```
ainterp 1.1.4  (c) 2001-2012 by Turku PET Centre

Interpolate TACs to an optimal time scale for simulations.

Command-line parameters:
  1) Datafile
  2) End time
  3) Interpolated datafile

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

End time is the length of the inter/extrapolated data. To interpolate to
the end of input data, set it to 0.

TAC file format is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: interpol, fr4sim, dfttime, dftframe, avgbolus, dftavg, fit2dat

Keywords: DFT, simulation

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```
algtimes 0.1.1  (c) 2006 by Turku PET Centre

Correct the sample times in Allogg ABSS on-line blood sampler data.
Use this, if sampling was accidentally started later than the PET scan.
If the new sampling start time is not given, the program lists information
on current sample times on the screen.

Usage:
  algtimes [Options] <Sampler datafile> [New sampling start time as hh:mm:ss]

Options:
 -o=<Filename>
    Filename for corrected sampler data; by default, original file is
    overwritten.
 -v[ersion]
 -build
    Print build information and exit.
 -h[elp]
    Print this text and exit.
 -silent
    Work silently; only warnings and error messages are printed in stdout.

See also: blo2kbq, injdifft, blotimes

Keywords: input, blood, sample times, injection time
```

```
Usage:alignlinear.exe standard_file reslice_file air_out -m model_menu_number
[options]
       Model Menu:
              3-D models:
                     6. rigid body 6 parameter model
                     7. global rescale 7 parameter model
                     9. traditional 9 parameter model (std must be on AC-PC line)
                    12. affine 12 parameter model
                    15. perspective 15 parameter model

              2-D models (constrained to in-plane, no interpolation):
                    23. 2-D rigid body 3 parameter model
                    24. 2-D global rescale 4 parameter model
                    25. 2-D affine/fixed determinant 5 parameter model
                    26. 2-D affine 6 parameter model
                    28. 2-D perspective 8 parameter model


       options: (defaults in parentheses)
       [-b1 FWHM_x(0.000000e+000) FWHM_y(0.000000e+000) FWHM_z(0.000000e+000)]
(standard file)
       [-b2 FWHM_x(0.000000e+000) FWHM_y(0.000000e+000) FWHM_z(0.000000e+000)]
(reslice file)
       [-c convergence_threshold(0.000010)]
       [-d] use static partitioning (like AIR3.0 and earlier)
       [-e1 standard_file_mask]
       [-e2 reslice_file_mask]
       [-f initialization_file]
       [-fs scaling_initialization_file]
       [-g termination_file [overwrite?(y/n)]]
       [-gs scaling_termination_file [overwrite?(y/n)]
       [-h halt_after_(5)_iterations_without_improvement]
       [-j] use non-positive definite Hessian matrices (not validated, use at your
own risk)
       [-p1 segment_standard_file_into_(1)_partitions]
       [-p2 segment_reslice_file_into_(1)_partitions]
       [-q] assume non-interaction of spatial parameter derivatives
       [-r repeated_iterations(25)]
       [-s initial_sampling(81) final_sampling(1) sampling_decrement_ratio(3)]
       [-t1 threshold_standard_file(7000)]
       [-t2 threshold_reslice_file(7000)]
       [-v] verbose reporting of interim results
       [-x cost_function(1)]
              1. standard deviation of ratio image
              2. least squares
              3. least squares with intensity rescaling
       [-z] (no additional argument; turns on pre-alignment interpolation)
```

```
ana2ecat 1.0.5  (c) 2003-2013 by Turku PET Centre

Conversion of Analyze 7.5 database(s) to ECAT 7 image volume or ECAT 6.3
image format.

Usage: ana2ecat [Options] <Analyze database OR path> [Output path]

Options:
 -7  Images are written in ECAT 7 format (default)
 -6  Images are written in ECAT 6.3 format
 -O=<output path>
     Data directory for ECAT images; by default current working directory
 -flip=<y|n>
     Override the default and environment variable ANALYZE_FLIP setting
     by always flipping/not flipping image in z-direction (planes).
     If environment variable is not set, then default is y.
     Images are always flipped in x,y-directions.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
Conversion of all Analyze files in directory S:\temp\neuro to ECAT 7
images in directory C:\data in PC/Windows:
   C:
   cd \data
   ana2ecat s:\temp\neuro

Program reads frame time information in SIF file, if that file is located
in the Analyze database directory and if it is named with *.sif extension.

Specific extensions to Analyze 7.5 format:
 -Scale factor to retain quantitation in image_dimension.funused1
 -Isotope halflife (sec) in image_dimension.funused3;
  this does not imply whether data is corrected for decay or not.
 -String in data_history.descrip tells whether data is corrected for decay;
  'Decay corrected.' or 'No decay correction.'

See also: ecat2ana, eframe, sif2ecat, e7emhdr, e7evhdr, flo2ecat, nii2ecat
and ImageConverter (.NET version) in
http://www.turkupetcentre.net/programs/tpc_csharp.html

Keywords: image processing, format conversion, ECAT, Analyze

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```
anabyteo 0.2.1  (c) 2003,2012 by Turku PET Center

Convert or show (by default) the byte order in Analyze 7.5 images.
Without options the current byte order is shown but not changed.

Usage: anabyteo [Options] <Analyze database name(s)>

Options:
 -L or -pc or -i
     Change byte order to little endian (PC Intel)
 -B or -sun or -sparc
     Change byte order to big endian (Sun Sparc, Motorola, PowerPC)
 -o=<directory>
     Converted files are plaved in specified directory, and original
     files are not overwritten
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only error and warning messages.

See also: ana2ecat, ecat2ana, ana_lhdr, ana_ehdr

Keywords: image processing, format conversion, Analyze, byte order

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```
ana_ehdr 0.2.1  (c) 2004,2013 by Turku PET Centre

Edit the information in Analyze 7.5 header file.
Note that frame times and isotope information are not stored in Analyze,
header but in SIF.

Usage: ana_ehdr [Options] <Header file> <field_name> := <field value>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only error and warning messages.

Example:
     ana_ehdr s2345dy1.hdr patient_id := 'Albert Einstein'

See also: ana_lhdr, nii_lhdr, iftlist, eframe

Keywords: image processing, Analyze, header

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```
ana_lhdr 0.1.2  (c) 2003-2013 by Turku PET Centre

List the information in Analyze 7.5 header.

Usage: ana_lhdr <Analyze file>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit

See also: ana2ecat, ecat2ana, ana_ehdr, anabyteo, nii_lhdr

Keywords: image processing, Analyze, header

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```
arlkup 2.1.4  (c) 1996-2013 by Turku PET Centre

Calculation of blood flow value look-up table from [O-15]H2O blood curve
for using with PET in vivo autoradiographic (ARG) method (1-5).

Command-line arguments must be given in this order:
  1) Blood datafile (calibrated and corrected for decay),
  2) Partition coefficient p [mL/mL],
  3) Maximal blood flow [mL/(min*100mL)],
  4) Integration start time [sec],
  5) Integration duration [sec],
  6) Size of the table (nr of rows),
  7) Filename for the look-up table

Options:
 -static=<y|N>
     The look-up table integral can be corrected for physical decay as
     single frame when static PET scan was performed (y), or dynamically
     (N, the default).
 -h or --help
     Print this message and exit
 --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

Example:
     arlkup s1456_blo.fit 0.8 50 0 120 5000 s1456.lkup

Times in blood datafile must be in seconds, and radioactivities in the same
units as are the calibration units of the PET image that will be converted
to the flow image.

Look-up table will contain 2 columns: integral [sec*kBq/mL] and flow
[mL/(min*100mL)].

References:
1. Raichle ME. Quantitative in vivo autoradiography with positron emission
   tomography. Brain Res Rev. 1979;1:47-68.
2. Herscovitch P, Markham J, Raichle ME. Brain blood flow measured with
   intravenous H215O. I. Theory and error analysis. J Nucl Med. 1983;
   24:782-789.
3. Raichle ME, Martin WRW, Herscovitch P, Mintun MA, Markham J. Brain blood
   flow measured with intravenous H215O. II. Implementation and validation.
   J Nucl Med. 1983;24:790-798.
4. Ruotsalainen U, Raitakari M, Nuutila P, Oikonen V, Sipila H, Teras M,
   Knuuti J, Bloomfield PM, Iida H. Quantitative blood flow measurement of
   skeletal muscle using oxygen-15-water and PET.  J Nucl Med. 1997;
   38:314-319.
5. http://www.turkupetcentre.net/analysis/doc/tracer/arg_h2o.html

See also: imgarg, fitdelay, imginteg, ecatlkup, dftlkup, ecatunit, imgflow

Keywords: perfusion, autoradiography, ARG, look-up table

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```
asc2flo 0.1.5  (c) 2005-2012 by Turku PET Centre

Reads numerical data from an ASCII file and writes those in a binary file
as 4-byte floats.
Numerical data can be stored on one or more lines, separated by
commas, tabs, or spaces.
Comment lines are allowed in the beginning of the file.

Usage:  asc2flo [Options] <ASCII file> [Binary file]

Options:
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

See also: flo2ecat, simcirc, dft2img, ecatadd, ecat2tif

Keywords: software testing, image processing, simulation

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you are welcome to redistribute it under GNU General Public License.
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```
avgbolus 1.4.6  (c) 2003-2013 by Turku PET Centre

Calculate an average curve of several bolus input curves with different
sample times. For simulations.

Usage:  avgbolus [Options] <bolus datafiles> <avg datafile>

Options:
 -nr=<Sample nr>
     Set the nr of samples to use for bolus appearance time; default is 2.
     Set nr=0, if different appearance time is not to be considered.
 -ns
     TACs are not scaled to a common AUC.
 -ne
     Standard deviations are not written in output file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1:
    avgbolus up????ap.kbq apmean.kbq
Example 2:
    dir /b *.kbq > filelist.txt
    avgbolus filelist.txt apmean.dat

Datafiles must contain a time column, and one or more concentration columns
separated by space(s) or tabulator(s). Only the first concentration column
is used in calculations.
If only one input datafile is given, it is assumed to contain a list of
bolus datafiles with paths if necessary. Tabs, commas and newlines can be
used to separate filenames in the list file.

Output datafile will contain three columns: time, avg concentration and s.d.
Program will determine the new sample times based on the shortest of input
datafiles.

Detailed program description:
 1) Read first curve from each datafile
 2) Replace NaNs with interpolated values.
 3) Determine bolus appearance time in each curve based on certain number
    of samples with highest slope.
 4) Move all curves in time to have a common appearance time.
 5) Search the bolus curve with shortest sampling duration.
 6) Calculate AUC from 0 to that time from all curves separately.
 7) Scale all bolus curves to have the same average AUC.
 8) Interpolate all bolus curves to common sample times.
 9) Calculate the mean and s.d. curve of all bolus curves.
10) Write the mean and s.d. data in a specified ASCII datafile.

See also: avgfract, dftavg, dftadd, interpol, dftadd, dft2svg

Keywords: DFT, simulation, modelling, input

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```
avgfract 1.1.2  (c) 2005-2012 by Turku PET Centre

Calculation of the mean of fraction curves. Data is not interpolated or
extrapolated. Resulting average datafile will contain a weight column;
weights represent the number of fractions from which each mean
value was calculated.

Usage: avgfract [Options] <Average datafile> <Fraction datafiles>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
  avgfract mean.rat ue*ap.rat

See also: metabcor, fit_hill, avgbolus, fr4sim, dftcalc, dftadd, dft2html

Keywords: DFT, input, simulation

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```
avgttac 0.1.4  (c) 2012,2013 by Turku PET Centre

Calculate average TACs from PET tissue time-activity curves of several PET
studies with equal sample (frame) times. Each regional TAC is processed
separately. All datafiles must contain the same regions.
TACs are not scaled in this process, therefore user must scale the data
to for example SUV or %ID before using this program.

Usage:  avgttac [Options] <Avg datafile> <TAC datafiles>

Options:
 -sd
     Regional standard deviations are written into avg datafile.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1:
    avgttac meansuv.dft *suv.dft
Example 2:
    dir /b *suv.dft > filelist.txt
    avgttac meansuv.dft filelist.txt

If only one input datafile is given, it is assumed to contain a list of
bolus datafiles with paths if necessary. Tabs, commas and newlines can be
used to separate filenames in the list file.

See also: avgbolus, avgfract, dftavg, dftsuv, dftsort, dftcut, dftren

Keywords: DFT, TAC, average, modelling

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b2m_mbf 1.2.4 (c) 1998-2013 by Turku PET Centre

Simulation of heart LV muscle and cavity PET TACs from arterial blood TAC
using the one-tissue compartment MBF model by Iida H et al. [1, 2]
as represented in [3].

Parameters:
  1) Blood H2O data
  2) Flow (mL/mL/min)
  3) Alpha
  4) Va
  5) Beta
  6) Result file for muscle and LV data

Example:
   b2m_mbf s3456ab.kbq 1.24 0.6 0.3 0.8 s3454.dft

For accurate results, blood input TAC should be noiseless and have very
short sampling intervals. Simulated curves can thereafter
be interpolated to represent PET frames using program fr4sim.

References:
1. Iida H, Rhodes CG, de Silva R, Yamamoto Y, Araujo LI, Maseri A, Jones T.
   Myocardial tissue fraction - correction for partial volume effects and
   measure of tissue viability. J Nucl Med 1991; 32:2169-2175.
2. Iida H, Rhodes CG, de Silva R, Araujo LI, Bloomfield P, Lammertsma AA,
   Jones T. Use of the left ventricular time-activity curve as a noninvasive
   input function in dynamic oxygen-15-water positron emission tomography.
   J Nucl Med 1992; 33:1669-1677.
3. Oikonen V. Model equations for myocardial perfusion studies with [15O]H2O
   PET. http://www.turkupetcentre.net/reports/tpcmod0005.pdf

See also: fitmbf, b2t_h2o, p2t_3c, fr4sim

Keywords: myocardium, perfusion, modelling, DFT

```
b2plasma 1.8.3  (c) 2002-2014 by Turku PET Centre

Converts blood time-activity curves (TACs) collected during a PET study
to plasma TACs, based on tracer-dependent population-based
RBC/plasma or plasma/blood ratio functions over time.

Usage:  b2plasma [Options] <Tracer> <Bloodfile> <HCr> <Plasmafile>

Options:
 -Log
     Log information is saved in output file.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

The following human PET tracer TACs can be converted:
  AH690
     ratio is assumed to follow a population average curve.
  AH691
     ratio is assumed to follow a population average curve.
  Carfentanil
     ratio is assumed to follow a population average curve
     (unpublished measurements from eight 70-min PET studies).
  FBPA
     ratio is assumed to rise from zero with slope 0.00888
     (unpublished measurement from 10 subjects).
  FDG
     ratio is assumed to be 0.8 in the beginning and to rise with
     slope 0.0012/min (Phelps ME et al. Ann Neurol 1979;6:371-388).
  FDOPA
     ratio is assumed to follow equation R(t)=(Rmax*t)/(Th+t),
     where Rmax=1.446 and Th=83.56 (unpublished results).
  Flu[mazenil]
     ratio is assumed to follow an average curve based on two
     subjects with assumed HCR=0.43.
  FTHA
     concentration in red blood cells is assumed to be zero.
  MEAIB
     ratio is assumed to rise from zero with slope 0.00398
     (unpublished measurement from 7 subjects).
  Metomidate or MTO
     concentration is the same in RBC and plasma water.
  ORM-B
     ratio is assumed to follow a population average curve
     (unpublished measurement from 6 subjects studied twice).
  Palm[itate]
     ratio is assumed to follow a population average curve
     (unpublished measurement from 8 subjects).
  PE2I
     ratio is assumed to follow a population average curve
     (unpublished measurements from ten 70-min PET studies).
  PIB or 6OHBTA1
     ratio is assumed to follow a population average curve,
     currently based on 15 subjects.
  PK11195
     ratio is assumed to follow a curve based on one
     subject with measured HCr.
For mice and rats (these conversion do not utilize hematocrit):
  MOUSEFDG
     plasma-to-blood ratio is assumed to follow the function published by
     Yu AS et al. J Nucl Med 2009;50(6):966-973.
  RATFDG
```

plasma-to-blood ratio is assumed to follow the function published by
Weber et al. Eur J Nucl Med 2002;29(3):319–323.

Codes for tracers that have below mentioned properties:
  norbc
    concentration in red blood cells is assumed to be zero.
  inwater
    concentration is the same in RBC and plasma water.

Times must be in minutes in data files, or seconds, if appropriately
specified inside the file. File format specification in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

The hematocrit (HCr, HCT) is normally between 0.40-0.51 in men and 0.36-0.47
in women. Note that HCr is lower in small vessels.

Example: estimate plasma curve from measured FDG blood TAC:
    b2plasma FDG i3344ab.kbq 0.38 i3344ap.kbq

See also: p2blood, b2rbc, bpr2cpr, dftcalc, dftcat, fit_bpr

Keywords: input, modelling, simulation, blood, plasma, RBC, hematocrit

```
b2rbc 2.0.5  (c) 1995-2013 by Turku PET Centre

Calculates the TAC of blood cells (erythrocytes, RBC) using
haematocrit (HCT), blood TAC and plasma TAC, based on equation

  Blood = HCT*RBC + (1-HCT)*Plasma

HCT is normally between 0.40-0.51 in men and 0.36-0.47 in women.

Usage:  b2rbc [Options] <Blood> <Plasma> <HCT> <RBC datafile>

Options:
 -h, --help
     Print this message and exit
 --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.
 --verbose
     Program prints more information about what it is doing.

See also: bpr2cpr, p2blood, b2plasma, dftcalc, fit_bpr

Keywords: input, modelling, simulation, RBC, plasma, blood

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```
b2t_h2o 3.1.1 (c) 1997-2013 by Turku PET Centre

Simulation of PET tissue time-radioactivity concentration curve (TAC)
in [O-15]H2O PET studies from decay corrected arterial blood TAC based on
the one-tissue compartment model.
By default, blood flow (perfusion) and tissue concentratios are
represented per PET volume (including vascular volume).

Command line parameters:
  1) Blood file (times in sec)
  2) Flow (mL/min/100mL)
  3) Partition coefficient of water (p)
  4) Extraction coefficient (1 - exp(-PS/f); normally 1.0)
  5-6) Vascular volume (%) and the arterial fraction of it (%)
  7) Tissue file

Options:
 -sub | -nosub
     TACs of sub-compartments (Ct, Cta, Ctv) are written (-sub, default)
     or not written (-nosub) into the output file
 -add
     Simulated TACs are added to an existing tissue data file.
     By default, existing file is overwritten.
 -fpt
     Blood flow (perfusion) is assumed to be given per perfusable tissue
     volume excluding vascular volume. TAC will still be simulated per
     regional PET volume including vascular volume.
 -voiname=<text>
     Enter a name (1-6 chars without spaces) for the simulated TAC
 -vena=<filename>
     Save the simulated venous blood TAC
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

Calculated tissue activities are written in the specified file with
these data columns:
  0) Time
  1) Total tissue activity (2+3+4)
  2) [H2O] in tissue
  3) Arterial [H2O] in tissue
  4) Venous [H2O] in tissue

See also: fit_h2o, p2t_3c, avgbolus, dfttime, dftadd, fr4sim, dftunit

Keywords: DFT, simulation, perfusion

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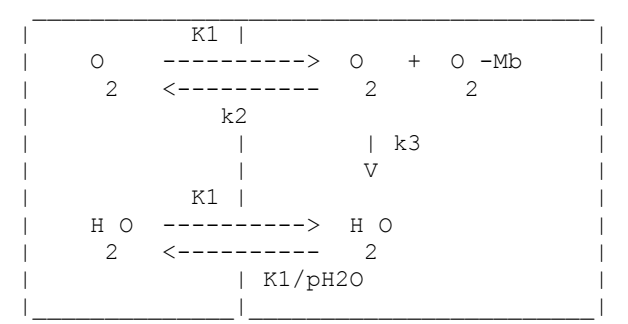
b2t_mo2 1.2.0 (c) 2002-2008 by Turku PET Centre

Simulates regional skeletal muscle PET radioactivity concentration curves in [O-15]O2 studies from decay corrected blood [O-15]O2 and [O-15]H2O curves using the following compartmental model dedicated for skeletal muscle (1-3):



Model definitions:
  K1=Flow (mL/min/dL), OER=k3/(k2+k3),
  Ki=Flow*OER (mL/min/dL),
  Metabolic rate of oxygen MRO2=Ki*[O2]a (mmol/min/dL)

Command line arguments:
  1) Blood O2 TAC file
  2) Blood H2O TAC file
  3) Flow, mL/(dL*min)
  4) Oxygen extraction fraction OER (fraction)
  5) Simulated tissue TAC file

General options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing
 -sub and -nosub
     With option -sub the TACs of all model compartments will be written in
     output tissue file, but with -nosub (default) only total tissue TAC
     will be saved
 -voiname=<text>
     Enter a name (1-6 chars without spaces) for the simulated TAC
 Options to set model parameters:
 -Vb=<Blood volume (%)>
     Set the simulated blood volume; default is 3.5%
 -Af=<Arterial proportion (%)>
     Set the simulated arterial proportion of total blood volume;
     default is 30%
 -pH2O=<value>
     Set the partition coefficient of water; default is 0.99
 -K1k2=<value>
     Set the K1/k2 for oxygen; by default the K1/k2 is estimated from
     OER and saturation curves for hemoglobin and myoglobin
 -Sao2=<value>
     Saturation of arterial blood hemoglobin; default is 0.97
 -p50Hb=<value>
     Half-saturation pressure for hemoglobin; default is 3.6 kPa
 -p50Mb=<value>
     Half-saturation pressure for myoglobin; default is 0.319 kPa
 -nHb=<value>
     Hill coefficient for hemoglobin; default is 2.7

-Mb=<value>
    Concentration of myoglobin in muscle; default is 4.7 mg/g
-Hb=<value>
    Concentration of hemoglobin in blood; default is 150 mg/g

Calculated tissue activities are written in the specified file with
these data columns. Columns 2-6 will be saved optionally (-sub):
  0) Time
  1) Total regional radioactivity concentration (2+3+4+5+6)
  2) Labeled [O2] in tissue region
  3) Labeled [H2O] in tissue region
  4) Concentration of arterial radioactivity in tissue region
  5) Venous labeled [O2] in tissue region
  6) Venous labeled [H2O] in tissue region

References:
1. Nuutila P, Peltoniemi P, Oikonen V, Larmola K, Kemppainen J, Takala T, Sipila H, Oksanen A, Ruotsalainen U, Bolli GB, Yki-Jarvinen H. Enhanced stimulation of glucose uptake by insulin increases exercise-stimulated glucose uptake in skeletal muscle in humans: studies using [15O]O2, [15O]H2O, [18F]fluoro-deoxy-glucose, and positron emission tomography. Diabetes 2000; 49:1084-1091.
2. Oikonen V, Nuutila P, Sipilä H, Tolvanen T, Peltoniemi P, Ruotsalainen U. Quantification of oxygen consumption in skeletal muscle with PET and oxygen-15 bolus. Eur J Nucl Med. 1998; 25: 1151.
3. Oikonen V. Modelling of low oxygen consumption. In: J. Knuuti, J. Rinne, P.Tenhonen (ed.), Medical Applications of Cyclotrons VIII. Abstracts of the VIII Symposium on the Medical Applications of Cyclotrons. Annales Universitatis Turkuensis D346:16, 1999.

See also: fit_mo2, o2metab, o2_p2w, fit_o2bl, avgbolus, fr4sim

Keywords: DFT, simulation, oxygen, skeletal muscle

bfset 1.0.0 (c) 2003,2005 by Turku PET Centre

Calculates a set of basis functions for simplified reference tissue model (SRTM) [1, 2]. Theta3=k2/(1+BP)+lambda.

Parameters:
  1) Reference region TAC file (*.dft, times in min)
  2) Min theta3 (1/min)
  3) Max theta3 (1/min)
  4) Number of basis functions to be calculated
  5) Isotope (C-11 or F-18)
  6) Result file (existing file is overwritten)

Reference region TAC is assumed to be decay corrected. Program requires the isotope to be able to calculate the non-decay corrected TAC.

Reference:
1. Lammertsma AA, Hume SP. Simplified reference tissue model for PET receptor studies. NeuroImage 1996;4:153-158.
2. Gunn RN, Lammertsma AA, Hume SP, Cunningham VJ. Parametric imaging of ligand-receptor binding in PET using a simplified reference region model. NeuroImage 1997;6:279-287.

See also: dft2ps, imgbfbp, regbfbp

```
blindinp 0.2.0 (c) 2010 by Turku PET Centre

Model-based estimation of plasma input curve from regional PET time-activity
curves (TACs).
This program is under early development and should not be used for any
serious purpose!

Command line arguments:
  1) Tissue TAC file (1)
  2) Filename for estimated input TAC (optional)

General options:
 -model=<k3|K1k2k3>
     Select the tissue uptake model; k3 by default
 -function=<P1|P2>
     Select the function for input curve; by default P1
 -blo=<Blood>
     If blood TAC is to considered in the modelling, then use this option
     to enter either the filename or TAC name of blood curve
 -fit=<Filename>
     Parameters of reference tissue function (2)
 -svg=<Filename>
     Plots of original and fitted TACs are written in specified file in
     Scalable Vector Graphics (SVG) 1.1 format (3)
     This option is functional only with certain options
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

Example:
     blindinp ua1807.dft ua1807inp.dft

References:
1. DFT format: http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. FIT format: http://www.turkupetcentre.net/analysis/doc/format_fit.html
3. SVG specification: http://www.w3.org/TR/SVG/

See also: dftreduc, dfteven, fitk3, fit2dat, blindref

Keywords: DFT, modelling, input

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you are welcome to redistribute it under GNU General Public License.
```

```
blo2kbq 3.8.1 (c) 1994-2012 by Turku PET Centre

Program for extraction and calibration of blood TACs measured using
automatic blood sampling systems (ABSS, "blood pump") (1).

Usage:  blo2kbq [Options] <Blood pump file>

Options:
 -c=<filename>
     Calibration coefficients for ABSS and well-counter should be specified
     with calibration file (2), given with option -c.
 -i=<isotope>
     If calibration file is given, then the isotope name
     (C-11, F-18, Ga-68, Ge-68 or O-15)
     must be entered (if not correctly specified inside pump file) so that
     the correct well-counter calibration factor can be used.
 -d[=<isotope>]
     Data is corrected for physical decay; isotope can optionally be
     given with this option.
 -start=<t>
     If ABSS measurement was not started at the time of injection,
     the delay t (sec) must be entered with option -start=<t>. If data
     collection was started before injection, enter a negative value for t;
     activities before that time are removed from the output data.
 -v[=<blood density>]
     With option -v activities are divided with the blood density 1.06
     to get kBq/g values, rather than kBq/mL. If blood density is different
     from default 1.06 g/mL, it can be entered after -v.
 -m[in]
     Sample times are written in minutes (in seconds by default).
 -l -r -t
     The counts or activity values are printed as an average of the two
     channels by default. With options -l and -r the left (ch2) or right (ch1)
     column is shown. With option -t both columns are shown.
 -z
     For reading of the measurement date, local time zone can be used with
     option -z instead of Greenwich main time (default).
 -o=<filename>
     Filename for corrected TAC data, can be entered with option -o.
     If not given, then files are written to the directory where input file
     was. Calibrated file is named *.kbq and non-calibrated *.dat by default.
 -s[canditronics], -a[llogg], -allogg2
     ABSS produces device-specific file formats; this option is needed
     if format can not be correctly identified from file extension
     (*.lis, *.bld, *.alg, or *.txt).
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
blo2kbq -i=O -d=O -c=S:/Lab/plasma/bsampler_calibration/pump_cal.dat sr452_blo.bld

References:
1.
http://www.turkupetcentre.fi/index.php?option=com_content&view=article&id=104&Itemid=
91&lang=en
2.
http://www.turkupetcentre.fi/index.php?option=com_content&view=article&id=151&Itemid=
91&lang=en

See also: blozero, blotimes, algtimes, blofch, dftcat, disp4dft, fitdelay
```

Keywords: blood, input, ABSS, online-sampler, blood pump, calibration

```
blobkg 1.1.1 (c) 2002-2009 by Turku PET Centre

Subtract constant background radioactivity in Scanditronics or GEMS on-line
blood sampler data.
Note that the original data file is overwritten.

Usage:  blobkg <Sampler datafile> <Time to use for correction (sec)>

Options:
 --dry
     Dry run: nothing is actually changed
 -h, --help
     Print this message and exit
 --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints lots of information about what it is doing.

The average of coincidence cps from 0 to specified time is calculated
and subtracted separately from both channels.
The background radioactivity is assumed to be stable during the assay.
Negative counts are not allowed, but set to zeroes; therefore some initial
phase background may remain after correction.

See also: blo2kbq, blotimes, blofch, bloexam, blozero, fitdelay

Keywords: input, blood, background, Scanditronics, online-sampler

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```

```
bloexam 1.1.1 (c) 2006-2009 by Turku PET Centre

Examines blood on-line sampler detector channels (Scanditronics and GEMS).
Program prints the following information on data files where the channel
ratio exceeds the predefined limit:
  column #1: measurement date
  column #2: Lower-to-higher channel ratio (the closer to 1 the better)
  column #3: channel 1 mean from ten highest overall measurements
  column #4: channel 2 mean from ten highest overall measurements
  column #5: file name

Usage:  bloexam [options] <name(s) of data file(s)>

Example:
     bloexam *.bld aivot//*.bld

Options:
 -limit=<limit for channel ratio>
     By default, limit is 0.7 (lower-to-higher channel)
 -h or --help
     Print this message and exit
 --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints lots of information about what it is doing.

See also: blofch, blo2kbq, blotimes, blozero

Keywords: blood, input, Scanditronics, online-sampler, channels, calibration

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```
blofch 2.0.2 (c) 2001-2009 by Turku PET Centre

This program verifies that both channels of Scanditronics or GEMS
on-line blood sampler (blood pump) have been functioning, and calculates
the ch1/ch2 coincidence count ratio.
Optionally, if one channel did not work or measured substantially lower
counts, then its values can be optionally replaced by values calculated
from the other channel using user-provided correct Ch1/Ch2 ratio.

Usage:  blofch [Options] <Sampler datafile> [Correct Ch1/Ch2]

Options:
 -h or --help
     Print this message and exit
 --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints lots of information about what it is doing.

See also: bloexam, blo2kbq, blotimes, blozero

Keywords: input, blood, Scanditronics, online-sampler, channels, calibration

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```

```
blolevel 0.0.4  (c) 2010 by Turku PET Centre

Non-linear fitting of one blood curve to match the level and timing
of another curve.
Check that sample and time units are specified inside data files, or,
if not specified, that the data is in the same units.

Usage:  blolevel [Options] <Datafile> <Reference file> <Matched datafile>

Options:
 -ir
     Matched data is saved and optionally plotted at sample times of
     reference data, but starting from zero time also in case of gap
     in the reference data
 -wf
     Weight by sampling interval
 -abs
     Sum of absolute differences is minimized instead of sum-of-squares
 -fast or -safe
     Speed up the fitting but increase the chance of failure, or
     increase the reliability at the cost of computing time
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing

See also: dftscale, crscale, dftunit, dfttime, dftcalc, dft2svg

Keywords: DFT, input, modelling, simulation

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```

```
blotimes 1.1.0 (c) 2006-2009 by Turku PET Centre

Correct or list the sample times in Scanditronics or GEMS on-line blood
sampler (blood pump) data (1).
Correct decay correction will bepossible only if blood sampling start time
is correct versus PET scan start time.

Usage:  blotimes <Sampler datafile> [New sampling start time as hh:mm:ss]

Options:
 -h, --help
     Print this message and exit
 --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.
 --verbose
     Program prints lots of information about what it is doing.

In Scanditronics data files the correct sampling start time is in the file
headers; however, in old Scanditronics data files the headers do not contain
time, but it is read from the first sample data line.
In GEMS data files the time in file headers is not the sampling start time,
but time is read from the first sample data line.
If new sampling time is given and it is different than the current sampling
start time, then all sample times in the sampler data file are changed.
If the new sampling start time is not given, the program lists information
on current sample times on the screen.

Example 1a: Blood sampler times are listed:
      blotimes us1165.bld
Example 1b: PET image scan start time is listed:
      egetstrt us1165.v
Example 1c: Obviously, blood sampler clock was not synchronized with PET,
therefore blood sample times must be corrected to PET scan start time:
      blotimes us1165.bld 10:25:58

References:
1. http://www.turkupetcentre.net/analysis/doc/pumpdata.html

See also: algtimes, blo2kbq, injdifft, egetstrt, blozero, blofch

Keywords: blood, input, sample times, Scanditronics, online-sampler

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```

blozero 1.0.2 (c) 2006,2009 by Turku PET Centre

Delete initial "bumps" in Scanditronics or GEMS on-line blood sampler curve
by setting the activities during the specified sample time range to zero.
Note that the original data file is overwritten.

Usage: blozero <Sampler datafile> <Zero start time> <Zero end time>

See also: blo2kbq, blotimes, blofch, bloexam, blobkg, fitdelay

Keywords: input, blood, background, Scanditronics, online-sampler

```
bpr2cpr 0.2.0  (c) 2008,2013 by Turku PET Centre

Converts blood-to-plasma (or optionally plasma-to-blood) ratio curve to
RBC-to-plasma (blood cell-to-plasma) using haematocrit (HCT),
based on equation

  Blood = HCT*RBC + (1-HCT)*Plasma

HCT is normally between 0.40-0.51 in men and 0.36-0.47 in women.

Usage:  bpr2cpr [Options] <BPR datafile> <HCT> <CPR datafile>

Options:
 -pbr
     Conversion is applied to plasma-to-blood ratio data
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: b2rbc, p2blood, b2plasma, dftcalc, dftcat

Keywords: input, modelling, simulation, RBC, plasma, blood

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```

```
convend 1.2.1  (c) 2001-2007 by Turku PET Centre

Program for byte order conversion of numerical values stored in flat
binary datafiles, between big endian (Sun Sparc, Motorola, PowerPC) and
little endian (PC/Intel) computers.

Usage: convend [Options] <base type> <Datafile> <Output file>

Options:
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

Accepted base types are: char, short, int, long, float and double.

See also: ecat2flo, flo2ecat, anabyteo

Keywords: ECAT, binary data, byte order, big endian, little endian

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you are welcome to redistribute it under GNU General Public License.
```

```
cpt2dft 0.7.1  (c) 2004-2013 by Turku PET Centre

Combines the regional PET TACs in CPT format into a single DFT file.
Data can also be saved in previous format, by setting output file
extension to '.roi.kbq'.
This program cannot currently read all CPT formats. It accepts standard
CPT files from Imagetool, Vinci and dft2cpt.
PET images scanned before 1993, and CPT files calculated from those, may
contain sum frames, which need to be removed before they can be processed
further.

Usage:  cpt2dft [Options] <CPT filename(s)> <Output filename>

Options:
 -cptunit=<Unit> or -auto
     If user knows for certain the calibration units in CPT files, it can
     be given to programs with option -cptunit, for example -cptunit=Bq/cc;
     with option -auto, program tries to guess the units
 -unit=<Unit>
     If CPT calibration unit is identified, the radioactivity concentrations
     may be converted to units specified with this option
 -d  Just frame mid times and activities are saved without any header
     information
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:  cpt2dft doe_john\*.cpt uit455.dft

References:
1. Regional time-radioactivity curves (TACs).
   http://www.turkupetcentre.net/analysis/doc/roi_tac.html
2. File formats in Turku PET Centre.
   http://www.turkupetcentre.net/analysis/doc/fileformat.html

See also: dftadd, dftren, dftunit, dftdecay, dft2csv, dft2svg, tsv2dft

Keywords: DFT, CPT, format conversion, tool, Imagetool, Vinci

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```

crscale 1.0.0 (c) 2006 by Turku PET Centre

Scales a count rate file into the level of a time activity curve (TAC)
in DFT file.
DFT file is assumed to contain two columns: time column and one TAC.
If more than one TACs exist, only the first one is used.
Data is interpolated, if necessary,
to the times of first file.
Output is written in DFT format or as plain data file depending of the
format of first data file.

Usage: crscale <count rate file> <dft file> <output file>

e.g.:   crscale s04064.img.cr s04064.dft s04064.cr.scaled

See also: dftcalc, fitdelay, dfttime, ecathead, dfthead, dft2ps, dftslope

Keywords: count rate curve, delay, DFT, modelling, input,

```
csv2dft 0.2.2  (c) 2007-2013 by Turku PET Centre

Converts time-activity curve (TAC) data in CSV file format [1]
in DFT file [2]. CSV (comma-separated values) files can be saved
for example in Excel.
Recent versions of TPC software can directly read CSV files.

Usage:  csv2dft [Options] <CSV file> [DFT file]

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Examples:
1. Convert one CSV file and enter the name for DFT file
     csv2dft 160410_ae426_TACBqml.csv ae426.dft
2. Convert all CSV files in current working directory in MS Windows
   command shell
     for %g in (*.csv) do csv2dft %g

References:
1. http://en.wikipedia.org/wiki/Comma-separated_values
2. http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: dft2csv, dftunit, dftlist, dftdel, dftadd, dftbreak, dftren

Keywords: DFT, CSV, tool, file format conversion

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```

```
csvconv 0.1.0  (c) 2013 by Turku PET Centre

Convert CSV files from international format to UK format and vice versa.
In international format the columns are separated by ';' and ',' is used
as decimal separator; in UK format the separators are ',' and '.',
respectively.

Usage:  csvconv [Options] <Command> <CSV file(s)>

Command:
  UK
     Convert all CSV files to UK format, if necessary  INT
     Convert all CSV files to international format, if necessary.
Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
  csvconv INT *.csv

See also: dft2csv, csv2dft

Keywords: CSV, Excel, tool, file format conversion

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```

```
cti2sif 2.1.0  (c) 2003-2013 by Turku PET Centre

Constructs a Scan Information File (SIF) from specified dynamic image
or sinogram in CTI ECAT 6.3 or 7.x format.

SIF can be used with Analyze and NIfTI image formats to retain
the frame time information.
Note that the count values in the resulting SIF file are not the same as
the values in SIF file retrieved from the scanner data, but similar
enough for usual purposes.

Usage: cti2sif [-Options] <Dynamic image/sinogram> <Name for SIF>

Options:
 -h or --help
     Print this message and exit
 --build or --version
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

Example:
     cti2sif ub7761dy1.v ub7761dy1.sif

See also: eframe, dftframe, esetstrt, ecattime

Keywords: image processing, ECAT, frame time, SIF, NIfTI, Analyze

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```
ctisort 2.0.1  (c) 1996-2012 by Turku PET Centre

Program sorts matrices in CTI ECAT 6.3 files.
Usually matrices need not be sorted, but some very simple software may
not fully support ECAT matrix list, in which case sorting may be necessary.
Note that program needs equal amount of disk space for temporary files!

Usage:  ctisort [Options] <ECAT file(s)>

Options:
 -planes | -frames
     Sort matrices primarily by plane (default) or by frame.
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only warnings and error messages.

See also: lmlist, lmhdr, lshdr, esplit

Keywords: image, ECAT, matrix, sort

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```

```
dft2csv 0.3.1  (c) 2010,2012 by Turku PET Centre

Converts PET tracer time-activity curve data in DFT format (1), or
IFT data, to CSV (comma-separated values) data, which can be easily imported
to other software, including Excel.

Usage:  dft2csv [Options] <DFT file> [CSV file]

Options:
 -separator=<<comma>|<semi-colon>|<tab>>
     By default comma is used as the separator, but semicolon or tabulator
     may be needed to import data to Excel or other software, depending
     on the localization settings. Use tabulator to import data to Origin.
     This setting affects also decimal points/commas.
 -header=<Yes|no>
     Descriptive title lines (if header information is available) can be
     included (default), or not included.
 -mid
     Frame mid time is written in CSV file instead of frame start and end.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Examples:
1. Convert one DFT file and enter the name for CSV file
     dft2svg ae426.dft ae426.csv
2. Convert all DFT files in current working directory in MS Windows
   command shell, using decimal commas and semi-colon as separator
     for %g in (*.dft) do dft2svg -separator=semi-colon %g

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. http://en.wikipedia.org/wiki/Comma-separated_values

See also: csv2dft, dft2res, dft2html, dft2pmod, dftunit

Keywords: DFT, IFT, CSV, Excel, file format conversion, tools

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```

```
dft2dat 1.2.5  (c) 2000-2009 by Turku PET Centre

Converts PET tracer time-activity curve data in DFT format (1) to pure
numeric data (with no header information or title lines), which can be
easily imported to other software.

Usage:  dft2dat [Options] <input file> [output file]

Options:
 -notime
     Data is written without sample times (and without header information)
 -ift
     Interfile-type headers are saved in output file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: dft2res, dft2html, dft2nci, dft2if, dft2idwc, dftadd, dftunit

Keywords: DFT, file format conversion, tools

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```
dft2frpl 0.1.1  (c) 2004,2006 by Turku PET Centre

Transforming DFT datafiles into suitable format for plotting with bars
representing both frame start and end times.

Usage:  dft2frpl [Options] <datafile> <output datafile>

Options:
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.

See also: dftframe, fr4sim, dft2ps, dft2svg, dft2html

Keywords: DFT, simulation, plotting, time frame

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```
dft2html 0.3.2 (c) 2004-2012 by Turku PET Centre

Program for converting DFT files into HTML table format.
Note that HTML format is only suitable for viewing and for transporting
data into spreadsheet software (Excel), but it is not accepted by analysis
software.

Usage: dft2html [Options] <DFT file> <HTML filename>

Options:
 -T  Table is always transposed (frames on columns, regions on lines).
 -O  Table is never transposed (frames on lines, regions on columns).
     By default, table is transposed if DFT contains less than 4 frames.
 -W[eights]
     Weights (if they exist) are included in HTML file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

See also: dft2csv, dft2dat, dft2res, dftlist, dftbreak, dftadd

Keywords: DFT, HTML, Excel, file format conversion

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you are welcome to redistribute it under GNU General Public License.
```

```
dft2img 1.6.5  (c) 2002-2013 by Turku PET Centre

Creates an image file in ECAT 6 or 7.2 format, with contents from the TACs
specified in a DFT file. Extension of output image filename (.img or .v)
determines which image format is used.
Image area is divided into equally sized rectangles, containing as pixel
values the regional TAC values.
Only one plane is written to image. Frames are written as specified in
the DFT file.

Usage:  dft2img [Options] <DFT file> <Output image> [ROI file]

If ROI filename is specified, the rectangular regions are defined in it.

Options:
 -s=<Advance|931|HR+|HRRT>
     Scanner, by default GE Advance.
 -z=<zoom>
     Reconstruction zoom factor, minimum and default is 1.41421356
 -tpl=<filename>
     Template image containing values [1,TAC nr]; ROIs are not saved
     with this option.
 -d=<image dimension>
     Image x,y-size in pixels; default 256; not effective with template.
 -n or -nodecay
     DFT data is not corrected for decay.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: flo2ecat, ecatadd, eframe, ecatunit, ecat2tif, img2dft

Keywords: image, simulation, software testing

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```
dft2pm 0.1.0  (c) 2007 by Turku PET Centre

Write the myocardial segments stored in DFT format into a file in ECAT 7
polar map format.

Usage:
  dft2pm [Options] <DFT filename> <ECAT file>

This program requires that following information (contents is of course
dependent on the polar map) is available in the DFT file:
# num_rings := 4
# sectors_per_ring := 6 6 4 1
# ring_position := 0 0.2 0.4 0.6
# ring_angle := 90 90 45 0

Options:
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

See also: pm2dft, dft2img, flo2ecat, asc2flo

Keywords: ECAT, polarmap, DFT, myocardium, file format conversion

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```
dft2pmod 0.2.3  (c) 2005,2012 by Turku PET Centre

Program for converting DFT files into PMOD TAC or BLD file format.

Usage: dft2pmod [Options] <DFT file(s)>

Options:
 -format=<<tac>|<bld>>
     File is saved in PET tissue (TAC) format, or in blood input (BLD)
     format, with corresponding filename extensions. By default program
     tries to determine the format automatically.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

See also: pmod2dft, dft2dat, dft2csv, dftbreak, dftadd

Keywords: DFT, PMOD, TAC, BLD, file format conversion

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```
dft2ps 0.6.1 (c) 2003-2009 by Turku PET Centre

Program for representing graphs of TACs in PostScript (PS) format.
If two DFT files are given, the program represents graphs where the TAC
from the first file (measured TAC) is plotted with symbols and
the TAC from the second file (fitted TAC) is plotted with lines.

Usage:  dft2ps [Options] <DFT file> <PS file> [2nd DFT file]

Options for changing graph settings:
 -p
     Each TAC is plotted on it's own page in PS file; By default, the first
     32 curves are plotted on one PS page, and the rest are not plotted
 -t
     Second DFT file is assumed to contain one plasma curve, which is
     plotted with all TACs in the first DFT file
 -x1=<startpoint of x-axis>
 -x2=<endpoint of x-axis>
 -y1=<startpoint of y-axis>
 -y2=<endpoint of y-axis>
General options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

Output filename must be specified by user and
it has to have the extension .ps

See also: fit2dat, dft2html, dft2dat, dftscale, crscale, dft2svg

Keywords: simulation, modelling, plotting, tool, DFT, PS, PostScript

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```
dft2res 1.0.5  (c) 2005-2012 Turku PET Centre

Program for converting DFT files into result file format.
This may be of use when regional values from parametric images need to
be processed further.

Usage: dft2res [Options] <DFT file(s)>

Options:
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

See also: rescoll, dft2csv, dft2html, img2dft

Keywords: results, DFT, modelling, conversion, tools

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```
dft2rfit 0.1.0  (c) 2006 by Turku PET Centre

Convert Turku PET Centre DFT (1) time-activity curve data into RFIT 4.4 (2)
compatible ROI or BLOOD format.

Usage:
  dft2rfit [Options] <DFT file(s)>

Options:
 -blood
     Files are converted to RFIT 4.4 bloodfile format.
     By default, ROI TAC file format is assumed.
 -sec or -min
     Sample times are known to be in seconds or minutes, but is not
     specified or is wrong in DFT files.
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.

References:
1. DFT specification:
   http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. RFIT web site:
   http://cfi.lbl.gov/cfi_software.html

See also: dft2dat, dft2idwc, dft2if, dft2pmod

Keywords: TAC, DFT, RFIT, input, tool, file format conversion

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```

```
dft2svg 0.3.5  (c) 2006-2013 by Turku PET Centre

Make XY plots of PET time-activity curves (TACs) in Scalable Vector Graphics
(SVG) 1.1. format; specification in http://www.w3.org/TR/SVG/
SVG files can be viewed with web browsers and processed further using for
example Batik, Gimp, and Inkscape.
TAC files can be given in DFT and PMOD formats.

Command-line arguments:
  1) Filename for SVG graphics file
  2-n) Filename(s) of TAC data

Command-line options:
 -L    TACs that are given after this option are plotted with lines only
 -S    TACs that are given after this option are plotted with symbols only
 -B    TACs that are given after this option are plotted with lines and
       symbols (default)
 -x1=<start of x axis>
 -x2=<end of x axis>
 -y1=<start of y axis>
 -y2=<end of y axis>
 -nmt, -nxt, -nyt
       Do not show main title or x or y axis titles
 -mt="<main title>"
       User-specified string to override any default main title
 -xt="<x axis title>"
       User-specified string to override any default x axis title
 -yt="<y axis title>"
       User-specified string to override any default y axis title
 -legend=<yes|No|auto>
       Show TAC legends (yes), do not show (no, default), or automatically
       determine whether to show or not (auto)
 -h or --help
       Print this message and exit
 -v, --version or --build
       Print software build information and exit
 --silent
       Program works silently, printing only warnings and error messages.

Normally, SVG graphics file should have extension .svg. Alternatively,
SVG graphics can be written inline in XHTML file by setting the extension
to .xhtml (for web browsers).

See also: fit2dat, dftscale, dftmax, dft2html, dft2csv

Keywords: simulation, modelling, plotting, tool, DFT, TAC, SVG, XML

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```
dftadd 1.6.6  (c) 2000-2012 Turku PET Centre

For adding specified region data from file2 to file1.
Files must have same number of frames.
If the number of region is not specified, all TACs are added.
If file1 does not exist, it will be created.

Usage:  dftadd [Options] <file1> <file2> [Number or name of VOI to add]

Options:
 -sn
     Copied region names are changed to contain the study number
 -ovr
     Existing file1 is overwritten
 -nt
     Program does not mind if the time or calibration units do not match
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example 1: Add regions with name 'striatum' from file a123_12.dft into
file a123_06.dft
     dftadd a123_06.dft a123_12.dft striatum

Example 2a: Combine all DFT files with study number s6789 into a new file
in MS Windows command prompt window
     for %g in (s6789*.dft) do dftadd combined.dft %g

Example 2b: Combine all putamen TACs from DFT files a*.dft into a new file
in MS Windows command prompt window
     for %g in (a*.dft) do dftadd -sn putamen.dft %g put

Example 3: To convert a plain data file into full DFT format create a new
new file with extension .dft
     dftadd -ovr new.dft plain.dat

See also: dftlist, dftdel, dftbreak, dftcat, dftavg, dftren, dftunit

Keywords: DFT, tool, simulation

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```
dftavg 1.4.4  (c) 2001-2012 by Turku PET Centre

Calculate a volume weighted average TAC of specified regions in a DFT file.

Usage: dftavg [options] <Datafile> [VOI names or numbers]

Options:
 -rm
     Remove the original TACs after averaging
 -h[emisphere]
     Average of hemispheres (dx and sin as the 2nd name field)
 --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

Example 1: Average TAC of all TACs named as 'cer':
     dftavg b123.dat cer

Example 2: Average TACs over planes of all regions separately;
           remove the original TACs with option -rm.
     dftavg -rm b123.dat

Example 3: Average of TAC numbers 4, 6 and 7:
     dftavg b123.dat 4 6 7

Example 4: Average of hemispheres (dx and sin) of all regions separately;
           remove the original TACs with option -rm.
     dftavg -hemisphere -rm b123.dat

See also: dftlist, dftdel, dftrmdpl, dftadd, avgttac, dftcalc, dftlevel

Keywords: DFT, modelling, tools, average

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```
dftbound 1.1.1  (c) 2004-2010 by Turku PET Centre

Subtract the reference region time-activity curve (TAC) from those
regional PET TACs that are not identified as reference regions.
Negative TAC values are preserved. Reference region TAC is excluded
from the output file by default.

Usage:  dftbound <Regional TAC file> <Reference region> <Output TAC file>

Options:
 -R  Reference region is written in output file
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

Example:
     dftbound ua273.dft cer ua273bnd.dft

See also: dftlist, dftavg, dftrmneg, dftadd, dftcalc, dftratio

Keywords: DFT, TAC, modelling, specific uptake

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```

```
dftcalc 1.4.9  (c) 1999-2014 by Turku PET Centre

Make arithmetic calculations with PET time-activity data in DFT or PMOD
format, see http://www.turkupetcentre.net/analysis/doc/format_dft.html
Operations can be made between two data files or between one file and
a constant value.

Usage:  dftcalc [Options] <datafile> <+|-|x|/> <value|2nd file> <output file>

Options:
 -h, --help
     Print this message and exit
 -nt
     Program does not mind if the time or calibration units do not match
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

Example 1: Add two to all activity concentrations in data.dft
     dftcalc data.dft + 2 sum.dft
Example 2: Subtract one curve from all curves in first data file
     dftcalc cortex.dft - reference.dft bound.dft

Data file can have one or more data columns. Second file may contain only
one column or as many columns as the first data file (if the column number
is different, only the first one is used); data is interpolated, if necessary,
to the times of first file.
If the second file contains only one frame, the value from that
frame will be used for all the frames of the first file.

See also: dftunit, dftbound, metabcor, dftsuv, dftratio, dftcbv, dftadd

Keywords: DFT, TAC, modelling, simulation, tools

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```
dftcat 1.4.6  (c) 2001-2013 by Turku PET Centre

Catenates the TACs from the second DFT file to the first one, or to a new
datafile. Sample times or correction for physical decay are not changed.

Usage:  dftcat <file1> <file2> [catenated file]

Options:
 -both | -first | -second | -cut=<time>
     In case of overlapping samples, either samples from both (-both),
     first (-first), or second (-second, default) TAC are saved in
     combined file, or specified cut time is used
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
     dftcat t455ap_pump.kbq t455ap_manual.kbq t455ap_combined.kbq

See also: dftcut, dftadd, dfttime, dftrmovl, inpstart, ecatcat, dftframe

Keywords: input, blood, modelling, tool, simulation

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```
dftcbv 1.1.2  (c) 2004-2014 by Turku PET Centre

Subtracts the contribution of vascular radioactivity from regional
PET TACs. Vascular volume fraction Vb can be given as a value that is
common to all regions, or as regional values in a TAC file, calculated
from a [O-15]CO study.

Usage:  dftcbv <Regional TAC file> <Blood TAC> <Vb> <Output TAC file>

Options:
 -n
     Negative TAC values are set to 0.
 -p
     Equation Ct=Cpet-Vb*Cb is applied; this is the default mode.
 -t
     Equation Ct=(Cpet-Vb*Cb)/(1-Vb) is applied.
 -sim
     Simulate the contribution of vascular radioactivity instead of
     correcting for it, calculating Cpet from Ct using equations above.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example 1:
     dftcbv uo372.dat uo372ab.kbq 0.045 uo372cbv.dat
Example 2:
     dftcbv uo372.dft uo372ab.kbq uo372vb.dft uo372cbv.dft

Vb values that are >=1.0 are assumed to be percentages.
Blood TAC can be given in a separate file, or as a region name inside
regional TAC file.

See also: imgcbv, p2blood, interpol, dftcalc, dft2csv

Keywords: DFT, modelling, vascular fraction, simulation

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```

```
dftcut 1.1.4  (c) 2001-2012 Turku PET Centre

For extracting specified time interval from PET time-activity
curves (TACs).

Usage:  dftcut [Options] <datafile> <start time> <end time> [output file]

 -h or --help
     Print this message and exit
 --build or --version
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only warnings and error messages.

See also: dftcat, dfttime, dftunit, dftframe, interpol, dftrmovl

Keywords: DFT, tool, simulation, frame time, time range

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```

```
dftdblf 1.0.2  (c) 2005,2008 by Turku PET Centre

Doubles the TAC sample number by making each sample/frame into two
by means of linear interpolation. This is mainly for simulation
and software testing purposes.

Parameters:
  1) Datafile
  2) Result file

Options:
 -mid
     Mid frame times are used even if frame start and end times are
     available
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

TAC file format is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: interpol, fr4sim, dftframe, dftinteg, dftcat, dftunit

Keywords: DFT, simulation, time frame

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```
dftdecay 4.2.0  (c) 1997-2013 by Turku PET Centre

Corrects PET TAC files for physical decay, or removes decay correction.

Usage: dftdecay [Options] <TAC file> [output file]

Options:
 -decay=<on|off>
     Correct the data for radioactive decay (on, default), or remove
     decay correction (off).
 -i=<Isotope code>
     If TAC file does not contain the isotope code, it can be specified with
     this option.
 -h or --help
     Print this message and exit.
 --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1: remove the correction for physical decay from a F-18 study,
           writing non-corrected data into a new file.
  dftdecay -decay=off -i=F-18 a123ap.dat a123ap_nodecay.dat

Example 2: correct the TAC data for radioactive decay, overwriting the data.
  dftdecay -decay=on -i=C-11 ia456dy1.dft

See also: dfttime, dftframe, dftunit, dft2csv, dft2svg, edecay

Keywords: DFT, input, physical decay, simulation, modelling

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```
dftdel 1.3.2  (c) 2001-2012 Turku PET Centre

For deleting the TACs of specified regions from a datafile.

Usage:  dftdel [Options] <datafile> <Numbers or names of VOIs>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

See also: dftlist, dftadd, dftren, dftbreak, dftrmdpl, dftvncor, dftcut

Keywords: DFT, tool

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```
dftdv 1.2.1  (c) 2000-2010 by Turku PET Centre

Calculates the ratio of tissue and plasma radioactivity curves, i.e.
distribution volume as a function of time.
Note that this is not the same as equilibrium distribution volume, but
it may become very close to it if the ratio reaches a steady phase.
Calibration units or adequate sampling time ranges or frequency
are not verified by the program.

Usage:  dftdv <Tissue file> <Plasma file> <Output datafile>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

Example:
     dftdv uo372.dft uo372ap.dat uo372dv.dft

See also: dftbound, dftratio, dftcalc, interpol, dft2svg, logan

Keywords: DFT, modelling

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```
dfteven 0.2.0  (c) 2009 Turku PET Centre

Even out the AUCs of regional TACs in DFT file.

Usage:  dfteven [Options] <Input file> [Output file]

Options:
 -scale=<AUC|mean>
     Scaling is based on TAC AUCs (default) or data point means.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: dftlist, dftdel, dftavg, avgbolus, avgfract, dftreduc, dftscale

Keywords: DFT, tool, simulation

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```
dftframe 2.0.4  (c) 2001-2012 by Turku PET Centre

Print or edit the frame times in regional TAC datafile (1).

By default, frame start times and lengths are printed on screen, and
optionally saved in the SIF file (2), if it does not exist.

If an existing SIF name is specified, the SIF frames are written into
regional TAC file.

Usage:  dftframe [Options] <TAC file> [SIF filename]

Options:
 -mid
     Frame mid time is written in TAC file instead of frame start and end
     times that are read from SIF
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

References:
1. TAC file: http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. SIF file: http://www.turkupetcentre.net/analysis/doc/sif.html

See also: eframe, dfttime, dftunit, interpol, dftcut, dftweigh, fr4sim

Keywords: DFT, SIF, tool, frame time

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```
dfthead 1.1.0  (c) 2001-2008 by Turku PET Centre

Calculates a weighted average TAC (head curve) of all regions in a DFT
file; by default it is included in the DFT file with name 'Head'.

Usage: dfthead <Datafile> [Filename for head curve]

Options:
 -h, --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints lots of information about what it is doing.

See also: ecathead, tocr, dft2dat, dftunit, dftdecay, fitdelay, dftweigh

Keywords: DFT, modelling, tool, head-curve, count-rate, time delay

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```
dfthncor 0.3.1  (c) 2004-2010 Turku PET Centre

For renaming the hemisphere field of TAC voinames in the datafile.
If voiname ends with _d or _s, that part is deleted, and hemisphere
is renamed as dx or sin.
Hemisphere names dx_m and sn are replaced by sin.

Usage:  dfthncor [Options] <datafile(s)>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

See also: dftlist, dftren, dftrenpl, dftvncor

Keywords: DFT, tool, hemispehere, roiname

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```

dftint 1.0.0 (c) 2004,2005 by Turku PET Centre

Program for linear (dot-to-dot) integration of PET time-activity curves.

Usage:

  dftint [Options] <datafile> [output file]

Options:
 -y, -i, -ii
  With options -y, -i and -ii the data can be interpolated, integrated,
  or the 2nd integral can be calculated. Default is integration.
 -fm, -fe
  Results are calculated at the frame mid (-fm) or frame end (-fe) times.
  Mid times is the default.

For accurate results, datafile should contain frame start and end times.

If output filename is not specified, the results are written to stdout.
Output is written in same format as the input DFT file.

See also: interpol, fr4sim, dfttime

Keywords: DFT, tools

```
dftinteg 0.1.3  (c) 2007-2013 by Turku PET Centre

Calculation of an AUC (integral over time) from regional or plasma TACs.

Usage:
  dftinteg [Options] <DFT file> <Start time> <Integration time> <AUC file>

Enter the start time and integration time in the same units that are in
the DFT file. Note that 3rd argument is not the integration end time.
Program will automatically set the integration start time and duration
based on the time range in the TAC file, if both are set to zero.
AUC/mean is by default written in DFT format, or in RES format if filename
has extension .res.

Options:
 -avg
     Average during specified range is calculated instead of AUC
 -h or --help
     Print this message and exit
 --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example 1: calculate AUC(32-302) with command
  dftinteg s5998dy1.dft 32 270 s5998int.dft
Example 2: integrate the regional TACs from a static or dynamic study
from the start time of the first frame to the end of the last frame:
  dftinteg a773dy1.dft 0 0 a773int.dft
Example 3: mean between 0 and 10 is calculated and saved in result format:
  dftinteg -avg ec4568.dft 0 10 ec4568_mean0-10.res

See also: interpol, dftratio, dftsuv, regfur, dftunit, imginteg, dftlevel

Keywords: DFT, modelling, AUC, autoradiography

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```

```
dftlevel 0.1.3 (c) 2010-2012 by Turku PET Centre

Calculation of sample mean over time frames in regional or blood
time-activity curves (TACs).
Mean is not weighted by frame duration or sampling intervals; for that
purpose use dftinteg with option -avg.

Parameters:
  1) TAC file (*.dft)
  2) Mean calculation start time
  3) Mean calculation end time
  4) Mean result file (*.dft or *.res)

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example:
     dftlevel ia15.dft 5 30 ia15level.dft

Mean calculation start and end times must be given in the same units that
are used in the data file.
Format of the accepted data file is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: dftinteg, interpol, dftframe, dfttime, dftavg, dftscale

Keywords: DFT, modelling, input, tools

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```

```
dftlist 1.4.7  (c) 1999-2013 by Turku PET Centre

Lists the volumes-of-interest (VOIs) of an DFT data file.
All VOI names are listed, if VOI name is not specified, and if e.g. 'cer'
is given, then only VOIs with name 'cer', 'Cer', or 'CER' are listed.
The activity concentrations are shown, if file contains <5 frames.

Usage:  dftlist [Options] <Datafile> [VOI name]

Options:
 -nv
     Do not print region volume.
 -NA
     Activity concentrations are never printed.
 -ift
     Interfile-type print.
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing no titles.

See also: dftren, dftdel, dft2csv, dft2dat, dft2res, iftlist, dft2svg

Keywords: DFT, tools, software testing

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```

```
dftlkup 0.1.1  (c) 2011 by Turku PET Centre

Replaces the y values in TAC file with the values from a given
look-up table.
The look-up table must contain two columns: program looks from the first
column a matching value for the TAC y value, and replaces the y
value with the value from the second column of the table.
Look-up table must be sorted in ascending order.
Histogram of the results is listed on the screen in verbose mode.

Usage:  dftlkup [options] <TAC file> <Look-up table> <Output file>

Output file is written in TAC (DFT) file format, unless filename
extension is *.res or *.htm(l).

Options:
 -c  If exact match in look-up table is not found, the closest value
     is selected; by default, value is interpolated from the table.
 --help or -h
     Print this message and exit
 --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

See also: ecatlkup, arlkup, dftinteg, dftcalc, dftunit, dft2csv

Keywords: DFT, perfusion, autoradiography, look-up table

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```

```
dftmatch 1.2.2  (c) 2005-2012 Turku PET Centre

Program for checking that two DFT files do have matching TAC contents;
this can be used for automating software and analysis tool testing.
Programs return code is 0, if files were matching, 10, if the files did
not match, and 1-9 in case of error.

Usage:  dftmatch [options] <File1> <File2>

Options:
-frames[=<Y|n>]
    Frames are checked (y, default) or not checked (n)
-conc[entrations][=<Y|n>]
    TAC values are checked (y, default) or not checked (n)
-regions[=<y|N>]
    Region names are checked (y) or not checked (n, default)
-timeunit[=<y|N>]
    Time unit is checked (y) or not checked (n, default)
-unit[=<y|N>]
    Concentration unit is checked (y) or not checked (n, default)
-studynr[=<Y|n>]
    Study number ir checked (y) or not checked (n, default)
-roughly
    Values are required to match roughly (99.9%), not exactly
-around
    Values are required to be around the same (90%), not exactly
-mean
    Mean of absolute concentration differences must be lower than the
    limit set with option -roughly or -around
-abs=<value>
    Absolute differences must not exceed the specified limit
-h or --help
    Print this message and exit
--build or --version
    Print software build information and exit
--verbose
    Program prints more information about what it is doing and shows
    detailed information on what did not match
--silent
    Program works silently, printing only warnings and error messages.

See also: dft2csv, dftunit, dftcalc, iftisval, resmatch, imgmatch

Keywords: DFT, software testing

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```

```
dftmax 0.3.5  (c) 2004-2013 by Turku PET Centre

Finds the maximum (or minimum) value in DFT datafile(s).

Usage: dftmax [Options] <DFT file(s)>

Options:
 -min
     Find the minimum value, instead of maximum
 -c[lean]
     Only the maximum or minimum value of ALL specified files is printed
 -time[=<y|N>]
     Both maximum value and time of maximum are printed (y) or only
     maximum value (n, default).
 -robust
     Search is limited to the longest range above and below median
 -h or --help
     Print this message and exit
 -v, --build or --version
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing.

See also: dftpeak, dftunit, dftframe, dft2csv, tacrange, dftmatch, dftlevel

Keywords: DFT, TAC, max, min

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```

```
dftnest 0.1.0 (c) 2013 by Turku PET Centre

Separate TACs from TACs of nested ROIs.

Format of the accepted data file is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html
File must contain the volume of each nested ROI.

Usage: dftnest [options] <Datafile> <Output file>

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: dftavg, dftadd, dftinteg, dftcalc

Keywords: DFT, modelling, tools

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```

```
dftpeak 0.1.1  (c) 2012 by Turku PET Centre

Finds the peak value in DFT datafile.

Usage: dftpeak [Options] <TAC file> <Result file>

Options:
 -decr=<Percentage>
     Time when TAC decreases to specified percentage of peak value is
     also estimated
 -h or --help
     Print this message and exit
 -v, --build or --version
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing.

See also: dftmax, dftframe, dftsuv, dftlevel, rescoll, inpstart

Keywords: DFT, TAC, max, min, peak

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```

dftratio 1.5.0 (c) 2003-2012 by Turku PET Centre

Calculates the regional tissue to reference tissue ratio, which is often
used as a robust and model independent index of receptor availability.
By default, ratio of AUCs is calculated as

$$\text{Ratio} = \frac{\text{Regional AUC}(t1..t2)}{\text{Reference AUC}(t1..t2)}$$

Data concentration units are cancelled out from the ratio. Therefore
the result is the same if it is calculated from original radioactivity
concentrations or SUV TACs (SUV ratios).

Parameters:
  1) Tissue TAC file
  2) Name of reference region in tissue file, or name of datafile
     containing the reference tissue TAC
  3-4) Start and end times for AUC calculation (t1 and t2) in minutes
  5) Result file (existing file is overwritten)
 [6) Ratio curve file (optional); only for plotting]

Options:
 -B Bound/free-ratio is calculated instead of Total/free;
     reference region TAC is first subtracted from other regional TACs.
 -M Bound TAC maximum value is searched between start and end times,
     and Bound/free ratio is calculated at this time point.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

The weights are not used in the calculations.

Example:
     dftratio ut1234.dft cer 40 60 ut1234ratio.res

See also: imgratio, dftcalc, dftdv, interpol, dftunit, dftsuv, rescoll

Keywords: TAC, DFT, modelling, AUC, ratio

```
dftreduc 0.1.1  (c) 2008,2009 Turku PET Centre

Reduce the number of regional TACs in DFT file by averaging similar TACs
Average TACs are sorted by AUC.

Usage:  dftreduc [Options] <Input file> <Output file>

Options:
 -nr=<number of resulting TACs>
     By default three TACs are created.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

See also: dftlist, dftdel, dftadd, dftbreak, dftavg, dftren, dfteven

Keywords: DFT, tool, simulation

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```

```
dftren 1.3.4  (c) 2001-2012 Turku PET Centre

Rename the regional TACs in the datafile.

Usage:
  dftren [Options] <datafile> <TAC nr or Name> <New name> <New hemisph> <New plane>

Set region nr to 0, if all TAC names are to be changed.
If name for hemisphere or plane is to be emptyed, enter character - or
an empty string "" or '', depending on the computer platform.
If some of the names is to be left unaltered, enter a . (dot).

Options:
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

See also: dftlist, dfthncor, dftrenpl, dftvncor, dftdel, dft2csv

Keywords: DFT, tool, rename, simulation

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```

```
dftrenpl 1.1.4  (c) 2002-2013 by Turku PET Centre

Renames the third field (which normally contains the PET plane number)
of regional names in TAC files.

Usage: dftrenpl [Options] <TAC file(s)>

Options:
 -seq[uential]
     By default, or with this option, the third name field is replaced by
     or set to a sequantial number, 000000, 000001, 000002, and so on.
     All regions are renamed.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: dftlist, dfthncor, dftren, dftvncor, dft2csv

Keywords: DFT, tool, simulation

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```

```
dftrepna 1.0.3  (c) 2003-2010 by Turku PET Centre

Replaces NaNs (missing or deleted samples) in DFT files by interpolation.

Usage: dftrepna [Options] <Datafile(s)>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

See also: dft2html, dft2dat, dft2res, dftlist

Keywords: DFT, tools, NA, NaN

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```

```
dftrmcmt 0.2.0  (c) 2005,2008 Turku PET Centre

Deleting comments and Interfile-type header information in DFT file(s).

Usage:  dftrmcmt [Options] <DFT file(s)>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing

See also: dft2dat, dft2html, dft2res

Keywords: DFT, file format conversion, tools

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```

dftrmdpl 0.3.1 (c) 2004-2008 Turku PET Centre

Removes regional TACs that are in duplicates in DFT files.
A duplicate TAC has the same region and hemisphere name and plane as
any of the previous TACs. This check is character upper/lower case
-insensitive.

Usage: dftrmdpl <file1> [file2] [file3] ...

See also: dftlist, dftdel, dftadd, dftbreak, dftren, dftrmovl

Keywords: DFT, tool

```
dftrmneg 1.1.1  (c) 2005,2010 Turku PET Centre

Program for deleting negative concentrations from TACs.
Negative values are replaced by zeroes.

Usage:  dftrmneg [Options] <DFT file(s)>

Options:
 -L=<lower limit>
     Lower limit for concentration values; by default 0.
 -U=<upper limit>
     Upper limit for concentration values; by default none.
 -replaceby=<limit|NA>
     When value is outside limits, is it replaced by the limit value
     (default), or marked as NA (not available).
 -del
     If all values in a row (frame) are outside limits or NA,
     the frame is deleted from file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: dftrmbkg, dftcbv, dftcut, dftlevel, ecatthrs

Keywords: DFT, input, tools, threshold

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```

dftrmovl 0.3.0 (c) 2004-2012 Turku PET Centre

Removes overlapping samples from blood or plasma TAC files.
If overlap exists, backup of the original file is saved as *.bak.
The first instance of overlapping samples is removed.

Usage: dftrmovl [Options] <file1> [file2] [file3] ...

Keywords: DFT, input, tool, frame time

See also: dftcut, dftrmdpl, dftcat, dftframe, dftrmneg, interpol

```
dftscale 0.3.1  (c) 2006-2010 by Turku PET Centre

Adjust two TACs into the same level to make visual comparison easier,
or adjust the TAC peak to specified value.

Usage 1: dftscale [Options] <Datafile1> <Datafile2> <Scaled datafile2>
Usage 2: dftscale [Options] <New peak value> <Datafile> <Scaled datafile>

Options:
 -x1=<start time>
     Time where AUC calculation is started (by default start of data)
 -x2=<end time>
     Time where AUC calculation is stopped (by default end of data)
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

The procedure for adjusting TACs in file2 to TACs in file1 is:
1. if times x1 and x2 are not set by user, then set these based on
   common time ranges in data1 and data2
2. calculate AUC1 between x1 and x2 in data1
3. calculate AUC2 between x1 and x2 in data2
4. calculate the scale factor as AUC1/AUC2
5. multiply data2 with the scale factor, and save the file.

The procedure for adjusting TAC peak is:
1. find the maximum TAC value
2. calculate the scale factor as peak/maximum
3. multiply data with the scale factor, and save the file.

See also: dftcalc, dftsuv, dftsums, dfteven, dftavg, dftmax, dft2svg

Keywords: modelling, simulation, input, plotting, scaling

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```

```
dftslope 0.5.1  (c) 2004-2011 by Turku PET Centre

Program for finding the highest slope of TAC(s) in a DFT file.
The intercept with x axis can be used as an estimate of tracer appearance
time, and can be used optionally (by specifying name for new DFT file) to
correct sample times so that the curve(s) start to rise at zero time.

Usage:
  dftslope [Options] <DFT file> <Nr of points for slope> [new DFT file]

Options:
 -xic
     Reports the average intercept with x axis (default)
 -slope
     Reports the highest slopes and their average
 -rmbkg
     Sample values before appearance time are set to zero
 -rise=<time>
     TAC(s) in new DFT start to rise at specified sample time (by default 0)
 -o=<filename>
     Reported values are written in specified file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

User should set the number of points for slope calculation, based on
visual inspection of the data. If number is set to 0, then program tries
to set the number automatically.

See also: fitdelay, dfttime, dftrmbkg, dft2svg, avgbolus

Keywords: DFT, input, time delay, modelling, simulation

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```

```
dftsm 0.1.0  (c) 2009 Turku PET Centre

Similarity measure (Pearson's correaltion coefficient) for PET
time-activity curves (TACs) in DFT file.

Usage:  dftsm [Options] <Input file>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: dftlist, dftadd, dftavg, dftreduc, dft2svg

Keywords: DFT, tool, similarity measure

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```
dftsmo 0.0.4  (c) 2007-2010 by Turku PET Centre

Smoothing of time-activity curve data using the method of Peter A Gorry (1).

Usage: dftsmo [Options] <DFT file> <Output file>

Options:
 -o=<order of polynomial>
     By default 2 (binomial polynomial); cubic polynomial may not work yet.
 -s=<order of differentiation>
     By default 0 (smoothing, no differentiation)
 -n=<Nr of points>
     Number of consecutive points, must be odd; by default 7
 -h or --help
     Print this message and exit.
 --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

References:
1. Gorry PA. General least-squares smoothing and differentiation of
   nonuniformly spaced data by the convolution method.
   Anal Chem. 1991;63:534-536.

See also: dft2svg, interpol, fr4sim

Keywords: DFT, noise, smoothing, derivation

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```

```
dftsort 0.3.1  (c) 2004-2012 by Turku PET Centre

Sort PET TAC data in DFT format (1) by the region name, by plane number,
or sample time.

Usage:  dftsort [Options] <datafile(s)>

Options:
 -sort=<name|plane|time>
     TACs are sorted by regional name (default) or plane, or TAC samples
     ("frames") are sorted by increasing sample time
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: dftlist, dftren, dftrenpl, dftvncor, dfthncor, dftcat, dft2csv

Keywords: DFT, tool, sorting

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```

```
dftstd 1.3.3  (c) 2001-2012 by Turku PET Centre

Program for calculation of standard deviation between regional TACs,
separately for each time frame.

With options -S and -C either SD (default) or CV can be computed.

Usage:  dftstd [Options] <Datafile> <SD file>

Options:
 -SD
     SD is calculated (default)
 -CV
     CV is calculated
 -AVG=<filename>
     Also average curve is calculated and written in specified file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: dftlist, var4dat, dftavg, avgbolus, avgttac, dftadd, dftweigh

Keywords: DFT, standard deviation, noise, simulation

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```

```
dftstudy 0.6.5  (c) 2004-2014 Turku PET Centre

Set or get the valid TPC study number in regional TAC (DFT) or
results (RES) file.
Study number can not exceed 10 characters, and it must not
contain spaces. A valid TPC study number contains 1-5 letters
(upper- or lowercase) followed by 1-5 digits.
Study number is automatically extracted from filename, if it does not
previously exist or is not given as an argument.

Usage:  dftstudy [Options] <datafile> [new study number]

Options:
 -fn[=<N>]
     Get study number from filename, optionally from the N first letters
     (max 10) of file name, excluding possible path and extension.
 -lower
     Convert study number letters to lowercase
 -df=<N>
     Delete the first N letters from study number
 -force
     Validity of new study number is not checked
 -value
     Print only the study number without file name
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

See also: dftunit, dftadd, rescoll

Keywords: DFT, RES, tool, simulation, study number

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```

```
dftsums 0.1.0  (c) 2006 by Turku PET Centre

Calculate the sum-of-squares (SS) of difference between two TACs.
The procedure is:
1. interpolate data2 to sample times in data1
2. calculate the square of difference at each sample time of data1
3. calculate the sum of squares

Usage:
  dftsums [Options] <Datafile1> <Datafile2> [Output file]

Options:
 -v[ersion]
 -build
    Print build information and exit.
 -h[elp]
    Print this text and exit.
 -silent
    Work silently; only warnings and error messages are printed in stdout.

See also: interpol, dftcalc, dftscale, dft2ps

Keywords: modelling, simulation, input
```

```
dftsuv 1.3.0 (c) 2004-2013 by Turku PET Centre

Calculation of standardized uptake values (SUV, DUR, DAR) from regional
time-activity curves (TAC), injected dose and subject weight.
SUV is calculated as a mean value between specified sample times.

Format of the accepted data file is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html
TAC radioactivity concentrations must be in kBq/mL, or in another units
that can be automatically converted into kBq/mL.

Instead of SUV, the percentage of injected dose per tissue volume
(%i.d./L) is calculated, if you set the subject weight (below) to 0.

Parameters:
  1) Tissue TAC file (*.dft); must be corrected for physical decay
  2) SUV calculation start time (min)
  3) SUV calculation end time (min)
  4) Injected dose (MBq)
  5) Subject weight (kg or liters)
  6) Result file

Options:
 -C=<Filename for SUV curve>
     Save regional SUVs from whole measurement time range.
 -D=<Tissue density (g/ml)>
     Calculate results per tissue mass instead of tissue volume.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1: calculate SUV40-60 and save SUV TAC with command
     dftsuv -c=uia15suv.dft uia15.dft 40 60 330 77 uia15suv40-60.res
Example 2: calculate SUV from available time range with command
     dftsuv uia15.dft 0 0 330 77 uia15suv.res

See also: dftinteg, dftframe, dfttime, dftcalc, dftunit, avgbolus, rescoll

Keywords: DFT, SUV, DUR, DAR, dose, modelling, tools

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```

```
dfttime 2.2.4  (c) 1999-2012 by Turku PET Centre

For changing sample times in regional or blood/plasma TAC files.
Samples with negative times are not saved.
Time must be given in the same units that are used in the datafile.

Usage: dfttime [Options] <input file> <[-]time value or file> <output file>

Time can be given as positive or negative value directly in the command
line, or in an ASCII file which contains a line with the time change value
in the following format: 'time_difference := time'.
Alternatively, time specified in file with 'Ta' or 'start_time' is
subtracted from sample times.

Options:
 -h or --help
     Print this message and exit
 -d[=<Isotope>]
     Physical decay correction is changed with change in sample times;
     without this option, radioactivity values are not changed.
     Accepted isotope codes are for example F-18, C-11, and O-15.
     Isotope code can also be specified in input file in format
     '# isotope := Isotope'.
     Note that this option will provide correct result only if time unit
     setting in datafile is correct.
 -keepnegat
     Samples with negative sample times are not removed from output.
 -keeptimes
     While correction for physical decay is changed with option -d, sample
     times will not be changed.
 -nogap
     Possible gap between time zero and first sample is filled.
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: dftframe, dftdecay, egetstrt, injdifft, dftunit, fitdelay

Keywords: DFT, modelling, simulation, late scan, input, time delay

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```

```
dftunit 0.5.4  (c) 2004-2012 by Turku PET Centre

Check (by default) or set (optionally) the data unit in PET TAC files
in DFT format.

Usage:  dftunit [Options] <TAC file(s)>

Options:
 -u[nit]=<New unit>
     This sets the unit; data values are however not changed
 -uc=<New unit> or -cu=<New unit>
     Conversion of data values and calibration unit
 -timeunit=<New time unit>
     This sets the sample time unit (min or sec); times are not changed
 -ctimeunit=<New time unit>
     Conversion of sample times and time unit
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

Conversions between the following calibration units are possible:
Bq/cc, kBq/cc, MBq/cc, nCi/cc
Note that mL is equal to cc (cubic centimeter).

See also: dftcalc, ecatunit, dftframe, dftmax

Keywords: DFT, calibration unit, simulation, format conversion

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```

```
dftvncor 0.2.2  (c) 2004-2012 Turku PET Centre

For renaming the voinames of regional TACs in the datafile to start
with a specified letter.
If voiname length would exceed 6 characters, the first letter is replaced.

Usage:  dftvncor [Options] <datafile> <letter>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

See also: dftlist, dftren, dftrenpl, dfthncor, dftsort

Keywords: DFT, tool, roiname

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```

```
dftweigh 2.3.1  (c) 2000-2013 by Turku PET Centre

Adds or removes the frame weighting information to DFT file for parameter
estimations. TACs in DFT file are assumed to be corrected for decay.
The relative weights are adjusted using a scan information file (SIF),
or TACs in DFT file (volume weighted average of all regions or given region);
in the latter case the units in DFT file must be set correctly.

Usage: dftweigh [Options] <DFT file> [SIF file | Region name]

Options:
 -rm
     Existing weights are removed
 -i=<Br-76|Cu-62|C-11|Ga-68|Ge-68|F-18|N-13|O-15|Rb-82>
     Isotope, in case it is not found inside SIF file.
     Isotope is only needed when SIF file is used.
 -L  Weights are not calculated, but existing weights are printed
     on screen.
 -sif=<Filename>
     SIF data based on DFT file is written in given file.
 -moderate=<value>
     Weights are moderated by adding (1/value)*max true counts to
     all counts, if (max trues)/value > (min trues). By default, value=100.
     You can set value to zero to apply full range of weights.
 -wf | -wfm
     Weights are based only on frame length or sampling interval.
     With -wfm the range of weights is reduced using option -moderate. -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Note that absolute weights cannot be calculated. Relative weights are
scaled so that average weight is 1.0.

Reference:
1. Mazoyer BM, Huesman RH, Budinger TF, Knittel BL. Dynamic PET data
   analysis. J Comput Assist Tomogr 1986; 10:645-653.

See also: siflist, sifcat, eframe, cti2sif, dftframe, sif2ecat, dftunit

Keywords: DFT, SIF, modelling, weighting

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```

```
disp4dft 3.2.3  (c) 1994-2013 by Turku PET Centre

Add dispersion effect to ideal data (ON), or correct a measured data set
for dispersion (OFF) [1, 2].
The time constant of the dispersion must be given in the same time units as
those that are used in the data file.
Program output is written in file in the same format as the input datafile.

Usage:
  disp4dft <ON|OFF> <Datafile> <Dispersion> <Output file>

Options:
 -L
    Dispersion time and other log information is written as comments in
    the corrected TAC file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
  disp4dft off us488blood.kbq 2.5 us488blood_disp.kbq

References:
 1. Iida H, Kanno I, Miura S, Murakami M, Takahashi K, Uemura K. Error
    analysis of a quantitative cerebral blood flow measurement using H215O
    autoradiography and positron emission tomography, with respect to the
    dispersion of the input function. J. Cereb. Blood Flow Metab. 1986;
    6:536-545.
 2. Oikonen V. Model equations for the dispersion of the input function in
    bolus infusion PET studies. TPCMOD0003 2002-09-03;
    http://www.turkupetcentre.net/reports/tpcmod0003.pdf

See also: dftunit, fit_winp, fitdelay, dft2svg

Keywords: modelling, simulation, input, blood, dispersion

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```

```
domany 0.4.2  (c) 2004-2006 by Turku PET Centre

Generates a set of commands for a set of PET studies, based on a command-
line with wildcards * and ?, and the matching data files.
File names must start with a valid study number (1-5 letters followed by
1-5 digits, e.g. 'uia7706').

Usage:
  domany [Options for domany] "<Command-line with wildcards>"

The whole command must be put within quotation marks; in some systems
double and/or single quotation marks can be used.
Program searches for files that match the first argument containing
wildcards * and ?, and then replaces with similar content the wildcards
in the following arguments, and generates the command-line for all files.
If an argument with wildcards should remain as such, put it inside quotes.

The file names for result files can be given with string STUDYNR in place
where the study number will be written by this program.

Options:
 -o=<File name>
    Commands are written in specified file; by default to stdout.
    If file exists, new commands are appended to it.
 -v[ersion]
 -build
    Print build information and exit.
 -h[elp]
    Print this text and exit.
 -silent
    Work silently; only warnings and error messages are printed in stdout.

For example, the following set of commands
  patlak pet\ut1234.dat plasma\ut1234ap.dat 10 60 ut1234.res
  patlak pet\ut1238.dat plasma\ut1238ap.dat 10 60 ut1238.res
  patlak pet\ut1239.dat plasma\ut1239ap.dat 10 60 ut1239.res
  patlak pet\ut1241.dat plasma\ut1241ap.dat 10 60 ut1241.res
  patlak pet\ut1242.dat plasma\ut1242ap.dat 10 60 ut1242.res
  patlak pet\ut1245.dat plasma\ut1245ap.dat 10 60 ut1245.res
  patlak pet\ut1246.dat plasma\ut1246ap.dat 10 60 ut1246.res
  patlak pet\ut1248.dat plasma\ut1248ap.dat 10 60 ut1248.res
  patlak pet\ut1248.dat plasma\ut1248ap.dat 10 60 ut1248.res
could be created by entering the following command:
  domany "patlak pet\ut????.dat plasma\ut????ap.dat 10 60 STUDYNR.res"
if these data files exist in the specified subdirectories.

See also: execlong

Keywords: tools, modelling, simulation
```

dtpa_c2s 1.0.1 (c) 2003,2005 by Turku PET Centre

Converts arterial blood Gd-DTPA concentration curve to SAT-turboFLASH
LV and myocardial (MC) MRI signal intensity curves.

Parameters:
  1) Datafile, containing Gd-DTPA concentration in blood
  2) Myocardial blood flow F (mL/mL/min)
  3) Extravascular extracellular volume fraction Ve (mL/mL)
  4) Venous blood volume fraction Vb (%)
  5) Delay time (sec)
  6) Omega*M0 for LV region
  7) Omega*M0 for myocardial region
  8) Signal intensity (output) file

Datafile must contain the following columns in this order:
  1) Sample time (sec)
  2) Gd-DTPA concentration
 [N) Myocardial regions are not used]

Options (with default values):
 -Alpha=8 (in degrees)
 -TR=0.0020
 -TI=0.055
 -R10b=0.67
 -R10myo=1.0
 -n=48
 -r1=4.3
 -E=0.5

Reference:
Larsson HBW, Rosenbaum S, Fritz-Hansen T. Quantification of the effect of
water exchange in dynamic contrast MRI perfusion measurements in the brain
and heart. Magn. Reson. Med. 2001;46:272-281.

See also: dtpa_s2c, fit_dtpa

Keywords: MRI, DFT, simulation, perfusion

dtpa_s2c 2.1.1 (c) 2002-2005 by Turku PET Centre

Converts SAT-turboFLASH LV MRI signal intensity curve to Gd-DTPA
arterial blood concentration curve.

Parameters:
  1) Datafile, containing measured LV signal
  2) Number of baseline samples (usually 3)
  3) Concentration (output) file

Datafile must contain the following columns in this order:
  1) Sample time (sec)
  2) LV signal
 [N) Myocardial regions are not used]

Options (with default values):
 -Alpha=8 (in degrees)
 -TR=0.0020
 -TI=0.055
 -R10b=0.67
 -n=48
 -r1=4.3
Options to use Omega*M0 factor measured in baseline study:
 -om=factor   ; factor is the Omega*M0 from baseline study
 -of=filename ; factor is read from the baseline concentration file

Reference:
Larsson HBW, Rosenbaum S, Fritz-Hansen T. Quantification of the effect of
water exchange in dynamic contrast MRI perfusion measurements in the brain
and heart. Magn. Reson. Med. 2001;46:272-281.

See also: dtpa_c2s, fit_dtpa

Keywords: MRI, DFT, simulation, perfusion

```
e63to7 0.9.7  (c) 2003-2012 by Turku PET Centre

Convert an ECAT 6.3 image or sinogram file to ECAT 7 format volume image
or 3D sinogram.

Usage: e63to7 [Options] <ECAT 6.3 file> [ECAT 7 file]

Options:
 -C=<o|B|M>
     Image calibration unit is changed from kBq/mL to Bq/mL (B, default)
     or MBq/mL (M), or the original unit is not changed (o).
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only warnings and error messages.

Examples:
1. Convert one image, let program give name to the ECAT7 file
     e63to7 is02345dy1.img
2. Convert one image, give a specific name to the ECAT7 file
     e63to7 is02345dy1.img is2345.v
3. Convert all images in current working directory in Windows command shell
     for %g in (*.img) do e63to7 %g

See also: e7to63, ecat2ana, ecat2flo, ecatadd, esplit, ecatunit

Keywords: image, ECAT, tool, modelling, file format conversion

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```

```
e7emhdr 0.3.1  (c) 2003-2010 by Turku PET Centre

Edits the information in the main header of an ECAT 7 file.

Usage: e7emhdr [Options] <ECAT file> <field_name> := <field value>
   or: e7emhdr [Options] <ECAT file> <header file>

Options:
 -h or --help
        Print this message and exit.
 --build or --version
        Print software build information and exit.
 --silent
        Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Header file can contain one or more mainheader field names and values
in interfile-like format, e.g.
  patient_name := Einstein Albert
  radiopharmaceutical := O-15 WATER
  study_description := brain scan
  facility_name := Turku PET Centre

Examples:
  e7emhdr s2345dy1.v patient_name := "Albert Einstein"
  e7emhdr s2345dy1.v s2345dy1.header

See also: lmhdr, lshdr, e7evhdr, lmlist, ecatunit, edecay

Keywords: ECAT7, image, header, tools

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```
e7eshdr 0.1.1  (c) 2007,2012 by Turku PET Centre

Edit the ECAT 7.x 3D scan file subheaders.

Usage: e7eshdr [options] <ECAT *.s file> <header file>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Header file can contain one or more subheader field names and values
in interfile-like format, e.g.
  scale_factor := 0.2
  x_resolution := 0.3375

See also: lshdr, lmlist, lmhdr, e7emhdr, e7evhdr

Keywords: ECAT7, scan, sinogram, header, tools

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```
e7evhdr 1.0.3  (c) 2005-2012 by Turku PET Centre

Edit the ECAT 7.x image volume file subheaders.

Usage: e7evhdr [options] <ECAT *.v file> <header file>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Header file can contain one or more subheader field names and values
in interfile-like format, e.g.
  x_pixel_size := 0.257426
  y_pixel_size := 0.257426
  z_pixel_size := 0.2425

See also: lshdr, e7emhdr, e7eshdr, lmlist, lmhdr

Keywords: ECAT7, image, header, tools

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```

```
e7to63 0.8.6  (c) 2003-2012 by Turku PET Centre

Convert ECAT 7.x sinogram or image volume file to ECAT 6.3 format.

Usage: e7to63 [Options] <ECAT 7.x file> [ECAT 6.3 file]

Options:
 -C=<o|k>
     Image calibration unit is changed from Bq/mL or MBq/mL to
     kBq/mL (k, default), or the original unit is preserved (o)
 -h or --help
     Print this message and exit
 --build or --version
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only warnings and error messages.

Examples:
1. Convert one image, let program give name to ECAT6 file
     e7to63 is02345.v
2. Convert one image, give a specific name to the ECAT6 file
     e7to63 is02345.v is2345dy1.img
3. Convert all images in current working directory in Windows command shell
     for %g in (*.v) do e7to63 %g

See also: e63to7, ecat2ana, ecat2flo, ecat2int, ecatadd, esplit, ecatunit

Keywords: image, ECAT, tool, modelling, file format conversion

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```
e7vplavg 1.0.0  (c) 2006 by Turku PET Centre

Combine the adjacent ECAT 7.x image volume planes to reduce
data size and noise.
If the number of image volume planes is not divisible by the number of
averaged adjacent planes, the leftover planes are excluded from the
resulting image volume.

Usage: e7vplavg [Options] <ECAT *.v file> <Resulting image volume file>

Options:
 -n=<Nr of adjacent planes that are averaged>
     Number of adjacent planes that are combined. By default, n=2.
 -first=<First included image plane>
     The first plane that is included in combined image volume.
     By default, 1.
 -last=<Last included image plane>
     The last plane that is included in combined image volume.
     By default, the last plane in the original image volume.
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.

See also: imgshrink, e7lmhdr, e7lmlist, esplit

Keywords: ECAT7, image, plane, tools

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```
eabaort 2.0.2  (c) 2005-2013 by Turku PET Centre

Extracts arterial input curve from human abdominal region of a dynamic
[O-15]H2O PET image by finding the aorta, and corrects it with
recovery coefficient based on method by Germano et al. (1).
The current method does also account for effect of background
radioactivity on recovery coefficient (3).

Supported file formats are ECAT 6.3, ECAT 7, NIfTI-1, and Analyze 7.5.
In case of NIfTI and Analyze image input, you need to add the frame
information to the blood data separately. This can be done with
program dftframe.
NOTICE: all image planes should contain a clear view of the abdominal
aorta that has not yet split into two vessels, and no other high spots;
crop the image before using this program.
NOTICE: It is recommended that either the full width half maximum (FWHM)
value or individually measured aorta diameter is specified as command-line
option, because both cannot be reliably estimated from a noisy image.
NOTICE: It is also recommended that the full width half maximum (FWHM)
value is determined for each scanner and reconstruction method.

Usage:  eabaort [Options] <PET image> <Blood file>

Options:
 -FWHM=<value|fit>
     Enter a fixed value for FWHM (mm); fitted by default.
     Results will not be reliable unless either FWHM or vessel diameter
     is measured and fixed.
 -diameter=<value>
     Enter a fixed value for inner vessel diameter (mm); fitted by default.
     Results will not be reliable unless either FWHM or vessel diameter
     is measured and fixed.
 -plane=<Mean|Median|Best>.
     Model is fitted separately to all image planes, and by default
     the mean FWHM and vessel diameter is used to estimate an average
     blood TAC using all image planes.
     With this option the median can be used instead of the mean, or
     blood TAC can be estimated only from the plane that provides
     the highest fitted peak.
 -model=<germano|gaussian>
     Select the PVE simulation method; Gaussian smoothing by default.
 -pixelsize=<value>
     Set image pixel size (mm) if image header does not valid pixel size.
 -fitsize=<value>
     Length (mm) of the fit square side. By default, 30x30mm square
     surrounding the peak pixel value is used in the fit.
 -sum=<filename>
     Save sum image subvolume which is used to fit vessel position.
 -sumfit=<filename>
     Save fitted sum image subvolume.
 -bkg=<filename>
     Model estimated background curve.
 -peak=<filename>
     Model estimated peak TAC (not corrected for recovery error).
 -subvol=<filename>
     Subrange of the original dynamic image used in fit; for testing.

Example 1: FWHM is measured, vessel diameter is estimated from image:
     eabaort -FWHM=6.3 -diameter=best s9876dy1.v s9876ab.dat

Example 2: vessel diameter is measured, FWHM is estimated from image:
     eabaort -FWHM=fit -diameter=19.2 s9876dy1.v s9876ab.dat

References:
1. Germano G, Chen BC, Huang S-C, Gambhir SS, Hoffman EJ, Phelps ME.
   Use of abdominal aorta for arterial input function determination
   in hepatic and renal PET studies. J Nucl Med 1992;33:613-620.
```

2. Scremin OU, Cuevas-Trisan RL, Scremin E, Brown CV, Mandelkern MA. Functional electrical stimulation effect on skeletal muscle blood flow measured with H215O positron emission tomography. Arch Phys Med Rehabil 1998;79:641-646.
3. Brix G, Belleman ME, Hauser H, Doll J. Recovery-koeffizienten zur quantifierung der arteriellen inputfunktion aus dynamischen PET-messungen: experimentelle und theoretische bestimmung. Nuklearmedizin 2002;41:184-190.

See also: fit_h2o, imgflow, fitdelay, fit_winp, imgbox, simiart

Keywords: input, image, modelling, abdominal aorta

rc2ki 1.1.0 (c) 2001,2005 by Turku PET Centre

For simulation of Influx constant (Ki) from rate constants k1-k3.

$$Ki = \frac{k1 * k3}{k2 + k3}$$

Parameters:
  1-3) k1 start, stop, and step
  4-6) k3 start, stop, and step
  7) k1/k2
  8) Result file

Result file will contain three columns: k1, k3 and Ki

Keywords: simulation

```
ecat2ana 1.0.5  (c) 2003-2013 by Turku PET Centre

Convert ECAT 6.3 images or ECAT 7 image volumes to Analyze 7.5 image format.

The resulting Analyze database consists of two files, Analyze image (*.img)
and header file (*.hdr).
Analyze image format does not contain information on the frame times.
Frame times can be retrieved from SIF file, which can be created optionally.
SIF can also be created later using program cti2sif.

By default, data is saved in big endian byte order (Sun Sparc).

Usage: ecat2ana [Options] <ECAT file(s)>

Options:
 -L[ittle] or -pc or -i
     Data is saved in little endian (PC Intel) byte order.
 -B[ig] or -sun or -sparc
     Data is saved in big endian (Sun Sparc, Motorola, PowerPC) byte order
     (default).
 -O=<output path>
     Data directory for Analyze files; by default the output directory
     ana_unix_files or ana_pc_files is created under input directory.
 -flip=<y|n>
     Override the default and environment variable ANALYZE_FLIP setting
     by always flipping/not flipping image in z-direction (planes).
     If environment variable is not set, then default is y.
     Images are always flipped in x,y-directions.
 -SIF
     SIF is saved with Analyze files; note that existing SIF will be
     overwritten.
 -frames
     Frames are saved as separate Analyze files.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --verbose
     Program prints more information about what it is doing.
 --silent
     Program works silently, printing only error and warning messages.

Example:
  ecat2ana *.v

Specific extensions to Analyze 7.5 format:
 -Scale factor to retain quantitation in image_dimension.funused1
 -Isotope halflife (sec) in image_dimension.funused3;
  this does not imply whether data is corrected for decay or not.
 -String in data_history.descrip tells whether data is corrected for decay;
  'Decay corrected.' or 'No decay correction.'

See also: ana2ecat, cti2sif, anabyteo, ana_lhdr, eframe, ecat2flo, ecat2nii
and ImageConverter (.NET version) in
http://www.turkupetcentre.net/programs/tpc_csharp.html

Keywords: image processing, format conversion, ECAT, Analyze

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you are welcome to redistribute it under GNU General Public License.
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```
ecat2flo 2.0.1  (c) 2003-2012 by Turku PET Centre

Extract the pixel data from ECAT 6.3 or 7.x matrices to a binary flat file
as 4-byte floats in this order of matrices:
All planes of first frame, then planes of 2nd frame, and so on.
Plane and frame number and matrix dimensions are written on screen
or in specified matrix information file, if filename for it is given.
The current platforms byte order (little or big endian) is used;
byte order can be swapped with program convend.

Usage:
  ecat2flo [Options] <ECAT file> <Output datafile> [Matrix information file]

Options:
 -inf=<Matrix information file>
     Plane and frame number and matrix dimensions x and y are written in
     specified text file; these numbers are needed when binary data
     is imported in another application program
 -b=<Nr of bins>
     Extract only specified nr of bins in sinogram leaving out bins from
     both sides
 -h or --help
     Print this message and exit
 --build, --version
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only error and warning messages.

See also: flo2ecat, convend, ecat2ana, ecatunit, eframe

Keywords: ECAT, image, sinogram, format conversion

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you are welcome to redistribute it under GNU General Public License.
```

```
ecat2nii 0.1.0  (c) 2013 by Turku PET Centre

Convert PET images from ECAT 6.3 or 7 to NIfTI-1 format.

Image byte order is determined by the computer where the program is run.
NIfTI image format does not contain information on the frame times.
Frame times can be retrieved from SIF file, which can be created optionally.
SIF can also be created later using program cti2sif.

Usage: ecat2nii [Options] <ECAT file(s)>

Options:
 -O=<output path>
     Data directory for NIfTI files, if other than the current working path.
 -dual
     Save the image in dual file format (the header and voxel data in
     separate files *.hdr and *.img); single file format (*.nii)
     is the default.
 -SIF
     SIF is saved with NIfTI; note that existing SIF will be overwritten.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --verbose
     Program prints more information about what it is doing.
 --silent
     Program works silently, printing only error and warning messages.

Example:
  ecat2nii *.v

See also: nii2ecat, cti2sif, nii_lhdr, eframe, ecat2flo, ecat2ana
and ImageConverter (.NET version) in
http://www.turkupetcentre.net/programs/tpc_csharp.html

Keywords: image processing, format conversion, ECAT, NIfTI

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```
ecat2tif 3.7.5  (c) 2002-2013 by Turku PET Centre

Extract the matrices of an ECAT 6.3 or ECAT 7 image or sinogram, or
NIfTI, Analyze 7.5, or microPET image, to TIFF 6.0 images.

Usage: ecat2tif [Options] <ECAT file> [Output TIFF file]

Options:
 -p=<Plane>
     A specified plane is extracted; by default all planes
 -f=<Frame>
     A specified frame is extracted; by default all frames
 -s[=Value]
     Color scale of output images is fixed from 0 to max of all
     image matrices, or from 0 to Value
 -L
     Log10 transform
 -L1
     Log10 transform, adding 1 to pixel values before transform
 -rb
     Apply rainbow colorscale instead of default grayscale
 -rbw
     Apply rainbow colorscale with white background
 -gr
     Apply grayscale (0=black, highest=white)
 -gi
     Apply inverse grayscale; default
 -th=<nr>
     Number of matrices tiled horizontally; set to a large value to draw
     all matrices in one row.
 -tv=<nr>
     Number of matrices tiled vertically; set to a large value to draw
     all matrices in one column.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example 1: Make TIF of plane 8 and frame 17, which is yet scaled to
the level of whole image maximum:
     ecat2tif -s -p=8 -f=17 s2345dy1.v s2345_pl08_fr17.tif
Example 2: Make TIF of all image matrices in rainbow color scale:
     ecat2tif -rb s2345sum.img s2345sum.tif
Example 3: Make TIF of all image matrices, scaling the colors to value 3:
     ecat2tif -S=3 a3456bp.v a3456bp.tif

See also: imgslice, ecatmax, ecatthrs, ecatunit, ecat2flo

Keywords: image, sinogram, TIFF, raster, tools

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```

```
ecatadd 2.0.0  (c) 2003-2012 by Turku PET Centre

For simulation of simple PET images for software testing;
Adds the contents of existing image files as new plane(s) and writes
the combined image as a new file.
Supports ECAT 6.3 and ECAT 7 formats.

Usage: ecatadd [Options] <combined file> <file1> <file2> [file3 ...]

Options:
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only warnings and error messages.

See also: ecatcat, dft2img, imgmove, flo2ecat, asc2flo, simcirc, esplit

Keywords: image, simulation, software testing

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```
ecatanon 4.3  (c) 1994-2007 by Turku PET Centre
Remove or encrypt patient information from ECAT 6.3 or 7 files
Usage: ecatanon <options> <file1> [file2...]
   --version, -V        Print version information
   --key <key>          Use encryption
   --name,    +n <name> Set patient name
   --no-name, -n        Remove patient name
   --file,    +f        Reset original filename to current name
   --no-file, -f        Remove original filename
   --id,      +i <name> Set patient id
   --no-id,   -i        Remove patient id
   --study,   +s <type> Set study type (ECAT7 only)
   --no-study -s        Remove study type (ECAT7 only)
   --no-upc   -u        Remove user process code
   --upc      +u <code> Set user process code
   --no-desc  -d        Remove study description
   --desc     +d <text> Set study description
   --no-age   -a        Remove patient age
   --age      +a        Set patient age
   --no-bd    -b        Remove patient birth date (ECAT7 only)
   --bd       +b <date> Set patient birth date or age (ECAT7 only,no encryption)

If an encryption key is specified, information is encrypted
instead of cleared. Note that the encryption is very weak and
should not be relied on for security.

See also: e7lmhdr, lmhdr, e7emhdr, iftcrypt

Keywords: image, patient anonymity, tool
```

```
ecatavg 0.3.0  (c) 2003,2006 by Turku PET Centre

Calculate an average of two or more ECAT 6.3 or 7 image or scan
files. ECAT files must contain same number of frames and planes.

Usage:
  ecatavg [Options] <Avg ECAT file> <ECAT file1> <ECAT file2> [more ECAT files]

Options:
 -sd=<Filename>
     Name for ECAT format file where standard deviations will be written.
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.

e.g. to calculate an average of all ECAT 7 images in current directory:
  ecatavg  average.v  *.v
e.g. to calculate average and S.D. of all perfusion images in ECAT 6.3
     format in a data directory:
  ecatavg  -SD=sd.img  average.img  /data/brain1/ua*flow.img

See also: ecatsum, ecatssum, esplit

Keywords: image, ECAT, modelling, simulation

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```
ecatcalc 1.6.1  (c) 2002-2013 by Turku PET Centre

Simple arithmetic calculations on ECAT 6.3 and ECAT 7 files.

Usage:
  ecatcalc [Options] <Image1> <Operation> <Image2|Const> <Output img>

, where
    Operation = +, -, x , /
    Const = Image1 is operated with this value

Options:
 -f or -frames
     All frames in image1 are processed with 1st frame of image2
 -m=<value> or -max=<value>
     Upper limit for output pixels
 -h or --help
     Print this message and exit
 --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

Examples:
     ecatcalc a999.flow.img - a1000.flow.img subtr.img
     ecatcalc o657dy1.v / 2.34 o657rda.v
     ecatcalc -f -m0.25 l333dy1.scn x l333.nrm l333dy1.corr.scn

Image1 and image2 must be in the same format, and they must have same
matrix size and plane numbers.
Data is not interpolated or corrected for physical decay, and thus it is
on the responsibility of the user to check that PET frame times are similar
and that physical decay and other corrections are appropriately considered.

See also: edecay, ecatunit, eframe, ecatcat, esplit, imginteg, ecat2tif

Keywords: ECAT, image, modelling, simulation

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```
ecatcat 3.2.2  (c) 1998-2012 by Turku PET Centre

Combines two or more dynamic ECAT 6.3 or 7.x images or sinograms.
This program can be used to catenate separate scans/images from one study,
when imaging session has been interrupted for some reason, or when
flat data with frames in separate files were converted to ECAT format.

Program corrects for decay and frame times to the start time of the first
specified image/sinogram. Use the original images or sinograms, if possible,
Input images must be decay corrected to the scan start time that is
specified in the main header and shown by this program.

Usage:
  ecatcat [Options] <file1> <file2> [file3 ...] <Catenated file>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: lmlist, eframe, lmhdr, sifcat, dftcat, esplit

Example:
     ecatcat a2345dy1.v a2345dy2.v a2345dy.v

Keywords: image processing, ECAT, tool, catenate

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```
ecatflip 1.4.0  (c) 2002-2013 by Turku PET Centre

Flips ECAT 6.3 or 7 file in X, Y, and/or Z direction(s).
By default, flipping in X and Y directions.

Usage:
  ecatflip [Options] <ECAT file> <Flipped ECAT file>

Options:
 -x
     Flip image in X direction (horizontally)
 -y
     Flip image in Y direction (vertically)
 -z
     Flip image in Z direction (image planes/slices)
 -up | -right
     Flip image to view it from above or right side
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

See also: esplit, img2cube, imgbox, imgslice, ecat2tif

Keywords: image, ECAT, tool, software testing

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```
ecathead 2.7.5  (c) 1995-2013 by Turku PET Centre

Program calculates the average TAC from all pixels in a PET image or scan
file in ECAT 6.3 or 7 format, or PET image in NIfTI-1 or Analyze format,
and writes it to a specified 'count-rate' file.
Count-rate file will be written with mid frame times in seconds, by default.
Frame start and end times are saved, if 'count-rate' file is named as
'*.dft', otherwise only frame mid times; option -format overrides this.
Decay correction is not changed: if image or sinogram is decay corrected,
head curve will be decay corrected, and vice versa.

Usage: ecathead [Options] <Dynamic image/sinogram> <Head curve>

Options:
 -thr[=<Threshold-%>,<<Nr of frames>|<a>|<fh>>]
     Count-rate curve is calculated from pixels exceeding the specified
     threshold level, or 10% level with only -thr.
     Specified number or default five last frames are used in determining
     threshold level; alternatively, with 'a' all frames, or with 'fh'
     the first half of frames are used in thresholding.
     Without -thr option all pixels are included.
 -m[in]
     Count-rate curve times are written in minutes (sec by default)
 -s[ec]
     Count-rate curve times are written in seconds (this is the default)
 -format=<cr|dft>
     File is written in 'count-rate' format with no titles and with frame
     mid times only, or, with title lines with PET frame start
     and end times (dft)
 -keepnegat
     Frames with negative mean value are not set to zero.
 -sum | -cps
     By default, mean of all or thresholded pixels is calculated;
     with option -sum the sum of pixel values is reported, or
     with option -cps the total radioactivity (not concentration).
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
     ecathead -thr=10,5 ub6789dy1.img ub6789dy1.head

See also: imgpext, img2dft, tocr, fitdelay, dftslope, eframe, dft2svg

Keywords: image, ECAT, time delay, count-rate, head-curve, input

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```
ecatlkup 2.2.4  (c) 1996-2013 by Turku PET Centre

Replaces the pixel values in PET image or scan file with the values
from a look-up table.
The look-up table must contain two columns: program looks from the first
column a matching value for the pixel value, and replaces the pixel
value with the value from the second column of the table.
Look-up table must be sorted in ascending order.
Histogram of the results is listed on the screen in verbose mode.

Usage:  ecatlkup <Input image> <Look-up table> <Output image>

Options:
 -c  If exact match in look-up table is not found, the closest value
     is selected; by default, value is interpolated from the table.
 -u=<unit id>
     Set image unit to a specified value: 0=unknown, 1=cnts/sec,
     2=counts, 3=kBq/mL, 4=sec*kBq/mL, 5=1/sec, 6=1/min, 7=mL/mL,
     8=mL/dL, 9=mL/(mL*min), 10=mL/(dL*min), 11=unitless, 12=nCi/mL,
     13=MBq/mL, 14=Bq/cc, 15=uCi/cc, 16=umol/(min*100g), 17=mg/(min*100g)
 -h or --help
     Print this message and exit
 --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

See also: arlkup, imginteg, ecatcalc, ecatunit, ecat2tif, dftlkup

Keywords: image, perfusion, autoradiography, look-up table

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```
ecatmax 0.3.0  (c) 2004-2010 by Turku PET Centre

Finds maximum value in PET image file(s) in ECAT 6.3 or 7.x format.

Usage: ecatmax [Options] <image file(s)>

Options:
 -min
     Minimum values are printed instead of maximum values
 -both
     Both max and min values are printed
 -clean
     Only the max and/or min value of all specified files is printed
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit

See also: ecatunit, eprofile, epxl2dft, lmhdr, lshdr, ecat2tif

Keywords: ECAT, image

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```

```
ecatssum 1.1.0  (c) 2006 by Turku PET Centre

  Software is used for calculating sum over specified frames or time interval
  in ECAT7 format 3D sinogram files. Sinogram data are treated as matrices and
  the original data format and header information are maintained. Software is
  optimized for large 3D sinogram files.

  Usage:
     ecatssum [options] <dynamic scn> <start frame> <end frame> <sum scn>

  Options:
    -t -T     start frame and end frame are given in milliseconds
    -f -F     force command line frame definition over main header frame info
    -s -S     run in silent mode
    -h -H     print usage and exit
    -v -V     print build information and exit

  Keywords: ECAT7, sinogram, sum

  E.g.: to extract frame 1 from dynamic sinogram:
     ecatssum HR+3D.S 1 1 HR+3D-frame1.S

  E.g.: to sum 5 frames starting from frame 15:
     ecatssum HR+3D.S 15 19 HR+3D-frames_15-19.S

  E.g.: to sum over time interval 1000 - 5000 milliseconds:
     ecatssum HR+3D.S 1000 5000 HR+3D-time1-5.S
```

```
ecatsum 1.4.3 (c) 2002-2007 by Turku PET Centre

Calculate an average over specified time frames of a dynamic
ECAT 6.3, ECAT 7 or Analyze 7.5 image. Will overwrite output
files without asking, if they exist.
If necessary, use program eframe to get a list of the time frames.

Usage:
  ecatsum [Options] <dynamic img/scn> <start frame> <end frame> <avg file>

Options:
 -i
     Integral image (activity x seconds) is calculated instead of an average.
 -s
     Sum image (sum of data matrix values) is calculated instead of an average.

Example: calculate average image over 5 frames starting from frame 14:
  ecatsum b123dy1.v 14 18 b123sum.v

See also: imginteg, ecatssum, eframe, lmlist, ecatunit

Keywords: ECAT, image, sum image, modelling

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```
ecatthrs 1.3.4  (c) 2002-2013 by Turku PET Centre

Threshold for PET image files in ECAT or Analyze format.
Program calculates an integral image/scan over time frames of a dynamic
image or scan file, finds the maximal integral value of all planes, and
cuts off (sets to zero) the pixels in dynamic image/scan which have lower
or higher integral than the specified threshold %.

Usage:
  ecatthrs [Options] <img file> <lower threshold %> <upper threshold %>
           <thresholded img file>  [mask file]

Options:
 -N=<nr of frames>
     Nr of frames from the end that are included in thresholding;
     by default, all frames are included
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example: threshold the background and cerebrospinal fluid:
     ecatthrs b123dy1.v 30 100 b123thres.v

Optional cutoff mask file will contain pixel values 1 (between threshold
values), and 0 (under lower or over upper threshold).

See also: eflexseg, imgdysmo, imgslim, esplit, img2dft, ecat2tif, ecatcalc

Keywords: image, threshold, mask

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```
ecattime 2.0.3  (c) 2002-2012 by Turku PET Centre

Changes the scan start and frame times in PET image or sinogram file in
ECAT 6.3 or 7 format to refer to the injection time instead of the original
delayed scan start time. Correction for physical decay is changed
accordingly in images, but not in sinograms.

Before using this program, PET image must be decay corrected to its
scan start time, but sinogram must not be corrected for decay.
Please note that file may be changed, but backup file is not made.

Usage:  ecattime [Options] <ECAT image or scan filename> [Time]

'Time' is either the time (min) from radiotracer injection to the PET scan
start time, or, the new scan start time.
If 'Time' is not entered, then program makes no changes to the data, but
only displays the current scan start time and time when the collection of
the first frame was started.

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1. PET scan is known to have started 30.2 min after tracer injection.
Times and decay will be corrected to the new scan start time:
     ecattime s2345dy1.v 30.2
Example 2. Injection time was 14:00:49, and PET times and decay will be
corrected to this new scan start time:
     ecattime s2345dy1.v 14:00:49

See also: edecay, eframe, egetstrt, ecatunit

Keywords: ECAT, image, physical decay, modelling

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```
ecatunit 0.3.2  (c) 2005-2013 by Turku PET Centre

For checking or setting data calibration units in ECAT images.
By default, the units are only shown, not changed.

Usage:  ecatunit [Options] <ECAT image(s)>

Options:
 -u=<New unit; e.g. Bq/cc or kBq/ml>
     Set the unit, but does NOT change the pixel values
 -us=<New unit; e.g. Bq/cc or kBq/ml>
     Set the unit only if unit is not originally defined in the image.
     This does NOT change the pixel values
 -uc=<New unit; e.g. Bq/cc or kBq/ml>
     Converts pixel values to the specified unit, e.g. kBq/ml to Bq/cc
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

The following unit conversions are tested (but also others may work):
  Bq/cc  -> kBq/ml
  nCi/ml -> kBq/ml
  MBq/ml -> kBq/ml
  kBq/ml -> Bq/cc

See also: dftunit, lmhdr, lshdr, e7emhdr, imgmax, ecatcalc, ecatlkup

Keywords: image, ECAT, calibration unit, tool, simulation

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```
edecay 1.3.4  (c) 2002-2012 by Turku PET Centre

Reports and changes the correction for physical decay in PET image and
sinogram data in ECAT 6.3 and 7.x format.

Usage: edecay [Options] <Image or Sinogram>

Options:
 -dd
     Correct PET data for physical decay.
 -rd
     Remove decay correction.
     Make sure that PET is decay corrected before this operation.
 -i=<O-15|N-13|C-11|F-18|Ge-68|Ga-68|Br-76|Rb-82|Cu-62>
     Changes or specifies the isotope.
     Any previous decay correction must be removed before this operation.
     Note that image may need to be recalibrated if isotope is changed;
     at least branching fraction needs to be corrected.
 -dc
     Add decay correction factors to the image data.
     This option does not add decay correction to the pixel values.
 -rc
     Remove decay correction factors from the image data.
     This option does not remove decay correction from the pixel values.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

If no option is specified, program reports the current state of decay
correction, but makes no changes to the data file.

See also: ecattime, eframe, egetstrt, esetstrt, ecatunit

Keywords: ECAT, image, physical decay, modelling, simulation

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```
efixplnr 2.1.0  (c) 2003-2012 by Turku PET Centre

Convert ECAT 6.3 or 7.x matrix numbers (planes, frames, gates
and/or beds) into continuous sequence, for instance, plane numbers
8,10,12 to 1,2,3.

Usage:
  efixplnr [Options] <ECAT file(s)>

Options:
 -planes=<Y|n>
     Plane numbers are changed to be continuous and start from 1
     (Y, default) or not changed (n).
 -frames=<y|N>
     Frame numbers are changed to be continuous and start from 1
     (y) or not changed (N, default).
 -gates=<y|N>
     Gate numbers are changed to be continuous and start from 1
     (y) or not changed (N, default).
 -Beds=<y|N>
     Bed numbers are changed to be continuous and start from 0
     (y) or not changed (N, default).
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

See also: esplit, e7vplavg, ecat2flo, ecat2ana, lmlist

Keywords: ECAT, matrixlist, image, sinogram, plane, frame, tools

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```
eflexseg 1.3.0  (c) 2002-2009 by Turku PET Centre

Flexible image segmentation (clustering) for dynamic PET image (1).
This program is for method testing purposes only!

Command-line arguments:
  1) Dynamic image file
  2) Threshold-% to exclude background and cerebrospinal fluid
  3) Max CV% allowed for pixels in the same cluster
  4) Threshold-% for correlation coefficient between cluster TACs
  5) Static cluster image
  6) Cluster TAC file (optional)

Options:
 -cf=<filename for correction factor image>
     ECAT format file will contain correction factors for individual
     pixels, calculated as (AUC of cluster avg TAC)/(AUC of pixel TAC)
 -sm=<filename for smoothed dynamic image>
     TACs in the original dynamic image are replaced by the cluster TACs
     which have been divided by the correction factors
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

Static cluster image will contain the cluster numbers as integers, where
0 represents pixels below TH%, and 1, 2, 3, ... represent clusters in
DECREASING order of TAC integrals.

Cluster TAC file is a DFT formatted ASCII file (2), containing the TACs of
individual clusters in the order 0, 1, 2, ...

Example:
     eflexseg b123dy1.v 30 5 50 b123cluster.v b123cluster.dat

References:
1. Bentourkia M. A flexible image segmentation prior to parametric
   estimation. Comput. Med. Imaging Graph. 2001;25:501-506.
2. DFT format http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: ecatthrs, imgdysmo, ecat2tif, ecat2ana, epxl2dft

Keywords: image, modelling, binding potential, basis function method

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```
eframe 1.4.6  (c) 2003-2012 by Turku PET Centre

Lists the time frame information of an ECAT 6.3 or 7.x file.
The frame start times and lengths can be saved in the specified frame file
in minutes.

If an existing Frame file is specified, the frame lengths or frame start
times and lengths (min) are read from it and are written in ECAT file;
Frame and ECAT file must contain an equal number of frames.
If SIF is provided and original ECAT file does not contain isotope or
scan start time, they are copied from the SIF.

Warning! Make sure that 'Frame file' does not exist, unless you want to
to change the frame times in ECAT file.

Usage: eframe [-Options] <ECAT file> [Frame file or SIF]

Options:
 -sec
     Program writes frame information to frame file in seconds.
 -min
     Program writes frame information to frame file in minutes;
     this is the default.
 -ift
     Frame file is written in interfile type format; currently
     this format is not supported in changing the frame times.
 -h or --help
     Print this message and exit.
 --build or --version
     Print software build information and exit.
 --silent
     Program works silently, printing only warnings and error messages.
 --verbose
     Program prints more information about what it is doing.

See also: esetstrt, egetstrt, ecattime, edecay, dftframe, ecathead

Keywords: image processing, ECAT, frame time, SIF

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```
egetstrt 1.0.3  (c) 2004-2010 by Turku PET Centre

Print the scan_start_time in ECAT 6.3 or 7.x files on screen (stdout).

Usage:
  egetstrt [Options] <ECAT file(s)>

Options:
 -o=<output filename>
     Output is written in given file; any existing file is overwritten.
 -d[=<min|sec>]
     Instead of scan start times, program lists the difference to the first
     one, either in seconds (sec) or in minutes (min); in minutes by default.
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

See also: ecattime, esetstrt, dfttime, injdifft, eframe

Keywords: image, input, IFT, tool, scan start time

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```

```
eprofile 0.4.1  (c) 2003-2012 by Turku PET Centre

Lists the x and y profiles of PET images at the pixel of maximum intensity
inside 4D image. Profiles are saved in DFT format; if image is dynamic,
then the profiles from every time frame are saved.

Command line arguments:
  1) PET image file
  2) Filename for x profile
  3) Filename for y profile

Options:
 -pxl=<x,y,z>
     Instead of maximum, calculate profiles at pixel (x,y,z), where
     x=column (starting from left, 1..width), y=row (starting from top,
     1..height), and z=plane (1..depth).
 -tif=<TIFF filename>
     Image matrix where profiles are calculated is saved as TIFF image
     showing the profile lines.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: epxl2dft, eroi2img, imgbox, esplit, ecatthrs, dft2csv

Keywords: image, profile, maximum

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```

```
epxl2dft 1.2.2  (c) 2003-2009 by Turku PET Centre

Extracts the TACs of specified pixel(s) in ECAT image or sinogram
and writes the TACs in DFT file.

Usage:
  epxl2dft [Options] <ECAT file> <DFT filename> [<pixel> [[...] pixel(s)]]

Options:
 -thr=<threshold%>
     Pixels with AUC less than (threshold/100 x max AUC) are omitted
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Pixel(s) must be defined in format x,y,z or 'x y z', where
x = column, starting from left, 1..width,
y = row, starting from top, 1..height, and
z = plane number, which may differ from sequential numbers.
A range of pixels can be defined with x1,y1,z1 ... x2,y2,z2.
If no pixels are specified, then all pixels are extracted.

Example 1: extract the TAC of image pixel [68,79,22]:
      epxl2dft ua6677dy1.v ua6677_pxl.dat 68,79,22
Example 2: extract the TACs of pixels inside specific image volume:
      epxl2dft ua6677dy1.v ua6677_pxl.dat 54,65,8 ... 59,71,9

See also: img2dft, imgpext, ecat2flo, imgslim, imgbox, dft2dat, dft2svg

Keywords: ECAT, image, pixel, sinogram, DFT, software testing

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```

```
esetstrt 1.0.3  (c) 2003-2010 by Turku PET Centre

Set the scan_start_time in ECAT 6.3 or 7.x files.
Note that this program does not change frame times or decay correction;
use this only if you know what you are doing.
Time is written in ECAT file as GMT, but local time should be given on
command line.

Usage:
  esetstrt [Options] <ECAT file> <YYYY-MM-DD> <hh:mm:ss>

Options:
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

Example:
  esetstrt a2345dy1.img 2003-12-25 23:15:03

See also: egetstrt, ecattime, ecatcat, edecay, lmhdr

Keywords: image, ECAT, tool

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```

```
esplit 0.3.3  (c) 2003-2012 by Turku PET Centre

Extracts specified frames and planes in ECAT 6.3 or 7.x matrix file
to a new file.

Usage:
  esplit <ECAT file> <frames> <planes> <Output ECAT file>

Options:
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
  esplit a02345dy1.img 1-20 4,6,8,10 a02345dy1_part.img

Note! The program interpretes ECAT 7 files as if they had only one plane.

See also: lmlist, eframe, ecatcat, imgbox, imgshrink, imgslim

Keywords: image, ECAT, tool, modelling

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```

```
extrapol 1.1.1  (c) 2003-2009 by Turku PET Centre

Extrapolates exponentially decreasing tail of PET plasma curves.
This is accomplished by fitting line to the end-part of the plot of the
natural logarithm of tracer concentration against time.
This approach may be applied to TACs which approach zero; thus this
cannot be used with tracers like radiowater.

Usage: extrapol [Options] <Plasmafile> <Last extrapolated time> <Output file>

Options:
 -e[nd]=<Fit end time>
     Start the search to fit end time; by default, the search for the best
     line fit is started from the last sample.
 -minnr=<Minimum nr of samples>
     Set the minimum number of samples used in searching the best fit;
     by default 3.
 -maxnr=<Maximum nr of samples>
     Set the maximum number of samples used in searching the best fit;
     by default all.
 -mintime=<Minimum time>
     Set a minimum time range used in searching the best fit.
 -svg=<Filename>
     Measured and extrapolated TACs are plotted in specified SVG file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Plasmafile must contain a time column, and one or more concentration columns
separated by space(s) or tabulator(s). File can also be in DFT format,
http://www.turkupetcentre.net/analysis/doc/format_dft.html
The last extrapolation time must be given in same units as are the sample
times in datafile.

See also: paucinf, avgbolus, fit_meb, fit_exp, fit_feng, fit2dat

Keywords: input, plasma, metabolite correction, modelling, simulation

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```

```
fit2dat 2.6.1  (c) 1996-2013 by Turku PET Centre

Program for calculating the PET time-activity curves (TACs) using
parameters of a mathematical function, which have been fitted to
the data previously.

Usage: fit2dat [Options] <Fitfile> <TAC file>

Fitfile must be in the DFT fit format; it contains the parameters
of the functions fitted to one or more PET TACs. Fitfile specifications:
http://www.turkupetcentre.net/analysis/doc/format_fit.html

Options:
 -i  Integrals of functions from zero to sample time are calculated;
     not available for all functions
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing
 The sample times, where function values are to be calculated, can
 be specified with one of the following options:
 -A[=<stop>]
     autointerpolate the data from 0 to stop time, or to fit range end time
     (default), with decreasing sample frequency
 -C=<start,stop,step>
     specify the first and last sample time, and the sample frequence
 -F=<file>
     specify a DFT file, which contains the time framing information
 -N=<nr>
     specify the number of sample points between fit start and end times
 -X=<x1,x2,x3,...>
     specify the sample times individually
 -R=<low,up,nr>
     Specified nr of random x values between low and up are generated
 -RST=<low,up,nr>
     Specified nr of random x values between low and up are generated
     with distribution biased towards low absolute values.

See also: fr4sim, fit_ppf, fit_sinf, fit_sigm, metabcor, fit2res

Keywords: DFT, simulation, input, interpolation, extrapolation

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you are welcome to redistribute it under GNU General Public License.
```

```
fit2res 0.2.3 (c) 2008-2013 by Turku PET Centre

Conversion of FIT files (1) to RES files (2).

Usage: fit2res [Options] <Name(s) of fit file(s)>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

References:
1. http://www.turkupetcentre.net/analysis/doc/format_fit.html
2. http://www.turkupetcentre.net/analysis/doc/format_res.html

See also: fit2dat, rescoll, resdiff, res2html, reslist, resmatch

Keywords: FIT, RES, simulation, tools, results

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```

fitdelay 2.0.3 (c) 1999-2009 by Turku PET Centre

For estimation and correction of the time delay (difference in appearance
times of radioactivity) between blood or plasma and PET time-activity
curves (TACs).

Program is based on the methods used by Meyer et al. (1) and
van den Hoff et al. (2):
The plasma/blood curve is shifted -60 - +60 sec, and a two-tissue
compartment model (with parameters K1, k2, k3, k4 and Vb) in multilinear
form (3) is fitted to the shifted TAC and each regional tissue TAC,
with the nonnegative least squares method (4).
For each region, the delay leading to the lowest sum-of-squares is selected;
the over-all delay value is calculated as a median of the regional delays.
Dispersion is not considered in this application.

Command-line arguments:
  1) Blood or plasma TAC filename
  2) Tissue TAC filename
  3) Fit time (s)
  4-5) Upto three additional blood or plasma files (optional)

Options:
 -o=<Filename>
 -o2=<Filename>
 -o3=<Filename>
 -o4=<Filename>
     Filename(s) for the time delay corrected TAC(s) can be speficied with
     these options; by default the file names for result files are formed as
     is told below.
 -timeunit=<min|sec>
     If datafile(s) do not contain the unit of sample times, it is
     recommended to specify it with this option. By default, units in data
     files are trusted.
 -format=<none|dft>
     Specify the output data format; none means that no title lines are saved.
 -fit=<Filename>
     Fitted best TACs are written is specified file.
 -model=<1|2>
     Select whether 1- or 2-tissue (default) compartment model is applied.
 -L[og]
     Time delay and other log information is written as comments in
     the corrected TAC file.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only warnings and error messages.

Example 1. Delay correction for C-11 or F-18 labeled tracer data, using
metabolite corrected plasma curve as input and count-rate data as tissue
and correcting also plasma metabolites and total blood for the delay-time:
   fitdelay ut345ap_pure.kbq ut345dy1.img.cr 1800 ut345ap_met.kbq ut345ab.kbq

Example 2. Delay correction for [O-15]water data, using regional tissue
curves as replacement for count-rate data:
   fitdelay ut111ab.kbq ut111dy1.dft 120

As tissue data, the scanner countrate curve is recommended, unless scanned
volume contains heart or large artery or vein where tracer was injected;
It may be possible to use also regional TACs, if datafile contains frame
start and end times. If tissue data contains background, remove it first
with dftrmbkg. The units of sample times should be specified in datafiles;
file format is specified in (5).

Estimated tracer appearance times in blood/plasma and tissue curves, and their differences (time delays and median time delay) are written in stdout. Delay corrected blood/plasma file is written with name *.delay.* ; the same correction can be applied to 1-3 additional files, for example plasma metabolite TACs.

References:

1. Meyer. Simultaneous correction for tracer arrival delay and dispersion in CBF measurements by the H215O autoradiographic method and dynamic PET. J Nucl Med 1989; 30:1069-1078.
2. van den Hoff et al. Accurate local blood flow measurements with dynamic PET: fast determination of input function delay and dispersion by multilinear minimization. J Nucl Med 1993; 34:1770-1777.
3. Blomqvist G. On the construction of functional maps in positron emission tomography. J Cereb Blood Flow Metab 1984; 4:629-632.
4. Lawson CL & Hanson RJ. Solving least squares problems. Prentice-Hall, 1974.
5. http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: dfttime, ecathead, dfthead, tocr, dftrmbkg, dftunit, fit_h2o

Keywords: dft, modelling, input, blood, time delay

```
fitedit 0.1.0  (c) 2013 by Turku PET Centre

Edit parameter value in FIT file 1, saving edited contents in file 2.

Usage:  fitedit [Options] <File1> <Par nr> <TAC nr> <Value> <File2>

Options:
 -h, --help
     Print this message and exit
 --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.
 --verbose
     Program prints more information about what it is doing.

See also: fit2res, fit2dat, metabcor, fit_ppf

Keywords: FIT, tools, input, simulation, metabolite correction

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```
fitglob 1.3.0 (c) 2002-2012 by Turku PET Centre

Non-linear fitting of compartmental model to plasma and tissue
time-activity curves (TACs) to estimate K1-k6 and Va using
Iterative Topografical Global Optimization routine (ITGO)
developed by Aimo Torn and Sami Viitanen (1, 2).

Command-line parameters:
  1) Parameter file (see below)
  2) Plasma file
  3) Blood file
  4) Tissue TAC file (*.dft)
  5) Fit end time (duration)
  6) Result file: parameters at global minimum

Options:
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example:
     fitglob par.set a919ap.dat a919ab.dat a919.dft 999 a919.res a919fit.dft

The parameter file contents must be exactly as follows:
  1) Model identifier:
     PR = parallel (receptor) model
          with parameters K1, K1/k2, k3, k3/k4, k5, k5/k6, Va
     P  = parallel (receptor) model
          with parameters K1, k2, k3, k4, k5, k6, Va
     SR = serial (metabolism) model
          with parameters K1, K1/k2, k3, k3/k4, k5, k5/k6, Va
     S  = serial (metabolism) model
          with parameters K1, k2, k3, k4, k5, k6, Va
     LR = kLoss model
          with parameters K1 K1/k2 k3 kLoss, Va
     L  = kLoss model
          with parameters K1, k2, k3, kLoss, Va
     KR = kLoss model2
          with parameters K1, K1/k2, k3, k3/k4, k5, k5/k6, kLoss, Va
     K  = kLoss model2
          with parameters K1, k2, k3, k4, k5, k6, kLoss, Va
  2) Lower and upper limits for each of the parameters
     Parameter can be fixed to a certain value by setting equal limits;
     fixing a ratio k3/k4 or k5/k6 to zero sets k4 or k6 to zero.
  3) Value of K1/F (0, if blood flow is not considered);
     the reduced venous blood activity and its dependence on blood flow can
     corrected by specifying the ratio K1/F.
  4) Number of points to sample in one iteration (prfmNr)
     If you don't know what to put here, set it to 0.

 Parameter file example 1:
 PR
 # K1
 0  0.5
 # K1/k2
 0.001 10.0
 # k3
 0  0.0
```

```
# k3/k4
0  0.0
# k5
0  0.2
# k5/k6
0.001 10.0
# Va
0  0.30
# K1/F
0
#prfmNr
100

Parameter file example 2:
KR
# K1
0  0.5
# K1/k2
0.001 10.0
# k3
0  0.0
# k3/k4
0  0.0
# k5
0  0.2
# k5/k6
0.001 10.0
# kLoss
0  0.2
# Va
0  0.30
# K1/F
0
#prfmNr
100
```

References:

1. Torn A, Viitanen S. Topografical global optimization. In: C.A. Floudas and P.M. Pardalos (eds.) Recent advances in Global Optimization, Princeton University Press, 1992.
2. Sederholm K. Globaali optimointi positroniemissiotomografia-kuvantamiseen liittyvässä mallintamisessa. Pro Gradu. Turun yliopisto, 2003; http://www.turkupetcentre.fi/gradu/sederholm.pdf

See also: fitk2, fitk3, fitk4, fitkloss, lhsol, p2t_v3c, dftweigh

Keywords: global optimization, compartment model, fitting, modelling

```
fith2met 0.2.0  (c) 2009,2012 Turku PET Centre

Fits the Hill type function to plasma fraction curves of parent tracer and
two metabolites. Functions fitted are:
Parent (unchanged) fraction:
  f(x) = 1 - (A*x^B)/(C+x^B)
Metabolite 1 fraction:
  f(x) = (f1*A*x^B)/(C+x^B)
Metabolite 2 fraction:
  f(x) = ((1-f1)*A*x^B)/(C+x^B)
, where 0<A<=1 , B>0 , C>0

Usage:  fith2met [Options] <Fraction file> [Fit file]

General options:
 -nd    Some fractions are known to exceed 1, not divided by 100.
 -delay[=<time>]
        Fit also delay time, or, set delay time (0 by default).
 -h or --help
        Print this message and exit.
 --build or --version
        Print software build information and exit.
 --silent
        Program works silently, printing only error and warning messages.
 --verbose
        Program prints more information about what it is doing.
Options to set weights:
 -W1    All weights are set to 1.0; by default, sample times are used to
        calculate weights unless weights are supplied in fraction file.
 -WP=<weight>, -WM1=<weight>, -WM2=<weight>
        Put additional or less weight to parent and/or metabolite fractions.

Fraction datafile must contain 3-4 columns, that is, sample times and
fractions of parent tracer and at least metabolite 1.
Weights can be specified as specified in DFT format (3);
any additional columns are ignored.
Lines that start with a '#' are not read from the datafile.

Program writes the fit start and end times, nr of points, WSS,
and parameters of the fitted function to the result (fit) file (4).

References:
1. Fitting the fractions of parent tracer in plasma.
   http://www.turkupetcentre.net/analysis/doc/fraction_fit.html
2. Wu S, Ogden RT, Mann JJ, Parsey RV. Optimal metabolite curve fitting for
   kinetic modeling of 11C-WAY-100635. J Nucl Med 2007;48:926-931.
3. DFT format. http://www.turkupetcentre.net/analysis/doc/format_dft.html
4. FIT format. http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit2dat, metabcor, fit_ppf, avgfract, dft2svg

Keywords: input, plasma, modelling, simulation, metabolite correction

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```

```
fitk2 1.3.4 (c) 2004-2013 by Turku PET Centre

Non-linear fitting of one-tissue compartment model to plasma and tissue
time-activity curves (TACs) to estimate K1, k2 and Vb.

Parameters:
  1) Plasma file (corrected for labeled metabolites)
  2) Blood file
  3) Tissue TAC file (*.dft)
  4) Fit end time (duration)
  5) Result file

Options:
 -lim[=<filename>]
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program.
     Without filename the default values are printed on screen.
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (Y, default),
     or not calculated (n).
     Program runs a lot faster if SD and CL are not calculated.
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (N, default).
 -Vb=<Vb(%)>
     Enter a fixed Vb; fitted by default.
 -<BPnd|BPp|DVR>=<Reference region name or filename>
     Optional reference region is used to calculate BPnd, BPp, or DVR;
     BPnd=DVroi/DVref-1, BPp=DVroi-DVref, and DVR=DVroi/DVref
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1: estimate K1, K1/k2 and Vb, no estimation of parameter SD
     fitk2 -sd=n a919ap.kbq a919ab.kbq a919.dft 60 a919k2.res

Example 2: estimate K1 and DV (=K1/k2); Vb is constrained to 0%%;
DVRs are calculated by dividing DVs by the DV of region 'cer'
     fitk2 -Vb=0 -R=cer p25apc.kbq none p25.dft 60 p25_k2.res

See also: logan, lhsoldv, fitk2di, fitk4, fit_h2o, p2t_v3c, dftweigh, dftcbv

Keywords: DFT, modelling, distribution volume, reversible uptake

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```
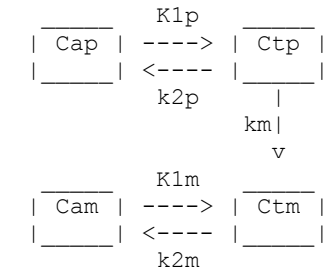

fitk2di 0.4.0 (c) 2010-2013 by Turku PET Centre

Non-linear fitting of dual input compartment model, with one tissue
compartment for both tracers (parent and metabolite):



Parameters:
  1) Parent plasma TAC file
  2) Metabolite plasma TAC file
  3) Blood TAC file (enter NONE if Vb is pre-corrected)
  4) Tissue TAC file
  5) Fit end time (duration)
  6) Result file

Options:
 -lim[=<filename>]
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program.
     Without filename the default values are printed on screen.
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y),
     or not calculated (N, default).
     Program runs a lot faster if SD and CL are not calculated.
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (N, default).
 -Vb=<Vb(%)>
     Enter a fixed Vb; fitted by default.
 -ref=<Reference region name or filename>
     Specified reference region is fitted using different set of model
     parameter constraints; not necessary if reference region is given
     with one of the following options -BPnd, -BPp, or -DVR.
 -<BPnd|BPp|DVR>=<Reference region name or filename>
     Optional reference region is used to calculate BPnd, BPp, or DVR;
     BPnd=DVroi/DVref-1, BPp=DVroi-DVref, and DVR=DVroi/DVref
 -refVfm=refVfp
     In reference region Vfm is set to equal Vfp=1.
 -mc=<Filename>
     Fit-based metabolite corrected regional TACs are written in DFT format.
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1: fitting with default settings
     fitk2di ia919apc.kbq ia919apm.kbq ia919ab.kbq ia919.dft 60 a919k2di.res

Example 2: Vb is constrained to 0%; DVRs are calculated by dividing DVs

by the DV of region 'cer'
```
     fitk2di -Vb=0 -R=cer p25apc.kbq p25apm.kbq none p25.dft 60 p25k2di.res
```

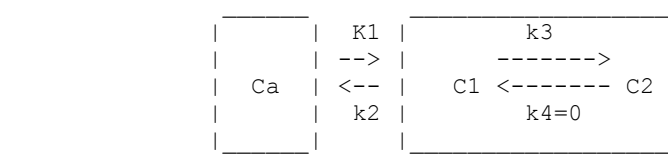
See also: fitk2, logan, fitk4, p2t_di, dftweigh, dftcbv

Keywords: DFT, modelling, distribution volume, reversible uptake, dual-input

```
fitk2wm 0.3.0 (c) 2004,2005 by Turku PET Centre

Non-linear fitting of one-tissue compartment model to plasma and
tissue time-activity curves (TACs) to estimate K1, k2 and Vb.
In addition, all regions are assumed to contain white matter (WM);
the WM volume fraction is also estimated as one of parameters.
Parameter estimates are restricted to the following values:
  Region     K1      K1/k2       fWM(%)  Vb(%)
  All        0 - 10  1e-5 - 500  0-75    0-8

Parameters:
  1) Plasma file (corrected for labeled metabolites)
  2) Blood file
  3) Tissue TAC file (*.dft)
  4) Name of WM region
  5) Fit end time (duration)
  6) Result file
  7) Fitted tissue TAC file (optional)
Options:
  -SD  Standard deviations are calculated and saved in results (default)
  -CL  95% Confidence limits are calculated and saved in results
  -n   SDs or confidence limits are not calculated nor reported
  -Vb=<Vb(%)>
       Enter a fixed Vb; fitted by default.
  -R=<Reference region name or filename>
       Optional reference region is used only to calculate DVR.

e.g.: fitk2wm a00919ap.kbq a00919ab.kbq a00919.dft wm 60 a00919k2.res
or:   fitk2wm -Vb=4.5 -R=cer p02apc.kbq p02ab.kbq p02.dft wm 60 p02k2.htm

See also: logan, lhsol, fitk2, fitk4, fit_h2o, p2t_v3c, dftweigh, dftcbv

Keywords: DFT, modelling, distribution volume, white matter
```

fitk3 3.3.4 (c) 2000-2013 by Turku PET Centre

Non-linear fitting of two-tissue compartment model to plasma and tissue
time-activity curves (TACs) to estimate K1, k2, k3, and optionally Vb.



Parameters:
  1) Plasma file (corrected for labeled metabolites)
  2) Blood file
  3) Tissue TAC file (*.dft)
  4) Fit end time (duration)
  5) Result file

Options:
 -lim[=<filename>]
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program.
     Without filename the default values are printed on screen.
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y),
     or not calculated (N, default).
     Program runs a lot faster if SD and CL are not calculated.
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (N, default).
 -Vb=<Vb(%)>
     Enter a fixed Vb; fitted by default.
 -r=<Reference region name or filename>
     Optional reference region is used to constrain K1/k2 in other regions;
     Also k3 is fitted to reference region data, thus any large region
     (for example cortex) can be used here.
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1: estimate K1, K1/k2, k3 and Vb
     fitk3 ua919ap.kbq ua919ab.kbq ua919.dft 60 ua919k3.res

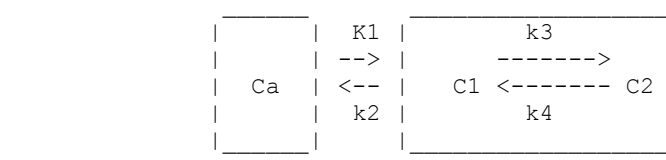
Example 2: estimate K1 and k3; Vb is constrained to 4.5%% and K1/k2 is
constrained to K1/k2 estimated from region 'occip'
     fitk3 -Vb=4.5 -r=occip ua919ap.kbq ua919ab.kbq ua919.dft 60 ua919.res

See also: patlak, lhsol, p2t_v3c, dftweigh, extrapol, dftcbv, rescoll

Keywords: TAC, modelling, irreversible uptake, k3, Ki

fitk4 3.2.4 (c) 2000-2013 by Turku PET Centre

Non-linear fitting of two-tissue compartment model to plasma and tissue
time-activity curves (TACs) to estimate K1, k2, k3, k4, and optionally Vb.



K1/k2 can be constrained to the value estimated in reference region.
By default 2-compartmental model is fitted to reference region.
Datafile(s) must be in DFT format. If tissue TAC file contains weights,
those are used in the fitting.

Parameters:
  1) Plasma file (corrected for labeled metabolites)
  2) Blood file
  3) Tissue TAC file (*.dft)
  4) Fit end time (duration)
  5) Result file

Options:
 -lim[=<filename>]
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program.
     Without filename the default values are printed on screen.
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y),
     or not calculated (N, default).
     Program runs a lot faster if SD and CL are not calculated.
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (N, default).
 -r=<Reference region name or filename>
     Optional reference region is used to constrain K1/k2.
 -rmod=<2|3>
     Specify the model (2- or 3-compartments) that is fitted to reference
     region data; by default 2-CM (1-tissue compartment model)
 -Vb=<Vb(%)>
     Enter a fixed Vb; fitted by default.
 -fk1k2=<<value> || <result filename>>
     K1/k2 is constrained to the given value in all regions; if result
     filename is entered, then K1/k2 is constrained to the median of
     K1/k2 values in the result file.
 -BPnd[=<reference region name>]
     BPnd is calculated as BPnd=VtROI/VtREF-1; reference region name
     is not needed if the same is specified with option -r.
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example 1: estimate K1, K1/k2, k3 and k3/k4; Vb is estimated;
Fitted curves are plotted with measured data in SVG file
  fitk4 -svg=a919fit.svg a919ap.kbq a919ap.kbq a919.dft 90 a919.res

Example 2: estimate K1, k3 and k3/k4; Vb is set to 1.5%%;
K1/k2 is constrained to K1/k2 estimated from region 'cer' with 2-CM
```
  fitk4 -Vb=1.5 -r=occip -rmod=2 ua919ap.kbq ua919ab.kbq ua919.dft 60 ua919.res
```

Example 3: constrain K1/k2 to the regional median; Vb is set to 4%%;
```
  fitk4 -Vb=4 ua919ap.kbq ua919ab.kbq ua919.dft 60 tmp.res
  fitk4 -Vb=4 -fk1k2=tmp.res ua919ap.kbq ua919ab.kbq ua919.dft 60 ua919fk1k2.res
```

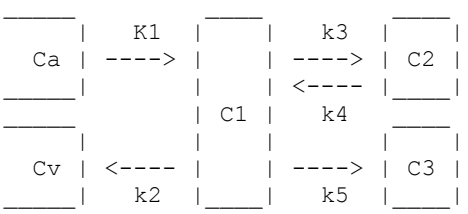
See also: logan, fitk2, fitk3, p2t_v3c, dftweigh, extrapol, dftcbv, rescoll

Keywords: TAC, modelling, binding potential, reversible uptake

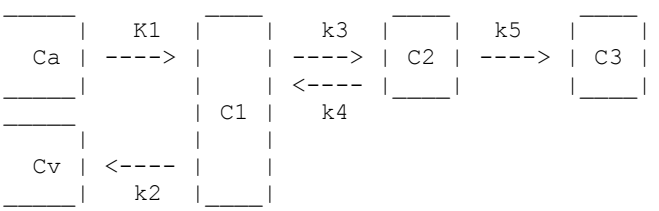
fitk5 0.2.2 (c) 2012-2013 by Turku PET Centre

Non-linear fitting of three-tissue compartment model to plasma and tissue time-activity curves (TACs) to estimate K1, k2, k3, k4, k5, and optionally Vb.

Model with two of tissue compartments in parallel:



Model with compartments in series:



Parameters:
1) Plasma file (corrected for labeled metabolites)
2) Blood file
3) Tissue TAC file (*.dft)
4) Fit end time (duration)
5) Result file

Options:
-lim[=<filename>]
Specify the constraints for model parameters;
This file with default values can be created by giving this option as the only command-line argument to this program.
Without filename the default values are printed on screen.
-SD[=<y|N>]
Standard deviations are calculated and saved in results (y), or not calculated (N, default).
Program runs a lot faster if SD and CL are not calculated.
-CL[=<y|N>]
95% Confidence limits are calculated and saved in results (y), or not calculated (N, default).
-model=<parallel|series>
Specify the model that is fitted to data; compartments in parallel (default) or in series.
-Vb=<Vb(%)>
Enter a fixed Vb; fitted by default.
-fit=<Filename>
Fitted regional TACs are written in DFT format.
-svg=<Filename>
Fitted and measured TACs are plotted in specified SVG file.
-h or --help
Print this message and exit.
--version or --build
Print software build information and exit.
--silent
Program works silently, printing only error and warning messages.
--verbose
Program prints more information about what it is doing.

Example 1: estimate K1, K1/k2, k3, k3/k4, k5, and Vb,
fitk5 ua919ap.kbq ua919ab.kbq ua919.dft 60 ua919k5.res

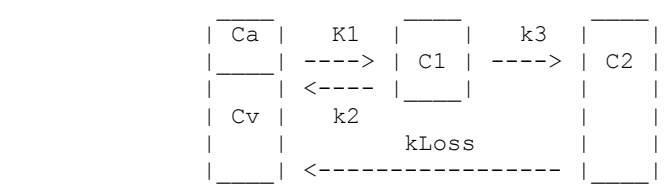
See also: patlak, p2t_v3c, fitk3, fitk4, dftweigh, dftcbv, rescoll

Keywords: TAC, modelling, irreversible uptake, k5, Ki

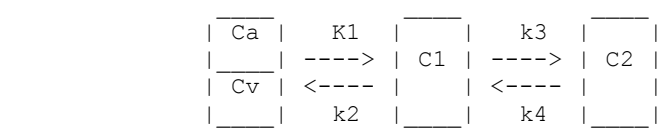
fitkloss 3.0.2 (c) 2002-2013 by Turku PET Centre

Non-linear fitting of two-tissue compartment model with kLoss or k4
to plasma and tissue time-activity curves (TACs) to estimate K1, k2, k3,
kLOSS or k4, and optionally Vb.

kLoss-model:



k4-model:



Parameters:
  1) Plasma file (corrected for labeled metabolites)
  2) Blood file
  3) Tissue TAC file
  4) Fit end time (duration)
  5) Result file

Options:
 -lim[=<filename>]
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program.
     Without filename the default values are printed on screen.
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y),
     or not calculated (N, default).
     Program runs a lot faster if SD and CL are not calculated.
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (N, default).
 -model=<k4|kloss>
     Specify the model that is fitted to data; kLoss model by default.
 -Vb=<Vb(%)>
     Enter a fixed vascular blood volume Vb; fitted by default.
 -f=<K1/F>
     K1/F-ratio; by default flow is ignored (F>>K1).
 -a=<fA%>
     Arterial volume fraction; 30 by default; effective only with -f.
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
     fitkloss s919ap.dat s919ab.dat s919.dft 999 s919.res

If datafile contains weights, those are used in the fitting.

Model parameters are written in the specified result file.

See also: dftweigh, fitk4, fitk3, patlak, logan, p2t_loss, dft2svg, rescoll

Keywords: TAC, modelling, loss rate, enzyme activity

```
fitmbf 2.3.0  (c) 1999-2013 by Turku PET Centre

Estimates the myocardial flow, alpha (PTF) and Va using Iida's MBF model
(1, 2) as represented in (3) from radiowater PET studies.
The same method is applied in Carimas, and for clinical work use of Carimas
is recommended; however, it is possible to save regional TACs in Carimas or
other sofware and used with this programs.

Parameters for the program:
  1) Regional TAC datafile (DFT or PMOD format)
  2) Beta value (from [O-15]CO study)
  3) Name of LV in TAC datafile
  4) Name of whole myocardium in TAC datafile
  5) Result file (5)

Options:
 -fA[lpha]
     Alpha is constrained to the Alpha estimate from a previous study
     (in basal conditions); option -F is obligatory with this.
 -fVa
     Va is constrained to the Va estimate from a previous study
     (in basal conditions); option -F is obligatory with this.
 -F=<Result file of basal study>
     Alpha and/or Va is constrained regionally to the estimate
     that is found in this result file.
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y),
     or not calculated (N, default).
     Program runs a lot faster if SD and CL are not calculated.
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (N, default).
 -Ca[=<filename>]
     Save arterial concentration curves, by default adding .ca to
     filename for regional TACs.
 -fit=<Filename>
     Fitted regional TACs are written in ASCII data file.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file (6).
 -rd=<y|n>
     Correction for physical decay is removed from the measured data
     during model calculation (y) or not removed (n, default). This may
     produce more accurate results when time frames are relatively long.
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Examples:
1. Calculation with no constraints:
     fitmbf s2345.dft 0.91 'lv Pl06' 'whole' s2345.res
2. Alpha (PTF) is constrained to estimates from basal study:
     fitmbf s2346.dft 0.91 'lv Pl05' whole s2346.res -fA -F=s2345.res

Existing result files are overwritten!

References:
1. Iida H, Rhodes CG, de Silva R, Yamamoto Y, Araujo LI, Maseri A, Jones T.
   Myocardial tissue fraction - correction for partial volume effects and
   measure of tissue viability. J Nucl Med 1991; 32:2169-2175.
2. Iida H, Rhodes CG, de Silva R, Araujo LI, Bloomfield P, Lammertsma AA,
   Jones T. Use of the left ventricular time-activity curve as a noninvasive
   input function in dynamic oxygen-15-water positron emission tomography.
```

J Nucl Med 1992; 33:1669-1677.
3. Oikonen V. Model equations for myocardial perfusion studies with [15O]H2O PET. http://www.turkupetcentre.net/reports/tpcmod0005.pdf
4. File format specification: DFT. http://www.turkupetcentre.net/formats/format_dft_1_0_0.pdf
5. File format specification: Result file. http://www.turkupetcentre.net/formats/format_res_1_0_0.pdf
6. Scalable Vector Graphics (SVG) 1.1 Specification. http://www.w3.org/TR/SVG/
7. Carimas. http://www.turkupetcentre.fi/carimas

See also: b2m_mbf, fit_h2o, dftunit, rescoll, res2html

Keywords: myocardium, perfusion, modelling, DFT

```
fitmetab 0.3.0  (c) 2007-2010 by Turku PET Centre

Fits the parameters of compartment model for plasma input metabolite
correction for PET (1, 2).
Two data files (3) are needed for the model fit: the total time-activity
concentration curve (parent tracer + radioactive metabolites), and the
measured fractions of parent tracer to total plasma activity.

Usage: fitmetab [Options] <Plasma file> <Fraction file> <Parameter file>

Options:
 -fract=<Filename>
     Write fitted fraction curve in specified file
 -parent=<Filename>
     Write the TAC of parent tracer in plasma in specified file
 -metab=<Filename>
     Write the TAC of metabolite in plasma in specified file
 -nd Some fractions are known to exceed 1, not divided by 100
 -model=<TPC|Huang>
     Select the metabolite model, either TPC (default), or Huang with
     single plasma metabolite
 -h or --help
     Print this message and exit
 --build or --version
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

If the sample times in plasma file are in seconds, the units of rate
constants will be specified as 1/sec.
For accurate results, plasma data should have a frequent sampling.

Parameter file will contain:
  -Name of metabolite model
  -Model parameter values
For example,
   model := TPCMOD0009C
   km := 0.8
   k1m := 0.5
   k2m := 0.4
   k3m := 0.1
   k4m := 0
Accepted metabolite models are:
  -TPC metabolite model (2)

References:
1. Lammertsma AA, Hume SP, Bench CJ, Luthra SK, Osman S, Jones T. Measurement
   of monoamine oxidase B activity using L-[11C]derenyl: Inclusion of
   compartmental analysis of plasma metabolites and a new model not requiring
   measurement of plasma metabolites. In: Quantification of Brain Function:
   Tracer Kinetics and Image Analysis in Brain PET (Uemura K, Lassen NA,
   Jones T, Kanno I, eds) Amsterdam, Excerpta Medica (pp) 313-318, 1993.
2. Oikonen V. New model for plasma metabolites.
   http://www.turkupetcentre.net/reports/tpcmod0009_app_c.pdf
3. DFT format. http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: metabcor, simmetab, fit_hill, fit_fexp, dft2svg

Keywords: DFT, input, metabolite correction, simulation

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you are welcome to redistribute it under GNU General Public License.
```

```
fitshape 2.3.0  (c) 2001-2009 by Turku PET Centre

Estimates the enzyme activity (k3) from regional brain PET studies
using the shape analysis method (1,2). This model assumes that:
  1) there is no metabolic product in the tissue at time 0
  2) metabolite is retained in tissue completely
  3) tissue radioactivity consists of parent tracer and metabolite, i.e.
     Ct(t) = Cs(t) + Cm(t)
  4) The increment of Cm during scan frame n can be calculated as:
     Cm(n)-Cm(n-1) = k3*Cs(n-1)*DT(n) , where DT is the duration of frame.

Command-line parameters:
  1) Tissue TAC file
  2) Fit time (in minutes from injection)
  3) Result file (existing file is overwritten)

Options:
 -h or --help
     Print this message and exit
 -smooth=<biexp|cexp|cbiexp|no>
     Tissue TACs will be smoothed by fitting to biexponential function
     as suggested in (2), or exponential function plus constant (default),
     or biexponential with constant; or not smoothed, in which case TACs
     should have been previously smoothed and interpolated to frequent
     sample times.
 -wf
     Weight by sampling interval.
 -step[size]=<time>
     Set the interpolated sample time frequency; 0.1 by default.
 -starttime=<time>
     Set the exponential fit start time (min); by default 3 min from
     injection, suitable for biexponential fits (2). For single exponential
     20 min or later is recommended unless option -wf is used.
 -svg=<Filename>
     Original data and fitted curves are plotted in specified file in
     Scalable Vector Graphics (SVG) 1.1 format;
     specification in http://www.w3.org/TR/SVG/
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -int=<Filename>
     Interpolated regional TACs are written in DFT format.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Format of the TAC data and result files are specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html and
http://www.turkupetcentre.net/analysis/doc/format_res.html

Example:
     fitshape -svg=ua1309shape.svg ua1309.dft 999 ua1309shape.res

References:
1. Koeppe RA, Frey KA, Snyder SE, Meyer P, Kilbourn MR, Kuhl DE.
   Kinetic modeling of N-[11C]methylpiperidin-4-yl propionate: alternatives
   for analysis of an irreversible positron emission tomography tracer for
   measurement of acetylcholinesterase activity in human brain.
   J Cereb Blood Flow Metab. 1999;19:1150-1163.
2. Tanaka N, Fukushi K, Shinotoh H, Nagatsuka S, Namba H, Iyo M, Aotsuka A,
   Ota T, Tanada S, Irie T. Positron emission tomographic measurement of
   brain acetylcholinesterase activity using N-[11C]methylpiperidin-4-yl
   acetate without arterial blood sampling: methodology of shape analysis
   and its diagnostic power for Alzheimer's disease.
   J Cereb Blood Flow Metab. 2001;21:295-306.
```

See also: simshape, fitk3, fit_trtm, rescoll

Keywords: DFT, modelling, reference input, enzyme activity, shape analysis

```
fit_bpr 0.2.0  (c) 2010-2012 by Turku PET Centre

Non-linear fitting of a function to sampled blood-to-plasma ratio data.

Usage: fit_bpr [Options] <Data file> <FIT file>

Options:
 -model=<igv|hillb|ihillb>
     Select the metabolite model; default is IGV
 -delay[=<time>]
     Fit also delay time, or, set delay time (0 by default)
 -bl=<baseline>
     Constrain baseline level to specified value; fitted by default
 -w1 All weights are set to 1.0 (no weighting); by default, weights in
     data file are used, if available
 -wf
     Weight by sampling interval
 -fast or -safe
     Speed up the fitting but increase the chance of failure, or
     increase the reliability at the cost of computing time
 -min=<ss|abs>
     Sum-of-squares (SS) is minimized by default, but optionally
     sum of absolute deviations can be selected
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Datafile can be any DFT file (1) which can include weights.
Program writes the fit start and end times, nr of points, WSS/n,
and parameters of the fitted function to the FIT file (2).

Example:
     fit_bpr -model=igv -svg=ia765bprat.svg ia765bp.rat ia765bprat.fit

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit2dat, dft2svg, avgfract, b2plasma, bpr2cpr, dftcat

Keywords: input, blood, plasma, modelling, simulation

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you are welcome to redistribute it under GNU General Public License.
```

```
fit_dei 0.4.0  (c) 2009 by Turku PET Centre

Fit multi-exponential with integral to PET time-activity curves (TACs).

Usage: fit_dei [Options] <TAC file> <Fit or Result file>

Options:
 -fit=<Filename>
     Fitted TACs are written in DFT format.
 -svg=<Filename>
     Measured and fitted TACs are plotted in SVG file.
 -wf
     Weight by sampling interval.
 -dlow=<time>
     Penalize non-integral part exceeding 0.001% and derivative exceeding
     0.1% after specified time.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints lots of information about what it is doing.

TAC file must be in DFT format (1). Function parameters are written in
fit (2) or result (3) format, depending on filename extension (.fit or .res).

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. http://www.turkupetcentre.net/analysis/doc/format_fit.html
3. http://www.turkupetcentre.net/analysis/doc/format_res.html

See also: fit_exp, fit_meb, fit_ek3, extrapol, fit2dat, dftcut

Keywords: DFT, simulation, shape analysis, extrapolation

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you are welcome to redistribute it under GNU General Public License.
```

fit_dtpa 3.3.5 (c) 2001-2010 by Turku PET Centre

Estimates the parameters of the myocardial perfusion model for Gd-DTPA
using regional signal intensity curves from LV and myocardium measured
with MRI and SAT-turboFLASH.
Fitted parameters are unidirectional influx constant Ki (mL/mL/min),
extravascular extracellular volume fraction Ve (mL/mL), venous blood
volume fraction Vb (%), and time delay dT (sec).

Parameters:
  1) Datafile, containing measurement data from myocardial region(s)
  2) LV datafile, or LV region name in previous datafile
  3) Number of baseline samples (usually 3)
  4) Fit duration (sec; time from beginning to use in fitting)
  5) Result file (overwritten, if existing)
 [6) Fitted SI datafile (optional)]

Options (with default or example values):
 -Alpha=8 (in degrees)
 -TR=0.0020
 -TI=0.055
 -R10myo=1.0
 -R10b=0.67
 -n=48
 -r1=4.3
 -HCT=0.38
 -E=0.50
 -Vb=6 ; if Vb is not set, it is fitted as one of the model parameters.
 -Vbmax=50 ; if Vb is fitted, the maximum for it can be changed with
         this option. Default is 50%.
 -dT=0 ; if dT is not set, it is fitted as one of the model parameters.
 -dTmin=0.5 ; if dT is fitted, the minimum for it can be changed with
         this option. Default is 0.5 s.
 -N   ; SD and 95% CLs are not calculated.
 -F=basal.res
         If specified, then the values of Omega*M0 are read from
         the results of the first study, and are used to calculate
         R10b and R10myo. This corrects the background from the first study.
         For this purpose, the result file must not be in HTML format.
 -FVe   Further, Ve is constrained to +-10% of the basal Ve value.
 -Vemin=0.10 ; minimum for Ve can be changed with this option. Default 0.10.
 -Vemax=0.40 ; maximum for Ve can be changed with this option. Default 0.40.
 -ODE=<am|conv>
         The second-order Adams-Moulton (am, default) or convolution (conv)
         is used to numerically solve the first-order ordinary differential
         equations.

Datafile(s) must contain the sample times (sec) in the first column, and
in the following columns the myocardial or LV signals.
Detailed description of the datafile format is available in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

Reference:
Larsson HBW, Rosenbaum S, Fritz-Hansen T. Quantification of the effect of
water exchange in dynamic contrast MRI perfusion measurements in the brain
and heart. Magn. Reson. Med. 2001;46:272-281.

See also: dtpa_s2c, dtpa_c2s

Keywords: MRI, DFT, modelling, perfusion

```
fit_exp 2.8.2  (c) 1994-2012 by Turku PET Centre

Non-linear fitting of the sum of 1-3 exponential functions to plasma and
tissue time-activity curves (TACs).

Function:

  f(x) = p1*exp(p2*x) + p3*exp(p4*x) + p5*exp(p6*x)

Usage:  fit_exp [Options] <TAC file> [Fit or Result file]

General options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.
Options for selecting the exponential function; selection between 1-3
exponentials can also be made by renaming the executable as
fit_3e, fit_2e or fit_1e :
 -3[e]
     Sum of three exponentials (default)
 -2[e]
     Sum of two exponentials
 -1[e]
     Single exponential function
 -nonneg
     p1, p3 and p5 are constrained to values >= 0
 -expneg
     p2, p4 and p6 are constrained to values <= 0.
Other options:
 -starttime=<<Time (min)>|Peak>
     Set the sample time from where fitting is started (0 by default),
     or 'peak' to start fitting from common peak time
 -endtime=<Time (min)>
     Set the sample time where fitting is stopped (last sample by default)
 -fit=<Filename>
     Fitted TACs are written in DFT format
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -autoname
     Names for fit file and fitted TAC file are set automatically
 -w1 All weights are set to 1.0 (no weighting)
 -wf Less frequent samples are given more weight.

TAC file must be in DFT format (1). Function parameters are written in
fit (2) or result (3) format, depending on filename extension (.fit or .res).

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. http://www.turkupetcentre.net/analysis/doc/format_fit.html
3. http://www.turkupetcentre.net/analysis/doc/format_res.html

See also: fit_fexp, fit_ratf, fit_hiad, fit2dat, extrapol, paucinf, dftcut

Keywords: DFT, input, simulation, extrapolation

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you are welcome to redistribute it under GNU General Public License.
```

```
fit_feng 1.4.1  (c) 2001-2011 by Turku PET Centre

Non-linear fitting of the model suggested by Feng et al (1) to PET plasma
time-activity curves.

Function:
  when t<=tau : y(t) = 0
  when t>tau:   y(t) = (p1*(t-tau)-p3-p5)*exp(p2*(t-tau))
                     + p3*exp(p4*(t-tau)) + p5*exp(p6*(t-tau))

Usage:  fit_feng [Options] <Datafile> <FIT file>

Options:
 -integ[ral]
     Given datafile represents the integral of fitted function
 -wf
     Weight by sampling interval
 -ext[ended] or -simpl[ified]
     Apply extended model (one extra exponential term with two more
     parameters) or simplified model (p5 and p6 fixed to zero)
 -ss
     Function approaches steady level; last exponent term is a constant,
     i.e. either p6 or p8 is 0
 -delay=<<value>|mean|median>
     Delay time (tau) is constrained to specified value or to mean or median
     of all TACs
 -fast or -safe
     Speed up the fitting but increase the chance of failure, or
     increase the reliability at the cost of computing time
 -cst=<Sample time>
     Earlier samples are not used in setting parameter constraints
     (but all samples are used in fitting); 0 by default
 -fit=<Filename>
     Fitted TACs are written in DFT format
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

Datafile can be any DFT file (2) which can include weights.
Program writes the fit start and end times, nr of points, WSS/n,
and parameters (p1, p2, p3, p4, p5, p6, tau) of the fitted function
to the FIT file (3).

Example 1: Fit function to plasma TAC and compute fitted curve
           between 0 and 60 min at 0.1 min intervals:
     fit_feng p455ap.kbq p455ap.fit
     fit2dat -c=0,60,0.1 p455ap.fit p455ap_new.kbq
Example 2: Fit function to plasma TAC and plot fitted and measured TACs
           in SVG format:
     fit_feng -svg=p455apfit.svg p455ap.kbq p455ap.fit

References:
1. Feng D, Huang S-C, Wang X. Models for computer simulation studies of input
   functions for tracer kinetic modeling with positron emission tomography.
   Int J Biomed Comput. 1993;32:95-110.
2. http://www.turkupetcentre.net/analysis/doc/format_dft.html
3. http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit2dat, fit_sinf, fit_exp, fit_ratf, fit_hiad
```

Keywords: DFT, input, modelling, simulation

fit_fexp 1.1.1 (c) 2006-2010 by Turku PET Centre

Fits the following exponential function to a fraction curve of unchanged
(parent) tracer in plasma, where fractions are between 0 and 1 (1,2).

$$f(x) = 1 - A * (2 - e^{-B*x} - e^{-C*x}) \quad \text{, where } 0<A<=1 \text{ , } B>0 \text{ , } C>0$$

Usage: fit_fexp [Options] <Fraction file> [Fit file]

General options:
 -ND   Some fractions are known to exceed 1, not divided by 100.
 -h or --help
        Print this message and exit.
 --build or --version
        Print software build information and exit.
 --silent
        Program works silently, printing only error and warning messages.
 --verbose
        Program prints more information about what it is doing.
Options to set weights:
 -W1   All weights are set to 1.0; by default, sample times are used to
        calculate weights unless weights are not supplied in fraction file.
 -WC   The last data column contains sample weights.

Fraction datafile must contain two columns, sample times and fractions
of parent tracer. Weights can be specified as specified in DFT format (4);
any additional columns are ignored.
Lines that start with a '#' are not read from the datafile.
Program writes the fit start and end times, nr of points, WSS/n,
and parameters of the fitted function to the FIT file (5).

References:
1. Fitting the fractions of parent tracer in plasma.
   http://www.turkupetcentre.net/analysis/doc/fraction_fit.html
2. Kropholler MA, Boellaard R, Schuitemaker A, van Berckel BNM, Luurtsema G,
   Windhorst AD, Lammertsma AA. Development of a tracer kinetic plasma input
   model for (R)-[11C]PK11195 brain studies. J Cereb Blood Flow Metab. 2005;
   25(7): 842-851.
4. http://www.turkupetcentre.net/analysis/doc/format_dft.html
5. http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit2dat, metabcor, avgfract, fit_hill, fit_ppf, fit_exp, dft2svg

Keywords: input, modelling, simulation, metabolite correction

```
fit_frtm 2.6.0  (c) 1999-2013 by Turku PET Centre

Estimates R1 (=K1/K1'), k2, k3, and BPnd (binding potential) using
the (full) reference tissue compartment model FRTM/RTCM (1,3). Assumption
is that K1/k2 is the same in all brain regions, but one-tissue compartment
model with plasma input does not need to fit the data satisfactorily
as is assumed in SRTM (2), and Cref(t) is not assumed to be the same as
Cfree(t) as is assumed in the ratio methods.
This program uses nonlinear regression in model fitting.

Parameters:
  1) Tissue TAC file
  2) Name of reference region in tissue file, or name of file
     containing reference tissue TAC
  3) Fit time (in minutes from injection)
  4) Result file (4)

Options:
 -DVR
     Instead of BPnd, program saves the DVR (=BPnd+1) values.
 -lim=<filename>
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program.
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y), or
     not calculated (n).
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (n).
 -fit=<Filename>
     Fitted regional TACs are written in file.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file (5).
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

If datafile contains weights, those are used in the fitting.
Values of R1, k2, and BPnd are written in the specified result file.
Fitted curves are written in DFT format, if filename is given.

Example 1: file a789.dft contains regions-of-interest and reference region,
with name 'cer all'. The whole time range is used in the fit.
     fit_frtm a789.dft 'cer all' 999 a789.res

Example 2: Reference region TAC is in a separate file, a789ref.dft.
Standard deviations and confidence limits are also estimated.
     fit_frtm -SD=y -CL=y a789.dft a789ref.dft 999 a789.res

References:
1. Cunningham VJ, Hume SP, Price GR, Ahier RG, Cremer JE, Jones AKP.
   Compartmental analysis of diprenorphine binding to opiate receptors
   in the rat in vivo and its comparison with equilibrium data in vitro.
   J Cereb Blood Flow Metab 1991;11:1-9.
2. Lammertsma AA, Hume SP. Simplified reference tissue model for PET
   receptor studies. NeuroImage 1996;4:153-158.
3. Oikonen V, Sederholm K. TPCMOD0002: Model equations for reference tissue
   compartmental models. http://www.turkupetcentre.net/reports/tpcmod0002.pdf
4. File format specification: Result file.
   http://www.turkupetcentre.net/formats/format_res_1_0_0.pdf
5. Scalable Vector Graphics (SVG) 1.1 Specification.
```

http://www.w3.org/TR/SVG/

See also: dftweigh, rescoll, logan, fit_srtm, regbfbp, r2t_rctm

Keywords: DFT, modelling, binding potential, BP, RTCM, reference input

```
fit_fwhm 0.1.1  (c) 2012 by Turku PET Centre

Estimation of FWHM from PET phantom measurements: RC at center of phantom
is measured from phantoms with different radius (1).

Usage: fit_fwhm [Options] <Data file> <FIT file>

Options:
 -svg=<Filename>
     Fitted and measured data are plotted in specified SVG file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Datafile must contain phantom radius (mm) as the first column and
the measured RC as the second column.

Example:
     fit_fwhm -svg=fwhmfit.svg rcphantom.dat rcphantom.fit

References:
1. Scremin OU, Cuevas-Trisan RL, Scremin E, Brown CV, Mandelkern MA.
   Functional electrical stimulation effect on skeletal muscle blood
   flow measured with H215O positron emission tomography. Arch Phys
   Med Rehabil 1998;79:641-646.

See also: eprofile, eabaort

Keywords: FWHM, resolution

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```
fit_gvar 1.2.1  (c) 2003-2008 by Turku PET Centre

Non-linear fitting of Gamma variate function with time delay term
to plasma and tissue time-activity curves (TACs) using iTGO.

Function:
         | 0                               , t < p4
  f(t) = |
         | p1*((t-p4)^p2)*exp(-(t-p4)/p3)  , t >= p4

Usage:  fit_gvar [Options] <Data file> <FIT file>

Options:
 -stoptime=<Fit end time>
     All data with sample time > stoptime is excluded from the fit.
 -thr=<Threshold%>
     Any time points that are less than Threshold% of the maximum after
     the peak of the curves is not used in the fit.
     Hint: try to set threshold close to 100, e.g. 99%, to get a good
     estimate of tracer appearance time.
 -auto
     Automatically sets the fit range from 0 to peak + at least one
     sample more, until WSS/n gets worse.
 -wf
     Weight by sampling interval
 -fast or -safe
     Speed up the fitting but increase the chance of failure, or
     increase the reliability at the cost of computing time
 -fit=<Filename>
     Fitted TACs are written in DFT format (1)
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing

Datafile can be any DFT file (1) which can include weights.
Program writes the fit start and end times, nr of points, WSS/n,
and parameters (p1, p2, p3, p4) of the fitted function
to the FIT file (2).

Example:
     fit_gvar -t=40 -svg=t876gvar.svg t876.dat t876gvar.fit

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit2dat, fit_feng, fit_exp, dftrmbkg

Keywords: DFT, input, modelling, simulation

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```

```
fit_h2o 4.2.0  (c) 1999-2013 by Turku PET Centre

Non-linear fitting of one-tissue compartmental water model to PET [O-15]H2O
study data.
The model parameters are blood flow (F), partition coefficient (pWater),
arterial blood volume (Va) and time delay (delayT). Venous radioactivity
is assumed to be the same as the tissue concentration.
Extraction factor of water is assumed to be 1.0.

The blood flow obtained using PET [O-15]H2O techniques reflects tissue
perfusion, since the method is dependent on the tissue exchange of
labelled water. Non-nutritive flow (blood flowing through arteriovenous
shunts) is not measured (Lammertsma & Jones, 1983).

Command line parameters:
  1) Blood H2O file
  2) Tissue TAC file (*.dft or *.tac)
  3) Fit duration (sec)
  4) Result file

Options:
 -ml or -dl
     In results the units of F and Va will be given per mL or per dL,
     respectively. By default, units are per dL.
 -fpt
     Blood flow (perfusion) is reported per perfusable tissue volume
     (PET volume minus vascular volume). By default perfusion is reported
     per PET volume.
 -input=<File name for new time delay corrected blood TAC>
     Input TAC sample times are corrected by the median of fitted time
     delay values; resulting input file can be used with imgflow, or
     as input to this program to have common time delay for all regions.
 -i=<filename>
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program.
     Parameter can be fixed to a certain value by setting its
     lower and upper limit to that value.
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y), or
     not calculated (n).
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (n).
 -Va=<Va(%)>
     Enter a fixed Va; fitted by default.
 -Delay=<Time delay (s)>
     Enter a fixed time delay; fitted by default.
 -pH2O=<Partition coefficient for water>
     Enter a fixed pH2O; fitted by default.
 -svg=<Filename>
     Plots of original and fitted TACs are written in specified file in
     Scalable Vector Graphics (SVG) 1.1 format; specification in
     http://www.w3.org/TR/SVG/
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -resid=<Filename>
     Weighted residual curves are written in DFT format.
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.
```

Example: fit_h2o uo1234bl.kbq uo1234.dft 999 uo1234f.res

Times must be in seconds in all PET data files.

References:
1. Lammertsma AA, Jones T. J Cereb Blood Flow Metab. 1983;3:416-424.

See also: b2t_h2o, imgflow, arlkup, water_input, fitk2

Keywords: DFT, modelling, perfusion, blood flow

```
fit_hiad 0.3.5  (c) 2008-2010 by Turku PET Centre

Fits the Hill and Hill derivative sum function to the PET
time-activity curves (TACs):
f(x) = A * { [n*xt^(n-1)]/[h^n+xt^n] - [n*xt^(2*n-1)]/[h^n+xt^n]^2
             + [k*xt^n]/[h^n+xt^n] }  , where xt=x-dt and n>=1

Usage:  fit_hiad [Options] <TAC file> [Fit parameter file]

Options:
 -Hill
     Hill function without Hill derivative is fitted;
     f(x) = (A*xt^n)/(h^n+xt^n)
 -fast or -safe
     Speed up the fitting but increase the chance of failure, or
     increase the reliability at the cost of computing time
 -W1
     All weights are set to 1.0; by default, sample times are used to
     calculate weights unless weights are not supplied in fraction file
 -k=<value>
     Parameter k is constrained to given value; setting k to zero causes
     the function to approach zero
 -dlow=<time>
     Penalize Hill derivative higher than 1% of total tissue activity
     after specified time
 -delay=<<value>|mean|median>
     Delay time (dt) is constrained to specified value or to mean or median
     of all TACs
 -fit=<Filename>
     Fitted TACs are written in DFT format
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

Program writes the fit start and end times, nr of points, WSS/n,
and parameters of the fitted function to the result (fit) file,
in format: http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit2dat, fit2res, dftweigh, dft2svg, regderiv, fit_exp, fit_ratf

Keywords: DFT, input, modelling, simulation

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you are welcome to redistribute it under GNU General Public License.
```

```
fit_hill 1.8.5  (c) 1999-2010 Turku PET Centre

Fits the following Hill function to a fraction curve of unchanged
(parent) tracer in plasma, where fractions are between 0 and 1 (1, 2).

                          B       B
         f(x) = 1 - (A * x ) / ( x + C )    , where 0<A<=1 , B>0 , C>0

Usage:  fit_hill [Options] <Fraction file> [Fit file]

General options:
 -ND    Some fractions are known to exceed 1, not divided by 100.
 -h or --help
        Print this message and exit.
 --build or --version
        Print software build information and exit.
 --silent
        Program works silently, printing only error and warning messages.
 --verbose
        Program prints more information about what it is doing.
Options to constrain the fit:
 -a=<value>
        Parameter A is fixed to given (population mean) value.
 -b=<value>
        Parameter B is fixed to given (population mean) value.
 -c=<value>
        Parameter C is fixed to given (population mean) value.
Options to refine the fitted function:
 -Asc | -Desc
        Fit an additional parameter D, so that
        f(x) = 1 - (A(1+Dx)x^B)/(x^B+C), where
        0<=D<=0.05 (Asc) or -0.05<=D<=0 (Desc).
 -Lwr   Fit function f(x) = A - (Ax^B)/(x^B+C) with usual constraints.
Options to set weights:
 -W1    All weights are set to 1.0; by default, sample times are used to
        calculate weights unless weights are not supplied in fraction file.
 -WC    The last data column contains sample weights.
 -WF    Multiply sample weights with sample times.

Fraction datafile must contain two columns, sample times and fractions
of parent tracer. Weights can be specified as specified in DFT format,
http://www.turkupetcentre.net/analysis/doc/format_dft.html ;
any additional columns are ignored.
Lines that start with a '#' are not read from the datafile.

Program writes the fit start and end times, nr of points, WSS/n,
and parameters of the fitted function to the result (fit) file,
in format: http://www.turkupetcentre.net/analysis/doc/format_fit.html

References:
1. Fitting the fractions of parent tracer in plasma.
   http://www.turkupetcentre.net/analysis/doc/fraction_fit.html
2. Wu S, Ogden RT, Mann JJ, Parsey RV. Optimal metabolite curve fitting for
   kinetic modeling of 11C-WAY-100635. J Nucl Med 2007;48:926-931.

See also: fit2dat, metabcor, avgfract, fit_sigm, fit_fexp, fit_ppf, dft2svg

Keywords: input, modelling, simulation, metabolite correction

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you are welcome to redistribute it under GNU General Public License.
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```
fit_meb 0.2.0  (c) 2009,2012 by Turku PET Centre

Fit mono-exponential decay function with background,
   f(t) = A*exp(-B*t) + C,
to PET time-activity curves (TACs).

Usage: fit_meb [Options] <TAC file> <Fit file>

Options:
 -starttime=<Time>
     Set the sample time from where fitting is started (0 by default).
 -w1 All weights are set to 1.0 (no weighting); by default, weights in
     data file are used, if available.
 -wf
     Weight by sampling interval.
 -fit=<Filename>
     Fitted TACs are written in DFT format.
 -svg=<Filename>
     Measured and extrapolated TACs are plotted in specified SVG file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

TAC file must be in DFT format (1). Function parameters are written in
Fit format (2).

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit_exp, fit_fexp, extrapol, fit2dat, dftcut, dftcat

Keywords: DFT, input, simulation, shape analysis, extrapolation

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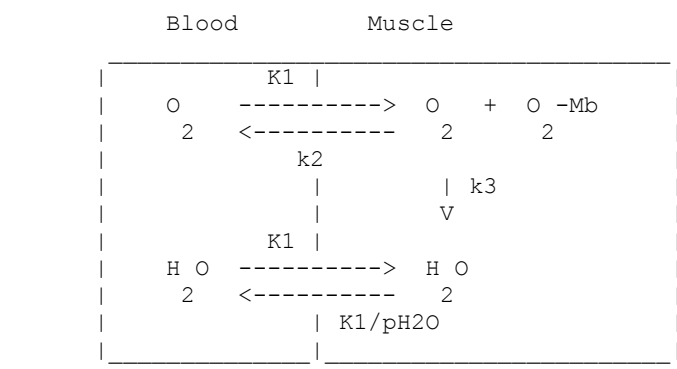
fit_mo2 3.0.0 (c) 1998-2008 by Turku PET Centre

Fits the following compartmental model dedicated for skeletal muscle (1, 2, 3)
to regional PET [O-15]O2 study data.
The model parameters are perfusion (Flow, K1), oxygen extraction ratio
(OER = K1/(k2+k3)), partition coefficients of oxygen and water (K1/k2 and
pH2O), blood volume fraction (Vb) and time delay (delayT).



Model definitions:
  K1=Flow (mL/min/dL), OER=k3/(k2+k3),
  Ki=Flow*OER (mL/min/dL),
  Metabolic rate of oxygen MRO2=Ki*[O2]a (mmol/min/dL)

Command line arguments:
  1) Blood O2 TAC file
  2) Blood H2O TAC file
  3) Muscle TAC file (*.dft)
  4) Fit duration (sec)
  5) Result file

General options:
 -SD[=<Y|n>]
     Standard deviations are calculated and saved in results (y), or
     not calculated (n).
 -CL[=<Y|n>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (n).
 -svg=<Filename>
     Plots of original and fitted TACs are written in specified file in
     Scalable Vector Graphics (SVG) 1.1 format; specification in
     http://www.w3.org/TR/SVG/
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing
 Options to set model parameters:
 -cO2a=<Arterial O2 concentration>
     Set the O2 content (mL O2/100 mL blood) of arterial blood to calculate
     rMRO2, for example -cO2a=19.8;
     if not specified, program can calculate only Ki for [O-15]O2
 -Af=<Arterial proportion (%)>
     Set the simulated arterial proportion of total blood volume;
     default is 30%
 Options for constraining model parameters:
 -i=<filename>
     Specify the constraints for model parameters;
     This file with default values can be created by giving this

option as the only command-line argument to this program.
Parameter can be fixed to a certain value by setting its
lower and upper limit to that value.

-Vb=<Blood volume (%)>
Set the regional blood volume; default is 3.5%

-pH2O=<value>
Set the partition coefficient of water; default is 0.99

-Flow=<value>
Set the regional perfusion (blood flow) value, e.g. based on [O-15]H2O
study, in units mL/100mL/min

-fK1k2
K1/k2 for oxygen is not estimated as a free parameter, but it is
calculated from OER and saturation curves for hemoglobin and myoglobin

-K1k2=<value>
Specify the K1/k2 for oxygen.

-Sao2=<value>
Saturation of arterial blood hemoglobin; default is 0.97

-p50Hb=<value>
Half-saturation pressure for hemoglobin; default is 3.6 kPa

-p50Mb=<value>
Half-saturation pressure for myoglobin; default is 0.319 kPa

-nHb=<value>
Hill coefficient for hemoglobin; default is 2.7

-Mb=<value>
Concentration of myoglobin in muscle; default is 4.7 mg/g

-Hb=<value>
Concentration of hemoglobin in blood; default is 150 mg/g

Example: fit_mo2 uo1235_o.kbq uo1235_w.kbq uo1235.dft 999 uo1235mo2.res

Times must be in seconds in all data files. File format is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

References:

1. Nuutila P, Peltoniemi P, Oikonen V, Larmola K, Kemppainen J, Takala T, Sipila H, Oksanen A, Ruotsalainen U, Bolli GB, Yki-Jarvinen H. Enhanced stimulation of glucose uptake by insulin increases exercise-stimulated glucose uptake in skeletal muscle in humans: studies using [15O]O2, [15O]H2O, [18F]fluoro-deoxy-glucose, and positron emission tomography. Diabetes 2000; 49:1084-1091.
2. Oikonen V, Nuutila P, Sipilä H, Tolvanen T, Peltoniemi P, Ruotsalainen U. Quantification of oxygen consumption in skeletal muscle with PET and oxygen-15 bolus. Eur J Nucl Med. 1998; 25: 1151.
3. Oikonen V. Modelling of low oxygen consumption. In: J. Knuuti, J. Rinne, P.Tenhonen (ed.), Medical Applications of Cyclotrons VIII. Abstracts of the VIII Symposium on the Medical Applications of Cyclotrons. Annales Universitatis Turkuensis D346:16, 1999.

See also: o2metab, o2_p2w, fit_o2bl, b2t_mo2, rescoll

Keywords: DFT, modelling, oxygen, skeletal muscle

```
fit_orm 0.4.8 (c) 2008-2010 by Turku PET Centre

Fits a model dedicated for ORM-B to regional PET study data.

Command line arguments:
  1) Plasma parent TAC file
  2) Plasma metabolite TAC file
  3) Blood TAC file
  4) Brain TAC file (*.dft)
  5) Fit duration (min)
  6) Result file

General options:
 -ref=<Region name or number>
 -wm=<Region name or number>
     White matter region is used to account for partial volume effect
     in all other regions
 -SD[=<Y|n>]
     Standard deviations are calculated and saved in results (y), or
     not calculated (n)
 -CL[=<Y|n>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (n)
 -svg=<Filename>
     Plots of original and fitted TACs are written in specified file in
     Scalable Vector Graphics (SVG) 1.1 format; specification in
     http://www.w3.org/TR/SVG/
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more of information about what it is doing
 Options to set model parameters:
 -Af=<Arterial proportion (%)>
     Set the simulated arterial proportion of total blood volume;
     default is 30%, minimum is 1%
 -fixvfp[=<y|N>]
     Vfp is constrained or not constrained to its estimate on reference
     region, if reference region is given with option -ref
 -fixmc1[=<y|N>]
     mc1 is constrained or not constrained to its estimate on reference
     region, if reference region is given with option -ref
 -fixmc2[=<y|N>]
     mc2 is constrained or not constrained to its estimate on reference
     region, if reference region is given with option -ref
 -fixvfm[=<y|N>]
     Vfm is constrained or not constrained to its estimate on reference
     region, if reference region is given with option -ref
 -mc1=<value>
     mc1 is constrained to specified value in all regions
 -mc2=<value>
     mc2 is constrained to specified value in all regions
 -irreversible
     Binding has an irreversible component (k4=0)
 -cm=1
     One-tissue compartment model is used for all regions (k3=k4=0).

See also: rescoll, metabcor, dftweigh, dftcalc, sim_orm, fitk4

Keywords: DFT, modelling

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you are welcome to redistribute it under GNU General Public License.

```
fit_ppf 2.0.10  (c) 2010-2013 Turku PET Centre

Fits an empirical function to plasma parent (unchanged) tracer
fraction curve (1), where the fractions are between 0 and 1.

Usage:  fit_ppf [Options] <Fraction file> [Fit file]

Options:
 -model=<PF | HILL | MPF | MHILL>
       Select the function (see descriptions below); default is HILL.
       Use MPF or MHILL to fit functions to 2-3 metabolite fraction curves
       instead of parent fraction curve.
 -min=<SS|ABS>
       Sum-of-squares (SS) is minimized by default, but optionally
       sum of absolute deviations (ABS) can be selected.
 -delaymin=<value>
       Set the lower limit for delay parameter.
 -mdelay=<separated | joint>
       Delay parameter for each metabolite is fitted separately, or
       all metabolites are assumed to share common delay time (default).
 -a=<value>, -b=<value>, -c=<value>, ...
       Specified parameter is fixed to given (population mean) value.
 -WC   The last data column contains sample weights.
 -W1   All weights are set to 1.0 (no weighting)
 -WF   Less frequent samples are given more weight.
 -WP=<weight>, -WM1=<weight>, -WM2=<weight>, -WM3=<weight>
       Put additional or less weight to parent and/or metabolite fractions.
 -ND   Some fractions are known to exceed 1, not divided by 100.
 -MRL  Error is returned if MRL check is not passed.
 -svg=<Filename>
       Fitted and measured TACs are plotted in specified SVG file.
 -h or --help
       Print this message and exit.
 --build or --version
       Print software build information and exit.
 --silent
       Program works silently, printing only error and warning messages.
 --verbose
       Program prints more information about what it is doing.

Fraction datafile must contain at least two columns: sample times and
fractions of parent tracer. Fractions of 1-3 metabolites can be given in
additional columns. Weights can be specified as specified in DFT format (2)
or with option -wc.
Program writes the fit start and end times, nr of points, WSS,
and parameters of the fitted function to the FIT file (3).

Available functions:
PF - extended power function (1,4,5)
  f(x) = {D^(-1/C) + (A*(x-E))^B }^-C , when x>E,
  f(x) = D                            , when x<=E ,
  where 0<A<=1, B>1.5, C>0, 0<D<=1, 0<=E.
  With option -d=1 this is essentially the same function as proposed in (4)
  or with options -b=2 -d=1 -e=0 the same as suggested in (5).
HILL - Extended Hill type function (1,6)
  f(x) = D - {(D-A)(x-E)^B}/{C+(x-E)^B} , when x>E,
  f(x) = D                              , when x<=E ,
  where 0<=A<=D, 1<=B, 0<C, 0<D<=1, 0<=E.
  With options -d=1 -e=0 this is the traditional Hill type function (6)
  f(x) = 1 - {(1-A)x^B}/(C+x^B)
MPF - Extended power function is fitted to 1-3 metabolite fractions.
MHILL - Extended Hill type function is fitted to 1-3 metabolite fractions.

References:
1. Fitting the fractions of parent tracer in plasma.
   http://www.turkupetcentre.net/analysis/doc/fraction_fit.html
2. http://www.turkupetcentre.net/analysis/doc/format_dft.html
```

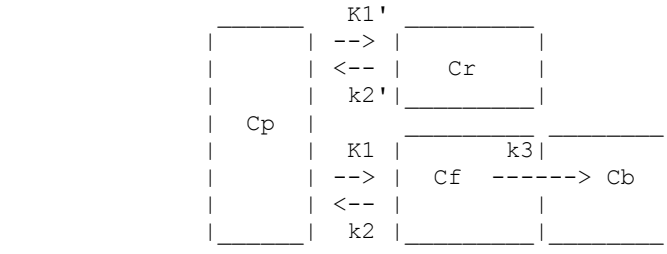
3. http://www.turkupetcentre.net/analysis/doc/format_fit.html
4. Meyer PT, Bier D, Holschbach MH, Boy C, Olsson RA, Coenen HH, Zilles K, Bauer A. Quantification of cerebral A1 adenosine receptors in humans using [18F]CPFPX and PET. J Cereb Blood Flow Metab. 2004;24(3):323-333.
5. Watabe H, Channing MA, Der MG, Adams HR, Jagoda E, Herscovitch P, Eckelman WC, Carson RE. Kinetic analysis of the 5-HT2A ligand ([11C]MDL 100,907. J Cereb Blood Flow Metab 2000;20:899-909.
6. Wu S, Ogden RT, Mann JJ, Parsey RV. Optimal metabolite curve fitting for kinetic modeling of 11C-WAY-100635. J Nucl Med 2007;48:926-931.

See also: fit2dat, metabcor, avgfract, fitedit, fit_fexp, fith2met, dft2svg

Keywords: input, plasma, modelling, simulation, metabolite correction

fit_rrtm 2.5.2 (c) 1999-2012 by Turku PET Centre

Estimates R1 (=K1/K1'), k2 and k3 applying the reduced reference tissue
compartment model, RRTM (1). This model is based on the full reference tissue
compartment model (2, 3), but here it is assumed that the binding or
metabolism of tracer is irreversible (k4=0) during the PET scanning.




```
  dCf(t) = R1*dCr(t) + k2*Cr(t) - (k2+k3)*Cf(t)
  dCb(t) = k3*Cf(t)
```

```
Command-line parameters:
  1) Tissue TAC file (4)
  2) Name or number of reference region in tissue file, or name of TAC file
     containing reference tissue TAC
  3) Fit time (in minutes from injection)
  4) Result file (5)
Options:
 -lim=<filename>
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y), or
     not calculated (n)
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (n)
 -fit=<Filename>
     Fitted regional TACs are written in DFT format (4).
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file (6).
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

If datafile contains weights, those are used in the fitting.
Values of R1, k2, and k3 are written in the specified result file.
Fitted curves are written in DFT format, if filename is given.

Example 1: file a789.dft contains regions-of-interest and reference region,
with name 'cereb'. The whole time range is used in the fit.
Fitted TACs are plotted in SVG format (7) in file a789rrtm.svg.
     fit_rrtm -svg=a789rrtm.svg a789.dft cereb 999 a789.res

Example 2: Reference region TAC is in a separate file, a789ref.dft.
Standard deviations and confidence limits are also estimated.
TAC data from injection to 60 min is used in the fitting.
     fit_rrtm -SD=y -CL=y a789.dft a789ref.dft 60 a789.res

Example 3a: Create a file containing default parameter limits:
     fit_rrtm -lim=rrtm.lim
```

Example 3b: Apply user-defined parameter constraints specified in rrtm.lim:
```
fit_rrtm -lim=rrtm.lim a789.dft cereb 999 a789.res
```

References:

1. Oikonen V. Model equations for reference tissue compartmental models. http://www.turkupetcentre.net/reports/tpcmod0002.pdf
2. Cunningham VJ, Hume SP, Price GR, Ahier RG, Cremer JE, Jones AKP. Compartmental analysis of diprenorphine binding to opiate receptors in the rat in vivo and its comparison with equilibrium data in vitro. J Cereb Blood Flow Metab 1991;11:1-9.
3. Lammertsma AA, Hume SP. Simplified reference tissue model for PET receptor studies. NeuroImage 1996;4:153-158.
4. File format specification: DFT. http://www.turkupetcentre.net/formats/format_dft_1_0_0.pdf
5. File format specification: Result file. http://www.turkupetcentre.net/formats/format_res_1_0_0.pdf
6. Scalable Vector Graphics (SVG) 1.1 Specification. http://www.w3.org/TR/SVG/

See also: dftweigh, patlak, fitk3, r2t_rtcm, rescoll

Keywords: DFT, modelling, irreversible uptake, reference tissue

```
fit_sigm 2.0.3 (c) 2006-2012 Turku PET Centre, University of Turku

Non-linear fitting of the Hill function (sigmoid function) to a (xi,yi)
curve data. Optionally, a background term B is added to the function:

       f(x) = (A * x^n ) / ( x^n + K ) + B , where A>=0, K>0, n>0, B>=0

Function for estimating EC50 from sigmoidal dose-response curve is obtained
by rearranging and marking n=HillSlope, A=Top-Bottom, B=Bottom, and
K=EC50^n :

       f(x) = Bottom + (Top-Bottom)/(1 + (EC50/x)^HillSlope)

With HillSlope constrained to 1 (see options below) the function reduces to
unconstrained one site binding hyperbola, f(x)=Top*x/(EC50+x).

Usage:  fit_sigm [Options] <Data file> <Fit file>

Options:
 -EC50
     EC50 is estimated by fitting sigmoidal dose-response curve function
     when drug concentrations are on a linear scale (not on a log scale);
     By default, parameter Top is fitted and Bottom is constrained to 0,
     which can be changed with options (see below)
 -w1 All weights are set to 1.0 (no weighting); by default, weights in
     data file are used, if available
 -wf
     Weight by sampling interval
 -n=<value>
     Parameter n or HillSlope is constrained to the given value; set -n=1
     to fit one site binding hyperbola
 -B  Parameter B or Bottom is fitted; by default B=0
 -B=<value>
     Parameter B or Bottom is constrained to the given value
 -A=<value>
     Parameter Top is constrained to the given value; currently this option
     does not affect parameter A in the default function
 -MRL
     Error is returned if MRL check is not passed
 -res=<Filename>
     Fitted parameters are also written in result file format (3)
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -fit=<Filename>
     Fitted TACs are written in DFT format
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Data file must contain at least 2 columns, sample times (or concentrations)
and measurement values (or receptor occupancies).
Weights can be specified as usual if data is in DFT format (1).

Program writes the fit start and end times, nr of points, WSS,
and parameters of the fitted function to the fit file (2).

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. http://www.turkupetcentre.net/analysis/doc/format_fit.html
3. http://www.turkupetcentre.net/analysis/doc/format_res.html

See also: fit_hiad, fit_ppf, fit_exp, fit_ratf, fit2dat, dft2csv
```

Keywords: curve fitting, Hill function, sigmoid, EC50, dose-response curve

```
fit_sinf 0.8.9  (c) 2005-2013 by Turku PET Centre

Fit the time-activity curve (TAC) of PET tracer in plasma or blood
to a four-to-ten parameter function (1). This function may be applied
when PET tracer is introduced into venous blood as a short infusion.
Function: f(t)=
  if t<=Ta :
     0
  if t>Ta and t<Ta+Ti :
     (1/Ti)*Sum[i=1..n, (Ai/Li)*(1-exp(-Li*(t-Ta)))]
  if t>=Ta+Ti :
     (1/Ti)*Sum[i=1..n, (Ai/Li)*(exp(-Li*(t-Ta-Ti)) - exp(-Li*(t-Ta)))]

Command-line arguments:
  1) TAC filename
  2) Filename for fitted function parameters (optional)

TAC data must be in DFT format (2). For a good fit, (radioactivity)
concentrations should be corrected for physical decay and
circulating metabolites.
Function parameters will be written in the parameter file (3).

Command-line options:
 -fast or -safe
     Speed up the fitting but increase the chance of failure, or
     increase the reliability at the cost of computing time.
 -fit=<Filename>
     Fitted TACs are written in DFT format
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -svg1=<Filename>
     Initial part of fitted and measured TACs are plotted in SVG file
 -svg2=<Filename>
     Lower part of fitted and measured TACs are plotted in SVG file
 -tau1=<Dispersion time constant (s)>
 -tau2=<2nd dispersion time constant (s)>
     Dispersion is added to function, also to saved curve and plot;
     curve without dispersion can be calculated from function parameters.
 -wf
     Weight by sampling interval.
 -min=<SS|ABS>
     Sum-of-squares (SS) is minimized by default, but optionally
     sum of absolute deviations can be selected.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing
Options for constraining the fit:
 -lim=<filename>
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program.
 -Ti=<infusion time>
     Duration of tracer infusion; 0, if short bolus.
 -Ta=<appearance time>
     Time when tracer concentration starts ascending.
 -n=<1|2|3|4|5|A>
     The nr of summed functions; A=determined by AIC (default).
     2 or 3 is usually recommended (much faster).

References:
1. Oakes ND et al. J Lipid Res. 1999;40:1155-1169.
2. http://www.turkupetcentre.net/analysis/doc/format_dft.html
```

3. http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit2dat, fit_feng, fit_winp, fit_exp, fit_ratf, extrapol

Keywords: input, modelling, simulation

```
fit_srtm 3.1.0  (c) 1999-2013 by Turku PET Centre

Estimates R1 (=K1/K1'), k2 and BPnd (binding potential) using simplified
reference tissue compartment model, SRTM (1,2,3). Assumptions are that
K1/k2 is the same in all brain regions, and that a one-tissue compartment
model with plasma input could fit the tissue curves satisfactorily.
This program uses nonlinear regression in model fitting.

Parameters:
  1) Tissue TAC file (in DFT, PMOD, or CSV format)
  2) Name of reference region in tissue file, or name of file
     containing reference tissue TAC
  3) Fit time (in minutes from injection)
  4) Result file (existing file is overwritten) (4)

Options:
 -DVR
     Instead of BPnd, program saves the DVR (=BPnd+1) values.
 -lim=<filename>
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program.
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y), or
     not calculated (n).
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (n).
 -fit=<Filename>
     Fitted regional TACs are written in file.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file (5).
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

If datafile contains weights, those are used in the fitting.
Values of R1, k2, and BPnd are written in the specified result file.
Fitted curves are written in DFT format, if filename is given.

Example 1: file a789.dft contains regions-of-interest and reference region,
with name 'cer all'. The whole time range is used in the fit.
     fit_srtm a789.dft 'cer all' 999 a789.res

Example 2: Reference region TAC is in a separate file, a789ref.dft.
Standard deviations and confidence limits are also estimated.
     fit_srtm -SD=y -CL=y a789.dft a789ref.dft 999 a789.res

References:
1. Cunningham VJ, Hume SP, Price GR, Ahier RG, Cremer JE, Jones AKP.
   Compartmental analysis of diprenorphine binding to opiate receptors
   in the rat in vivo and its comparison with equilibrium data in vitro.
   J Cereb Blood Flow Metab 1991;11:1-9.
2. Lammertsma AA, Hume SP. Simplified reference tissue model for PET
   receptor studies. Neuroimage 1996;4:153-158.
3. Oikonen V, Sederholm K. TPCMOD0002: Model equations for reference tissue
   compartmental models. http://www.turkupetcentre.net/reports/tpcmod0002.pdf
4. File format specification: Result file.
   http://www.turkupetcentre.net/formats/format_res_1_0_0.pdf
5. Scalable Vector Graphics (SVG) 1.1 Specification.
   http://www.w3.org/TR/SVG/
```

See also: dftweigh, rescoll, logan, regbfbp, fit_frtm, r2t_rtcm

Keywords: DFT, modelling, binding potential, BP, SRTM, reference input

```
fit_tac 0.1.0  (c) 2008 by Turku PET Centre

Non-linear fitting of an exponential sum function to PET tissue
time-activity curves (TACs).

Function:
  when t<=tau: y(t) = 0
  when t>tau:  y(t) = (p1*(t-tau)-p3)*exp(p2*(t-tau)) + p3*exp(p4*(t-tau))
                     +(p5*(t-tau)-p7)*exp(p6*(t-tau)) + p7*exp(p8*(t-tau))

Usage:  fit_tac [Options] <Datafile> <FIT file>

Options:
 -function=<MFENG|MLUNQ|LUNQ|MGVAR|HGVAR|HMGVA|WEIB>
     Select the function; by default MFENG (above)
 -wf
     Weight by sampling interval
 -fast or -safe
     Speed up the fitting but increase the chance of failure, or
     increase the reliability at the cost of computing time
 -fit=<Filename>
     Fitted TACs are written in DFT format
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing

Datafile can be any DFT file (1) which can include weights.
Program writes the fit start and end times, nr of points, WSS/n,
and parameters (p1, p2, p3, p4, p5, p6, p7, p8, tau) of the fitted function
to the FIT file (2).

Example 1: Fit function to plasma TAC and compute fitted curve
           between 0 and 60 min at 0.1 min intervals:
     fit_tac p455ap.kbq p455ap.fit
     fit2dat -c=0,60,0.1 p455ap.fit p455ap_new.kbq
Example 2: Fit function to plasma TAC and plot fitted and measured TACs
           in SVG format:
     fit_tac -svg=p455apfit.svg p455ap.kbq p455ap.fit

References:
1. http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit2dat, fit_feng, fit_sinf, fit_exp, fit_ratf, fit_hiad

Keywords: DFT, input, modelling, simulation

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you are welcome to redistribute it under GNU General Public License.
```
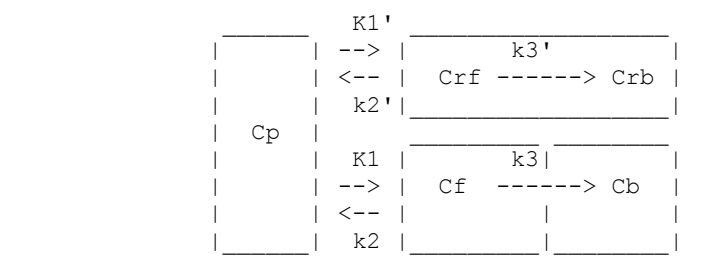

```
fit_trtm 2.6.3  (c) 1999-2012 by Turku PET Centre

Estimates R1 (=K1/K1'), k2' and k3 (assumption: k4=0) using transport-
limited reference tissue compartment model, TRTM (1). This model
is based on the reference tissue compartment model (2), but here it is
assumed that in reference tissue k3'>>k2', and thus the uptake in it is
limited only by transport into tissue (3,4).
```



$$Cr(t) = Crf(t) + Crb(t) \; ; \quad Ct(t) = Cf(t) + Cb(t)$$

$$dCt(t) = R1*dCr(t) + (R1*k3)*Cr(t) - (R1*k2'+k3)*Ct(t)$$

```
Command-line parameters:
  1) Tissue TAC file (5)
  2) Name or number of reference region in tissue file, or name of TAC file
     containing reference tissue TAC
  3) Fit time (in minutes from injection)
  4) Result file (existing file is overwritten) (6)
Options:
 -rk2=<<value>|mean|median>
     Constrain k2' to specified <value>, or to mean or median of regional
     k2' values excluding reference region(s)
 -lim=<filename>
     Specify the constraints for model parameters;
     This file with default values can be created by giving this
     option as the only command-line argument to this program
 -SD[=<y|N>]
     Standard deviations are calculated and saved in results (y), or
     not calculated (n)
 -CL[=<y|N>]
     95% Confidence limits are calculated and saved in results (y), or
     not calculated (n)
 -fit=<Filename>
     Fitted regional TACs are written in DFT format (5).
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file (7).
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

If datafile contains weights, those are used in the fitting.

Example 1: file a789.dft contains regions-of-interest and reference region,
with name 'putam'. The whole time range is used in the fit.
Fitted TACs are plotted in SVG format (7) in file a789trtm.svg.
     fit_trtm -svg=a789trtm.svg a789.dft putam 999 a789.res

Example 2: Reference region TAC is in a separate file, a789ref.dft.
Standard deviations and confidence limits are also estimated.
TAC data from injection to 60 min is used in the fitting.
     fit_trtm -SD=y -CL=y a789.dft a789ref.dft 60 a789.res

Example 3a: Create a file containing default parameter limits:
```

```
     fit_trtm -lim=trtm.lim

Example 3b: Apply user-defined parameter constraints specified in trtm.lim:
     fit_trtm -lim=trtm.lim a789.dft putam 999 a789.res
```

References:

1. Oikonen V. Model equations for reference tissue compartmental models. http://www.turkupetcentre.net/reports/tpcmod0002.pdf
2. Cunningham VJ, Hume SP, Price GR, Ahier RG, Cremer JE, Jones AKP. Compartmental analysis of diprenorphine binding to opiate receptors in the rat in vivo and its comparison with equilibrium data in vitro. J Cereb Blood Flow Metab 1991;11:1-9.
3. Herholz K, Lercher M, Wienhard K, Bauer B, Lenz O, Heiss W-D. PET measurement of cerebral acetylcholine esterase activity without blood sampling. Eur J Nucl Med 2001;28:472-477.
4. Nagatsuka S, Fukushi K, Shinotoh H, Namba H, Iyo M, Tanaka N, Aotsuka A, Ota T, Tanada S, Irie T. Kinetic analysis of [11C]MP4A using a high-radioactivity brain region that represents an integrated input function for measurement of cerebral acetylcholinesterase activity without arterial blood sampling. J Cereb Blood Flow Metab 2001; 21: 1354-1366.
5. File format specification: DFT. http://www.turkupetcentre.net/formats/format_dft_1_0_0.pdf
6. File format specification: Result file. http://www.turkupetcentre.net/formats/format_res_1_0_0.pdf
7. Scalable Vector Graphics (SVG) 1.1 Specification. http://www.w3.org/TR/SVG/

See also: dftweigh, fitk3, fitshape, lhtrtm, r2t_rtcm, rescoll

Keywords: DFT, modelling, irreversible uptake, reference tissue

```
fit_wcdf 0.1.4  (c) 2008-2010 by Turku PET Centre

Fits the WCDF and WCDF derivative sum function to the PET
time-activity curves (TACs).

Usage:  fit_wcdf [Options] <TAC file> [Fit parameter file]

Options:
 -CDF
     WCDF function without its derivative is fitted
 -fast or -safe
     Speed up the fitting but increase the chance of failure, or
     increase the reliability at the cost of computing time
 -W1
     All weights are set to 1.0; by default, sample times are used to
     calculate weights unless weights are not supplied in fraction file
 -k=<value>
     Parameter k is constrained to given value; setting k to zero causes
     the function to approach zero
 -dlow=<time>
     Penalize WCDF derivative higher than 1/10000 of total tissue activity
     after specified time
 -delay=<<value>|mean|median>
     Delay time (dt) is constrained to specified value or to mean or median
     of all TACs
 -fit=<Filename>
     Fitted TACs are written in DFT format
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

Program writes the fit start and end times, nr of points, WSS/n,
and parameters of the fitted function to the result (fit) file,
in format: http://www.turkupetcentre.net/analysis/doc/format_fit.html

See also: fit2dat, fit2res, dftweigh, dft2svg, regderiv, fit_hiad

Keywords: DFT, input, modelling, simulation

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you are welcome to redistribute it under GNU General Public License.
```

```
fit_winp 0.3.3  (c) 2010,2012 by Turku PET Centre

Fit blood time-activity curve (TAC) from PET [O-15]H2O study
to a six (1) or four parameter (2) function, when radiowater is
given to patient as a short infusion.

Command-line arguments:
  1) Plasma TAC filename
  2) Filename for fitted function parameters (optional)

Plasma data (3) must contain two columns: sample times and (radioactivity)
concentrations which preferably are corrected for physical decay and
circulating metabolites. Extra columns are ignored.
Function parameters will be written in the parameter file (4); note that
these describe dispersion corrected curve, if dispersion time constants
are specified.

Command-line options:
 -tau1=<Dispersion time constant (s)>
 -tau2=<2nd dispersion time constant (s)>
     Dispersion (5) is added to function, also to saved curve and plot
 -func=<331|332>
     Select the function to be fitted; 331 is the default
 -MRL
     Error is returned if MRL check is not passed
 -fast or -safe
     Speed up the fitting but increase the chance of failure, or
     increase the reliability at the cost of computing time
 -wf
     Weight by sampling interval
 -fit=<Filename>
     Fitted TAC is written in DFT format
 -dcfit=<Filename>
     Fitted dispersion corrected (5) TAC is written in DFT format;
     can only be used when dispersion time constant is set
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing
Options for constraining the fit:
 -Ti=<infusion time (s)>
     Duration of tracer infusion; 0, if short bolus
 -Ta=<appearance time (s)>
     Time when tracer concentration starts ascending.

References:
1. Oakes ND et al. J Lipid Res. 1999;40:1155-1169.
2. Kudomi N et al. Eur J Nucl Med Mol Imaging 2008;35:1899-1911.
3. http://www.turkupetcentre.net/analysis/doc/format_dft.html
4. http://www.turkupetcentre.net/analysis/doc/format_fit.html
5. Iida H et al. J Cereb Blood Flow Metab. 1986;6:536-545.

See also: fit2dat, fit_sinf, fit_feng, disp4dft, dfttime, fitdelay

Keywords: input, modelling, simulation, dispersion, radiowater

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```
flo2ecat 2.0.1  (c) 2003-2012 by Turku PET Centre

Construct an ECAT PET image or sinogram from pixel values stored as 4-byte
floats in a binary flat file.
Data must be stored in this matrix order: all planes of the 1st frame,
2nd frame, and so on.
The format of the output file is determined from its filename extension
(*.v, *.s, *.i, *.img or *.scn).
The byte order of binary data is assumed to be the same as in current
platform; use option -e to change byte order, if necessary.

Usage: flo2ecat [Options] <Datafile> <Output ECAT file>
                          [<planeNr> <frameNr> <dimx> <dimy>]

Options:
 -t=<Advance|931|HR+|HRRT>
     Set scanner specific parameters in headers
 -r=<reconstruction zoom>
     Set reconstruction zoom in image headers (only for images)
 -inf=<Matrix information file> or -f=<Matrix information file>
     ASCII file containing the number of planes and frames, and x and y
     dimensions
 -z[ero]
     Zero hot spots outside of FOV (only for images)
 -b=<Nr of bins>
     Nr of bins in the output sinogram; use this to add (nr-dim1)/2 bins
     filled with zeroes to both sides of sinogram
 -p  Transpose the data, i.e. switch x and y axis
 -e  Switch the byte order between little and big endian
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Examples:
     flo2ecat -t=Advance xyz.dat xyz.scn 35 1 281 336
     flo2ecat -t=HRRT -inf=qwe.inf qwe.dat qwe.v

See also: ecat2flo, asc2flo, ana2ecat, e7emhdr, eframe, sif2ecat, ecatflip

Keywords: ECAT, image, sinogram, format conversion, software testing

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```

```
fr4sim 3.9.2  (c) 1998-2012 by Turku PET Centre

Simulation programs calculate tissue curve values with short sample
time intervals. This program sums up those points within specified time
frames to simulate a measured PET tissue uptake curve.

Usage:
  fr4sim [Options] <datafile> <frames data> <output datafile> [isotope]

Options:
 -i  Calculates integrals at frame mid times, instead of averages;
     not available with [isotope].
 -ii Calculates 2nd integrals at frame mid times, instead of averages;
     not available with [isotope].
 -sec or -min
     Sample times are known to be in seconds or minutes, but is not
     specified or is wrong in DFT files.
 -mid
     Frame mid time is written in output file instead of start and end times
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Input datafile can contain one or more data columns in any DFT format (1).
Frames data can be in SIF format (2). Alternatively, frames data file can
consist of one or two columns of data, containing either
1) frame durations or 2) frame start times and frame durations;
time units must be same as in the datafile. Frames are allowed to overlap.

If the isotope is specified, the correction for physical decay is at first
removed, then PET framing is simulated, and after that the framed data
is decay corrected again, based on the frame start time and length as is
the normal procedure when collecting PET image data.
Check that time units are correct when using this possibility.

Output is written in DFT format (1) depending on the format of the input.

References:
1. TAC file: http://www.turkupetcentre.net/analysis/doc/format_dft.html
2. SIF file: http://www.turkupetcentre.net/analysis/doc/sif.html

See also: dftframe, dfttime, dftdecay, dftunit, interpol, extrapol, dftint

Keywords: DFT, simulation, time frame, SIF, interpolation

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```

```
fvar4dat 1.4.0  (c) 2002-2012 by Turku PET Centre

Program for adding Gaussian noise to PET time-activity (TAC) data
using equations (1, 2):
  SD(t) = TAC(t) * sqrt(Pc/(TAC(t)*exp(-lambda*t)*deltat)
  TAC_noisy(t) = TAC(t) + SD(t)*G(0,1) ,
where Pc is the proportionality constant that determines the level,
of noise, Deltat is the scan frame length, and G(0,1) is a pseudo random
number from a gaussian distribution with zero mean and SD of one.

TAC data must be in DFT (3) or PMOD format, and it must contain frame start
and end times. TACs are assumed to be decay corrected.

Usage:
  fvar4dat <Datafile> <Pc> <Isotope> <Output file>

Options:
 -S[eed]=<seed for random number generator>
     Computer clock is used by default
 -sec
     If datafile does not contain time unit, times are by default assumed to
     be in minutes. Use this option to set time unit to sec.
 -R=<nr of repeats>
     Specified number of output files (*_NNNN.*) with different set of
     noise are created
 -common=<y|N>
     Common noise SD based on TAC mean is used (y) or not used (n, default)
 -minsd=<SD>
     Set a minimum SD to add a minimum level of noise also to the TAC
     time frames with no activity
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

If the output filename extension is *.sd or *.cv, then noise is not added
but calculated values of SD or CV (for noise) are saved instead.

TAC file format is specified in

References:
1. Chen K, Huang SC, Yu DC. Phys Med Biol 1991;36:1183-1200.
2. Varga J, Szabo Z. J Cereb Blood Flow Metab 2002;22:240-244.
3. http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: var4dat, mvar4dat, wvar4dat, dftstd, avgttac, dft2csv, fvar4img

Keywords: TAC, DFT, noise, simulation

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```
fvar4img 1.3.0  (c) 2003-2012 by Turku PET Centre

Program for adding Gaussian noise to dynamic PET image
using equations (1, 2):
  SD(t) = TAC(t) * sqrt(Pc/(TAC(t)*exp(-lambda*t)*deltat)
  TAC_noisy(t) = TAC(t) + SD(t)*G(0,1) ,
where Pc is the proportionality constant that determines the level,
of noise, TAC(t) is the mean activity concentration in the image frame,
Deltat is the scan frame length, and G(0,1) is a pseudo random
number from a gaussian distribution with zero mean and SD of one.

Image must be in ECAT (6.3 or 7) format, or Analyze 7.5 format with SIF.
Image is assumed to be decay corrected to zero time.

Usage:
  fvar4img [Options] <image file> <Pc> <output image>

Options:
 -seed=<seed for random number generator>
     Computer clock is used by default
 -i=<O-15|N-13|C-11|F-18|Ge-68|Ga-68|Br-76|Rb-82|Cu-62>
     Specifies the isotope
 -minsd=<SD>
     Set a minimum SD to add a minimum level of noise also to the image
     frames with no activity
 -efile=<TAC filename>
     Save image mean TAC and SD that were used in noise simulation
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
     fvar4img -i=C-11 simulated.v 5.0 noisy.v

References:
1. Chen K, Huang SC, Yu DC. Phys Med Biol 1991;36:1183-1200.
2. Varga J, Szabo Z. J Cereb Blood Flow Metab 2002;22:240-244.

See also: dft2img, flo2ecat, eframe, edecay, fvar4dat, ecat2tif

Keywords: image, simulation, noise

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```

```
halflife 1.0.1  (c) 2007,2012 by Turku PET Centre

List the PET isotopes and their half-lives (min) that are identified by
most TPC software.

Usage: halflife [Options] [> Outputfile]

Options:
 -i=<Isotope code>
 -lambda
     Lambda value is listed.
 -sec
     Half-lives are listed in seconds and lambdas 1/sec.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

See also: dftdecay, edecay, dfttime, ecattime

Keywords: physical decay, decay correction, halflife, isotope

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```

heartcor 1.1.0 (c) 2007-2013 by Turku PET Centre

Correction of regional tissue and blood time-activity curves (TACs)
measured with PET for recovery and spillover fractions, and contribution
of blood activity in vascular space (10%) (Henze et al., 1983).
This method works properly, if regions-of-interest (ROIs) are drawn
in the middle of cavity and muscle, excluding the border areas.
Method is valid when cavity radius >> wall thickness and FWHM/2.36.

Command-line parameters:
  1) Datafile that contains at least three columns: sample times and TACs
     of myocardial cavity and myocardium. Corrections based on these TACs
     are applied to any additional TACs in the file; for file format
     see http://www.turkupetcentre.net/analysis/doc/format_dft.html
  2) Name or number of regional TAC representing cavity/blood
  3) Name or number of regional TAC representing whole myocardium
     surrounding cavity
  4) Diameter of cavity (mm)
  5) Myocardial wall thickness (mm)
  6) Image resolution in PET image (FWHM, mm)
  7) Output datafile

Options:
 -Vb=<Vascular volume fraction>
     Set vascular volume fraction (0-0.9) in tissue; by default Vb=0.1
 -sim[ulate]
     Recovery and spillover errors are simulated and added to initially,
     non-affected data, originating from compartment model simulations
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.

Example:
     heartcor s6368dy.dft lv myo 52 10 10 s6368dy_cor.dft

Reference:
1. Henze E, Huang S-C, Ratib O, Hoffman E, Phelps ME, Schelbert HR.
   Measurements of regional tissue and blood-pool radiotracer
   concentrations from serial tomographic images of the heart.
   J Nucl Med. 1983;24:987-996.

See also: fitmbf, patlak, logan, simimyoc

Keywords: myocardium, cavity, spill-over, recovery, modelling, simulation

```
hist4dat 2.1.2  (c) 1996-2012 by Turku PET Centre, University of Turku

Calculate a histogram from all values that are given in an ASCII data
file; file can contain data on one or several lines, separated by
commas and/or spaces. Only point can be used as decimal separator.
Resulting histogram file contains the middle value of bin in first column,
and the proportion (0-1) of values in the bin in the next column
or in several columns when option -s is used.
Program also prints on console the mean, sd, cv, and nr of data points.

Usage:  hist4dat [Options] <Data file> <Histogram file>

Options:
 -b=<Binsize> or -p=<Binsize as % of median>
     Set the bin size using these options; by default, bin size is 20%
     of median.
 -N  Histogram is calculated from normalized data (divided by their mean).
 -d  Nr of values in each bin is written in histogram file; proportion
     of them is written by default.
 -s  Separate histograms for each column (empty values in data file must
     be marked with dots).
 -sf=<File for sorted data>
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: imgpext, epxl2dft, dft2dat, ecat2flo, dft2svg

Keywords: image, pixel, histogram, statistics, simulation

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you are welcome to redistribute it under GNU General Public License.
```

hm4mpa 1.4.0 (c) 2000-2008 by Turku PET Centre

Estimates the brain ACh esterase (AChE) activity (k3) from regional
time-activity concentration curves (TACs) using a reference tissue input
model dedicated to [C-11]MP4A brain PET studies (1).

The model assumptions are:
  1) hydrolysis is irreversible (k4=0)
  2) In reference tissue (striatal or cerebellum region) hydrolysis is very
     rapid (k3>>k2)
  3) Plasma activity can be approximated by mono-exponential function
  4) Hydrolysis is very rapid in plasma (compared to tissue).
Note that because of these assumptions the method cannot be used to analyze
AChE inhibitor studies.

In this method, first a ratio curve (tissue relative to reference tissue)
is calculated. Then a function R(t)=A*exp(-k*t)+B is fitted to the ratio
curve. The k3 is solved from the fitted parameters as k3=(B*k)/(A+B).

Command-line parameters:
  1) Tissue TAC file
  2) Name or number of reference region in tissue file, or name of file
     containing reference tissue TAC
  3) Fit time (in minutes from injection)
  4) Result file (existing file is overwritten)

Options:
 -h or --help
     Print this message and exit
 -svg=<Filename>
     Fitted and calculated ratio curves are plotted in specified file in
     Scalable Vector Graphics (SVG) 1.1 format;
     specification in http://www.w3.org/TR/SVG/
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

Format of the TAC data and result files are specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html and
http://www.turkupetcentre.net/analysis/doc/format_res.html
If tissue TAC file contains weights, those are used in the fitting;
weighting the data is recommended.

Example 1: File b4457.dft contains the TACs of regions-of-interest and
reference region with name PUTAM. The whole time range is used in the fit.
Fits are plotted in file b4457hm.svg.
     hm4mpa -svg=b4457hm.svg b4457.dft putam 999 b4457.res

References:
1. Herholz K, Lercher M, Wienhard K, Bauer B, Lenz O, Heiss W-D.
   PET measurement of cerebral acetylcholine esterase activity without blood
   sampling. Eur J Nucl Med 2001; 28(4):472-477.

See also: dftweigh, dftratio, fit_trtm, r2t_rtcm, rescoll

Keywords: DFT, modelling, reference input, enzyme activity, AChE

```
hrp2sif 1.0.0  (c) 2005 by Turku PET Centre

Makes a scan information file (SIF) based on information in HR+ scan files
(sinograms, *.S) in ECAT 7.x format.

Usage: hrp2sif [Options] <HR+ sinogram file> <SIF file>

e.g.: hrp2sif  meikalainen_234_69d_de7.S  uia02345dy1.sif

Options:
 -h  Print this text and exit.
 -v  Print program build information and exit.
 -test[=<print level>]
     Print more or less details during the process.

See also: cti2sif, dftweigh, sifcat

Keywords: SIF, HR+, scan file, modelling
```

```
hrpcr 1.1.2 (c) 2005-2007 by Turku PET Centre

Convert ECAT HR+ head-curve (.r file), containing countrate (CR) data,
to count-rate (.cr) file format, that is suitable for correction of
time-delay between blood/plasma and tissue TACs.
CR data will be corrected for physical decay.

Usage: hrpcr [Options] <HR+ count-rate filename> <Isotope> [CR filename]

Options:
 -m[in]
     Sample times are written in minutes.
 -s[ec]
     Sample times are written in seconds;
     by default in sec for O-15, O-14, and Rb-82, otherwise in min.
 -c[opy]
     If file is not in original HR+ format, it is still saved with new name.
 -format=<cr|dft>
     File is written in 'count-rate' format with no titles (cr), or,
     with title lines (dft, default)
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.
 -test[=<print level>]
     Print more or less details during the process.

See also: tocr, fitdelay, dftslope, crscale, dft2ps, dftdecay, ecathead

Keywords: ECAT HR+, modelling, time delay, count-rate, head-curve

Note: This program is not updated supported, please use tocr instead!

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you are welcome to redistribute it under GNU General Public License.
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```
htmlfind 0.3.1 (c) 2003-2012 by Turku PET Centre

Program for searching HTML and XHTML code in a specified file or in every
file with extensions *.htm, *.html and *.xhtml that are found under
specified path. Optionally, the (X)HTML code fragment can be changed to
the given text in every place where it is found.

Usage:  htmlfind [Options] <Path or HTML file> <Search text>

Options:
 -replace <Substitute text>
     Search text is replaced by specified text in every instance;
     substitute must not contain certain special characters like '&'
 -replace-from-file <Filename>
     Search text is replaced in every instance by the contents of
     the specified ASCII text file, including new line characters;
     text length must not exceed 2047 characters
 -case[-sensitive]
     Search is case-sensitive. By default, upper-and lowercase letters
     are considered equal
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

Example 1: Command for finding out if and where the specified HTML file
contains HTML code fragment '<a href=':
     htmlfind webpage.html "<a href="

Example 2: Command for replacing a web address with another in all HTML
files which can be found in the current directory and below it:
     htmlfind . www.old.fi -replace www.new.fi

Keywords: HTML, tools

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you are welcome to redistribute it under GNU General Public License.
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```
hypotime 0.1.1  (c) 2009 by Turku PET Centre

Hypotime method (1) for dynamic PET images in ECAT 6.3 or 7.2 format.
This method maps the washout of PET radioligands which are very fast cleared
from circulation, as for example [C-11]WAY-100635.

Parameters:
  1) Dynamic image file
  2) Hypotime image file

Options:
 -thr=<threshold%>
     Pixels with AUC less than (threshold/100 x max AUC) are set to zero.
     Default is 0 %.
 -T=<time>
     By default Hypotime measure is calculated at the end of last PET frame.
     This option can be used to set an earlier time point.
 -dt
     Hypotime measure is divided by T, and then 0.5 is subtracted, resulting
     into image with values between 0.0 (absent washout) and 0.5 (infinitely
     high washout rate).
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

Example:
     hypotime -thr=7 -dt ua2918dy1.v ua2918ht.v

References:
1. Moeller M, Rodell A, Gjedde A. Parametric mapping of 5HT1A receptor
   sites in the human brain with the Hypotime method: theory and normal
   values. J Nucl Med. 2009; 50: 1229-1236.

See also: imgbox, imgshrink, ecat2tif

Keywords: image, modelling, reversible uptake, hypotime method

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```

```
if2e7 2.2.4 (c) 2006 by Turku PET Centre

SYNTAX:
if2e7
      [--version] [-v] [-m] [-x] [-t scanner]
      [-a [anonyName]] [-d dd mm yyyy] [-f f1,..,fn] [-i isotope]
      [-c calibfactor] [-s slicesensfile] [-u units]
      [-r startplane endplane] [-p pixel x0 y0] [-w startframe endframe]
      [-o outfile] [-q maxpixel] interfile_image

The program converts interfile images to ECAT7 format.
The Output images are quantified if there is calibration information available.

-a [anonyName] anonymous. Erases patient information from the output image
               (patient name, ID and birth date). <anonyName> will be
               placed in the 'patient name' filed, if specified.
-c calibfactor factor which scales counts/s to Bq/ml
-d dd mm yyyy  date of scan. Obsolete as it can be taken from the header.
               The date must be in the format dd mm yyyy, e.g. '-d 31 1 1999'
-f f1,..,fn    framing information. Obsolete as it can be taken from the header.
               Frame length of frame 1 to n in sec, numbers are sperated by ','.
               Example: '-f 120,300,300' for 3 frames with 2min, 5min and 5min
-i isotope     Obsolete as it can be taken from the header.
               <isotope> can be 'C-11', 'O-15', 'F-18' 'Ga-68' or 'Ge-68'
-m             multiplies matrix pixel values with <calibFactor>.
               Obsolete as image tools (MEDx, Vinci, YaIT) and the conversion
               program to Analyse format do the calibration internally.
-p pixel x0 y0 reduces the size of the ECAT7 image. This is useful for
               studies, where the outer parts of a plane contain only '0's.
               The new image centre will be at pixel (<x0>/<y0>). The pixel size
               is unchanged. <pixel> is the x-y-dimension of the ECAT7 image.
               Example: '-p 64 128 128' for a 64x64 image cut out of the
               centre of a 256x256 image.
-q maxpixel    set maximal pixel value to specified value.
               Example: '-q 0.015' for recommended 0.015 cnts/s.
-r start end   reduces the number of slices in the ECAT7 image. This is
               useful for studies where most planes contain only '0's.
               <start> is the number of the first plane to take <end> the
               number of the last. (First plane is plane 0)
               Example: '-r 0 9' for the first 10 slices only
-s filename    reads the slice sensitivity values from file <filename>.
               The file has to be an ASCII file with lines 'keyword := value'.
               'calibration factor' and 'efficient factor for plane x', where
               'x' are integers (i.e. plane numbers, starting with plane 0),
               are the only relevant keywords. ';' marks a comment line.
               Example for a slice sensitivity file:
                  ; This is a slice sensitivity file, 3D OSEM, 5 iter, 14 subs

                  ; calibration factor in (Bq/ml)/(counts/s)
                  calibration factor := 6.52630e+06
                  ; plane := value
                  efficient factor for plane 0 := 0.985115
                  efficient factor for plane 1 := 1.01314
-t scanner     sets defaults for several scanner specific fields like plane
               separation, bin size, number of planes etc. and determines
               the kind of interfile format. Options for <scanner> are 'HRRT'.
               If not specified it is taken form the image file name extension;
               '.i' for HRRT.
-u units       data units in the calibrated ECAT7 image.
               Options for <units> are 'Bq/ml', 'kBq/ml' (default) and 'MBq/ml'
-v             verbose mode. Prints useful information to screen.
--version      print build information and exit(0).
-w start end   reduces the number of frames in the ECAT7 image. This is
               useful if one needs only a part of a dynamic study.
               <start> is the number of the first frame to take <end> the
               number of the last. (First frame is frame 1)
               Example: '-w 1 3' for the first 3 frames only
-x             supress all corrections (also decay and duration)
```

Explicit command line switches override the values from the header.

The interfile_image filename is expected to consist of several fields
separated by '_'. The last '.' is the beginning of the file name extension.
HRRT-image filenames have the form RB9999_bla_framex_bla.i. The first field is
expected to be the study name. Dynamic studies must contain a field 'framex'.
The extension for the header is '.i.hdr' (e.g. RB9999_bla_framex_bla.i.hdr).

It is enough to specify one image (frame) in the command line as the programm
looks for all other frames (e.g. RB9999_bla_framex_bla.i).

```
if2e7
      [--version] [-v] [-m] [-x] [-t scanner]
      [-a [anonyName]] [-d dd mm yyyy] [-f f1,..,fn] [-i isotope]
      [-c calibfactor] [-s slicesensfile] [-u units]
      [-r startplane endplane] [-p pixel x0 y0] [-w startframe endframe]
      [-o outfile] [-q maxpixel] interfile_image
```

See also: run_if2e7, e7lmhdr, e7lshdr, e7emhdr

Keywords: Interfile, ECAT7, HRRT

```
iftadd 1.0.1  (c) 2004,2010 by Turku PET Centre

Inserts the items with specified key name from Interfile-type file2 to
file1. If no key names are specified, then all items are copied.
If file1 does not exist, it will be created.

Usage:  iftadd [Options] <file1> <file2> [key1 [key2...]]

Options:
 -ovr
    When key name exists, the key and and its value are replaced
 -nodupl
    When key name exists, the new key and its value are not inserted
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

Example:
     iftadd patname.hdr iea345.hdr patient_name

See also: iftlist, iftdel, iftisval

Keywords: header, IFT, tool

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```

```
iftdel 1.0.1 (c) 2004-2010 by Turku PET Centre

Deletes the items with specified key names from an Interfile-type file.

Usage:  iftdel [Options] <filename> [key1 [key2...]]

Options:
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

Example:
     iftdel iea345.hdr patient_name

See also: iftlist, iftadd, iftisval

Keywords: header, IFT, tool

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```

```
iftisval 1.1.2 (c) 2005-2013 by Turku PET Centre

Check whether specified Interfile-type key and value exist in a text file,
for example:
     CALIBRATED := Yes
Key and value are case-insensitive.
Program returns code 0, if key, and optional value, are found,
code 10, if key is not found, and 11, if key was found but without
matching value.

Usage:  iftisval [options] <filename> [key [value]]

Options:
-lt | -gt | -abs=<limit>
    Values are tested numerically (not as text), to be less (-lt) or
    greater (-gt) than the given value, or the absolute difference is not
    allowed to exceed the specified limit (-abs=<limit>)
-h or --help
    Print this message and exit
-v or --version or --build
    Print software build information and exit
--silent
    Program works silently, printing only warnings and error messages
--verbose
    Program prints more information about what it is doing.

Example 1:
     iftisval iea345ab.kbq calibrated yes
Example 2:
     iftisval -abs=0.02 header.dat halflife 2.05

See also: iftmatch, iftlist, iftadd, reslist, resmatch, dftmatch, imgmatch

Keywords: header, IFT, tool, software testing

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```

```
iftlist 1.0.4  (c) 2004-2011 Turku PET Centre

List on screen the specified or all key names and values in
an Interfile-type file.

Usage:  iftlist [Options] <filename> [key1 [key2...]]

Options:
 -a[ll]
     List all values, also those with no key name
 -value
     Print only the key value(s) without key name(s)
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

Example:
     iftlist iea345.hdr patient_name

See also: iftadd, iftdel, iftisval

Keywords: header, IFT, tool

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```

```
iftmatch 0.2.0 (c) 2013 by Turku PET Centre

Verify that the contents in two IFT files is similar.
By default, all contents (keys and values) are tested, but by specifying
a key, only values of that that key are tested. If the second IFT file
has a different key name, then it can be specified as the second key name.

IFT files are text files with key and (optional) value at each line,
for example:
   calibrated := yes
   calibration_coefficient := 6.78901E-005

Key and value strings are case-insensitive. Lines may be in any order,
except that if more than one key instances are found, the order of the
values must be the same.

Program returns 0, if match is found, 1-9 in case of an error, or
10, if matching key or value is not found.

Usage:  iftmatch [options] <filename1> <filename2> [key [key2]]

Options:
-lt | -gt | -abs=<limit>
    Values in file 1 and 2 are tested numerically (not as text), to be less
    (-lt) or greater (-gt) in file 1 than in file 2, or the absolute
    difference is not allowed to exceed the specified limit (-abs=<limit>)
--help
    Print this message and exit
--version or --build
    Print software build information and exit
--silent
    Program works silently, printing only warnings and error messages
--verbose
    Program prints more information about what it is doing.

Example 2:
     iftmatch data1.ift data2.ift
Example 2:
     iftmatch iea345header.txt validheader.txt calibrated
Example 3:
     iftmatch -abs=0.02 iea345hdr.txt validhdr.txt halflife
Example 4:
     iftmatch -abs=0.02 iea345hdr.txt validhdr.txt half-life halflife

See also: iftisval, reslist, dftlist, lmhdr, resmatch, iftlist

Keywords: IFT, tool, software testing

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```

```
img2cube 0.1.1  (c) 2010,2012 by Turku PET Centre

Resamples PET image to a cube with equal 3D dimensions of each voxel
and equal dimensions in image volume. Note that some smoothing occurs in
the process, and currently the use of should be limited to making
illustrations of image data.
By default (if <new dim> is set to 0) the highest dimension in original
image is used.

Usage:
  img2cube [options] <image file> <new dim> <slice image file>

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: imgslim, esplit, imgshrink, imgbox, imgslice, e7vplavg, ecat2tif

Keywords: image processing, ECAT, tool

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```
img2dft 4.1.3  (c) 1996-2013 by Turku PET Centre

Calculates regional time-radioactivity concentration curves (TACs) from
a PET image in ECAT 6.3, ECAT 7.x, or Analyze 7.5 format, when
regions-of-interests (ROIs) are given in ECAT 6.3 format ROI files (1) or
as mask image. Regional TACs are written in output file in DFT format (2).
If filename for output file is not specified, it will be saved in the
default path replacing the extension of image filename with '.dft'.

Note that versions 4.x and after apply image upscaling for selecting
pixels inside ROIs; this might lead to smaller ROI volumes and therefore
affect also the ROI averages and variances.

Usage:  img2dft [Options] <Image> <ROI file(s) or Mask image> [Output file]

Options:
 -P[=<planes>]
      Calculate all ROIs on all planes, or on specified plane;
      by default, ROIs are calculated only on planes where they were drawn.
      Effective only with ROI files.
 -V[=<sd|cv>]
      Calculates also the variances inside ROI(s) and saves those in
      a *.var file. With options -Vsd and -Vcv standard deviation or
      coefficient of variation (%) is calculated and saved as *.sd or *.cv
      file, respectively.
      Effective only with ROI files.
 -tm  Write time frame mid times instead of start and end times.
 -median
      Calculates ROI median instead of ROI average.
      Effective only with ROI files.
 -lms Calculates least median of squares estimate instead of ROI average.
      Effective only with ROI files.
 -lts Calculates least trimmed square estimate instead of ROI average.
      Effective only with ROI files.
 -h or --help
      Print this message and exit.
 --version or --build
      Print software build information and exit.
 --silent
      Program works silently, printing only error and warning messages.
 --verbose
      Program prints more information about what it is doing.

Options -median, -lms and -lts can only be used for parametric images.

Example 1:
      img2dft a1204dy1.img a1204*.roi a1204dy1.dft
Example 2:
      img2dft -P=4,6,8,10 us4321dy1.img us4321*.roi
Example 3:
      img2dft -V=sd uo286suv.v uo286*.roi
Example 4:
      img2dft uo286suv.v uo286mask.v

References:
1. http://www.turkupetcentre.net/analysis/doc/format_roi.html
2. http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: roilist, lmlist, eroi2img, roipxl, ecatthrs, dft2csv, dft2res

Keywords: image, ROI, mask, ECAT, TAC, analysis, modelling

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you are welcome to redistribute it under GNU General Public License.
```

```
imgafind 0.0.1  (c) 2009 by Turku PET Centre

Trial program to find the locations of arteries in dynamic PET image.

Usage: imgafind <Image file> <Template image>

Options:
 -peak=<filename>
     Pixel peak values are saved as image
 -time=<filename>
     Pixel peak times are saved as image
 -ratio=<filename>
     Pixel peak value/time ratios are saved as image
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

See also: eabaort, ecatthrs, eflexseg, imgdysmo

Keywords: image, input, blood, aorta

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```
imgbfbp 0.6.10  (c) 2003-2014 by Turku PET Centre

Computation of parametric images of binding potential (BPnd) from
dynamic PET images in ECAT, NIfTI, or Analyze format applying simplified
reference tissue model (SRTM) [1]. The model is solved using the basis
function approach [2], similar to the RPM program.
Note that default limits for theta3 are suitable for [C-11]raclopride;
for other tracers the limits need to be set using command-line options.
Parameters:
  1) Dynamic image file (corrected for decay)
  2) Reference region TAC file (times in minutes!)
  3) Parametric BP image file
  4) SIF file (optional)

Example:
     imgbfbp ua2918dy1.v ua2918cer.dft ua2918bp.v

Options:
 -R1=<filename>
     Programs computes also an R1 image
 -k2=<filename>
     Programs computes also a k2 image
 -min=<value (1/min)>
     Set minimum value for theta3; it must be >= k2min/(1+BPmax)+lambda.
     Default is 0.06 min-1. Lambda for F-18 is 0.0063 and for C-11 0.034.
 -max=<value (1/min)>
     Set maximum value for theta3; it must be <= k2max+lambda.
     Default is 0.60 min-1.
 -nr=<value>
     Set number of basis functions; default is 500, minimum 100.
 -bf=<filename>
     Basis function curves are written in specified file.
 -wss=<filename>
     Weighted sum-of-squares are written in specified image file.
 -err=<filename>
     Pixels with their theta3 in its min or max value are written
     in the specified imagefile with values 1 and 2, respectively,
     others with value 0.
 -thr=<threshold%>
     Pixels with AUC less than (threshold/100 x ref AUC) are set to zero;
     default is 0%
 -DVR
     Instead of BP, program saves the DVR (=BP+1) values.
 -noneg
     Pixels with negative BP values are set to zero.
 -end=<Fit end time (min)>
     Use data from 0 to end time; by default, model is fitted to all frames.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Fit is always weighted, either based on the counts in SIF provided by
user, or if SIF is not provided, then weights are estimated based on
mean radioactivity concentration in the dynamic image, and estimated SIF
is written with default filename.

References:
1. Lammertsma AA, Hume SP. Simplified reference tissue model for PET
   receptor studies. NeuroImage 1996;4:153-158.
2. Gunn RN, Lammertsma AA, Hume SP, Cunningham VJ. Parametric imaging of
   ligand-receptor binding in PET using a simplified reference region
   model. NeuroImage 1997;6:279-287.
```

See also: ecatunit, eframe, cti2sif, dftweigh, edecay, ecat2tif, regbfbp

Keywords: image, modelling, binding potential, basis function method

```
imgbfh2o 0.2.0  (c) 2013 by Turku PET Centre

Estimation of rate constants K1, k2 and Va from dynamic PET image in
ECAT 6.3, ECAT 7.x, NIfTI-1, or Analyze 7.5 file format using
one-tissue compartment model (1), solved using the basis function
approach (2, 3).

When applied to dynamic [O-15]H2O studies, the resulting K1 image
equals perfusion (blood flow) image. K1 image can be divided by tissue
density (g/mL) (option -density) and multiplied by 100 (option -dl)
to achieve the blood flow image in units (mL blood)/((100 g tissue) * min).

When applied to dynamic [O-15]O2 brain studies, the resulting K1 image
can be converted to oxygen consumption image by multiplying it by
arterial oxygen concentration [4] (ml O2 / dL blood) to get the
parametric image in units mL O2 / ((100 ml tissue) * min).
The model assumptions hold only when oxygen consumption is 1-6.7
ml O2/(100g * min) and fit time is set to 300 s or less [4].

Parameters:
  1) Blood TAC file (corrected for decay and delay, times in seconds!)
  2) Dynamic image file (corrected for decay)
  3) Fit time (s)
  4) Parametric K1 (flow) image file

General options:
 -ml or -dl
     Units in flow and Va images will be given per mL or per dL,
     respectively. By default, units are per mL.
 -density[=<value>]
     With option -density the flow is calculated per gram or 100g tissue.
     Tissue density can be changed from the default 1.04 g/ml.
 -Vd=<filename>
     Parametric K1/k2 (Vd, apparent p) image is saved.
 -k2=<filename>
     Parametric k2 image is saved; in some situations perfusion calculation
     from k2 can be more accurate than the default assumption of f=K1.
     Perfusion can be calculated from k2 using equation f=k2*pH2O, where
     pH2O is the physiological partiton coefficient of water in tissue.
 -Va=<filename>
     Parametric Va image is saved.
     Set -Va=0, if Va=0 is assumed (pre-corrected); otherwise Va is fitted.
 -wss=<filename>
     Weighted sum-of-squares are written in specified image file.
 -thr=<threshold%>
     Pixels with AUC less than (threshold/100 x input AUC) are set to zero;
     default is 0%
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Options for setting basis functions:
 -k2min=<Min k2> and -k2max=<Max k2>
     Enter the minimum and maximum k2 in units ml/(ml*min).
 -fmin=<Min K1> and -fmax=<Max K1>
     Enter the minimum and maximum perfusion value; defaults are
     0.005 and 4.0 ml/(ml*min), respectively.
 -pmin=<Min p> and -max=<pmax>
     Enter the minimum and maximum value for apparent partition coefficient
     for water; defaults are 0.3 and 1.0 ml/ml, respectively.
 -nr=<value>
     Set number of basis functions; default is 500, minimum 100.
```

```
 -bf=<filename>
     Basis function curves are written in specified file.
 -err=<filename>
     Pixels with their k2 in its min or max value (calculated from min and
     max K1 and p values) in the specified imagefile with values 1 and 2,
     respectively, others with value 0.

Example 1. Calculation of perfusion and arterial blood volume image,
           stopping fit at 180 s:
  imgbfh2o -Va=s2345va.img s2345abfit.kbq s2345dy1.v 180 s2345flow.v

By default, the units of pixel values in the blood flow (K1) image is
(mL blood)/((mL tissue) * min), in Vd image (mL blood)/(mL tissue),
in k2 image 1/min, and in Va image (mL blood/mL tissue),
but the blood flow and Va units can be changed with above listed options.

References:
1. Lammertsma AA, Jones T. J Cereb Blood Flow Metab. 1983;3:416-424.
2. Gunn RN et al. NeuroImage 1997;6:279-287.
3. Boellaard R et al. Mol Imaging Biol. 2005;7:273-285.
4. Ohta S, et al. J Cereb Blood Flow Metab. 1992;12:179-192.

See also: imgflow, arlkup, regbfh2o, fit_h2o, ecatunit, fitdelay, imgcbv

Keywords: image, modelling, perfusion, radiowater, basis function method

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```

```
imgbkg 1.2.1  (c) 2002-2012 by Turku PET Centre

Subtracts the background radioactivity from a dynamic PET image
using the last time frame of an image scanned before new injection,
assuming that tracer concentration from the 1st scan does not change
after the last frame. Physical decay is corrected according to scan
start and frame times.
Different branching ratio between isotopes is corrected for a few common
PET isotopes.
ECAT 6.3 and 7.2 image formats are supported.
Image data must be decay corrected to scan start times.

Usage:
  imgbkg [Options] <Image file> <Background image> <Result image>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: edecay, ecatcalc, lmhdr, egetstrt, esetstrt, ecathead

Keywords: image, ECAT, background, tool

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```

imgbound 1.2.0 (c) 2003,2005 by Turku PET Centre

Subtraction of reference region TAC from dynamic PET image in
ECAT 6.3 or 7.x 2D format.
Main use is in the analysis of [F-18]FDOPA studies prior to the multiple
time graphical analysis (MTGA) with plasma input.

Parameters:
  1) Dynamic image file
  2) Output image file
  3) Reference region TAC file
  4) Reference region name, if file contains more than one TAC

e.g.: imgbound ua2618dy1.img ua2618dy1_spec.img ua2618dy1.dft 'cer avg'

Note that the reference region TAC and dynamic image must have exactly same
time frames.

See also: imgki, ecatcalc, imgratio

Keywords: image, modelling, specific uptake

```
imgbox 0.1.4  (c) 2009-2013 by Turku PET Centre

Extracts a box-like volume of 3D/4D PET image.
Image is processed frame-by-frame, thus it can process even large files.
Note that no backup is made of any previous output file.

Usage: imgbox <Image file> [<Volume definition file> <Output image file>]

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Volume definition file is an ASCII text file, which containts pixel
coordinates (x y z; 1..dimension) of the two opposite corners of
the extracted image volume, for example:
     corner1 := 63 57 26
     corner2 := 84 71 44
If only input image filename is given, then program prints the image
dimensions.

See also: imgslim, esplit, e7vplavg, imgshrink, epxl2dft, eroi2img

Keywords: image processing, tool, modelling

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```
imgcbv 0.3.2  (c) 2004-2013 by Turku PET Centre

Subtraction of the contribution of vascular radioactivity from dynamic PET
image. Vascular volume fraction Vb can be given as a single value
that is common to all image pixels, or as separate value for each image
pixel in a (smoothed) Vb image, usually calculated from a [O-15]CO study.

Parameters:
  1) Dynamic image file (corrected for decay)
  2) Blood TAC file (times in minutes)
  3) Vb value or Vb image file (fraction, not percentage)
  4) Output image file

Options:
 -p or -t
     Equation Ct=Cpet-Vb*Cb (-P, default), or Ct=(Cpet-Vb*Cb)/(1-Vb) (-T)
     is applied in the correction
 -n
     Negative TAC values are preserved; by default those are set to zero
 -bl=<Output filename for blood TAC>
     If datafile for blood TAC interpolated to PET frame times is needed
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

Example 1: Vascular volume fraction in all tissue is assumed to be 0.04:
     imgcbv ua2918dy1.img ua2918ab.kbq 0.04 ua2918cbv.img
Example 2: Vascular volume fraction is given in specific image file:
     imgcbv ua2918dy1.v ua2918ab.kbq ua2918vb.v ua2918cbv.v

See also: dftcbv, ecatcalc, p2blood, ecatunit, dftunit, imgmax

Keywords: image, modelling, vascular fraction

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```

imgckin 0.1.0 (c) 2009 by Turku PET Centre

Compares kinetics of time-activity curves (TACs) between given TAC and
pixels in PET image.
First, each image pixel TAC is scaled to the same AUC as given TAC;
then similarity between TACs is determined with runs test (1);
if p<0.05, then TAC kinetics are significantly different, but if p is
close to 1, they are similar.

Parameters:
  1) Dynamic PET image file
  2) Reference TAC file
  3) Lower limit for AUC scale difference (image/reference)
  4) Upper limit for AUC scale difference
  5) Runs test p image file

Options:
 -h, --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints lots of information about what it is doing.

Example:
     imgckin ua2918dy1.v ua2918cer.dft 0.5 10 ua2918rt.v

References:
1. Cobelli C, Forster D, Toffolo G. Tracer Kinetics in Biomedical
   Research: From Data to Model. Kluwer Academic Publishers, 2002.

See also: dftrunst, imginteg, ecatcalc, ecatthrs, ecat2tif

Keywords: image, modelling, input, runs test

```
imgcorrl 0.2.4  (c) 2005,2007 by Turku PET Centre

Calculation of correlation between two (parametric) PET images in
ECAT 6.3 or ECAT 7 format.

Usage:
  imgcorrl [Options] <Image #1> <Image #2> <Result file>

e.g.: imgcorrl  ua2918dvr.img  ua2918bp.img  ua2918cor.res

Options:
 -diff
     Difference between pixel values (#2 - #1) is compared to the mean,
     as suggested by Bland & Altman (1)
 -resid=<filename>
     Residuals (predicted_image2 - image2) are calculated for each pixel,
     then forced in between -restr*SD and +restr*SD, and saved in
     specified file in the same format as image1 (2)
 -scaled
     Residuals are scaled to 0-100
 -pred=<filename>
     predicted_image2 is saved in specified file
 -restr=<limit>
     Restriction limits for residuals can be changed with this option;
     By default, restr=2.0
 -L1=<lower limit>
     Pixels whose values in image #1 are less than limit are excluded
     from correlation
 -L2=<lower limit>
     Pixels whose values in image #2 are less than limit are excluded
     from correlation
 -lowthr=<lower threshold%>
     Set lower cut-off threshold (percent of maximum)
 -upthr=<upper threshold%>
     Set upper cut-off threshold (percent of maximum)
 -f1=<frame>
     If image #1 contains more than one time frame, the frame used in
     correlation can be specified with this option; 1 by default
 -f2=<frame>
     If image #2 contains more than one time frame, the frame used in
     correlation can be specified with this option; 1 by default
 -pf=<filename>
     Pixel values are written in ASCII file as two columns for plotting
     with other software. Warning: file may be too large for most programs
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

References:
1. Bland JM, Altman DG. Statistical methods for assessing agreement
   between two methods of clinical measurement. Lancet 1986; i: 307-310.
2. Naum A, Oikonen V, Sundell J, Engblom E, Koistinen J, Ylitalo A,
   Någren K, Airaksinen J, Iozzo P, Nuutila P, Knuuti J. Additional Visual
   Analysis Tool (AVAT) in PET imaging. (manuscript).

See also: ecat2flo, imgpext, rescoll, imgshrink, e7vplavg, ecatcalc, ecat2tif

Keywords: image, modelling, correlation, residual, linear regression

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```

```
imgdv 1.3.5  (c) 2003-2013 by Turku PET Centre

Estimation of distribution volume (Vt) or distribution volume ratio (DVR)
from dynamic PET images in ECAT 6.3, 7.x, NIfTI-1, or Analyze 7.5 format,
applying model independent graphical analysis approach of Logan et al
[1, 2, 3] for reversible tracer uptake or binding.
Simple non-iterative perpendicular line fitting algorithm [4] is applied
in determination of the slope of the Logan plot.

Parameters:
  1) Input file (Plasma or Reference region TAC; times in minutes)
  2) Dynamic image file
  3) Linear fit start time (0 for automatic determination)
  4) Parametric image file

Options:
 -k2=<k2 of reference region>
     With reference region input it may be necessary to specify also the
     population average for reference region k2 [2]
 -Thr=<threshold%>
     Pixels with AUC less than (threshold/100 x max AUC) are set to zero.
     Default is 0 %
 -max=<Max value>
     Upper limit for Vt or DVR values; by default set pixel-wise
     to 10x the AUC ratio.
 -min=<Min value>
     Lower limit for Vt or DVR values; 0 by default.
 -F  Remove parametric pixel values that are over 4x higher than
     their closest neighbours.
 -E=<Fit end time (min)>
     Never use data after fit end time.
 -V=<filename>
     Y axis intercepts times -1 are written as an image in specified file.
 -N=<filename>
     Numbers of selected plot data points are written as an image.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example:
     imgdv ua3818ap.kbq ua3818dy1.v 20 ua3818dv.v

The unit of pixel values in the parametric Vt image is
(mL plasma)/(mL tissue), and DVR images are unitless.

In theory, DVR equals BP+1, and therefore a binding potential image can
be computed from DVR image by subtraction of unity, e.g. using program
ecatcalc. However, this may lead to a large number of pixels with negative
values that may hamper the further statistical or visual analysis.

References:
1. Logan J, Fowler JS, Volkow ND, Wolf AP, Dewey SL, Schlyer DJ,
   MacGregor RR, Hitzemann R, Bendriem B, Gatley SJ, Christman DR.
   Graphical analysis of reversible radioligand binding from time-activity
   measurements applied to [N-11C-methyl]-(-)-cocaine PET studies in human
   subjects. J Cereb Blood Flow Metab 1990; 10: 740-747.
2. Logan J, Fowler JS, Volkow ND, Wang GJ, Ding YS, Alexoff DL.
   Distribution volume ratios without blood sampling from graphical
   analysis of PET data. J Cereb Blood Flow Metab. 1996; 16: 834-840.
3. Logan J. Graphical analysis of PET data applied to reversible and
   irreversible tracers. Nucl Med Biol 2000; 27:661-670.
4. Varga J & Szabo Z. Modified regression model for the Logan plot.
```

J Cereb Blood Flow Metab 2002; 22:240-244.

See also: imgbfbp, imglhdv, ecat2tif, logan

Keywords: image, modelling, distribution volume

```
imgdysmo 1.4.0  (c) 2003-2009 by Turku PET Centre

Smoothing of dynamic PET images in ECAT 6.3 and 7 format.
Replaces pixel TACs with an average TAC of up to 5x5x5 neighbouring pixels
which are selected based on the MRL (maximum run length) and AUC difference.

Usage:
  imgdysmo [Options] <dynamic img> <smoothed image>

Example:
  imgdysmo  b00123dy1.img  b00123dy1smoothed.img

Options:
 -m=<3|5>
     Set filter mask to 3x3x3 or 5x5x5 pixels (default)
 -s=<1|2|3|4|5>
     Set smoothing strength: 1=min, 2=default, 5=max
 -a=<nr>
     Set the nr of pixels to average inside smoothing mask;
     by default this is set automatically based on the mask size
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

Note that before application, the quantitativity of the regional results
must be validated using appropriate material from similar PET studies.

See also: ecatthrs, ebkgrm, eflexseg, fvar4img

Keywords: ECAT, image, smoothing, modelling

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```

```
imgfiltg 0.4.0  (c) 2006-2013 by Turku PET Centre

Program for applying 2D or 3D Gaussian filter for a static or dynamic PET
image (ECAT 6.3, 7.x or Analyze 7.5 format).
SD of Gaussian filter must be specified by user, and SD=FWHM/2.355.
2D convolution is slow in case of large image and large filter size,
but more accurate than fast 2D and 3D algorithms.

Command line arguments:
  1) dynamic PET image file
  2) Gaussian filtered image file
  3) SD of Gaussian filter (by default in pixels; see below)

Options:
 -method=<<2D>|<fast2D>|<fast3D>>
     Specify the Gaussian filtering method; default is the 2D convolution
     method which is slow but accurate; fast2D is a less accurate but fast
     2D Gaussian convolution algorithm with IIR approximation;
     fast3d is 3D Gaussian convolution algorithm with IIR approximation.
 -border=<fill|zero>
     Image is extrapolated symmetrically before smoothing (fill, default),
     or data outside image borders is assumed to be zeroes (zero).
     Applies only to 2D method.
 -fsize=<filter size>[pxl|mm|cm]
     Size of filter kernel, by default 6*SD; size can be be given in pixels
     (default), mm, or cm. Final size in pixels will be automatically
     changed to the next odd number.
     Applies only to 2D method.
 -steps=<nr>
     More steps provides better accuracy but longer execution time;
     default is 4. Applies only to fast2D and fast3D methods.
 -pixelsize=<value>
     Set image pixel size (mm), if missing or wrong in image data.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example #1a: Gaussian SD in pixels
  imgfiltg s5998dy1.v s5998dy1_filt.v 6pxl
Example #1b: Gaussian with SD of 6 millimeters and 40 mm filter size
  imgfiltg -fsize=40mm s5998dy1.v s5998dy1_filt.v 6mm

See also: imgdysmo, eflexseg, ecatthrs, ebkgrm, fvar4img, prfpeak, fitprfs

Keywords: image, gaussian, filter, FWHM

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```

```
imgflow 0.8.10  (c) 2003-2013 by Turku PET Centre

Estimation of rate constants K1, k2 and Va from dynamic PET image in
ECAT 6.3, ECAT 7.x, NIfTI-1, or Analyze 7.5 file format using
linearized two-compartment model [1].
Lawson-Hanson non-negative least squares (NNLS) [2] are used to solve
general linear least squares functions.

When applied to dynamic [O-15]H2O studies, the resulting K1 image
equals perfusion (blood flow) image. K1 image can be divided by tissue
density (g/mL) (option -density) and multiplied by 100 (option -dl)
to achieve the blood flow image in units (mL blood)/((100 g tissue) * min).

When applied to dynamic [O-15]O2 brain studies, the resulting K1 image
can be converted to oxygen consumption image by multiplying it by
arterial oxygen concentration [3] (ml O2 / dL blood) to get the
parametric image in units mL O2 / ((100 ml tissue) * min).
The model assumptions hold only when oxygen consumption is 1-6.7
ml O2/(100g * min) and fit time is set to 300 s or less [3].

Parameters:
  1) Blood TAC file (corrected for decay and delay, times in seconds!)
  2) Dynamic image file
  3) Fit time (s)
  4) Parametric K1 (flow) image file

Options:
 -k2=<filename>
     Parametric k2 image is saved; in some situations perfusion calculation
     from k2 can be more accurate than the default assumption of f=K1.
     Perfusion can be calculated from k2 using equation f=k2*pH2O, where
     pH2O is the physiological partiton coefficient of water in tissue.
 -Va=<filename>
     Parametric Va image is saved.
     Set -Va=0, if Va=0 is assumed; otherwise Va is always fitted.
 -Vd=<filename>
     Parametric K1/k2 image (apparent pH2O) is saved.
 -thr=<threshold%>
     Pixels with AUC less than (threshold/100 x max AUC) are set to zero.
     Default is 5%.
 -max=<Max value>
     Upper limit for flow values in final units.
 -filter
     Remove parametric pixel values that are over 4x higher than
     their closest neighbours.
 -noneg
     Pixels where K1 estimates are negative are fitted again with
     constraint Va=0.
 -ml or -dl
     Units in flow and Va images will be given per mL or per dL,
     respectively. By default, units are per mL.
 -density[=<value>]
     With option -density the flow is calculated per gram or 100g tissue.
     Tissue density can be changed from the default 1.04 g/ml.
 -h or --help
     Print this message and exit.
 -v, --version, or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only warnings and error messages.
 --verbose
     Program prints more information about what it is doing.

By default, the units of pixel values in the flow (K1) image is
(mL blood)/((mL tissue) * min), in DV image (mL blood)/(mL tissue),
in k2 image 1/min, and in Va image (mL blood/mL tissue),
but the flow and Va units can be changed with above listed options.
```

Example 1. Calculation of perfusion and arterial blood volume image,
stopping fit at 180 s:

```
imgflow -Va=s2345va.v s2345abfit.kbq s2345dy1.v 180 s2345flow.v
```

Example 2. Dynamic image is precorrected for vascular activity,
and all available data is used:

```
imgflow -Va=0 s2345abfit.kbq s2345dy1_vacorr.v 9999 s2345flow.v
```

References:

1. Blomqvist G. On the construction of functional maps in positron emission tomography. J Cereb Blood Flow Metab. 1984;4:629-632.
2. Lawson CL & Hanson RJ. Solving least squares problems. Prentice-Hall, 1974.
3. Ohta S, Meyer E, Thompson CJ, Gjedde A. Oxygen consumption of the living human brain measured after a single inhalation of positron emitting oxygen. J Cereb Blood Flow Metab. 1992;12:179-192.

See also: imgbfh2o, imgcbv, fit_h2o, b2t_h2o, imglhdv, fitdelay, eabaort

Keywords: image, modelling, perfusion, blood flow, radiowater

```
imgform 0.1.1  (c) 2012,2013 by Turku PET Centre

Determines the format and type of PET image file. Information is written
on stdout, or in a file if filename for that is given by user.

File format is also returned as exit code. Exit code is 0 if format was not
identified and <0 in case of an error.

Usage:  imgform [Options] <Image file> [Filename for information]

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit

See also: lmhdr, nii_lhdr, ana_lhdr, e63to7, ana2ecat, upet2e7, nii2ecat

Keywords: image, file format

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```

```
imgfur 1.0.3  (c) 2007-2012 by Turku PET Centre

Calculation of Fractional Uptake Rate (FUR) or FUR-based Metabolic Rate (MR)
image from static or dynamic PET image in ECAT 6.3 or 7.2 format.
Information on FUR in:
http://www.turkupetcentre.net/modelling/methods/fur.html

Parameters:
  1) Input file (Plasma TAC)
  2) PET image file
  3-4) FUR calculation start and stop time (min);
     set both to zero to use the whole time range from PET image data
  5) FUR or MR image file

Options for calculation of metabolic rate:
 -Ca=<value>
     Concentration of native substrate in arterial plasma (mM),
     for example plasma glucose in [18F]FDG studies.
     With this option the metabolic rate (umol/(min*100 g)) is calculated.
 -LC=<value>
     Lumped Constant in MR calculation; default is 1.0.
 -density=<value>
     Tissue density in MR calculation; default is 1.0 g/ml.

General options:
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1. Calculation of FUR image from a dynamic image from 45 to 60 min:
     imgfur ua2918ap.kbq ua2918dy1.v 45 60 ua2918fur.v

Example 2. Calculation of glucose uptake image, when tissue density is 1.04,
plasma glucose concentration is 5.2 mM, lumped constant is 0.52, from
a static (one frame) image:
     imgfur -density=1.04 -Ca=5.2 -LC=0.52 a864ap.kbq a864dy1.v 0 0 a864mrglu.v

Format of the plasma data file is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

The unit of pixel values in the FUR image is
(mL plasma)/(min*(mL tissue)) by default, and umol/(min*100 g) in metabolic
rate image.

See also: imgki, imginteg, ecatcalc, ecattime, ecat2tif, regfur

Keywords: image, modelling, FUR, retention index, irreversible uptake

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```

```
imginteg 1.3.3  (c) 2005-2013 by Turku PET Centre

Calculation of an AUC (integral over time) image from PET image
in ECAT 6.3, 7.x, NIfTI-1, or Analyze 7.5 format.
Analyze and NIfTI image must have SIF in the same folder.
In case of static image, the matrix values are simply multiplied by the
frame duration.
The pixel values of resulting integral image will be in units of
radioactivity concentration times sec.

Command line arguments:
  1) PET image
  2) AUC calculation start time (sec)
  3) AUC calculation duration (sec)
  4) AUC image file

Options:
 -avg
     Average during specified range is calculated instead of AUC
 -min
     AUC times are given in minutes instead of seconds
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Program will automatically set the integration start time or duration
based on the time range in the image, if either is set to zero.

Example 1: calculate integral image between 32 and 302 seconds after
scan start with command
  imginteg s5998dy1.v 32 270 s5998int.v

Example 2: integrate a static or dynamic image from the start time of
the first frame to the end of the last frame:
  imginteg a773dy1.v 0 0 a773int.v

Example 3: integrate a dynamic image from 600 seconds to the end of
the last frame:
  imginteg a773dy1.v 600 0 a773int.v

See also: ecatunit, ecattime, ecatsum, ecatcalc, imgratio, ecatlkup

Keywords: image, modelling, autoradiography, perfusion, SUV

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```
imgki 1.5.6  (c) 2003-2012 by Turku PET Centre

Estimation of influx constant (Ki) from dynamic PET images in ECAT 6.3
or 7.2 format applying multiple time graphical analysis (MTGA) approach of
Gjedde [1] and Patlak & Blasberg [2, 3] for irreversible tracer uptake.
Simple non-iterative perpendicular line fitting algorithm [4] is applied.

Parameters:
  1) Input file (Plasma or Reference region TAC; times in minutes)
  2) Dynamic image file
  3) Linear fit start time in minutes (0 for automatic determination)
  4) Parametric image file

Options:
 -Ca=<value>
     Concentration of native substrate in arterial plasma (mM),
     e.g. glucose in [18F]FDG studies.
     With this option the metabolic rate (umol/(min*100 g)) is calculated.
 -LC=<value>
     Lumped Constant; default is 0.52.
     This or default LC is used in calculation of metabolic rate.
 -density=<value>
     Tissue density; default is 1.04 g/ml.
     This or default density is used only in calculation of metabolic rate.
 -thr=<threshold%>
     Pixels with AUC less than (threshold/100 x max AUC) are set to zero.
     Default is 0 %.
 -max=<Max value>
     Upper limit for Ki values.
 -filter
     Remove parametric pixel values that are over 4x higher than
     their closest neighbours.
 -end=<Fit end time (min)>
     Never use data after fit end time.
 -v=<filename>
     Y axis intercepts are written as an image in specified file.
 -n=<filename>
     Numbers of selected plot data points are written as an image.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

Example 1. Calculation of Ki image, starting linear fit from 20 minutes:
     imgki ua2918ap.kbq ua2918dy1.v 20 ua2918ki.v

Example 2. Calculation of glucose uptake image, when tissue density is 1.02,
           plasma glucose concentration is 5.2 mM, lumped constant is 1.0,
           starting linear fit from 10 minutes after radiotracer injection:
     imgki -density=1.02 -Ca=5.2 -LC=1.0 s8642ap.kbq s8642dy1.v 10 s8642ki.v

Format of the input data file is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

The unit of pixel values in the parametric (Ki) image is
(mL plasma)/(min*(mL tissue)) by default, and umol/(min*100 g) in metabolic
rate image.

To calculate Ki images from [18F]FDOPA studies with plasma input:
subtract reference region TAC from dynamic image before using this program.

References:
1. Gjedde A. Calculation of cerebral glucose phosphorylation from brain
   uptake of glucose analogs in vivo: a re-examination. Brain Res. 1982;
   257:237-274.
```

2. Patlak CS, Blasberg RG, Fenstermacher JD. Graphical evaluation of blood-to-brain transfer constants from multiple-time uptake data. J Cereb Blood Flow Metab 1983;3:1-7.
3. Patlak CS, Blasberg RG. Graphical evaluation of blood-to-brain transfer constants from multiple-time uptake data. Generalizations J Cereb Blood Flow Metab 1985;5:584-590.
4. Varga J & Szabo Z. Modified regression model for the Logan plot. J Cereb Blood Flow Metab 2002; 22:240-244.

See also: imgfur, imgbound, imglhki, ecat2tif, patlak

Keywords: image, modelling, irreversible uptake, metabolic rate

```
imglhdv 1.4.3  (c) 2002-2012 by Turku PET Centre

Estimation of distribution volume (DV) from dynamic PET images in
ECAT 6.3 or 7.x format applying Lawson-Hanson non-negative least squares
(NNLS) [1] to solve general linear least squares functions.
DV is estimated directly without division from one- or two-tissue
compartment model [2,3,4].

Parameters:
  1) Plasma file (times in minutes!)
  2) Dynamic image file
  3) Parametric image file

e.g.: imglhdv  ua2918ap.kbq  ua2918dy1.v  ua2918dv.v

Options for model selection:
 -A  Automatic selection of model for separate pixels
 -1  Force one-tissue compartment model for all pixels
 -2  Force two-tissue compartment model for all pixels
 -0  Akaike weighted average of 1- and 2-tissue
     compartment model results [5,6] (default)
 -M  Selected model is written as second 'frame' in the parametric image.

Other command line options:
 -T=<threshold%>
     Pixels with AUC less than (threshold/100 x plasma AUC) are set to zero.
     default is 0%
 -E=<Fit end time (min)>
     Use data from 0 to end time; by default, model is fitted to all frames.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

The unit of pixel values in the DV image is (ml blood)/(ml tissue).

References:
1. Lawson CL & Hanson RJ. Solving least squares problems.
   Prentice-Hall, 1974.
2. Zhou Y, Brasic J, Endres CJ, Kuwabara H, Kimes A, Contoreggi C, Maini A,
   Ernst M, Wong DF. Binding potential image based statistical mapping for
   detection of dopamine release by [11C]raclopride dynamic PET.
   NeuroImage 2002;16(3):S91.
3. Zhou Y, Brasic JR, Ye W, Dogan AS, Hilton J, Singer HS, Wong DF.
   Quantification of cerebral serotonin binding in normal controls and
   subjects with Tourette's syndrome using [11C]MDL 100,907 and
   (+)[11C]McN 5652 dynamic PET with parametric imaging approach.
   NeuroImage 2004;22(Suppl 2):T98.
4. Hagelberg N, Aalto S, Kajander J, Oikonen V, Hinkka S, Någren K,
   Hietala J, Scheinin H. Alfentanil increases cortical dopamine D2/D3
   receptor binding in healthy subjects. Pain 2004;109:86-93.
5. Turkheimer FE, Hinz R, Cunningham VJ. On the undecidability among
   kinetic models: from model selection to model averaging. J Cereb Blood
   Flow Metab 2003; 23: 490-498.
6. Sederholm K. Model averaging with Akaike weights. TPCMOD0016 2003-04-07.
   http://www.turkupetcentre.net/reports/tpcmod0016.pdf

See also: imgdv, ecat2tif, lhsoldv, logan

Keywords: image, modelling, distribution volume, NNLS

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```
imglhk3 0.8.9  (c) 2003-2010 by Turku PET Centre

Estimation of rate constant k3 from dynamic PET images in ECAT 6.3 or 7.x
format using linearized three-compartment model with rate constants K1, k2
and k3 (1) and, if required, also vascular volume fraction Vb, applying
Lawson-Hanson non-negative least squares (NNLS) to solve general linear
least squares functions (2).

Parameters:
  1) Plasma file (sample times in minutes!)
  2) Dynamic image file
  3) Parametric k3 image file

Options:
 -Thr=<threshold%>
     Pixels with AUC less than (threshold/100 x max AUC) are set to zero.
     Default is 5 %
 -ThrDV=<threshold%>
     DV and k3 in pixels with DV less than (threshold/100 x DV) are
     set to zero. By default, this threshold is not applied.
 -DV=<filename>
     Parametric K1/(k2+k3) image is saved
 -K1=<filename>
     Parametric K1 image is saved
 -k2=<filename>
     Parametric k2 image is saved
 -Ki=<filename>
     Parametric Ki image is saved
 -Vb=<filename>
     Parametric Vb image is saved
 -alt
     Alternative method to estimate k3; Ki is fixed
 -F  Remove parametric pixel values that are over 4x higher than
     their closest neighbours
 -E=<Fit end time (min)>
     Use data from 0 to end time; by default, model is fitted to all frames
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

Example 1b: Vb is assumed negligible:
     imglhk3 ua2917ap.kbq ua2917dy1.v ua2917k3.v
Example 1b: Vb is fitted as one of the model parameters:
     imglhk3 -Vb=ua2917vb.v ua2917ap.kbq ua2917dy1.v ua2917k3.v
Example 1c: Vb is pre-corrected:
     imgcbv ua2917dy1.v ua2917ab.kbq 0.04 ua2917dy1_cbv.v
     imglhk3 ua2917ap.kbq ua2917dy1_cbv.v ua2917k3.v
Example 2: K1, DV, and k3 images are saved:
     imglhk3 -K1=ua2917k1.v -DV=ua2917dv.v ua2917ap.kbq ua2917dy1.v ua2917k3.v
Example 3: k3 pixel values are set to zero if DV is less than 10% of DVmax:
     imglhk3 -ThrDV=10 ua2917ap.kbq ua2917dy1.v ua2917k3.v

The vascular volume is considered in the model setting only if filename
for Vb image is given. Otherwise the contribution of vasculature to the
total radioactivity concentration is assumed to be negligible.
Note that this model can correctly estimate Vb only if
-plasma does not contain any labelled metabolites
-plasma and blood curves are similar in shape.
Alternatively, vascular volume can be pre-corrected with imgcbv.

The units of pixel values in the parametric images are 1/min for k3,
ml/(min*ml) for K1 and Ki, and ml/ml for DV and Vb.
```

References:
1. Blomqvist G. On the construction of functional maps in positron
   emission tomography. J Cereb Blood Flow Metab 1984;4:629-632.
2. Lawson CL & Hanson RJ. Solving least squares problems.
   Prentice-Hall, 1974.

See also: imgcbv, imglhki, imglk3, imglhlk3, ecat2tif, lhsolvk3, lhsolk3

Keywords: image, modelling, irreversible uptake, enzyme activity

```
imglhki 1.3.1  (c) 2002-2012 by Turku PET Centre

Estimation of influx rate constant (Ki) from dynamic PET images in
ECAT 6.3 or 7.x format applying Lawson-Hanson non-negative least squares
(NNLS) [1] to solve general linear least squares functions.
Ki is estimated directly without division [2] from one- or two-tissue
compartment model.

Parameters:
  1) Plasma file (times in minutes!)
  2) Dynamic image file
  3) Parametric image file

e.g.: imglhki  ua2918ap.kbq  ua2918dy1.v  ua2918ki.v

Options for model selection:
 -A  Automatic selection of model for separate pixels
 -1  Force one-tissue compartment model for all pixels
 -2  Force two-tissue compartment model for all pixels
 -0  Akaike weighted average of 1- and 2-tissue
     compartment model results [3]  (default)
 -M  Selected model is written as second 'frame' in the parametric image.

Other command line options:
 -T=<threshold%>
     Pixels with AUC less than (threshold/100 x plasma AUC) are set to zero.
     default is 0%
 -E=<Fit end time (min)>
     Use data from 0 to end time; by default, model is fitted to all frames.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

The unit of pixel values in the parametric image is ml/(min*ml).

References:
1. Lawson CL & Hanson RJ. Solving least squares problems.
   Prentice-Hall, 1974.
2. Zhou Y, Brasic J, Endres CJ, Kuwabara H, Kimes A, Contoreggi C, Maini A,
   Ernst M, Wong DF. Binding potential image based statistical mapping for
   detection of dopamine release by [11C]raclopride dynamic PET.
   NeuroImage 2002;16:S91.
3. Turkheimer FE, Hinz R, Cunningham VJ. On the undecidability among
   kinetic models: from model selection to model averaging. J Cereb Blood
   Flow Metab 2003; 23: 490-498.

See also: imgki, ecat2tif, lhsolki, patlak

Keywords: image, modelling, influx rate, NNLS

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```

imglhlk3 0.3.1 (c) 2003,2005 by Turku PET Centre

Estimation of three-compartment model term lambda*k3 for irreversible
PET tracers [2, 4] from dynamic PET images in ECAT 6.3 or 7.x format.
A modification of the method of Blomqvist [1] is applied and Lawson-Hanson
non-negative least squares (NNLS) [3] is used to solve the resulting
general linear least squares functions for Ki and K1.
Lambda*k3 is solved as lambda*k3 = Ki*K1/(K1-Ki) [2]. Ki/K1 is constrained
to <0.9.

Lambda*k3 is more robust parameter than k3, because
-like lambda=K1/k2 it is independent of blood flow [2]
-it is independent of nonspecific binding which appears in both k2 and k3
 and is cancelled out in k3/k2 [4]
However, lambda*k3 is dependent on plasma protein binding [4].

Program parameters:
  1) Plasma file (times in minutes!)
  2) Dynamic image file
  3) Parametric lambda*k3 image file
  4) Parametric Vb image file (optional)

Options:
 -T=<threshold%>
     Pixels with AUC less than (threshold/100 x mean AUC) are set to zero.
     Default is 0 %
 -Ki=<filename>
     Parametric Ki image is saved.
 -K1=<filename>
     Parametric K1 image is saved.
 -F Remove parametric pixel values that are over 4x higher than
     their closest neighbours.
 -E=<Fit end time (min)>
     Use data from 0 to end time; by default, model is fitted to all frames.

e.g.: imglhlk3 ua2917ap.kbq ua2917dy1.v ua2917lk3.v -K1=ua2917k1.v

The vascular volume is considered in the model setting only if filename
for Vb image is given. Otherwise the contribution of vasculature to the
total radioactivity concentration is assumed to be negligible.
Note that this model can correctly estimate Vb only if
-plasma does not contain any labelled metabolites
-plasma and blood curves are similar in shape.

The units of pixel values in the parametric images are ml/(min*ml) for
lambda*k3, Ki and K1, and ml/ml for Vb.

References:
1. Blomqvist G. On the construction of functional maps in positron
   emission tomography. J Cereb Blood Flow Metab 1984;4:629-632.
2. Fowler JS, Volkow ND, Cilento R, Wang G-J, Felder C, Logan J.
   Comparison of brain glucose metabolism and monoamine oxidase B (MAO B)
   in traumatic brain injury. Clin Pos Imag 1999;2:71-79.
3. Lawson CL & Hanson RJ. Solving least squares problems.
   Prentice-Hall, 1974.
4. Logan J, Fowler JS, Ding Y-S, Franceschi D, Wang G-J, Volkow ND,
   Felder C, Alexoff D. Strategy for the formation of parametric images
   under conditions of low injected radioactivity applied to PET studies
   with the irreversible monoamine oxidase A tracers [11C]clorgyline and
   deuterium-substituted [11C]clorgyline. J Cereb Blood Flow Metab 2002;
   22:1367-1376.

See also: imglhk3, ecat2tif, lhsolvk3, lhsolk3

Keywords: image, modelling, irreversible uptake

imglk3 0.1.0 (c) 2006 by Turku PET Centre

Estimation of lambda*k3 (lambda=K1/k2) from dynamic PET images in ECAT 6.3
or 7.x format applying the irreversibe two-tissue compartment model [1, 2]:
1) Ki is calculated using the average of graphical analysis (Gjedde-Patlak)
   slopes between time range tGA1-tGA2 (see below).
2) K1 is estimated with bilinear regression between time ranges 0-tBR1
   and 0-tBR2 [2].
3) Lambda*k3 is calculated as lambda*k3=K1*Ki/(K1-Ki).

Parameters:
  1) Input file (Arterial plasma corrected for metabolites and delay time;
     times in minutes)
  2) Dynamic PET image file
  3) tGA1 (Gjedde-Patlak linear fit start time; min)
  4) Lambda*k3 image file

Options:
 -Thr=<threshold%>
     Pixels with AUC less than (threshold/100 x max AUC) are set to zero.
     Default is 10 %
 -K1=<filename>
     K1 image is saved.
 -Ki=<filename>
     Ki image is saved.
 -F Remove parametric pixel values that are over 4x higher than
     their closest neighbours.
 -tGA2=<time>
     Gjedde-Patlak linear fit end time (min).
     By default, all PET data is used.
 -tBR1=<time (min)>
     K1 results are calculated starting from range 0-tBR1; by default, 5 min.
 -tBR2=<time (min)>
     K1 results are calculated until range 0-tBR2; by default, 18 min.
 -h or --help
     Print this message and exit
 -v, --build or --version
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.

e.g.: imglk3 ua2918ap.parent.kbq ua2918dy1.v 6 ua2918lk3.v

References:
1. Fowler JS, Volkow ND, Wang GJ, Logan J, Pappas N, Shea C, MacGregor R.
   Age-related increases in brain monoamine oxidase B in living healthy
   human subjects. Neurobiol Aging 1997; 18: 431-435.
2. Logan J, Fowler JS, Volkow ND, Wang G-J, MacGregor RR, Shea C.
   Reproducibility of repeated measures of deuterium substituted
   [11C]L-deprenyl ([11C]L-deprenyl-D2) binding in the human brain.
   Nucl Med Biol 2000; 27:43-49.

See also: imgcbv, imglhlk3, imglhk3, ecat2tif

Keywords: image, modelling, irreversible uptake

```
imgmatch 1.1.2  (c) 2006-2013 by Turku PET Centre

Program for checking if two PET images are equal.
Returns 0 if files match and a nonzero value otherwise.
ECAT 6.3 and 7, NIfTI-1, Analyze 7.5 and microPET formats are (partially)
supported.
Program is meant mainly for testing purposes.

Usage:
  imgmatch [Options] <Image1> <Image2>

Options:
 -header=<y|N>
     All values in the headers (excluding transformation parameters)
     are required to match (y) or not tested (n, default).
 -transform=<y|N>
     Transformation parameters in the headers are required to match (y),
     or not tested (n, default).
 -planes=<Y|n>
     Planes numbers are required to match (y, default) or not tested (n).
 -frames=<Y|n>
     Frame times are required to match (y, default) or not tested (n).
 -abs=<value>
     Absolute result differences must not exceed the specified limit value;
     by default no difference is allowed.
 -roughly
     Pixel values are required to match roughly (99.9%), not exactly.
 -around
     Pixel values are required to be around the same (90%), not exactly.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Image1 and image2 must be in the same format, and they must have same
matrix size and plane numbers.

See also: dftmatch, resmatch, ecatcalc, ecatunit, ecatmax, ecat2tif

Keywords: Image, ECAT, Analyze, tools, software testing

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```
imgmax 0.4.0  (c) 2004-2013 by Turku PET Centre

Finds maximum value in PET image file(s) in ECAT 6.3 or 7.x, NIfTI-1,
or Analyze 7.5 format.

Usage: imgmax [Options] <image file(s)>

Options:
 -min
     Minimum values are printed instead of maximum values
 -both
     Both max and min values are printed
 -clean
     Only the max and/or min value of all specified files is printed
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit

See also: ecatunit, eprofile, epxl2dft, lmhdr, lshdr, eframe, ecat2tif

Keywords: ECAT, NIfTI, Analyze, image, max, min

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```

```
imgmove 0.1.2  (c) 2004,2012 by Turku PET Centre

Moving specified image frames in x,y-directions. Only for simulation use:
this is not valid method for movement correction, because attenuation
correction is not moved accordingly.

Usage: imgmove [Options] <Parameters>

Parameters:
  1) Dynamic image file (ECAT or Analyze)
  2) Movement in pixels in x direction (negative=left)
  3) Movement in pixels in y direction (negative=down)
  4) Frame numbers which are moved
  5) Output image file

Options:
 -fill
     New image area is filled with neighbouring pixel values
     (by default with zeroes).
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --verbose
     Program prints more information about what it is doing.
 --silent
     Program works silently, printing only error and warning messages.

Example:
     imgmove ua2918dy1.v 0 2 14-16 ua2918dy1mov.v

See also: dft2img, flo2ecat, eframe, lmhdr, ecat2tif
Keywords: simulation, software testing, ECAT, Analyze

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```
imgpext 3.2.0  (c) 1996-2006 by Turku PET Centre

 Extracts the individual pixel values of an CTI ECAT 6.3 or 7 image plane
 and frame, either all or those within specified regions.
 Values are written in stdout (on screen).

 Usage:  imgpext [flags] [options] <Image file> [ROI file]

 Flags:
   -h -H      print this message and exit
   -v -V      print build information and exit
   -s -S      run in silent mode

 Options:
   -p -P      apply ROIs to all image planes.
   -i -I      print out pixel indices in format
              matrix[1..planeNr][1..rowNr][1..colNr][1..frameNr].
   -m <val>   print only values greater than <val>

 Parameters:
   <Image file>   input image filename
   [ROI file]     ROI file to be applied

 Keywords: ECAT, ROI

 See also: imgpreport
```

```
imgratio 1.0.3  (c) 2005-2009 by Turku PET Centre

Computation of AUC ratio image from dynamic PET image in
ECAT 6.3, 7.x or Analyze 7.5 format and reference region TAC.

Parameters:
  1) Dynamic image file
  2) Reference region TAC file
  3) Time (min) where ratio calculation starts
  4) Time (min) where ratio calculation ends
  5) Ratio image file

Options:
 -h, --help
     Print this message and exit
 -Bound
     Instead of VOXEL/REF, (VOXEL-REF)/REF ratio is calculated
 -Thr=<threshold%>
     Pixels with AUC less than (threshold/100 x ref AUC) are set to zero;
     default is 10%
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints lots of information about what it is doing.

Example:
     imgratio ua2918dy1.img ua2918cer.dft 60 90 ua2918ratio.img

See also: dftratio, imginteg, ecatcalc, ecat2tif, ecatunit, dftunit

Keywords: image, modelling

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```
imgshrink 1.1.1  (c) 2006-2012 by Turku PET Centre

Program for shrinking the size of a dynamic or static PET image to take
less memory and disk space, and to reduce computation time when testing
pixel-by-pixel modeling methods.ECAT 6.3, 7.x and Analyze 7.5 formats are accepted.
Eight neighbouring pixels are averaged into one pixel; thus image size
will be shrunk into 1/8 of the size of the original image.

Command line arguments:
  1) PET image file
  2) Shrunk image file

Options:
 -z=<Yes|no>
     Nr of image planes (z dimension) is halved (default) or not changed
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages

Example:
  imgshrink i5998dy1.v i5998dy1_shrinked.v

See also: imgslim, e7vplavg, esplit, imgbox, imginteg

Keywords: ECAT7, image, tools, modelling

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```
imgslice 0.1.1  (c) 2010,2012 by Turku PET Centre

Extract one slice from a PET image. Note that some smoothing occurs in
the process, and currently the use of should be limited to making
illustrations of image data.

Usage:
  imgslice [options] <image file> <filename for image slice>

Options:
 -plane[=<slice>]
 -column[=<slice>]
 -row[=<slice>]
     Specified slice (by default mid slice) of image planes (default),
     columns, and/or rows is extracted.
 -dim=<new image dimension>
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example 1: make a TIFF image of parametric image from a central slice in
three directions
    imgslice -plane -column -row ia123bp.v ia123bp_slices.v
    img2tif -s -rb -th=3 ia123bp_slices.v ia123bp_slices.tif

See also: imgslim, esplit, imgshrink, img2cube, e7vplavg, ecat2tif, ecat2flo

Keywords: image processing, ECAT, tool

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```

```
imgslim 0.2.1  (c) 2008-2013 by Turku PET Centre

Slice off empty parts in dynamic ECAT and NIfTI images.
Note that no backup is made of any previous output file.

Usage: imgslim <Image file> <Output image file>

Options:
 -limit=<value>
     Slices where average pixel value is less than the limit value
     are cut off; by default 0.1
 -keepframes | -slimframes
     Selects whether time frames can be sliced off
     (by default, frames are always kept)
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: imgbox, esplit, e7vplavg, imginteg, imgshrink, ecatunit

Keywords: image processing, ECAT, compression

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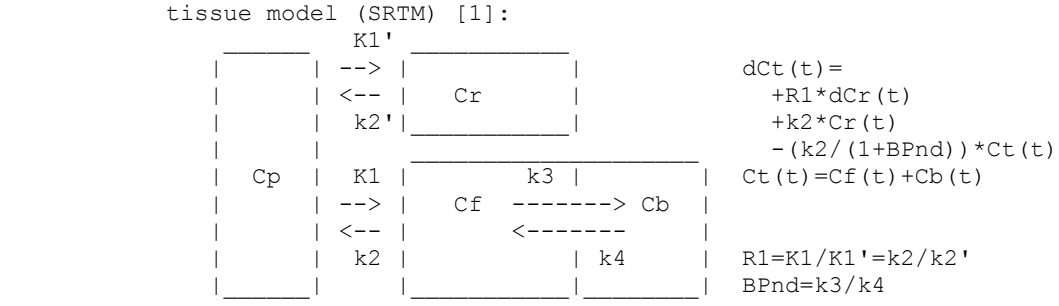
imgsrtm 1.4.4 (c) 2003-2013 by Turku PET Centre

Computation of parametric images of binding potential (BPnd) from dynamic PET images in ECAT, NIfTI, or Analyze format applying simplified reference tissue model (SRTM) [1]:



The model is transformed to general linear least squares functions [2], which are solved using Lawson-Hanson non-negative least squares (NNLS) algorithm [3]. BPnd is estimated directly without division [4].

Parameters:
  1) Dynamic image file (corrected for decay)
  2) Reference region TAC file
  3) Parametric BPnd image file

Options:
 -SRTM2
     STRM2 method (5) is applied; in brief, traditional SRTM method is used first to calculate median k2' from all pixels where BPnd>0; then SRTM is run another time with fixed k2'
 -R1=<filename>
     Program computes also an R1 image
 -k2=<filename>
     Program computes also a k2 image
 -k2s=<filename>
     Program computes also a k2' image
 -theta3=<filename> or -t3=<filename>
     Program computes also a theta3 image; theta3 = k2/(1+BPnd)+lambda
 -rp=<filename>
     Program writes regression parameters in the specified image file
 -dual=<filename> or -du=<filename>
     Program writes number of i in set p in NNLS dual solution vector in the specified image file
 -thr=<threshold%>
     Pixels with AUC less than (threshold/100 x ref AUC) are set to zero
     default is 0%
 -DVR
     Instead of BP, program saves the DVR (=BPnd+1) values
 -end=<Fit end time (min)>
     Use data from 0 to end time; by default, model is fitted to all frames
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
     imgsrtm ua2918dy1.v ua2918cer.dft ua2918bp.v

References:
1. Lammertsma AA, Hume SP. Simplified reference tissue model for PET receptor studies. NeuroImage 1996;4:153-158.
2. Blomqvist G. On the construction of functional maps in positron emission tomography. J Cereb Blood Flow Metab 1984;4:629-632.

3. Lawson CL & Hanson RJ. Solving least squares problems. Prentice-Hall, 1974.
4. Zhou Y, Brasic J, Endres CJ, Kuwabara H, Kimes A, Contoreggi C, Maini A, Ernst M, Wong DF. Binding potential image based statistical mapping for detection of dopamine release by [11C]raclopride dynamic PET. NeuroImage 2002;16:S91.
5. Wu Y, Carson RE. Noise reduction in the simplified reference tissue model for neuroreceptor functional imaging. J Cereb Blood Flow Metab. 2002;22:1440-1452.

See also: imgdv, imgbfbp, ecat2tif, imgratio, ecatunit

Keywords: image, modelling, binding potential, SRTM, SRTM2

```
imgsuv 0.1.2  (c) 2011-2013 by Turku PET Centre

Calculation of a SUV (standardized uptake value) image from PET image
in ECAT 6.3 and 7.x, NIfTI, and Analyze 7.5 format.
SUV in image pixels is calculated as mean value in specified time range.
Before calculation, make sure that radioactivity concentration units in PET
image header are correct. Analyze and NIfTI images do not contain units,
therefore unit kBq/mL is assumed.
Image data and injected dose must be decay corrected to the same time
(usually the tracer injection time).

Command line arguments:
  1) PET image
  2) SUV calculation start time (min)
  3) SUV calculation end time (min)
  4) Injected dose (MBq)
  5) Subject weight (kg)
  6) SUV image file

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Instead of SUV (g/mL), the percentage of injected dose per tissue volume
(%i.d./L) is calculated, if you set the subject weight to 0.

If SUV calculation start and end times are set to zero, then no average
over time is calculated, but the (dynamic) PET image is saved
in SUV or %i.d./L units.

See also: ecatunit, ecattime, imginteg, ecatcalc, eframe, dftsuv

Keywords: image, modelling, SUV, DUR, DAR, dose

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```
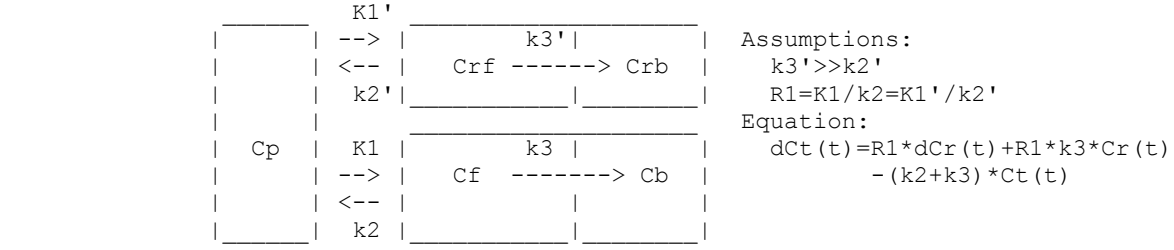

imgtrtm 0.1.3 (c) 2010 by Turku PET Centre

Computation of parametric images of k3 from dynamic PET images in
ECAT or Analyze format applying transport-limited reference
tissue model for irreversible uptake, TRTM (1). This model
is based on the reference tissue compartment model (2,3), but here it is
assumed that in reference tissue k3'>>k2', and thus the uptake in it is
limited only by transport into tissue (4,5).



The model is transformed to general linear least squares functions (6),
which are solved using Lawson-Hanson non-negative least squares (NNLS)
algorithm (7).

Parameters:
  1) Dynamic image file (corrected for decay)
  2) Reference region TAC file
  3) Parametric BPnd image file

Options:
 -R1=<filename>
     Program computes also an R1 image
 -k2=<filename>
     Program computes also a k2 image
 -k2s=<filename>
     Program computes also a k2' image
 -DV=<filename>
     Parametric R1*k2/(k2+k3) image is saved
 -rp=<filename>
     Program writes regression parameters in the specified image file
 -dual=<filename> or -du=<filename>
     Program writes number of i in set p in NNLS dual solution vector in
     the specified image file
 -thr=<threshold%>
     Pixels with AUC less than (threshold/100 x ref AUC) are set to zero
     default is 0%
 -thrR1=<threshold>
     Pixels with R1 less than specified threshold value are set to zero in
     parametric maps. By default, this threshold is not applied.
 -thrDV=<threshold%>
     DV (=R1*k2/(k2+k3)) and k3 in pixels with DV less than
     (threshold/100 x DVmax) are set to zero.
     By default, this threshold is not applied.
 -end=<Fit end time (min)>
     Use data from 0 to end time; by default, model is fitted to all frames
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example 1: k3 map is computed with default settings
     imgtrtm ua5212dy1.v ua5212put.dft ua5212k3.v

Example 2: Pixel values in k3 map are set to zero when R1 is lower than

the specified R1 threshold level:

```
imgtrtm -thrR1=0.7 -R1=ua5212r1.v ua5212dy1.v ua5212put.dft ua5212k3.v
```

Example 3: k3 pixel values are set to zero when TAC AUC is less than 5% of reference region AUC, or when DV is less than 10% of DVmax:

```
imgtrtm -thr=5 -thrdv=10 ua5212dy1.v ua5212put.dft ua5212k3.v
```

References:

1. Oikonen V. Model equations for reference tissue compartmental models. http://www.turkupetcentre.net/reports/tpcmod0002.pdf
2. Cunningham VJ, Hume SP, Price GR, Ahier RG, Cremer JE, Jones AKP. Compartmental analysis of diprenorphine binding to opiate receptors in the rat in vivo and its comparison with equilibrium data in vitro. J Cereb Blood Flow Metab 1991;11:1-9.
3. Lammertsma AA, Hume SP. Simplified reference tissue model for PET receptor studies. NeuroImage 1996;4:153-158.
4. Herholz K, Lercher M, Wienhard K, Bauer B, Lenz O, Heiss W-D. PET measurement of cerebral acetylcholine esterase activity without blood sampling. Eur J Nucl Med 2001;28:472-477.
5. Nagatsuka S, Fukushi K, Shinotoh H, Namba H, Iyo M, Tanaka N, Aotsuka A, Ota T, Tanada S, Irie T. Kinetic analysis of [11C]MP4A using a high-radioactivity brain region that represents an integrated input function for measurement of cerebral acetylcholinesterase activity without arterial blood sampling. J Cereb Blood Flow Metab 2001; 21: 1354-1366.
6. Blomqvist G. On the construction of functional maps in positron emission tomography. J Cereb Blood Flow Metab 1984;4:629-632.
7. Lawson CL & Hanson RJ. Solving least squares problems. Prentice-Hall, 1974.

See also: fit_trtm, lhtrtm, imglhk3, ecat2tif, ecatunit

Keywords: image, modelling, irreversible uptake, reference tissue

```
injdifft 1.0.2 (c) 2006,2008 Turku PET Centre

Calculate time difference between zero times of PET scan and blood data.
Zero times are given in two text files in format
scan_start_time := YYYY-MM-DD hh:mm:ss, or
injection_time := YYYY-MM-DD hh:mm:ss.

The result, time difference (time2-time1 in seconds) will be written in
stdout or specified file in format
time_difference := <time2-time1>.

Usage:  injdifft [options] <timefile1> <timefile2> [output file]

Options:
 -min | -sec
     Time difference is written in minutes or in seconds (default)
 -small
     Software ignores time differences of multiples of one hour, that may
     have been caused by wrong time zone or daylight saving setting in
     either of the zero times
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

Example:
     injdifft -small s95432dy1.v.ift s95432blo.kbq s95432.dift

See also: egetstrt, blo2kbq, iftlist, dfttime, blotimes

Keywords: input, IFT, tool

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you are welcome to redistribute it under GNU General Public License.
```

```
inpstart 0.1.1  (c) 2012 by Turku PET Centre

Verify that peak is not missed in an input TAC file.
Return code is zero, if no problems were encountered.
This may be used in scripts for a rough test if venous plasma TAC can
be used as input in Patlak analysis, but it must not replace visual
inspection.

Usage:  inpstart [Options] <TAC file(s)>

Options:
 -fix
     Minor problems are corrected; always check the result before use.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

Example 1: check that specified data files are suitable as input TACs
     inpstart *vp.kbq

See also: dftframe, dfttime, avgbolus, dftcat, interpol

Keywords: DFT, input, peak, zero

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you are welcome to redistribute it under GNU General Public License.
```

```
interpol 2.6.1  (c) 1993-2013 by Turku PET Centre

Program for linear (dot-to-dot) interpolation and integration of time-
activity curves (TACs).

Usage:  interpol [Options] <datafile> [output file]

Options:
 -y or -i or -ii
     TACs are interpolated (-y, default), integrated (-i), or the 2nd
     integral (-ii) is calculated.
 -X=<x1;x2;...> or -C=<start;stop;step> or -F=<xfile>
     The sample times for interpolated or integral TACs can be specified with
     these options; if none of these is given, the sample times of the
     original datafile are used. Definite sample times can be given after
     -X; regular sample timing can be specified using option -C; with -F the
     sample times can be read from any DFT file.
 -A=[t]
     Input TACs are interpolated and integrated with sample (0,0) or (t,0)
     as their first measurement points.
 -0=<y|F>
     Input TACs are interpolated and integrated with sample (0,y) added
     if TAC starts later than at zero time. With option -0=F the first
     existing sample value is used as y value.
 -header=<Yes|no>
     Descriptive title lines (if header information is available) can be
     included (default), or not included.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Input data is considered to be non-framed even if it contains frame
start and end times; if necessary, frame mid times are used.
The interpolated or integrated values are calculated exactly at the
specified sample times, except when the start and end times of PET frames
are given with -F=<xfile>; then the time frame average values or integrals
at the frame mid time are calculated.

If output filename is not specified, the results are written to stdout.
Output is written in same TAC file format as the input file;
http://www.turkupetcentre.net/petanalysis/format_tpc_dft.html

See also: dftinteg, fr4sim, dftframe, ainterp, dftcut, extrapol, dftsuv

Keywords: DFT, tools, modelling, simulation, AUC, interpolation

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you are welcome to redistribute it under GNU General Public License.
```

```
lassenp 0.1.1  (c) 2010,2011 by Turku PET Centre

Calculates drug occupancy from distribution volumes of PET tracer
without reference region using Lassen plot (1,2).

Usage:  lassenp [Options] <DV-result file1> <DV-result file2> <Occ file>

Options:
 -c1=<Drug concentration in study 1>
 -c2=<Drug concentration in study 2>
     Occupancy is calculated without baseline study (not yet implemented)
 -svg=<Filename>
     Plot is written in specified file in Scalable Vector Graphics format
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

References:
1. Lassen NA, Bartenstein PA, Lammertsma AA, Prevett MC, Turton DR,
   Luthra SK, Osman S, Bloomfield PM, Jones T, Patsalos PN, O'Connell MT,
   Duncan JS, Andersen JV. Benzodiazepine receptor quantification in vivo
   in humans using [11C]flumazenil and PET: application of the steady-state
   principle. J Cereb Blood Flow Metab. 1995;15:152-165.
2. Cunningham VJ, Rabiner EA, Slifstein M, Laruelle M, Gunn RN. Measuring
   drug occupancy in the absence of a reference region: the Lassen plot
   re-visited. J Cereb Blood Flow Metab. 2010;30:46-50.

See also: logan, fitk4, reslist, resdel, rescoll, resdiff

Keywords: modelling, receptor occupancy, Lassen plot, distribution volume

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you are welcome to redistribute it under GNU General Public License.
```
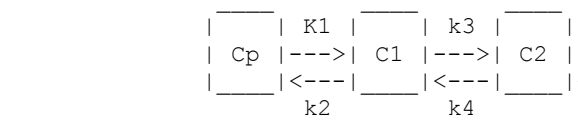
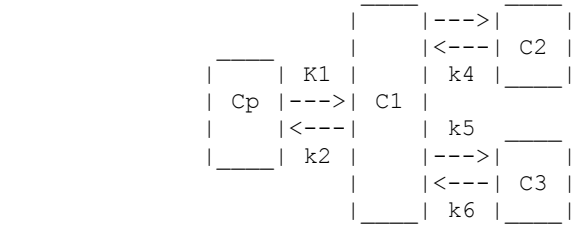

lhsol 2.0.2 (c) 2002-2012 by Turku PET Centre

Fitting of full or reduced compartmental model to plasma and tissue
time-activity curves (TACs) to estimate the model parameters:



compartments in series (s)



compartments in parallel (p)

Compartmental models are transformed into general linear least squares
functions (1, 2, 3), which are solved using Lawson-Hanson non-negative
least squares (NNLS) algorithm (4). Linear parameters are always >=0,
but compartmental model parameters may get negative estimates.
Note that rate constants and macroparameters are represented per volume
(measured by PET) including vascular volume.

Usage: lhsol <Model> <Plasma file> <Tissue file> <Fit time> <Result file>

, where Model is one of these strings:
     k1 (for assuming k2=k3=k4=k5=k6=0)
     k2 (for assuming k3=k4=k5=k6=0)
     k3 (for assuming k4=k5=k6=0)
     k4 (for assuming k5=k6=0)
     k5s (for assuming k6=0 and compartments in series)
     k6s (compartments in series)
     k5p (for assuming k6=0 and compartments in parallel)
For model 'k6p' many of model parameters could not be solved.

Options:
 -Vp=<ignored|fitted>
     Vp is ignored (default) or fitted; note that plasma curve is assumed
     to represent vascular blood curve, which is usually not true.
 -w1 | -wf
     Sample weights are set to 1 (-w1) or to frame lengths (-wf);
     by default weights in tissue data file are used, if available.
 -mid[=<y|N>]
     Mid frame times are used (y) or not used (n, default) even if frame
     start and end times are available.
 -fit=<Filename>
     Fitted regional TACs are written in DFT format.
 -svg=<Filename>
     Fitted and measured TACs are plotted in specified SVG file.
 -par=<Filename>
     Parameters of linear model are saved in result format.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

References:
1. Blomqvist G. On the construction of functional maps in positron emission
   tomography. J Cereb Blood Flow Metab 1984;4:629-632.

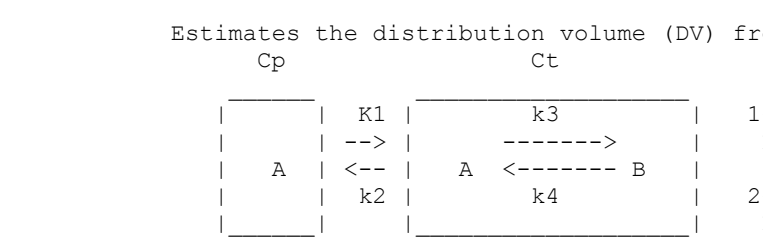
2. Gjedde A, Wong DF. Modeling neuroreceptor binding of radioligands
   in vivo. In: Quantitative imaging: neuroreceptors, neurotransmitters,
   and enzymes. (Eds. Frost JJ, Wagner HM Jr). Raven Press, 1990, 51-79.
3. Oikonen V. Multilinear solution for 4-compartment model:
   I. Tissue compartments in series.
   http://www.turkupetcentre.net/reports/tpcmod0023.pdf
4. Lawson CL & Hanson RJ. Solving least squares problems.
   Prentice-Hall, 1974.

See also: dftcbv, patlak, logan, lhsolki, lhsoldv, fitk2, fitk3, fitk4

Keywords: DFT, modelling, compartmental model, multilinear fit, NNLS

lhsoldv 1.4.3 (c) 2002-2012 by Turku PET Centre

Estimates the distribution volume (DV) from compartmental model:



The model is transformed to general linear least squares functions [1], which are solved using Lawson-Hanson non-negative least squares (NNLS) algorithm [2]. DV is estimated directly without division [3,4,5].

Parameters:
  1) Metabolite corrected plasma file
  2) Tissue TAC file (*.dft)
  3) Fit end time (duration)
  4) Result file (existing file is overwritten)

Options:
 -ref=<reference region name>
     When reference region is defined, DVR can be calculated as DVroi/DVref
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.
Options for selection of model:
 -0 Akaike weighted avg of 1- and 2-tissue compartment model results [6,7]
 -1 Force one-tissue compartment model for all regions
 -2 Force two-tissue compartment model for all regions
 -A Automatic selection of model for separate regions (default)

Example:
     lhsoldv ua2918ap_pure.kbq ua2918.dft 90 ua2918dv.res

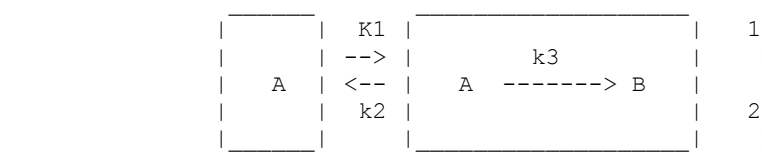
References:
1. Blomqvist G. On the construction of functional maps in positron emission tomography. J Cereb Blood Flow Metab 1984;4:629-632.
2. Lawson CL & Hanson RJ. Solving least squares problems. Prentice-Hall, 1974.
3. Zhou Y, Brasic J, Endres CJ, Kuwabara H, Kimes A, Contoreggi C, Maini A, Ernst M, Wong DF. Binding potential image based statistical mapping for detection of dopamine release by [11C]raclopride dynamic PET. NeuroImage 2002;16(3):S91.
4. Zhou Y, Brasic JR, Ye W, Dogan AS, Hilton J, Singer HS, Wong DF. Quantification of cerebral serotonin binding in normal controls and subjects with Tourette's syndrome using [11C]MDL 100,907 and (+)[11C]McN 5652 dynamic PET with parametric imaging approach. NeuroImage 2004;22(Suppl 2):T98.
5. Hagelberg N, Aalto S, Kajander J, Oikonen V, Hinkka S, Någren K, Hietala J, Scheinin H. Alfentanil increases cortical dopamine D2/D3 receptor binding in healthy subjects. Pain 2004;109:86-93.
6. Turkheimer FE, Hinz R, Cunningham VJ. On the undecidability among kinetic models: from model selection to model averaging. J Cereb Blood Flow Metab 2003; 23: 490-498.
7. Sederholm K. Model averaging with Akaike weights. TPCMOD0016 2003-04-07. http://www.turkupetcentre.net/reports/tpcmod0016.pdf

See also: dftcbv, dftweigh, dft2svg, logan, fitk2, fitk4, imglhdv, rescoll

Keywords: DFT, modelling, distribution volume, Vt, NNLS

lhsolki 1.3.0 (c) 2002-2005 by Turku PET Centre

Estimates the influx rate constant (Ki) from compartmental model:



The model is transformed to general linear least squares functions [1], which are solved using Lawson-Hanson non-negative least squares (NNLS) algorithm [2]. Ki is estimated directly without division [3].

Parameters:
  1) Metabolite corrected plasma file
  2) Tissue TAC file (*.dft)
  3) Fit end time (duration)
  4) Result file (existing file is overwritten)

e.g.: lhsolki ub2917ap_pure.kbq ub2917.dft 90 ub2917ki.res

Options:
 -0 Akaike weighted avg of 1- and 2-tissue compartment model results [4,5]
 -1 Force one-tissue compartment model for all regions
 -2 Force two-tissue compartment model for all regions (default)
 -A Automatic selection of model for separate regions

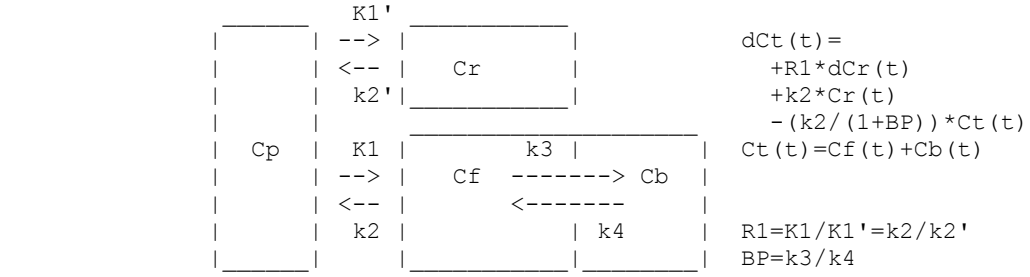
References:
1. Blomqvist G. On the construction of functional maps in positron emission tomography. J Cereb Blood Flow Metab 1984;4:629-632.
2. Lawson CL & Hanson RJ. Solving least squares problems. Prentice-Hall, 1974.
3. Zhou Y, Brasic J, Endres CJ, Kuwabara H, Kimes A, Contoreggi C, Maini A, Ernst M, Wong DF. Binding potential image based statistical mapping for detection of dopamine release by [11C]raclopride dynamic PET. NeuroImage 2002;16:S91.
4. Turkheimer FE, Hinz R, Cunningham VJ. On the undecidability among kinetic models: from model selection to model averaging. J Cereb Blood Flow Metab 2003; 23: 490-498.
5. Sederholm K. TPCMOD0016 2003-03-20.

See also: dftcbv, dftweigh, dft2ps, patlak, fitk3, imglhki

Keywords: DFT, modelling, irreversible uptake

lhsrtm 2.0.2 (c) 2002-2005 by Turku PET Centre

Estimates the BP from simplified reference tissue model [1]:



The model is transformed to general linear least squares functions [2], which are solved using Lawson-Hanson non-negative least squares (NNLS) algorithm [3]. BP is estimated directly without division [4], but if fitted TACs are saved, those are calculated from original model setting.

Parameters:
  1) Tissue TAC file (*.dft)
  2) Name of reference region in tissue file, or name of file
     containing reference tissue TAC
  3) Fit end time (duration)
  4) Result file (existing file is overwritten)
  5) Fitted regional TAC file (optional)

Options:
 -DVR
    Reports BP+1=DVR instead of BP.
 -mid[=<y|n>]
    Mid frame times are used (y) or not used (n, default) even if frame
    start and end times are available.

References:
1. Lammertsma AA, Hume SP. Simplified reference tissue model for PET
   receptor studies. NeuroImage 1996;4:153-158.
2. Blomqvist G. On the construction of functional maps in positron emission
   tomography. J Cereb Blood Flow Metab 1984;4:629-632.
3. Lawson CL & Hanson RJ. Solving least squares problems.
   Prentice-Hall, 1974.
4. Zhou Y, Brasic J, Endres CJ, Kuwabara H, Kimes A, Contoreggi C, Maini A,
   Ernst M, Wong DF. Binding potential image based statistical mapping for
   detection of dopamine release by [11C]raclopride dynamic PET.
   NeuroImage 2002;16:S91.
5. Oikonen V. Model equations for reference tissue compartmental models.
   http://www.turkupetcentre.net/reports/tpcmod0002.pdf

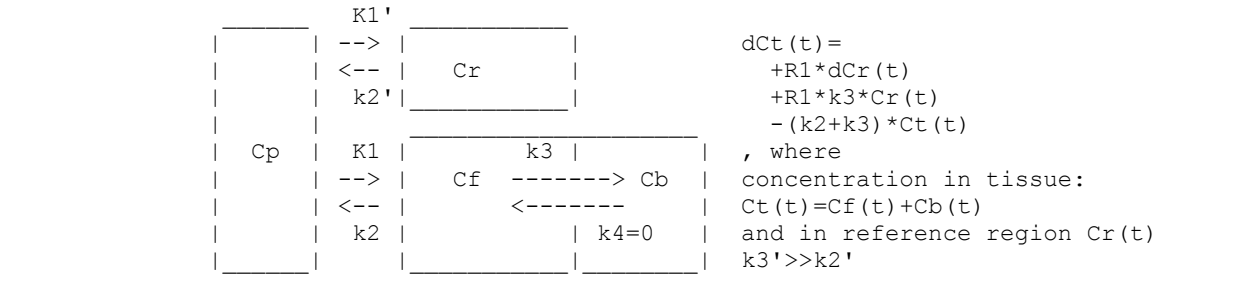
Warning! BP seems to be underestimated with noisy data.
Weights are used if found in TAC data file.

See also: dftweigh, logan, regbfbp, imgsrtm, fit_srtm, dft2ps

Keywords: DFT, modelling, binding potential, distribution volume

lhtrtm 0.3.3 (c) 2003-2008 by Turku PET Centre

Estimates the k3 from transport-limited reference tissue model for
irreversible tracer uptake [1,2].



The model is transformed to general linear least squares functions [2,3],
which are solved using Lawson-Hanson non-negative least squares (NNLS)
algorithm [4]. The k3 can be estimated from either original model
setting [5], or directly without division, but if fitted TACs are saved,
those are always calculated from original model setting.

Parameters:
  1) Regional tissue TAC file (*.dft)
  2) Name of reference region in tissue file, or name of file
     containing reference tissue TAC
  3) Fit end time (min from injection)
  4) Result file (existing file is overwritten)
  5) Fitted regional TAC file (optional)

Options:
 -k3=<original|direct>
     k3 is estimated either from original model setting (original, default)
     or from rearranged model without division (direct)
 -mid[=<y|n>]
     Middle frame times are used (y, default) or not used (n) even if frame
     start and end times are available
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing

Weights are used if found in TAC data file.

References:
1. Herholz K, Lercher M, Wienhard K, Bauer B, Lenz O, Heiss W-D.
   PET measurement of cerebral acetylcholine esterase activity without
   blood sampling. Eur J Nucl Med 2001;28:472-477.
2. Nagatsuka S, Fukushi K, Shinotoh H, Namba H, Iyo M, Tanaka N, Aotsuka A,
   Ota T, Tanada S, Irie T. Kinetic analysis of [11C]MP4A using a high-
   radioactivity brain region that represents an integrated input function
   for measurement of cerebral acetylcholinesterase activity without
   arterial blood sampling. J Cereb Blood Flow Metab 2001; 21: 1354-1366.
3. Blomqvist G. On the construction of functional maps in positron emission
   tomography. J Cereb Blood Flow Metab 1984;4:629-632.
4. Lawson CL & Hanson RJ. Solving least squares problems.
   Prentice-Hall, 1974.
5. Oikonen V. Model equations for reference tissue compartmental models.
   http://www.turkupetcentre.net/reports/tpcmod0002.pdf

See also: fit_trtm, fitk3, dftweigh, r2t_rtcm, dft2svg

Keywords: DFT, modelling, irreversible uptake, reference tissue

```
liverinp 1.0.2  (c) 2003-2013 by Turku PET Centre

Input for liver models consists of two parts: portal vein and hepatic artery.
This program calculates a weighted average of TACs of portal vein and
hepatic artery.

Command-line arguments for the program:
 1) Filename for portal vein TAC
 2) Filename for hepatic artery TAC
 3) Proportion of portal vein input
 4) Filename for output TAC (weighted average)

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing no titles.

Example:
  liverinp ue65pv.kbq ue65ha.kbq 0.90 ue65hi.kbq

See also: dftcalc, interpol, dftcat, dft2csv

Keywords: input, modelling, simulation, liver

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you are welcome to redistribute it under GNU General Public License.
```

```
lmhdr 2.2.2  (c) 1996-2012 by Turku PET Centre

List the information in the main header of an ECAT 6.3 or 7.x file.

Usage: lmhdr [Options] <ECAT file>

Options:
 -h or --help
     Print this message and exit.
 --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example:
     lmhdr s2345dy1.img

See also: lshdr, lmlist, egetstrt, ecatunit, e7emhdr

Keywords: ECAT, header

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```
lmlist 2.2.2  (c) 1996-2012 by Turku PET Centre

List the matrices of an ECAT 6.3 or 7.x file.

Usage: lmlist [Options] <ECAT file>

Options:
 -h or --help
     Print this message and exit.
 --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

e.g.: lmlist s2345dy1.v

See also: esplit, efixplnr, ecatadd, lmhdr, lshdr, ecat2flo, ecat2ana

Keywords: ECAT, matrixlist, header, tool

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```

```
logan 2.0.11 (c) 2000-2013 by Turku PET Centre

Calculates the distribution volume Vt or distribution volume ratio (DVR=BP+1)
using multiple-time graphical analysis (MTGA) for reversible PET
ligands (Logan plot) (1,2,3) from regional PET time-activity curves (TACs).

Parameters:
  1) Tissue TAC file
  2) Name of plasma file OR reference region name in TAC file
  3-4) Start and end times for linear fit
  5) Result file (existing file is overwritten)

Options:
 -k2=<reference region k2>
     With reference region input, the population average of reference
     region k2 (or k2/(1+k5/k6) in 3-compartment model) is set.
 -BPnd
     With reference input, BPnd (=DVR-1) is reported instead of DVR
 -BPnd=<reference region name>
     With plasma input, BPnd can be calculated as DVroi/DVref-1
 -DVR=<reference region name>
     With plasma input, DVR can be calculated as DVroi/DVref
 -BPp=<reference region name>
     With plasma input, BPp can be calculated as DVroi-DVref
 -sd=<y|n>
     Standard deviations are saved (y, default) or not saved (n) in results.
 -mid[=<y|n>]
     Mid frame times are used (y) or not used (n, default) even if frame
     start and end times are available.
 -svg=<Filename>
     Plots are written in specified file in Scalable Vector Graphics (SVG) 1.1
     format; specification in http://www.w3.org/TR/SVG/
 -plotdata=<Filename>
     Data for plots is written in specified file in XHTML table format for
     easy importing in Excel or OpenOffice spreadsheet, where the data can
     be viewed; if filename extension is .dft, data is written in DFT format
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Options for selecting the least-squares line fit method:
 -C  Traditional regression model
 -M  Median of two-point slopes and intercepts (Cornish-Bowden)
 -P  Perpendicular regression model (4)
 -R  Iterative method (York 1966, Lybanon 1984, Reed 1992); default
  If tissue file contains weights, the iterative method (-R) is weighted.
  With other fitting methods the weights are not used.
  With options -C and -R program can automatically find the linear plot
  range, if fit start time is set to zero.

Example 1: tissue curves are in ut2345.dft and plasma curve in ut2345ap.dat;
fitted data range is from 10 to 60 min; standard deviations are not needed:
     logan -nosd ut2345.dft ut2345ap.dat 10 60 ut2345.res

Example 2: tissue curves in ut1234.dft, including reference region 'cer';
reference tissue k2 is assume to equal 0.163;
plot is saved for viewing in ut1234pplot.svg:
     logan -svg=ut2345lplot.svg ut2345.dft cer -k2=0.163 20 60 ut2345.res

References:
1. Logan J, Fowler JS, Volkow ND, Wolf AP, Dewey SL, Schlyer DJ,
   MacGregor RR, Hitzemann R, Bendriem B, Gatley SJ, Christman DR.
```

Graphical analysis of reversible radioligand binding from time-activity measurements applied to [N-11C-methyl]-(-)-cocaine PET studies in human subjects. J Cereb Blood Flow Metab 1990; 10: 740-747.
2. Logan J, Fowler JS, Volkow ND, Wang GJ, Ding YS, Alexoff DL. Distribution volume ratios without blood sampling from graphical analysis of PET data. J Cereb Blood Flow Metab. 1996; 16: 834-840.
3. Logan J. Graphical analysis of PET data applied to reversible and irreversible tracers. Nucl Med Biol 2000; 27:661-670.
4. Varga J & Szabo Z. Modified regression model for the Logan plot. J Cereb Blood Flow Metab 2002; 22:240-244.

See also: imgdv, fitk4, lhsoldv, patlak, rescoll, res2html

Keywords: DFT, modelling, distribution volume, DVR

```
lshdr 2.2.3  (c) 1996-2012 by Turku PET Centre

List the subheader(s) of an ECAT 6.3 or 7.x file.

Usage: lshdr [Options] <ECAT file> [plane [frame]]

Options:
 -h or --help
     Print this message and exit.
 --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

e.g.: lshdr s2345dy1.v 1 1

See also: lmhdr, lmlist, eframe, egetstrt, ecatunit, e7evhdr

Keywords: ECAT, header, tool

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you are welcome to redistribute it under GNU General Public License.
```

```
mapmin 1.0.2  (c) 2002-2007 by Turku PET Centre

Program studies the map of WSS minima of non-linear compartmental models
applied to PET tissue and plasma data.
The following procedure until the frequency of finding new minima gets
lower than a specified value:
  1) make initial parameter values using randon number generator
  2) make delta values using randon number generator
  3) find local minimum using Powell-Brent or Hooke-Jeeves method
  4) save minimum, if differs from the previous saved ones
  5) repeat from 1) until the stop criteria are fulfilled.

Command-line parameters:
  1) Parameter file (see below)
  2) Plasma file
  3) Blood file
  4) Tissue TAC file (*.dft)
  5) Fit end time (duration)
  6) Report file: list of all minima
  7) Result file: parameters at global minimum

e.g.:
mapmin par.set a00919ap.dat a00919ab.dat a00919.dft 999 a00919.log a00919.res

The parameter file contents must be exactly as follows:  1) Model identifier:
     PR= parallel (receptor) model
         with parameters Va, K1, K1/k2, k3, k3/k4, k5, k5/k6
     P = parallel (raceptor) model
         with parameters Va, K1, k2, k3, k4, k5, k6
     SR= serial (metabolism) model
         with parameters Va, K1, K1/k2, k3, k3/k4, k5, k5/k6
     S=  serial (metabolism) model
         with parameters Va, K1, k2, k3, k4, k5, k6
     LR= kLoss model
         with parameters Va, K1 K1/k2 k3 kLoss
     L = kLoss model
         with parameters Va, K1, k2, k3, kLoss
  2) Lower and upper limits for each of the parameters
     Parameter can be fixed to a certain value by setting equal limits;
     fixing a ratio k3/k4 or k5/k6 to zero sets k4 or k6 to zero.
  3) Value of K1/F (0, if blood flow is not considered)
  4) Number of sampled points (prfmNr)

Results are appended to the end of files, if they exist already.
Fitted curves are written in DFT format, if filename is given.
```

```
metabcor 1.3.9  (c) 1996-2013 by Turku PET Centre

Calculate TACs of authentic (unchanged) tracer and radioactive
metabolite(s) from measured plasma TAC and fractions of authentic tracer.
For more information, read
http://www.turkupetcentre.net/analysis/doc/metab_corr.html

Usage: metabcor [Options] <Plasma datafile> <Fraction datafile>

Fraction file can have either of two formats:
 1) it can contain the sample times, and the fraction(s) of authentic
    tracer, and optionally the fractions of different metabolites; or
 2) parameters of a mathematical function fitted to the fraction curves.

By default, result TACs are written in files named as *_pure.* and
*_met.*, and if several metabolites exist, the following as *_met2.*
and *_met3.*

Options:
 -fnpure=<file name for parent tracer TAC>
 -fnmet=<file name for plasma metabolite TAC>
 -fnmet2=<file name for the second plasma metabolite TAC>
 -fnmet3=<file name for the 3rd plasma metabolite TAC>
 -pure=<id>
        The result file is named by adding specified id text before file
        extension, instead of the default '_pure'.
 -met=<id>
        The result file is named by adding specified id text before file
        name extension, instead of the default '_met'.
 -met2=<id>
        The result file is named by adding specified id text before file
        name extension, instead of the default '_met2'.
 -met3=<id>
        The result file is named by adding specified id text before file
        name extension, instead of the default '_met3'.
 -h or --help
        Print this message and exit.
 --build or --version
        Print software build information and exit.
 --silent
        Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: fit_ppf, fit_fexp, fit2dat, dft2svg, dftcalc

Keywords: input, plasma, modelling, metabolite correction

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you are welcome to redistribute it under GNU General Public License.
```

mkcalhdr 1.0.0 (c) 2005-2006 by Turku PET Centre

Calculates calibration factor. Assumes that there is a cylindrical phantom
with 20 cm diameter in the FOV. Resulting calibration header file is written
in file STUDY_RECMETHOD_iMNsXY_sS.cal.hdr, where STUDY is the part of the
calibration study name preceding delimiter "_", "-", "." or space, RECMETHOD is
the utilised reconstruction method, iMN is the number of iterations preceded
by char i, sXY is the number of subsets preceded by char s and sS is the span
preceded by char s. If calibration is calculated for 128 x 128 matrix size, suffix
m128 is appended in header file name.

Efficient factor for each plane is calculated as mean over planes 19-189 divided by
plane average. Efficient factor is set to zero for planes 0-5 and 200-206.

Usage: mkcalhdr [-Options] -a <A> <interfile image(s) separated with space>

Options:
  -h -H   print usage and exit
  -v -V   print version and exit
  -s -S   calculate standard deviation in VoI

Parameters:
  -a A (required) A is the activity concentration at scan start time in Bq/ml.

Keywords: image processing, quantification, calibration, interfile

See also: if2e7, run_if2e7

mpatlak 1.1.2 (c) 2002-2005 by Turku PET Centre

Calculates the influx (uptake) rate constant Ki, using modified Gjedde-Patlak plot (1, 2, 3). Modification by Vesa Oikonen (unpublished).

Parameters:
  1) Tissue TAC file
  2) Name of plasma file OR reference region name in TAC file
  3-4) Start and end times for linear fit
  5) Result file (existing file is overwritten)
 [6) Filename for plot data (optional)]

Options:
 -N SDs are not saved in the results.
 -mid[=<y|n>]
     Mid frame times are used (y) or not used (n, default) even if frame
     start and end times are available.

e.g. mpatlak ut1234.dat ut1234ap.dat 10 60 ut1234.res
 or mpatlak ut1234.dft cer 10 60 ut1234.res ut1234mplot.htm

Least-squares line fit method can be selected with following options:
-C   Traditional regression model (default)
-M   Median of two-point slopes and intercepts (Cornish-Bowden)
-P   Perpendicular regression model (4)
-R   Iterative method (York 1966, Lybanon 1984, Reed 1992)

In current program version, the weights are not used in the fit.

References:
1. Gjedde A. Calculation of cerebral glucose phosphorylation from brain
   uptake of glucose analogs in vivo: a re-examination. Brain Res. 1982;
   257:237-274.
2. Patlak CS, Blasberg RG, Fenstermacher JD. Graphical evaluation of
   blood-to-brain transfer constants from multiple-time uptake data.
   J Cereb Blood Flow Metab 1983;3:1-7.
3. Patlak CS, Blasberg RG. Graphical evaluation of blood-to-brain transfer
   constants from multiple-time uptake data. Generalizations.
   J Cereb Blood Flow Metab 1985;5:584-590.
4. Varga J & Szabo Z. Modified regression model for the Logan plot.
   J Cereb Blood Flow Metab 2002; 22:240-244.

See also: patlak, fitk3, lhsolki, rescoll

Keywords: DFT, modelling, irreversible uptake, net influx

```
mvar4dat 1.1.1  (c) 2001-2008 by Turku PET Centre

Program for adding Gaussian noise to time-activity data.
Variance (SD) for each time frame is specified in SD file.
SD file can be made e.g. with program dftstd.

Usage:  mvar4dat <Datafile> <SD file> <Output file>

Options:
 -S[eed]=<seed for random number generator>
     Computer clock is used by default
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

TAC file format is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: dftstd, var4dat, fvar4dat, wvar4dat, rescoll

Keywords: DFT, noise, simulation

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you are welcome to redistribute it under GNU General Public License.
```

```
nii2ecat 0.1.1  (c) 2013 by Turku PET Centre

Conversion of NIfTI-1 PET image database(s) to ECAT 7 image volume
image format.

Usage: nii2ecat [Options] <NIfTI database OR path>

Options:
 -O=<output path>
     Data directory for ECAT images; by default current working directory
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
Conversion of all NIfTI images in directory S:\temp\neuro to ECAT 7
images in directory C:\data in PC/Windows:
   C:
   cd \data
   nii2ecat s:\temp\neuro

NIfTI file(s) must be named as *.nii (single format) or *.hdr and *.img
(dual format).
Program reads frame time information in SIF file, if that file is located
in the NIfTI database directory and if it is named with *.sif extension.

See also: eframe, sif2ecat, e7emhdr, e7evhdr, flo2ecat, ana2ecat
and ImageConverter (.NET version) in
http://www.turkupetcentre.net/programs/tpc_csharp.html

Keywords: image processing, format conversion, ECAT, NIfTI

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you are welcome to redistribute it under GNU General Public License.
```

```
nii_ehdr 0.1.0  (c) 2013 by Turku PET Centre

Edit the information in NIfTI-1 image header.
New contents are given in an ASCII text file with one or more header fields
in the same format as is the output of nii_lhdr.
Use this program only if you are familiar with NIfTI format; note that
no backup is created.

Usage: nii_ehdr <NIfTI file> <Header content file>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing
 --silent
     Program works silently, printing only error and warning messages.

Example: copy header contents from image1.nii to image2.nii
     nii_lhdr image1.nii > header.dat
     nii_ehdr image2.nii header.dat

See also: nii_lhdr, iftlist, iftdel, iftadd, ana_lhdr

Keywords: image processing, NIfTI, header

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you are welcome to redistribute it under GNU General Public License.
```

```
nii_lhdr 0.1.1  (c) 2013 by Turku PET Centre

List the information in NIfTI-1 image header. Optionally, only the specified
header field is printed.

Usage: nii_lhdr <NIfTI file> [Header field name]

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit

See also: nii_ehdr, ana_lhdr, ana_ehdr, iftlist

Keywords: image processing, NIfTI, header

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you are welcome to redistribute it under GNU General Public License.
```

o2metab 1.3.0 (c) 2002,2008 by Turku PET Centre

Calculates the blood time-activity curves (TACs) of labelled water and
oxygen from arterial blood TAC measured after [O-15]O2 bolus using
a dedicated [O-15]O2 metabolite model (1, 2) to be used as input in
oxygen-15 model.

Command-line arguments:
  1) Arterial blood TAC file (corrected for decay, sample times in sec)
  and optionally either:
  2) Parameter file (produced by fit_o2bl version 1.2 or later)
  or:
  2) model parameter k1 (1/sec)
  3) model parameter k3 (1/sec)
  4) model parameter k4 (1/sec)
  5) model parameter delay (sec)

Options:
 -o2w
     Simulates the blood [O-15]H2O TAC from [O-15]O2 TAC which is in this
     case provided as input.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints lots of information about what it is doing.

Labeled oxygen and water TACs are written in the same folder than blood TAC
is, with _o and _w added in the filename before extension.

Example 1: calculation of oxygen and water curves with default model
           parameters
  o2metab s4455blo.kbq

Example 2: calculation of oxygen and water curves with user-specified
           model parameters
  o2metab s4455blo.kbq 1.307e-3 2.034e-3 0 0

Example 3: simulation of water curve from oxygen curve with default model
           parameters
  o2metab -o2w s4455blo_o.kbq

References:
1. Huang S-C et al. Modelling approach for separating blood time-activity
   curves in positron emission tomographic studies.
   Phys Med Biol. 1991;36(6):749-761.
2. Iida H et al. Modelling approach to eliminate the need to separate
   arterial plasma in oxygen-15 inhalation positron emission tomography.
   J Nucl Med. 1993;34:1333-1340.

See also: fit_o2bl, o2_p2w, fit_mo2, metabcor, dft2svg

Keywords: DFT, input, blood, metabolite correction, oxygen

o2_p2w 2.0.0 (c) 2002,2013 by Turku PET Centre

Convert measured arterial plasma TAC from a [O-15]O2 PET study
to blood [O-15]H2O TAC (1).

Usage:
  o2_p2w [Options] <Plasma TAC file> <Blood H2O file>

Options:
 -HCT=<Hematocrit>
     Specify the hematocrit; when specified, the plasma-to-blood ratio
     is calculated using it, assuming that water contents of RBCs and
     plasma are 0.73 and 0.94, respectively.
 -PBR=<Plasma-to-blood ratio>
     Specify the plasma-to-blood ratio; by default 1.12; effective only
     when HCT is not given.
 -SCT=<Sample collect time>
     Plasma sample collection time (usually 20 s) should be given for
     accurate fit with fit_o2bl.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

References:
1. Lubberink M, Wong YY, Raijmakers PGHM, Schuit RC, Luurtsema G,
   Boellaard R, Knaapen P, Vonk-Noordegraaf A, Lammertsma AA. Myocardial
   oxygen extraction fraction measured using bolus inhalation of 15O-oxygen
   gas and dynamic PET. J Nucl Med. 2011;52(1):60-66.

See also: fit_o2bl, o2metab, b2t_mo2, fit_mo2, dft2svg, dft2csv

Keywords: input, oxygen, blood, metabolite correction

```
p2blood 1.8.3  (c) 2002-2014 by Turku PET Centre

Converts plasma time-activity curves (TACs) collected during a PET study
to blood TACs, based on tracer-dependent population-based
RBC/plasma or plasma/blood ratio functions over time.

Usage:  p2blood [Options] <Tracer> <Plasmafile> <HCr> <Bloodfile>

Options:
 -Log
     Log information is saved in output file.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

The following human PET tracer TACs can be converted:
  AH690
     ratio is assumed to follow a population average curve.
  AH691
     ratio is assumed to follow a population average curve.
  Carfentanil
     ratio is assumed to follow a population average curve
     (unpublished measurements from eight 70-min PET studies).
  FBPA
     ratio is assumed to rise from zero with slope 0.00888
     (unpublished measurement from 10 subjects).
  FDG
     ratio is assumed to be 0.8 in the beginning and to rise with
     slope 0.0012/min (Phelps ME et al. Ann Neurol 1979;6:371-388).
  FDOPA
     ratio is assumed to follow equation R(t)=(Rmax*t)/(Th+t),
     where Rmax=1.446 and Th=83.56 (unpublished results).
  Flu[mazenil]
     ratio is assumed to follow an average curve based on two
     subjects with assumed HCR=0.43.
  FTHA
     concentration in red blood cells is assumed to be zero.
  MEAIB
     ratio is assumed to rise from zero with slope 0.00398
     (unpublished measurement from 7 subjects).
  Metomidate or MTO
     concentration is the same in RBC and plasma water.
  ORM-B
     ratio is assumed to follow a population average curve
     (unpublished measurement from 6 subjects studied twice).
  Palm[itate]
     ratio is assumed to follow a population average curve
     (unpublished measurement from 8 subjects).
  PE2I
     ratio is assumed to follow a population average curve
     (unpublished measurements from ten 70-min PET studies).
  PIB or 6OHBTA1
     ratio is assumed to follow a population average curve,
     currently based on 15 subjects.
  PK11195
     ratio is assumed to follow a curve based on one
     subject with measured HCr.
For mice and rats (these conversion do not utilize hematocrit):
  MOUSEFDG
     plasma-to-blood ratio is assumed to follow the function published by
     Yu AS et al. J Nucl Med 2009;50(6):966-973.
  RATFDG
```

plasma-to-blood ratio is assumed to follow the function published by
Weber et al. Eur J Nucl Med 2002;29(3):319-323.

Codes for tracers that have below mentioned properties:
  norbc
    concentration in red blood cells is assumed to be zero.
  inwater
    concentration is the same in RBC and plasma water.

Times must be in minutes in data files, or seconds, if appropriately
specified inside the file. File format specification in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

The hematocrit (HCr, HCT) is normally between 0.40-0.51 in men and 0.36-0.47
in women. Note that HCr is lower in small vessels.

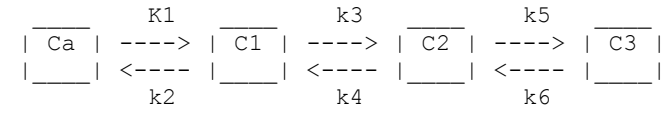
Example: estimate blood curve from measured FDG plasma TAC:
    p2blood FDG i3344ap.kbq 0.38 i3344ab.kbq

See also: b2plasma, b2rbc, dftcalc, dftcbv, imgcbv, fit_bpr

Keywords: input, modelling, simulation, blood, plasma, RBC, hematocrit

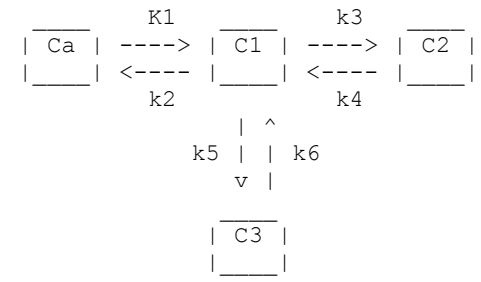
p2t_3c 1.2.1 (c) 2001-2013 by Turku PET Centre

Simulation of PET tissue time-radioactivity concentration curve (TAC)
from arterial plasma (Ca) TAC based on three-tissue compartmental model,
where the compartments are in series (default):




```
  dC1(t)/dt = K1*Ca(T) - (k2+k3)*C1(T) + k4*C2(T)
  dC2(t)/dt = k3*C1(T) - (k4+k5)*C2(T) + k6*C3(T)
  dC3(t)/dt = k5*C2(T) - k6*C3(T)
  Ct(T) = C1(T) + C2(T) + C3(T)
```

, or, optionally, three-tissue compartmental model, where the 2nd and 3rd
tissue compartments are parallel, often used to represent specific and
non-specific binding:




```
  dC1(t)/dt = K1*Ca(T) - (k2+k3+k5)*C1(T) + k4*C2(T) + k6*C3(T)
  dC2(t)/dt = k3*C1(T) - k4*C2(T)
  dC3(t)/dt = k5*C1(T) - k6*C3(T)
  Ct(T) = C1(T) + C2(T) + C3(T)
```

Parameters:
  1) Plasma TAC filename
  2-7) K1, k2, k3, k4, k5, k6
  8) Filename for simulated TACs

Options:
 -paral[lel]
     Model with parallel compartments C2 and C3 is applied.
 -ser[ies]
     Model with compartments C1, C2, and C3 in series is applied (default).
 -sub | -nosub
     TACs of sub-compartments (C1, C2 and C3) are written (-sub, default)
     or not written (-nosub) into the output file.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

If the times in plasma file are in seconds, the units of rate constants
must be specified as 1/sec.
For accurate results, plasma TAC should have very short sampling intervals.
To reduce the model, k5 or k3 can be set to 0.

Simulated TACs are written in ASCII format with columns:
  1) Sample time
  2) Total tissue activity concentration (Ct)
  3) Activity concentration in 1st tissue compartment (C1)
  4) Activity concentration in 2nd tissue compartment (C2)

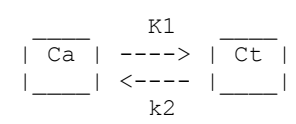
5) Activity concentration in 3rd tissue compartment (C3)

See also: p2t_v3c, p2t_di, dftadd, dftren, fr4sim, dft2csv, dft2img

Keywords: DFT, simulation, modelling, compartmental model

p2t_conv 1.0.1 (c) 2005,2006 by Turku PET Centre

Simulation of PET tissue time-radioactivity concentration curve (TAC)
from arterial plasma (Ca) TAC based on one-tissue compartmental model.



Ct(T) = K1*Ca(T) (x) exp[-k2*T]
, where (x) denotes the operation of convolution

Parameters:
  1) Plasma TAC filename
  2-3) k1, k2
  8) Filename for simulated TACs

Options:
 -h or --help
     Print this message and exit
 -v, --build, or --version
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.

If the times in plasma file are in seconds, the units of rate constants
must be specified as 1/sec.

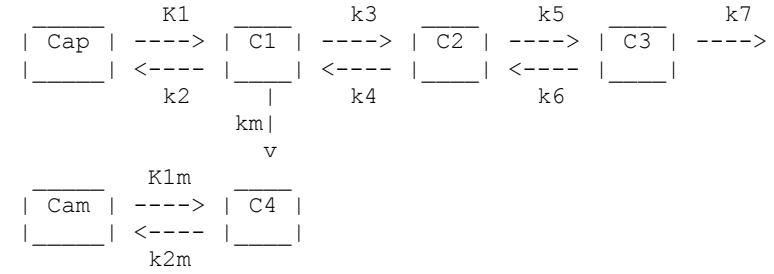
See also: p2t_3c

Keywords: DFT, simulation

p2t_di 0.1.1 (c) 2013 by Turku PET Centre

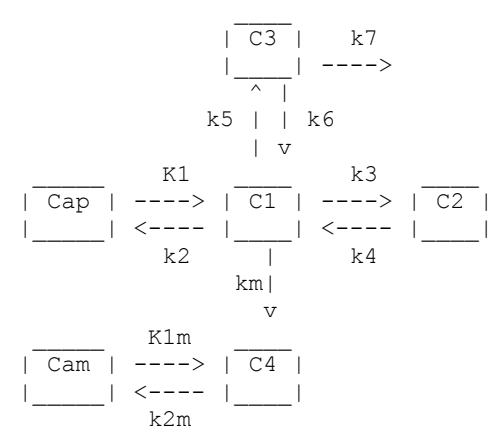
Simulation of PET tissue time-radioactivity concentration curve (TAC) using dual-input four-tissue compartmental model. Input consists of parent tracer and metabolite concentration curves in arterial plasma (Cap and Cam) and total radioactivity concentration in arterial blood (Cb).

Tissue compartments for parent tracer are in series [1] (by default):




```
  dC1(t)/dt = K1*Cap(T) - (k2+k3+km)*C1(T) + k4*C2(T)
  dC2(t)/dt = k3*C1(T) - (k4+k5)*C2(T) + k6*C3(T)
  dC3(t)/dt = k5*C2(T) - (k6+k7)*C3(T)
  dC4(t)/dt = K1m*Cam(T) + km*C1(T) - k2m*C4(T)
  Ct(T) = C1(T) + C2(T) + C3(T) + C4(T)
  Cvb(T) = Cab(T) - dCt(t)/dt / f
  Cpet(T)= Vb*fA*Cab(T) + Vb*(1-fA)*Cvb(T) + (1-Vb)*Ct(T)
```

, or, optionally, the 2nd and 3rd tissue compartments are parallel [2], often used to represent specific and non-specific binding:




```
  dC1(t)/dt = K1*Ca(T) - (k2+k3+k5+km)*C1(T) + k4*C2(T) + k6*C3(T)
  dC2(t)/dt = k3*C1(T) - k4*C2(T)
  dC3(t)/dt = k5*C2(T) - (k6+k7)*C3(T)
  dC4(t)/dt = K1m*Cam(T) + km*C1(T) - k2m*C4(T)
  Ct(T) = C1(T) + C2(T) + C3(T) + C4(T)
  Cvb(T) = Cab(T) - dCt(t)/dt / f
  Cpet(T)= Vb*fA*Cab(T) + Vb*(1-fA)*Cvb(T) + (1-Vb)*Ct(T)
```

Command-line arguments:
  1) Plasma parent TAC filename
  2) Plasma metabolite TAC filename
  3) Blood TAC filename
  4-13) Rate constants K1, k2, k3, k4, k5, k6, k7, km, K1m, and k2m
  14) Vascular volume fraction Vb (%)
  15) Filename for simulated TACs

Options:
 -paral[lel]
     Model with parallel compartments C2 and C3 is applied.

```
 -ser[ies]
     Model with compartments C1, C2, and C3 in series is applied (default).
 -f=<Perfusion (ml/(min*ml) or ml/(sec*ml))>
     Difference between concentrations in venous and arterial blood can
     be simulated if tissue perfusion (f>K1) is specified with this option
     and arterial fraction of vascular volume is set with option -fA;
     by default it is assumed that venous and arterial activities are
     the same (f>>K1).
 -fA=<Arterial fraction of vascular volume (%)>
     Difference between concentrations in venous and arterial blood can
     be simulated if arterial fraction of vascular volume is specified with
     this option and tissue perfusion is set with option -f;
     by default it is assumed that Vb consists of only arterial blood.
 -sub | -nosub
     TACs of sub-compartments (C1, C2 and C3) are written (-sub)
     or not written (-nosub, default) into the output file.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

If the times in plasma file are in seconds, the units of rate constants
(k's) and blood flow (f) must also be specified as 1/sec.
For accurate results, plasma TAC should have very short sampling intervals.
To reduce the model, k7, k5, and k3 can be set to 0.

Simulated TACs are written in ASCII format with columns:
  1) Sample time
  2) Total tissue activity concentration (Cpet)
  3) Activity concentration in 1st tissue compartment, (1-Vb)*C1
  4) Activity concentration in 2nd tissue compartment, (1-Vb)*C2
  5) Activity concentration in 3rd tissue compartment, (1-Vb)*C3
  6) Activity concentration in 4th tissue compartment, (1-Vb)*C4
  7) Arterial concentration to tissue activity, Vb*fA*Cab (optional)
  8) Venous contribution to tissue activity, Vb*(1-fA)*Cvb (optional)

References:
1. TPCMOD0001 Appendix B.
2. TPCMOD0001 Appendix C.

See also: p2t_v3c, dftadd, dftren, fr4sim, dft2csv, dft2img

Keywords: DFT, simulation, modelling, compartmental model, dual-input

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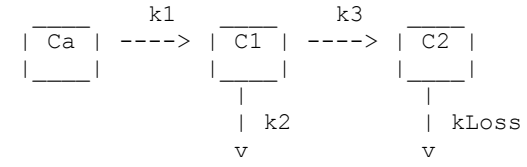
you are welcome to redistribute it under GNU General Public License.
```

p2t_loss 1.2.0 (c) 2001-2012 by Turku PET Centre

Simulation of PET tissue time-radioactivity concentration curve (TAC)
from arterial plasma (Ca) TAC, based on two-tissue compartmental model
with a loss of tracer from the second compartment to plasma.




```
  dC1(t)/dt = K1*Ca(T) - (k2+k3)*C1(T)
  dC2(t)/dt = k3*C1(T) - kLoss*C2(T)
  Ct(T) = C1(T) + C2(T) + C3(T)
```

Parameters:
  1) Plasma TAC filename
  2-5) k1, k2, k3, kLoss
  6) Filename for simulated TACs

Options:
 -sub | -nosub
     TACs of sub-compartments (C1 and C2) are written (-sub, default)
     or not written (-nosub) into the output file.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

If the times in plasma file are in seconds, the units of rate constants
must be specified as 1/sec.
For accurate results, plasma TAC should have very short sampling intervals.

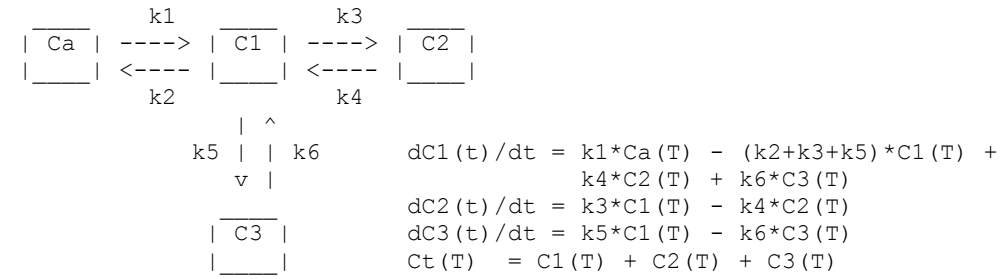
Results are saved in DFT format, where the TACs are:
  1) Total tissue activity concentration (Ct)
  2) Activity concentration in 1st tissue compartment (C1)
  3) Activity concentration in 2nd tissue compartment (C2)

See also: p2t_3c, p2t_v3c, dftadd, dftren, fr4sim, dft2csv, dft2img

Keywords: DFT, simulation, compartmental model, loss rate

p2t_p3c 1.1.1 (c) 2001-2006 by Turku PET Centre

Simulation of PET tissue time-radioactivity concentration curve (TAC)
from arterial plasma (Ca) TAC based on three-tissue compartmental model,
where the second and third compartments are parallel, often used to
represent specific and non-specific binding.



Parameters:
  1) Plasma TAC filename
  2-7) k1, k2, k3, k4, k5, k6
  8) Filename for simulated TACs

Options:
 -nosub
     TACs of sub-compartments (C1, C2 and C3) are not written into output file.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

If the times in plasma file are in seconds, the units of rate constants
must be specified as 1/sec.
For accurate results, plasma data should have very short (e.g. 0.1 min)
time 'frames'.
To reduce the model, k5 and/or k3 can be set to 0.

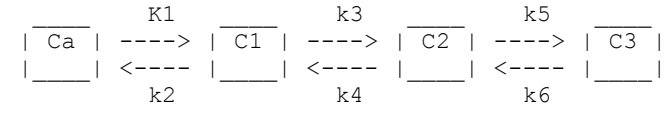
Results are saved in DFT format, where the TACs are:
  1) Total tissue activity concentration (Ct)
  2) Activity concentration in 1st tissue compartment (C1)
  3) Activity concentration in 2nd tissue compartment (C2)
  4) Activity concentration in 3rd tissue compartment (C3)

See also: p2t_3c, p2t_vp3c, dftadd, dftren, fr4sim, dft2img

Keywords: DFT, simulation

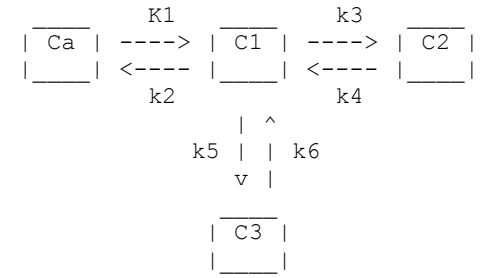
p2t_v3c 1.2.1 (c) 2001-2013 by Turku PET Centre

Simulation of PET tissue time-radioactivity concentration curve (TAC)
from arterial plasma (Ca) and blood (Cb) TACs, based on three-tissue
compartmental model, where the compartments are in series (default):




```
  dC1(t)/dt = K1*Ca(T) - (k2+k3)*C1(T) + k4*C2(T)
  dC2(t)/dt = k3*C1(T) - (k4+k5)*C2(T) + k6*C3(T)
  dC3(t)/dt = k5*C2(T) - k6*C3(T)
  Ct(T) = C1(T) + C2(T) + C3(T)
  Cvb(T) = Cab(T) - dCt(t)/dt / f
  Cpet(T)= Vb*fA*Cab(T) + Vb*(1-fA)*Cvb(T) + (1-Vb)*Ct(T)
```

, or, optionally, three-tissue compartmental model, where the 2nd and 3rd
tissue compartments are parallel, often used to represent specific and
non-specific binding:




```
  dC1(t)/dt = K1*Ca(T) - (k2+k3+k5)*C1(T) + k4*C2(T) + k6*C3(T)
  dC2(t)/dt = k3*C1(T) - k4*C2(T)
  dC3(t)/dt = k5*C1(T) - k6*C3(T)
  Ct(T) = C1(T) + C2(T) + C3(T)
  Cvb(T) = Cab(T) - dCt(t)/dt / f
  Cpet(T)= Vb*fA*Cab(T) + Vb*(1-fA)*Cvb(T) + (1-Vb)*Ct(T)
```

Command-line arguments:
  1) Plasma TAC filename
  2) Blood TAC filename
  3-8) K1, k2, k3, k4, k5, k6
  9) Blood flow f (ml/(min*ml)); set to 0 to assume that f>>K1 and Cvb=Cab
  10) Vascular volume fraction Vb (%)
  11) Arterial fraction of vascular volume fA (%)
  12) Filename for simulated TACs

Options:
 -paral[lel]
     Model with parallel compartments C2 and C3 is applied.
 -ser[ies]
     Model with compartments C1, C2, and C3 in series is applied (default).
 -sub | -nosub
     TACs of sub-compartments (C1, C2 and C3) are written (-sub, default)
     or not written (-nosub) into the output file.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

If the times in plasma file are in seconds, the units of rate constants

(k's) and blood flow (f) must also be specified as 1/sec.
For accurate results, plasma TAC should have very short sampling intervals.
To reduce the model, k5 or k3 can be set to 0.

Simulated TACs are written in ASCII format with columns:
  1) Sample time
  2) Total tissue activity concentration (Cpet)
  3) Activity concentration in 1st tissue compartment, (1-Vb)*C1
  4) Activity concentration in 2nd tissue compartment, (1-Vb)*C2
  5) Activity concentration in 3rd tissue compartment, (1-Vb)*C3
  6) Arterial concentration to tissue activity, Vb*fA*Cab
  7) Venous contribution to tissue activity, Vb*(1-fA)*Cvb

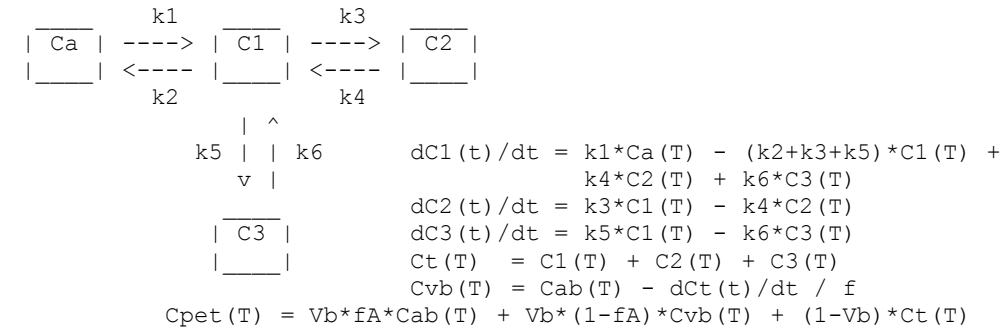
References:
1. TPCMOD0001.

See also: p2t_3c, p2t_di, dftadd, dftren, fr4sim, dft2csv, dft2img

Keywords: DFT, simulation, modelling, compartmental model

p2t_vp3c 1.1.0 (c) 2001,2005 by Turku PET Centre

Simulation of PET tissue time-radioactivity concentration curve (TAC)
from arterial plasma (Ca) and blood (Cb) TACs, based on three-tissue
compartmental model, where the second and third compartments are parallel,
often used to represent specific and non-specific binding.



Parameters:
  1) Plasma TAC filename
  2) Blood TAC filename
  3-8) k1, k2, k3, k4, k5, k6
  9) Blood flow f (ml/(min*ml));
     set to 0 to assume that f>>K1 and Cvb=Cab
  10) Vascular volume fraction Vb (%)
  11) Arterial fraction of vasclar volume fA (%)
  12) Filename for simulated TACs

Options:
  -nosub
   TACs of sub-compartments are not written into output file.

If the times in plasma file are in seconds, the units of rate constants
(k's) and blood flow (f) must be specified as 1/sec.
For accurate results, plasma data should have very short (e.g. 0.1 min)
time 'frames'.
To reduce the model, k5 or k3 can be set to 0.

Results are saved in DFT format, where the TACs are:
  1) Total tissue activity concentration (Cpet)
  2) Activity concentration in 1st tissue compartment, (1-Vb)*C1
  3) Activity concentration in 2nd tissue compartment, (1-Vb)*C2
  4) Activity concentration in 3rd tissue compartment, (1-Vb)*C3
  5) Arterial concentrationcontribution to tissue activity, Vb*fA*Cab
  6) Venous contribution to tissue activity, Vb*(1-fA)*Cvb

See also: p2t_v3c, p2t_p3c, dftadd, dftren, fr4sim, dft2img

Keywords: DFT, simulation

```
parsexml 2.0.1  (c) 2005-2012 by Turku PET Centre

Software is used for extracting fields from XML-files. Uses expat library.

Usage:
    parsexml [options] <field name> <XML document>

Options:
   -h --help     print usage and exit
   -v --version  print version and exit

Keywords: XML, format

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you are welcome to redistribute it under GNU General Public License.
```

```
patlak 1.8.10  (c) 2001-2013 by Turku PET Centre

Calculates the influx (uptake) rate constant Ki (ml/(min*ml)) as slope of
the Gjedde-Patlak plot (1,2,3) from regional PET time-activity curves (TACs).

Parameters:
  1) Tissue TAC file
  2) Name of plasma file OR reference region name in TAC file
  3-4) Start and end times for linear fit (min)
  5) Result file (existing file is overwritten)

Options for calculation of metabolic rate:
 -Ca=<value>
     Concentration of native substrate in arterial plasma (mM),
     for example plasma glucose in [18F]FDG studies.
     With this option the metabolic rate (umol/(min*100 g)) is calculated.
 -LC=<value>
     Lumped Constant in MR calculation; default is 1.0.
 -density=<value>
 -d=<value>
     Tissue density in MR calculation; default is 1.0 g/ml.

General options:
 -ic=<y axis intercept>
     Force y axis intercept to specified value; for FUR or Ri calculation
     use regfur.
 -sd=<y|n>
     Standard deviations are saved (y, default) or not saved (n) in results.
 -mid=<Y|n>
     Frame middle times are used (y), or not used (n, default), even if frame
     start and end times are available. For compatibility with old software.
 -svg=<Filename>
     Plots are written in specified file in Scalable Vector Graphics (SVG) 1.1
     format; specification in http://www.w3.org/TR/SVG/
 -plotdata=<Filename>
     Data for plots is written in specified file in XHTML table format for
     easy importing in Excel or OpenOffice spreadsheet, where the data can
     be viewed; if filename extension is .dft, data is written in DFT format
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Options for selecting the least-squares line fit method:
 -C  Traditional regression model (default)
 -M  Median of two-point slopes and intercepts (Cornish-Bowden)
 -P  Perpendicular regression model (4)
 -R  Iterative method (York 1966, Lybanon 1984, Reed 1992)
In the present software version, the weights are not used in the fit.

Example 1: tissue curves are in ut1234.dat and plasma curve in ut1234ap.dat;
fitted data range is from 10 to 60 min; standard deviations are not needed:
     patlak -nosd ut1234.dat ut1234ap.dat 10 60 ut1234.res

Example 2: tissue curves in ut1234.dft, including reference region 'cer';
plot is saved for viewing in ut1234pplot.svg:
     patlak -svg=ut1234pplot.svg ut1234.dft cer 10 60 ut1234.res

References:
1. Gjedde A. Calculation of cerebral glucose phosphorylation from brain
   uptake of glucose analogs in vivo: a re-examination. Brain Res. 1982;
   257:237-274.
2. Patlak CS, Blasberg RG, Fenstermacher JD. Graphical evaluation of
```

blood-to-brain transfer constants from multiple-time uptake data.
J Cereb Blood Flow Metab 1983;3:1-7.
3. Patlak CS, Blasberg RG. Graphical evaluation of blood-to-brain transfer constants from multiple-time uptake data. Generalizations.
J Cereb Blood Flow Metab 1985;5:584-590.
4. Varga J & Szabo Z. Modified regression model for the Logan plot.
J Cereb Blood Flow Metab 2002; 22:240-244.

See also: imgki, fitk3, fitkloss, lhsolki, regfur, logan, rescoll, dfttime

Keywords: DFT, modelling, irreversible uptake, net influx rate, Ki

```
paucinf 1.4.2  (c) 2002-2009 Turku PET Centre

Estimates the half-life (t1/2) and elimination rate constant (kEL) of
a PET tracer in plasma, and the AUC of plasma time-activity curve from
0 to infinite time. AUC can be used e.g. to estimate the total clearance of
PET tracer after a single intravenous dose:
          Dose
   Cl = --------
     T  AUC
           0-Inf
The natural logarithm of tracer concentration is plotted against time
from bolus infusion. The plot becomes linear in the end phase, as the
tracer is eliminated according to the laws of first-order reaction
kinetics. The slope of the linear part of the plot equals -kEL.

Usage:  paucinf <Plasmafile> [Result file]

Options:
 -end=<sample time>
     Use data from 0 to given time in the line fit; by default
     search for the best line fit extends to the last sample
 -start=<sample time>
     Use data from given time to end in the line fit; by default,
     the search for the best line fit extends to the first sample
 -winnonlin
     Best line fit is searched using algorithm that gives similar results
     to WinNonlin with the same simple model
 -svg=<Filename>
     Plots of log transformed TACs and fitted lines are written in specified
     file in Scalable Vector Graphics (SVG) 1.1 format; specification in
     http://www.w3.org/TR/SVG/
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Plasmafile must contain a time column, and one or more concentration columns
separated by space(s) or tabulator(s). The result is printed on screen.

See also: extrapol, interpol, fit_exp, fit2dat

Keywords: input, modelling, pharmacokinetics, clearance, elimination rate

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```

```
pdoc2htm 1.4.3 (c) 2002-2013 by Turku PET Centre

Convert the information text, printed by command-line programs,
to XHTML 1.0 format.
For software developed in Turku PET Centre, these documents are stored
in http://www.turkupetcentre.net/programs/doc/

Usage: pdoc2htm <Text file> [HTML filename]

Options:
 -L  Sets HTML-links for 'See also:' list
 -validator=<yes|no>
     Link to W3C XHTML validator is added or not added (default)
 -GPL=<yes|no>
     Link to GNU GPL is added (default) or not added
 -XML
     Document is saved in XML format for automatic program listing;
     options -L, -validator, and -gpl are not effective
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

Example:
  program --help > temp.txt
  pdoc2htm temp.txt program.html

See also: progvers, adddate

Keywords: programming, tools

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you are welcome to redistribute it under GNU General Public License.
```

```
pet2pet 1.2  (c) 2004 by Turku PET Center

This program is used to fit PET image into PET image.
PET images can be in ECAT 6.3 or ECAT 7 format.

Usage: pet2pet.exe <pet1 file>  <pet2 file>  <new pet file> [options]

e.g.: pet2pet dy1.img dy2.img new.img

For more information type 'pet2pet.exe o'.
```

```
pm2dft 0.1.0  (c) 2007 by Turku PET Centre

Extracts the sectors in every ring of a ECAT 7 polar map into DFT file.

Usage:
  pm2dft [Options] <ECAT file> <DFT filename>

This program writes the following information (contents is dependent on the
polar map) in DFT file as comments; this is needed if DFT file is converted
back to ECAT 7 polar map:
# num_rings := 4
# sectors_per_ring := 6 6 4 1
# ring_position := 0 0.2 0.4 0.6
# ring_angle := 90 90 45 0

Options:
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

See also: dft2pm, img2dft, ecat2flo, imgpext, epxl2dft

Keywords: ECAT, polarmap, DFT, myocardium, file format conversion

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```

```
pmod2dft 0.1.2  (c) 2012 by Turku PET Centre

Program for converting PMOD TAC and BLD files into DFT format.

Other programs are able to read PMOD files directly, if they are built
with libtpccurveio version 2.1.0 or later (check with option --build).
Note that programs built with earlier libtpccurve version may seem to read
PMOD files directly, but result may not be correct.

Usage: pmod2dft [Options] <PMOD file(s)>

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

See also: dft2pmod, dft2csv, dftbreak, dftadd, dftunit, dftframe

Keywords: DFT, PMOD, TAC, BLD, file format conversion

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you are welcome to redistribute it under GNU General Public License.
```

```
ppet2dft 0.1.1  (c) 2011 by Turku PET Centre

Convert regional time-activity curve (TAC) data created using PPET software
(1) saved as *.tac files into DFT format (2).

Usage:
  ppet2dft [Options] <PPET *.tac file(s)>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing
 --dry
     Dry run: nothing is actually written on disk.

Example: Convert all PPET TAC files to DFT files:
     ppet2dft *.tac

References:
1. Boellaard R, Yaqub M, Lubberink M, Lammertsma A. PPET: A software tool
   for kinetic and parametric analyses of dynamic PET studies.
   NeuroImage 2006;31(Suppl 2):T62.
2. DFT format http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: dft2csv, dft2idwc, dft2dat, dft2html, dftunit, dft2svg

Keywords: PPET, DFT, TAC, format conversion, tool

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you are welcome to redistribute it under GNU General Public License.
```

```
progvers 0.4.2  (c) 2005-2012 by Turku PET Centre, University of Turku

Program for extracting program version information from an executable
program file into a text file in format:
program_name = xxx
program_version = x.y.z
compilation_date = YYYY-MM-DD hh:mm:ss
etc

Usage:  progvers [options] <program name> [Output filename]

Options:
 -opt=<command-line option>
        Option which tells the program to display build information.
 --version
 --build
        Print build information and exit.
 --help
        Print this text and exit.

See also: adddate, pdoc2htm

Keywords: software development, tools

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you are welcome to redistribute it under GNU General Public License.
```

```
qrsolv 0.1.0  (c) 2012 by Turku PET Centre

Solves overdetermined linear least square problem using QR.

Usage:  qrsolv [Options] <matrix A> <vector B>

Options:
 -begin=<x start>
 -end=<x stop>
     Restrict the data range used in the linear fitting
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Matrix A and vector B can be given in DFT format; samples times are ignored
but sample number must be the same in both files.

See also: lhsol, lhsoldv, lhsolki

Keywords: QR, linear model, LSQ

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```

r2t_rtcm 1.1.4 (c) 2001-2013 by Turku PET Centre

Simulation of PET tissue time-radioactivity concentration curve (TAC) from reference tissue TAC based on a selected reference tissue input compartment model.

Available reference tissue input models and model parameters:
  FRTM; (Full) reference tissue model; R1, k2, k3, BP [1]
  SRTM: Simplified reference tissue model; R1, k2, BP [2]
  RRTM: Reduced reference tissue model; R1, k2, k3 (k4=0)
  TRTM: Transport-limited reference tissue model; R1, k2, k3 [3]

Parameters:
  1) Model (FRTM|SRTM|RRTM|TRTM)
  2) Name of file containing (only) the reference tissue TAC
  3-5/6) Model parameters
  6/7) Filename for the simulated TAC

Simulated TACs are saved in DFT format, where columns are:
  1) Total tissue activity (Ct)
  2) Activity in 1st tissue compartment (Cf)
  3) Activity in 2nd tissue compartment (Cb)

Options:
 -nosub
     TACs of sub-compartments (Cf and Cb) are not written into output file.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

References:
1. Cunningham VJ, Hume SP, Price GR, Ahier RG, Cremer JE, Jones AKP.
   Compartmental analysis of diprenorphine binding to opiate receptors
   in the rat in vivo and its comparison with equilibrium data in vitro.
   J Cereb Blood Flow Metab 1991;11:1-9.
2. Lammertsma AA, Hume SP. Simplified reference tissue model for PET
   receptor studies. NeuroImage 1996;4:153-158.
3. Herholz K, Lercher M, Wienhard K, Bauer B, Lenz O, Heiss W-D.
   PET measurement of cerebral acetylcholine esterase activity without
   blood sampling. Eur J Nucl Med 2001;28:472-477.

See also: fit_frtm, fit_srtm, fit_rrtm, fit_trtm, dftadd, fr4sim

Keywords: DFT, modelling, simulation, reference tissue, reference input

rc2ki 1.1.0 (c) 2001,2005 by Turku PET Centre

For simulation of Influx constant (Ki) from rate constants k1-k3.

$$Ki = \frac{k1 * k3}{k2 + k3}$$

Parameters:
  1-3) k1 start, stop, and step
  4-6) k3 start, stop, and step
  7) k1/k2
  8) Result file

Result file will contain three columns: k1, k3 and Ki

Keywords: simulation

```
re4dist 1.0.1  (c) 2005 by Turku PET Centre

Calculates robust estimates from data values,
which must be in an ASCII file - each distribution on it's own column.
Results are printed into a file.

Usage: re4dist <Data file> <Result file>

The data file is assumed to have spaces or tabs between columns,
'.' as decimalpoint (not ',') and '.' marking empty values
(e.g. at the end of the shorter columns, when lenght of columns differ).
```

```
regbfbp 0.5.1  (c) 2003-2013 by Turku PET Centre

Estimate the binding potential (BP) from simplified reference tissue
model [1]. The model is solved using the basis function approach [2],
similar to the RPM program for producing BP images.

Parameters:
  1) Tissue TAC file (must be corrected for radioactive decay)
  2) Name of reference region in tissue file, or name of file
     containing reference tissue TAC
  3) Isotope (C-11, F-18, ...)
  4) Result file (existing file is overwritten)

Tissue TAC file must contain weights.

Options:
 -min=<value (1/min)>
     Set minimum value for theta3; it must be >= k2min/(1+BPmax)+lambda.
     Default is 0.01 min-1. Lambda for F-18 is 0.0063 and for C-11 0.034.
 -max=<value (1/min)>
     Set maximum value for theta3; it must be <= k2max+lambda.
     Default is 0.60 min-1.
 -nr=<value>
     Set number of basis functions; default is 5000.
 -bf=<filename>
     Basis functions are written in specified DFT file.
 -E=<Fit end time (min)>
     Use data from 0 to end time; by default, model is fitted to all frames.
 -DVR
     Instead of BP, program saves the DVR (=BP+1) values.
 -svg=<Filename>
     Plots of original and fitted TACs are written in specified file in
     Scalable Vector Graphics (SVG) 1.1 format; specification in
     http://www.w3.org/TR/SVG/
 -fit=<Filename>
     Fitted regional TACs are written in specified file.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

References:
1. Lammertsma AA, Hume SP. Simplified reference tissue model for PET
   receptor studies. NeuroImage 1996;4:153-158.
2. Gunn RN, Lammertsma AA, Hume SP, Cunningham VJ. Parametric imaging of
   ligand-receptor binding in PET using a simplified reference region
   model. NeuroImage 1997;6:279-287.

See also: dftweigh, dftdecay, logan, lhsrtm, imgbfbp, fitk2

Keywords: DFT, modelling, binding potential

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```

```
regbfh2o 0.2.0  (c) 2013 by Turku PET Centre

Basis function (BS) fitting of one-tissue compartmental water model to
PET [O-15]H2O study data (Boellaard et al., 2005).
The model parameters are blood flow (F), partition coefficient (pWater),
arterial blood volume (Va) and time delay (delayT). Venous radioactivity
is assumed to be the same as the tissue concentration.
Extraction factor of water is assumed to be 1.0.

The blood flow obtained using PET [O-15]H2O techniques reflects tissue
perfusion, since the method is dependent on the tissue exchange of
labelled water. Non-nutritive flow (blood flowing through arteriovenous
shunts) is not measured (Lammertsma & Jones, 1983).

Command line parameters:
  1) Blood H2O file (corrected for time delay and physical decay)
  2) Tissue TAC file (corrected for physical decay)
  3) Fit duration (sec)
  4) Result file

General options:
 -ml or -dl
     In results the units of F and Va will be given per mL or per dL,
     respectively. By default, units are per dL.
 -fpt
     Blood flow (perfusion) is reported per perfusable tissue volume
     (PET volume minus vascular volume). By default perfusion is reported
     per PET volume.
 -Va=<Va(%)>
     Enter a fixed Va; fitted by default.
 -pH2O=<Partition coefficient for water>
     Enter the true partition coefficient for water to report perfusion as
     F=k2*pH2O instead of default F=K1; apparent pH2O is fitted in any case.
 -svg=<Filename>
     Plots of original and fitted TACs are written in specified file in
     Scalable Vector Graphics (SVG) 1.1 format; specification in
     http://www.w3.org/TR/SVG/
 -fit=<Filename>
     Fitted regional TACs are written in specified file.
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Options for setting basis functions:
 -k2min=<Min k2> and -k2max=<Max k2>
     Enter the minimum and maximum k2 in units 1/min (for example
     0.01 and 2.5).
 -fmin=<Min K1> and -fmax=<Max K1>
     Enter the minimum and maximum perfusion value; defaults are
     0.5 and 400 ml/(dl*min), respectively.
 -pmin=<Min p> and -max=<pmax>
     Enter the minimum and maximum value for apparent partition coefficient
     for water; defaults are 0.3 and 1.0 ml/ml, respectively.
 -nr=<value>
     Set number of basis functions; default is 5000.
 -bf=<filename>
     Basis function curves are written in specified file.

Example:  regbfh2o uo1234bl.kbq uo1234.dft 999 uo1234f.res

Times must be in seconds in all PET data files, unless specified inside
the files.
```

References:
1. Boellaard R et al. Mol Imaging Biol. 2005;7:273-285.
2. Lammertsma AA, Jones T. J Cereb Blood Flow Metab. 1983;3:416-424.

See also: b2t_h2o, fit_h2o, regbfh2o, imgflow, arlkup, fitk2, dftweigh

Keywords: DFT, TAC, modelling, perfusion, blood flow, radiowater

```
regderiv 0.2.0 (c) 2008,2011 by Turku PET Centre

Calculation of derivatives of regional PET time-activity curves (TACs).
Resulting derivative curves are noisy because of the simple
calculation method.

Command line arguments:
  1) Regional TAC file
  2) Filename for derivatives

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

Example:
     regderiv ua1807.dft ua1807deriv.dft

TAC file format is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: dftframe, dftinteg, dftslope, dftadd, dftdel, dft2svg

Keywords: DFT, simulation

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```
regfur 1.2.0  (c) 2007-2013 by Turku PET Centre

Calculation of Fractional Uptake Rate (FUR) or FUR-based Metabolic Rate (MR)
from regional PET TACs. Information on FUR in:
http://www.turkupetcentre.net/modelling/methods/fur.html

Parameters:
  1) Input file (Plasma TAC)
  2) Regional TAC file
  3-4) FUR calculation start and stop time (min);
     set both to zero to use the whole time range from regional data
  5) FUR or MR result file

Options for calculation of metabolic rate:
 -Ca=<value>
     Concentration of native substrate in arterial plasma (mM),
     for example plasma glucose in [18F]FDG studies.
     With this option the metabolic rate (umol/(min*100 g)) is calculated.
 -LC=<value>
     Lumped Constant in MR calculation; default is 1.0.
 -density=<value>
 -d=<value>
     Tissue density in MR calculation; default is 1.0 g/ml.

General options:
 -curve=<filename>
     FUR as a function of time is written in specified file; this can be
     used to study the time-dependence of FUR estimates.
 -it=<Time (min)>
     Input AUC is normally calculated from 0 to the middle time of FUR
     calculation time; in special cases this option can be used to
     calculate it from 0 to the specified time instead.
 -deriv[ative]
     Tentative option for calculating FUR as ratio of tissue derivative and
     plasma. This does not affect the FUR curve made with option -curve.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing

Example 1. Calculation of FUR from dynamic PET data from 45 to 60 min:
     regfur ua2918ap.kbq ua2918dy1.dft 45 60 ua2918fur.res

Example 2. Calculation of glucose uptake, when tissue density is 1.04,
plasma glucose concentration is 5.2 mM, lumped constant is 0.52, from
a static (one frame) scan:
     regfur -Ca=5.2 -LC=0.52 -d=1.04 a864ap.kbq a864dy1.dft 0 0 a864mrglu.res

FUR and MR results are saved in result file format by default, but if
filename extension is set to .dft or .html, results are saved in
regional TAC or HTML table format, respectively.
Format of the supported plasma and regional TAC data files are specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html and result file
in http://www.turkupetcentre.net/analysis/doc/format_res.html

The unit of FUR is (mL plasma)/(min*(mL tissue)) by default, and
umol/(min*100 g) if metabolic rate is calculated.

See also: patlak, dftinteg, dftcalc, dfttime, dftsuv, rescoll, imgfur

Keywords: DFT, modelling, FUR, retention index, irreversible uptake

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```
res2html 1.2.3 (c) 2002-2012 by Turku PET Centre

Program for converting result files to (X)HTML table format.
If filename is omitted, then it is named automatically by replacing
original extension with .htm.

Usage: res2html [Options] <Result file> [HTML filename]

Options:
 -n[osd]
     SDs and CVs are not saved into HTML file.
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.

See also: reslist, rescoll, dft2res, fit2res, dft2html

Keywords: HTML, results, modelling, conversion, tools

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```
resai 1.2.3  (c) 2002-2013 by Turku PET Centre

Program for calculating Asymmetry Index (AI) from PET results
saved in RES format (1).

                         (dx - sin)
  Asymmetry index AI = ------------ x 100
                       (dx + sin)/2

The right and left hemisphere is recognized from the following strings:
  dx, dex, dexter, right, rgt, sn, sin, sinist, left, lft
Only the first set of results in one file is used.
Input result file must not be in HTML format.

Usage: resai <Results file> <AI results file>

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example:
  resai ut6789ki.res ut6789kiai.res

If the AI result file (output) extension is .htm(l), then data
are saved in HTML table format.

References:
1. http://www.turkupetcentre.net/analysis/doc/format_res.html

See also: reslist, rescoll, resdiff, dft2res, fit2res, resdel, dfthncor

Keywords: result, AI, asymmetry

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```
rescoll 2.2.3 (c) 2002-2012 by Turku PET Centre

Collects the model analysis results from a set of PET studies, and
by default tabulates regional results and means with standard deviations;
then results of only one model analysis program can be used at a time.

Usage: rescoll [Options] <Collection file> <Two or more result files>

Options:
 -s[ort]
     Results will be sorted by study number
 -strict
     Quits with error when normally a warning would be displayed
 -list
     Regional results are not collected but result files are just
     tabulated into one HTML file
 -par[ameter]
     Regional and individual results are collected for each parameter
     (not yet tested)
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing

Example:
     rescoll patlakmeans.html ua4???ki.res

The collected data is saved in tables in XHTML 1.1 format, therefore the
collection filename extension has to be .htm(l).
File can then be viewed and printed with a web browser or Excel.
In Excel the data can be also be processed further and saved in Excel
format.

See also: reslist, resdiff, dft2res, fit2res, resmatch, resdel

Keywords: result, tabulation, reporting, modelling, simulation, tool

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```
resdel 0.4.2  (c) 2004-2012 by Turku PET Centre

Remove region(s) from result file (1).
If output filename is not given, input file is modified.

Usage:  resdel <result file> <numbers or names of regions>

Options:
 -o=<output file>
    Remaining results are written in specified file;
    By default, input file is modified.
 -h or --help
    Print this message and exit.
 --version or --build
    Print software build information and exit.
 --silent
    Program works silently, printing only error and warning messages.
 --verbose
    Program prints more information about what it is doing.
 --dry
    Dry run: nothing is actually written on disk.

References:
1. http://www.turkupetcentre.net/analysis/doc/format_res.html

See also: reslist, resrmdpl, res2html, resplsta, rescoll, resdiff

Keywords: RES, results, tools, modelling

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```

```
resdiff 1.1.4  (c) 2004-2012 by Turku PET Centre

Calculate difference between results in two result files as percent change
in file2 from file1 using equation 100%*(result2-result1)/|result1|.
If file name for %-difference is not given, output is printed
on screen (stdout).

Usage:  resdiff [options] <file1> <file2> [%-difference file]

Options
 -occ[upance]
 -inh[ibition]
     Occupance or inhibition percentage is calculated, that is,
     100%*(result1-result2)/result1.
 -nocheck
     Result files are allowed to contain different parameters and
     region names.
 -round
     Differences are rounded to the nearest integer percentage.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: reslist, rescoll, res2html, dft2res, fit2res, resmatch, resdel

Keywords: result, modelling, simulation, occupance, inhibition

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```
reslist 1.3.0 (c) 2003-2013 by Turku PET Centre

Lists the user-specified regional results on screen.
Note: result file must not be in HTML format.

Usage: reslist [Options] <Results file> [VOI name]

Options:
 -n
     CL or SD values are not shown
 -ift
     Results are listed in IFT format
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit.

Example: reslist ut6789ki.res put

See also: resdel, rescoll, resmatch, res2html, fit2res, resrmdpl, iftisval

Keywords: RES, FIT, IFT, results, tools

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```

```
resmatch 1.1.7  (c) 2006-2012 Turku PET Centre

Program for verifying that two result files do have matching contents;
this can be used for automating software and analysis tool testing.
Programs return code is 0, if files were matching, 10, if the files did
not match, and 1-9 in case of error.

Usage:  resmatch [Options] <File1> <File2>

Options:
 -header=<y|N>
     Header fields are verified (y) or not verified (n, default)
 -param[eters]=<y|N>
     Parameter names are verified (y) or not verified (n, default)
 -regions=<y|N>
     Region names are verified (y) or not verified (n, default)
 -res[ults]=<List of result column numbers (e.g. -res=1-2 or -res=1,3)>
     By default all result values are verified. With this option,
     only selected columns (or none with -res=0) are verified.
 -roughly
     Result values are required to match roughly (<2% difference allowed).
 -around
     Results are required to be around the same (<10% difference allowed).
 -abs=<value>
     Absolute result differences must not exceed the specified limit value
 -errors=<Y|n>
     Result errors (SD, CL) are verified (y, default) or not verified (n)
 -h or --help
     Print this message and exit.
 -v, --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: reslist, res2html, resdel, resdiff, fit2res, dftmatch, imgmatch

Keywords: results, tools, software testing

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```

```
resplsta 1.2.0 (c) 2002-2012 by Turku PET Centre

Program for calculating results statistics over planes.
Reads the regional results from a result file, and calculates averages
medians and SDs between different planes.
Only the statistics are saved.
Only the first set of results in one file is used.
Input result file must not be in HTML format.

Usage: resplsta [Options] <Results> <Statistics file>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
     resplsta ut6789patlak.res ut6789patlakavg.html

If the statistics result file (output) extension is .htm(l), then data
are saved in HTML table format.
Existing file will be overwritten.

See also: rescoll, reslist, resdel, resrmdpl

Keywords: result, simulation, tool, statistics

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```
resrank 0.2.1  (c) 2011,2012 by Turku PET Centre

This program determines the regional order of a user-defined parameter
and saves the order as a new column in the result file (1).
If name of a new result file is not given, then original file is
overwritten.
Input result file must not be in HTML format.

Usage: resrank [Options] <Results file> [New results file]

Options:
 -res[ults]=<Result column number(s)>
     List of result column numbers (e.g. -res=1-2 or -res=1,3) which are
     separately ranked; by default the first result column is ranked.
 -scale
     Instead of rank, the scale of each region is saved, with 1 for the
     region with the lowest value and 1000 for the highest.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example:
  resrank -res=3 ut6789srtm.res

If the new result file (output) extension is .htm(l), then data
are saved in HTML table format.

References:
1. http://www.turkupetcentre.net/analysis/doc/format_res.html

See also: reslist, rescoll, resdel, resdiff, dft2res, fit2res

Keywords: result, order, rank

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```

```
resrmdpl 0.2.1  (c) 2004,2012 by Turku PET Centre

Removes regions that are in duplicates in result (RES) files.
A duplicate has the same region name as any of the previous regions.
This check is character upper/lower case -insensitive.

Usage:  resrmdpl [Options] <file1> [file2] [file3] ...

Options:
 --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages
 --verbose
     Program prints more information about what it is doing.

See also: reslist, resdel

Keywords: results, tools

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```
ressort 0.1.1  (c) 2011,2012 by Turku PET Centre

Sort the results is RES file format (1) by the region name.
Input result file must not be in HTML format.

Usage: ressort [Options] <Result file(s)>

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example:
  ressort ut6789srtm.res

If the new result file (output) extension is .htm(l), then data
are saved in HTML table format.

References:
1. http://www.turkupetcentre.net/analysis/doc/format_res.html

See also: reslist, rescoll, resrank, resdel, resdiff, dft2res, fit2res

Keywords: RES, result, tool, sorting

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```

```
sif2tac 0.1.0  (c) 2013 by Turku PET Centre

Convert PET SIF to TAC format, either DFT, PMOD TAC, or HTML table,
depending on the output filename extension.

Usage:  sif2tac [Options] <SIF name> <TAC filename>

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: siflist, dftframe, eframe, dft2svg, dft2csv, dfthead, fr4sim

Keywords: DFT, TAC, SIF, tool, frame time

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```
sifcat 1.1.0  (c) 2000-2013 by Turku PET Centre

Catenates the scan information files (SIF) from interrupted PET studies
into a single SIF file.

Usage: sifcat [Options] <Combined SIF file> <SIF files>

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: siflist, sifisot, eframe, dftframe, sif2tac, dftweigh, ecatcat

Keywords: image, SIF, tool

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```
sifisot 1.0.2  (c) 2005-2013 by Turku PET Centre

Adds isotope to the scan information files (SIF), if they do not contain
it already. If isotope code is not given by user, then program shows
the current isotope setting.

Usage: sifisot <SIF file(s)> [Isotope code]

Options:
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example:
     sifisot *.sif C-11

See also: siflist, eframe, dftframe, dftweigh, sifcat

Keywords: image, SIF, physical decay, isotope

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```

```
siflist 1.1.3  (c) 2000-2013 by Turku PET Centre

Lists the information in a SIF file.

Usage: siflist [Options] <SIF file>

Options:
 -i=<Br76|Cu62|C11|Ga68|Ge68|F18|N13|O15|Rb2>
     Isotope, in case it is needed but not given inside SIF file.
 -decay=<corrected|non-corrected>
     Weights are calculated for TACs corrected or non-corrected (default)
     for physical decay.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

See also: sif2tac, sifcat, sifisot, hrp2sif, eframe, dftframe, dftweigh

Keywords: image, SIF, frame time

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```

```
simcirc 0.3.0  (c) 2012 by Turku PET Centre

Draw circle in x,y matrix with 1 inside circle and 0 outside of it
for simple simulations, SW testing, and creating ROI masks.

Command line arguments:
  1) dimension
  2) diameter
  3) output filename

Options:
 -separator=<<comma>|<semi-colon>|<tab>|<space>>
     By default tab is used as the separator, but comma, semicolon or space
     may be needed to import data to other software.
 -format=<<ascii>|<float>|<short>>
     By default data is written in ASCII text format, but optionally
     it can be written in binary flat file as floats or short ints.
 -diam2=<2nd diameter>
     If the second diameter is specified, then a ring is created.
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example #1:
  simcirc 256 224 circle.txt
Example #2:
  simcirc -format=float 256 64 circle.bin
  flo2ecat -t=hrrt circle.bin circle.v 1 1 256 256

See also: asc2flo, flo2ecat, simiart, ecatcalc, ecatlkup, ecatadd, ecatcat

Keywords: simulation, image, software testing

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```

```
simiart 0.2.2  (c) 2012 by Turku PET Centre

Simulate dynamic PET image plane with background activity surrounding
a circular object that is assumed to be extending across image planes
(bar or vessel) with spill-over and spill-in effects.
The defalt method is based on Germano et al. JNM 1992; 33: 613-620.
This method is only valid for vessels with very large diameter.
To simulate the circular vessel correctly in 2D image matrix use
the equations in Brix et al. Nuklearmedizin 2002;41:184-190 instead;
however, that would require numerical solution to double integrals
Alternative method applies Gaussian 2D smoothing.

Usage:  simiart [Options] <Blood TAC file> <Bkg TAC file> <Image file>

Options:
 -dim=<Image x and y dimension in pixels>
     Set image dimension; by default 128
 -pxlsize=<Voxel size (mm)>
     Set image voxel size; by default 1 mm
 -diameter=<Vessel diameter (mm)>
     Set vessel diameter; by default 25 mm; vessel border is simulated
     by simple cutoff, thus diameter should be several pixels -fwhm=<FWHM (mm)>
     Set image resolution; by default 8 mm
 -xpos=<vessel position (mm)>
     Set vessel distance from centre of image; by default 0 mm;
     negative distance moves vessel to the left, positive to the right
 -ypos=<vessel position (mm)>
     Set vessel distance from centre of image; by default 0 mm
     negative distance moves vessel upwards, positive downwards
 -bar | -gaussian
     Select the spill-over and spill-in simulation method (bar by default)
 -h or --help
     Print this message and exit.
 --version or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only error and warning messages.
 --verbose
     Program prints more information about what it is doing.

Example #1:
  simiart blood.dat background.dft vessel.v
Example #2:
  simiart -fwhm=4.3 blood.dat background.dft vessel.v

See also: fvar4sim, imgfiltg, ecatadd, ecatcalc, simcirc, flo2ecat

Keywords: simulation, image, software testing, vessel, input

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```
simimyoc 0.2.0  (c) 2013 by Turku PET Centre

Simulate dynamic PET image of heart. Approach is very simplistic and
only applicable to software testing and basic simulations:
only one image plane is produced, containing a ring representing myocardial
muscle surrounding LV cavity.

Usage:  simimyoc [Options] <TAC data file> <Image file>

TAC data file must contain the time-activity curves of myocardial muscle,
blood in LV cavity, and optionally background surrounding the heart.
Sample times in TAC file are used as time frames of the simulated image.

Options:
 -dim=<Image x and y dimension in pixels>
     Set image dimension; by default 128
 -3D
     Simulation in 3D (note that computation may take time)
 -pxlsize=<Voxel size (mm)>
     Set image voxel size; by default 1 mm
 -fwhm=<FWHM (mm)>
     Set image resolution; by default 8 mm
 -thickness=<Myocardial wall thickness (mm)>
     Set (relaxed) myocardial wall thickness; by default 10 mm
 -diameter=<Max LV cavity diameter (mm)>
     Set maximal LV cavity diameter; by default 52 mm
 -diamin=<Min LV cavity diameter (fraction)>
     Set minimum LV cavity diameter as fraction of max diameter;
     by default 0.62
 -bif=<Image filename>
     Save heart beat phases separately as image planes
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example #1:
  simimyoc tacs.dat myoc.v

See also: fvar4sim, imgfiltg, ecatadd, ecatcalc, heartcor

Keywords: simulation, image, software testing, myocardium, LV

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```

```
simmetab 0.2.0  (c) 2007,2011 by Turku PET Centre

Simulation of PET plasma time-radioactivity concentration curve (TAC)
of parent tracer and its metabolite from total arterial plasma (Ca) TAC
based on compartment model (1).

Usage: simmetab [Options] <Plasma file> <Parameter file> <Parent TAC file>

Options:
 -metab=<Filename>
     Write plasma metabolite TAC in specified file
 -h or --help
     Print this message and exit
 -v, --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages.

If the times in plasma file are in seconds, the units of rate constants
must be specified as 1/sec.
For accurate results, plasma data should have very frequent sampling.

Parameter file must contain (at least):
  -Name of metabolite model
  -Model parameter values
For example,
   model := TPCMOD0009C
   km := 0.8
   k1m := 0.5
   k2m := 0.4
   k3m := 0.1
   k4m := 0
Accepted metabolite models are:
  -TPC metabolite model (2)

References:
1. Lammertsma AA, Hume SP, Bench CJ, Luthra SK, Osman S, Jones T. Measurement
   of monoamine oxidase B activity using L-[11C]derenyl: Inclusion of
   compartmental analysis of plasma metabolites and a new model not requiring
   measurement of plasma metabolites. In: Quantification of Brain Function:
   Tracer Kinetics and Image Analysis in Brain PET (Uemura K, Lassen NA,
   Jones T, Kanno I, eds) Amsterdam, Excerpta Medica (pp) 313-318, 1993.
2. Oikonen V. New model for plasma metabolites.
   http://www.turkupetcentre.net/reports/tpcmod0009_app_c.pdf

See also: metabcor, fit_ppf, dft2svg

Keywords: DFT, input, metabolite correction, simulation

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```

simshape 2.0.0 (c) 2001,2008 by Turku PET Centre

Simulates the time-activity curves (TACs) of authentic, Cs(t), and
metabolized, Cm(t), radiotracer using the measured total tissue curve,
Ct(t), and rate constant k3, based on the shape analysis method (1,2).

Command-line parameters:
  1) Tissue TAC file
  2) k3
  3) Filename for simulated Cm(t)

Options:
 -h or --help
     Print this message and exit
 -int=<Filename>
     Interpolated regional TACs are written in DFT format.
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

Format of the TAC data are specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

Example: metabolite TAC in tissue is simulated first, saving also the
fitted and interpolated total tissue TAC, then the TAC of
authentic tracer is calculated by subtraction, and finally all curves
are plotted in SVG format:
     simshape -int=ua1309ct.dft ua1309.dft 0.070 ua1309cm.dft
     dftcalc ua1309ct.dft - ua1309cm.dft ua1309cs.dft
     dft2svg ua1309sa.svg -s ua1309.dft -l ua1309ct.dft ua1309cs.dft ua1309cm.dft

References:
1. Koeppe RA, Frey KA, Snyder SE, Meyer P, Kilbourn MR, Kuhl DE.
   Kinetic modeling of N-[11C]methylpiperidin-4-yl propionate: alternatives
   for analysis of an irreversible positron emission tomography tracer for
   measurement of acetylcholinesterase activity in human brain.
   J Cereb Blood Flow Metab. 1999;19:1150-1163.
2. Tanaka N, Fukushi K, Shinotoh H, Nagatsuka S, Namba H, Iyo M, Aotsuka A,
   Ota T, Tanada S, Irie T. Positron emission tomographic measurement of
   brain acetylcholinesterase activity using N-[11C]methylpiperidin-4-yl
   acetate without arterial blood sampling: methodology of shape analysis
   and its diagnostic power for Alzheimer's disease.
   J Cereb Blood Flow Metab. 2001;21:295-306.

See also: fitshape, fitk3, fit_trtm, dftcalc, dft2svg, dftdel, dftadd

Keywords: DFT, simulation, reference input, enzyme activity, shape analysis

```
sim_orm 0.3.3 (c) 2008-2010 by Turku PET Centre

Fits a model dedicated for ORM-B to regional PET study data.

Usage: sim_orm [Options] <Parent plasma TAC> <Metabolite plasma TAC>
               <Blood TAC> <Model parameters> <Simulated TAC>

 Options to set model parameters:
 -2tcm | -distr
     Select compartmental model:
     -2tm2 (default): two-tissue compartmental model, with parameters
      K1p, Vfp, k3p, Vbp, K1m, Vfm, Vb(%)
     -distr: one-tissue compartmental model with normal distribution
      of rate constants, with parameters K1p, Vfp, K1m, Vfm, CV, Vb(%)
 -Af=<Arterial proportion (%)>
     Set the simulated arterial proportion of total blood volume;
     default is 30%, minimum is 1%
General options:
 -sub
     TACs of sub-compartments are written into output file;
     this is the default
 -nosub
     TACs of sub-compartments are not written into output file
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing

See also: fit_orm, dftadd, dftren, fr4sim, p2t_3c, p2t_v3c, dft2svg

Keywords: DFT, simulation

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```

```
spa2pro 2.0.0 (c) 2003-2005 by Turku PET Centre

For program testing and simulation.
Transforms the given image in spatial domain to a sinogram in Radon domain.
Uses the tranformation functions in the reconstruction utilities library
libtpcrec.

Usage: spa2pro [Options and Arguments] <Image> <Sinogram>

Options:
1) Discretization model; default 0/1 model.
   -m<0[,s] (0/1, with s sublors if given)
      1[,s] (length of intersection, with s sublors if given)
      2 (exact area)
      3 (linear interpolation)
     4 (nearest neighbour)>
2) Fit input image to [-1,1]x[-1,1].
   -f
3) Run in noisy verbose mode.
   -n
4) Print build information and exit.
   -v -V

Arguments:
1) View number; by default determined from the input image.
   -a<number>
2) Bin number; by default determined from the input image.
   For methods 3 and 4 bin number must divide the image dimension.
   -b<number>

Input files:
1) Image: image volume in ECAT or Interfile format. Image format is
   determined from the file name extension;
   ECAT = .v and .img
   Interfile = .i (+.i.hdr)
2) Sinogram: sinogram in ECAT or Interfile format. Sinogram format is
   decided from the file name extension;
   ECAT = .s, .S and .scn
   Interfile = .i

Keywords: reconstruction, simulation, ECAT, interfile
```

```
stn_chck 1.0.0  (c) 2006 by Turku PET Centre

Validate the specified study number. A valid TPC study number consists of
1-5 letters (upper- or lowercase) followed by 1-5 digits.

Usage:  stn_check [options] <study number>

Options:
 -h or --help
     Print this message and exit
 -build or --version
     Print software build information and exit
 -silent
     Program works silently, printing only warnings and error messages.

See also: dftstudy

Keywords: study number

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```

```
taclist 2.0.0  (c) 1999-2013 by Turku PET Centre

Lists the volumes-of-interest (VOIs) of a TAC data file.
All VOI names are listed, if VOI name is not specified, and if e.g. 'cer'
is given, then only VOIs with name 'cer', 'Cer', or 'CER' are listed.
The activity concentrations are shown, if file contains <5 time frames.

Usage:  taclist [Options] <Datafile> [VOI name(s)]

Options:
 -nv
     Do not print region volume.
 -NA
     Activity concentrations are never printed.
 -ift
     Interfile-type print.
 -h or --help
     Print this message and exit
 -v, --version, or --build
     Print software build information and exit
 --silent
     Program works silently, printing no titles.

See also: dftren, dftdel, dft2csv, dft2dat, dft2res, iftlist, dft2svg

Keywords: TAC, tools, software testing

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```

```
tacmultx 0.1.0  (c) 2012 Turku PET Centre

For multiplying the x column(s) in TAC file by user-specified operand.
Resulting TAC can be written into new file, or original can be overwritten.

Usage:  tacmultx [Options] <file> <operand> [output file]

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: tacsetx, dftlist, dftadd, dftframe, dftunit, dft2csv

Keywords: DFT, TAC, tool, simulation

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```

```
tacrange 0.1.1  (c) 2013 by Turku PET Centre

Finds the time range in TAC datafile(s) in DFT, CSV, PMOD, or SIF formats.

Usage: tacrange [Options] <TAC file(s)>

Options:
 -unit=<sec|min>
     Times are shown in seconds, or minutes (default)
 -h or --help
     Print this message and exit
 -v, --build or --version
     Print software build information and exit
 --verbose
     Program prints more information about what it is doing.

See also: dftframe, dftmax, inpstart, dftunit, iftisval, tacsetx

Keywords: DFT, TAC, SIF, max, min

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```

```
tacsetx 0.1.0  (c) 2012 Turku PET Centre

For adding specified TAC from file2 as x (time) column to file1.
Files must have same number of samples.

Usage:  tacsetx [Options] <file1> <file2> <Number or name of TAC to add>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

See also: dftlist, dftadd, dftframe, dftunit, dft2csv

Keywords: DFT, TAC, tool, simulation

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```

```
tacsort 0.4.0  (c) 2004-2013 by Turku PET Centre

Sort PET TAC data by the region name or sample time.

Usage:  tacsort [Options] <TAC file(s)>

Options:
 -sort=<name|time>
     TACs are sorted by regional name (default) or TAC samples
     ("frames") are sorted by increasing sample time
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example:
  tacsort -sort=time *.tac

See also: dftlist, dftren, dftrenpl, dftvncor, dfthncor, dftcat, dft2csv

Keywords: TAC, tool, sorting, frame time

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```
tocr 0.2.0 (c) 2007-2010 by Turku PET Centre

Convert the head-curve data file from ECAT HR+ (*.r) or HRRT (*.hc)
to count-rate (.cr) file format, that is suitable for correction of
time-delay between blood/plasma and tissue TACs.
CR data will be corrected for physical decay.

Usage: tocr [Options] <Head-curve filename> <Isotope> [CR filename]

Options:
 -m[in]
     Sample times are written in minutes.
 -s[ec]
     Sample times are written in seconds;
     by default in sec for O-15, O-14, and Rb-82, otherwise in min.
 -c[opy]
     If file is not in HR+ or HRRT head-curve format, it is still saved
     with new name.
 -format=<cr|dft>
     File is written in 'count-rate' format with no titles (cr), or,
     with title lines (dft, default)
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing
 -test[=<print level>]
     Print more or less details during the process.

See also: fitdelay, ecathead, dfthead, dftscale, dft2svg, dftdecay

Keywords: ECAT HR+, HRRT, modelling, time delay, count-rate, head-curve

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```

```
tsv2dft 0.2.1  (c) 2006,2009 by Turku PET Centre

Convert regional time-activity curve (TAC) data created in Amide (a Medical
Imaging Data Examiner)(1) saved as *.tsv files into DFT format (2).

Usage:
  tsv2dft [Options] <Amide *.tsv file(s)>

Options:
 -min | -sec
     Convert time units to minutes or seconds; by default in seconds.
 -unit=<unit string>
     TSV file does not contain information on the calibration units.
     If you know the units, set it with this option, for example
     -unit=Bq/mL
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing
 --dry
     Dry run: nothing is actually changed.

Example: Convert all TSV files to DFT files; sample times are converted
     to minutes, and concentrations are known to be in units Bq/mL:
     tsv2dft -min -unit=Bq/mL *.tsv

References:
1. Amide web site http://amide.sourceforge.net/
2. DFT format http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: xel2dft, cpt2dft, idwc2dft, if2dft, csv2dft, dftunit

Keywords: Amide, DFT, TAC, format conversion, tool

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```

```
upet2e7 0.2.4  (c) 2009-2012 by Turku PET Centre

Conversion of Siemens Inveon/MicroPET CT or PET image to ECAT 7
image volume format. Please note that a .NET image format conversion
tool with GUI (ImageConverter) is also available.
MicroPET image consists of two files with extension .img and .hdr;
both are required in conversion.
Note that also Analyze 7.5 images consist of equally named two files.

Usage: upet2e7 [Options] <MicroPET image> [ECAT filename]

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

Example 1:
     upet2e7 ae72.pet.img ae72.v

See also: upet2sif, flo2ecat, ana2ecat, eframe, e7emhdr, e7evhdr

Keywords: image processing, format conversion, ECAT, MicroPET, Inveon

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```

```
upet2sif 0.1.0  (c) 2009 by Turku PET Centre

Constructs a scan information file (SIF) from Inveon/microPET image header.
MicroPET image consists of two files with extension .img and .hdr;
only header file is needed here.

Usage: upet2sif [Options] <MicroPET header file> <SIF filename>

Options:
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

Example:
     upet2sif ae72.pet.img.hdr ae72.sif

References:
1. Scan Information File. http://www.turkupetcentre.net/analysis/doc/sif.html

See also: cti2sif, hrp2sif, dftweigh, siflist, sifcat, sif2ecat, upet2e7

Keywords: SIF, modelling, weighting, MicroPET, Inveon

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```
var4dat 1.3.2  (c) 1999-2012 by Turku PET Centre

Program for adding Gaussian noise to time-activity data.
If optional isotope letter is specified, variance is increased by decay.
If datafile contains weights, then the specified amount of variance is
added to frames with weight=1, and higher or lower variance to those
frames with lower or higher weight.

Usage:
  var4dat <CV%> <Data file> <Output file> [Isotope code]

Options:
 -S[eed]=<seed for random number generator>
     Computer clock is used by default
 -sec
     If datafile does not contain time unit, times are by default assumed to
     be in minutes. Use this option to set time unit to sec.
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints more information about what it is doing.

TAC file format is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: fvar4dat, mvar4dat, wvar4dat, dftstd, avgttac, dft2csv, rescoll

Keywords: DFT, noise, simulation

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you are welcome to redistribute it under GNU General Public License.
```

```
vox_icc 1.0.0  (c) 2005 by Turku PET Centre

Inter Class Correlation calculation of ECAT 6.3, ECAT 7 or Analyze7.5 files.

Usage:
  vox_icc <Image1> <Image2> [<Image3 Image4>... <Image2N-1 Image2N>]

e.g.:  vox_icc ecat63a.img ecat63b.img
       vox_icc analyze75a.img analyze75b.img analyze75c.img analyze75d.img

Images must be in same format, and they must have same
matrix size and plane numbers. Output file will have 'icc' as basename
```

```
vox_occu 1.0.0  (c) 2005 by Turku PET Centre

Occupancy calculation of two ECAT 6.3, ECAT 7 or Analyze7.5 files.

Usage:
  vox_occu <Image1> <Image2> [output]

e.g.:  vox_occu ecat63a.img ecat63b.img
       vox_occu ecat63a.img ecat63b.img output.img

Image1 and image2 must be in same format, and they must have same
matrix size and plane numbers. Output file will have Image1's header.
Output filename will be format occu_<Image1> unless optional output
parameter is used.
```

```
  vox_sd 1.0.0  (c) 2005 by Turku PET Centre

  Bias corretec standard deviation calculation of ECAT 6.3, ECAT 7 or Analyze7.5
files.

  Usage:
    vox_sd <Image1> [<Image2> ... <ImageN>]

  e.g.:  vox_sd ecat63a.img ecat63b.img
         vox_sd ecat63a.img ecat63b.img output.img

  Images must be in same format, and they must have same
  matrix size and plane numbers. Output file will have 'sd' as basename
  Output filename will be format unless optional output
  parameter is used.
```

```
vox_variab 1.0.0  (c) 2005 by Turku PET Centre

Variability calculation of two ECAT 6.3, ECAT 7 or Analyze7.5 files.

Usage:
  vox_variab <Image1> <Image2> [output]

e.g.:  vox_variab ecat63a.img ecat63b.img
       vox_variab ecat63a.img ecat63b.img output.img

Image1 and image2 must be in same format, and they must have same
matrix size and plane numbers. Output file will have Image1's header.
Output filename will be format variab_<Image1> unless optional output
parameter is used.
```

```
wizcorr 2.0.0  (c) 1995-2006 by Turku PET Centre

Corrects the Wizard 1480 3" assay data files with wrong isotope setting.
The isotope code, and physical decay correction to the assay start time,
are corrected.

Usage:
  wizcorr <New isotope code> <Assay filename(s)>

Options:
 -h[elp]
     Print this message and exit
 -build or --v
     Print software build information and exit
 -silent
     Program works silently, printing only warnings and error messages.
 --dry
     Dry run: nothing is actually changed.

e.g.:
wizcorr C-11 S:\lab\plasma\A02__5??.T

See also:

Keywords: BAM, Wizard gamma counter, assay, decay correction
```

```
wizdat2t 0.1.0  (c) 2006 by Turku PET Centre

Reformats the new Wizard 1480 3" assay data files (*.dat) to older assay
file format (*.t).
Original .dat files are preserved, .t files are created in the same path.

Usage:
  wizdat2t <Assay filename(s)>

Options:
 -h or --help
     Print this message and exit
 -v or --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only warnings and error messages.
 --dry
     Dry run: nothing is actually changed.

e.g.:
wizdat2t S:\lab\plasma\A05__875.dat

See also: wizcorr

Keywords: BAM, Wizard gamma counter, assay, format conversion
```

wrapper 1.0.2 (c) 2005-2012 Turku PET Centre

A wrapper program to execute the latest version of the program
it is named after. Programs should adhere to the following naming scheme:
program_name_0_0_0.extension
, where 0_0_0 is the version number, and extension is usually .exe, but
it is not required.

See also: progvers, adddate, pdoc2htm

Keywords: software development, tools

```
wvar4dat 1.2.1  (c) 2002-2008 by Turku PET Centre

Program for adding Gaussian noise to time-activity data.
SD is assumed to be equal to (noise level)*sqrt(1/weight), and
the weights must be included in the DFT datafile (e.g. dftweigh).

Usage:  wvar4dat <Datafile> <Noise level> <Output file>

Options:
 -S[eed]=<seed for random number generator>
     Computer clock is used by default
 -h or --help
     Print this message and exit
 --version or --build
     Print software build information and exit
 --silent
     Program works silently, printing only error and warning messages
 --verbose
     Program prints lots of information about what it is doing.

TAC file format is specified in
http://www.turkupetcentre.net/analysis/doc/format_dft.html

See also: dftweigh, var4dat, fvar4dat, wvar4dat, dftstd, rescoll

Keywords: DFT, noise, simulation

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you are welcome to redistribute it under GNU General Public License.
```

```
xel2dft 0.2.3  (c) 2006-2009 by Turku PET Centre

Convert regional time-activity curve (TAC) data from GEMS Xeleris
to DFT format.

Usage:
  xel2dft [Options] <Xeleris TAC file(s)>

Options:
 -e=<Extension for output file(s)>
     Specify the file name extension for the converted files. By default,
     extension is '.dft'.
     NOT YET APPLIED.
 -o=<Single output filename>
     All Xeleris TAC files are converted and combined into one DFT file.
     NOT YET APPLIED.
 -min | -sec
     Convert time units to minutes or seconds, if needed.
 -unit=<units>
     If Xeleris TAC calibration units are identified, the radioactivity
     concentrations can be converted to units specified with this option.
 -h or --help
     Print this message and exit.
 -v, --version, or --build
     Print software build information and exit.
 --silent
     Program works silently, printing only warnings and error messages.
 --verbose
     Program prints lots of information about what it is doing.
 --dry
     Dry run: nothing is actually changed.

Example:
     xel2dft *.tac

See also: csv2dft, cpt2dft, idwc2dft, if2dft, dftren, dftadd

Keywords: Xeleris, DFT, TAC, format conversion, tool, PET-CT

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you are welcome to redistribute it under GNU General Public License.
```

```
yokoi 1.2.3  (c) 2002-2005 by Turku PET Centre

Calculates the distribution volume DV or DVR (=BP+1) using multiple-time
graphical analysis (MTGA) for reversible PET ligands (Yokoi plot) (1).

Parameters:
  1) Tissue TAC file
  2) Name of plasma file OR reference region name in TAC file
  3-4) Start and end times for linear fit
  5) Result file (existing file is overwritten)
 [6) Filename for plot data and fitted lines (optional) ]

Options:
 -N
     SDs are not saved.
 -mid[=<y|n>]
     Mid frame times are used (y) or not used (n, default) even if frame
     start and end times are available.
 Least-squares line fit method can be selected with following options:
 -C  Traditional regression model
 -M  Median of two-point slopes and intercepts (Cornish-Bowden)
 -P  Perpendicular regression model (2)
 -R  Iterative method (York 1966, Lybanon 1984, Reed 1992); default
  If tissue file contains weights, the iterative method (-R) is weighted.
  With other fitting methods the weights are not used.
  With options -C and -R program can automatically find the linear plot
  range, if fit start time is set to zero.

e.g. yokoi ut2345.dat ut2345ap.dat 10 60 ut2345.res
 or  yokoi ut2345.dft cer 20 60 ut2345.res ut2345yplot.htm

References:
1. Yokoi T, Iida H, Itoh H, Kanno I. A new graphic plot analysis for
   cerebral blood flow and partition coefficient with iodine-123-
   iodoamphetamine and dynamic SPECT validation studies using
   oxygen-15-water and PET. J Nucl Med. 1993; 34(3): 498-505.
2. Varga J & Szabo Z. Modified regression model for the Logan plot.
   J Cereb Blood Flow Metab 2002; 22:240-244.

See also: logan, fitk4, lhsoldv, patlak, rescoll

Keywords: DFT, modelling, distribution volume, Yokoi plot
```