[^{11}C]PE2I PET data

Original data

Three 63-min PET studies from different subjects were kindly presented from the Karolinska Institutet. Data includes total radioactivity concentration in blood and plasma and metabolite corrected plasma concentration, dynamic PET images, MRI images, and regional time-radioactivity curves (TAC) from caudatus, putamen, striatum and cerebellum. Image time frames are 3x1, 4x3 and 8x6 min. The three subjects/studies are identified as “jkar”, “joma”, and “maut”. Activities are in units nCi/ml.

Definition of new ROIs and calculation of regional TACs

Work was done and documented by Jussi Hirvonen:

cti2sif 1.1 (c) 2003 by Turku PET Centre
- obtaining sif files from ECAT image files

ecatsum 1.3 (c) 2002, 2003 by Turku PET Centre
- creating sum images over all frames (1-15) and over first 5 frames for MRI-PET coregistration

ecat2ana 0.6 2003, 2004 by Turku PET Centre
- conversion between CTI Matrix 6.3 and Analyze 7.5 MRI and PET images
- data saved in little indian byte order (PC Intel)
- keeping decay correction in PET images
- result Analyze 7.5. files in neurological convention (right-is-right)

MRIcro 1.37 build 4 (Chris Rorden)
- changing MRI images z-dimension in Analyze 7.5 header from 1.000 to 3.125

SPM2 (Friston et al, 1995) running on Matlab 6.5 for Windows, build 13, (Math Works, Natick, MA).
- coregistration of MRI images to summed (frames 1-5) PET images
- coregistration procedure: normalized mutual information method

Imadeus Academic 1.20 (build 395) (c) 2001-2004 Forima Inc., Turku, Finland
- x-flipped Analyze 7.5 images (resulting in radiological convention, right-is-left)
- ROIs in caudate (cau, 4-5 planes), putamen (put, 3-4 planes), thalamus (tha, 4-5 planes), cerebellum (cer, 6 planes), substantia nigra (sn, 1 plane), white matter (wm, 3-4 planes), anterior cingulate cortex (ac, 5 planes), dorsolateral prefrontal cortex, 5 planes), occipital cortex (occ, 5 planes)
- output files contain activities for sides (dx, sn) separately and for combinations (weighted average of dx&sn)

- frame start & end times in output files
- activity values: nCi/ml (*-v3-nci.dft) and kBq/ml (*-v3-kbq.dft)

Corrections to the data

Weighting: Regional data was weighted using program dftweigh 1.5. SIF files were not available, therefore the average of regional curves was used to calculate the relative weight factors.

Delay correction: Based on visual inspection of plasma and tissue curves, delay correction was considered necessary. Countrate curve was not available, therefore "head curves" were first calculated from dynamic images using program ecathead 2.5 with options `-m -thr=10,5` (thresholding out pixels less than 10% of max value during 5 last frames). Decay correction was then made using program `fitdelay 1.7` with fit time of 20 minutes. The delay times were 14, 14 and 10 s for the three studies, respectively; Jučaité et al. (manuscript) mentions that delay time in a material of eight men was about 10 s.

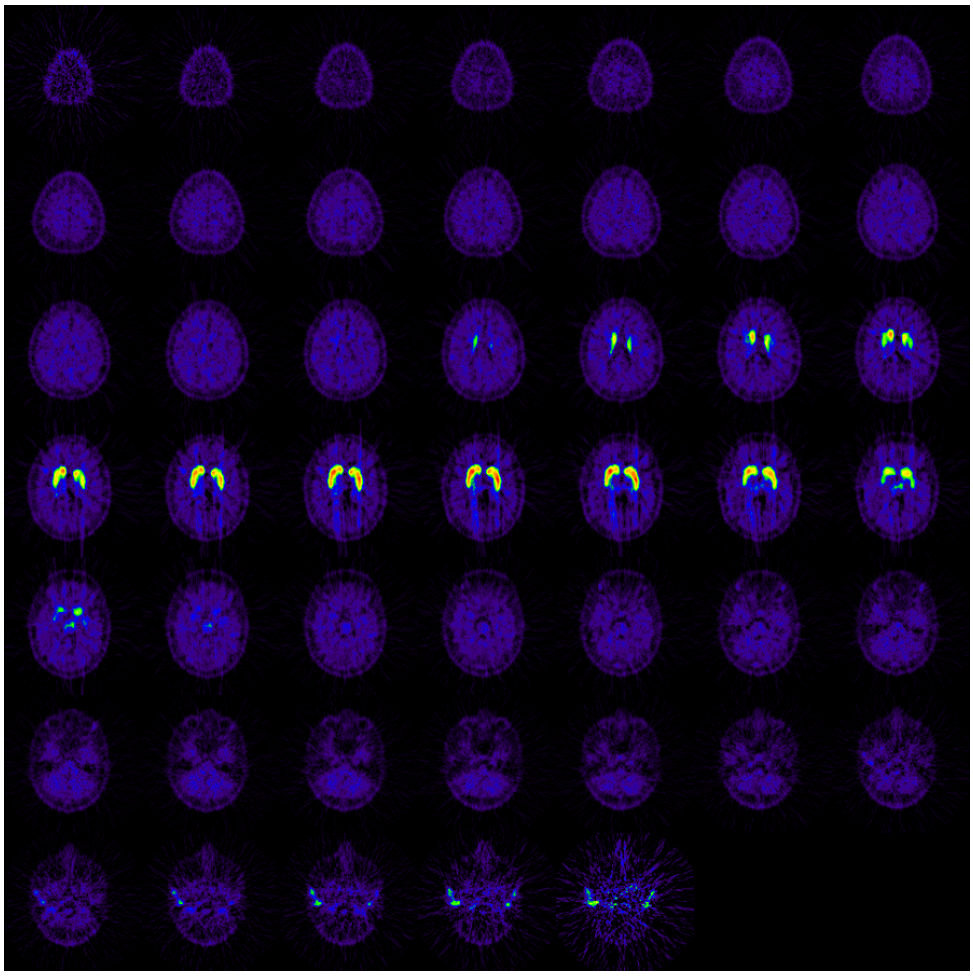
Blood volume fraction (V_B) cannot be fitted, because the first PET frames are too long for this purpose. To correct for the vascular activity, V_B was assumed to be 4.5% in all brain regions. Because the first-pass extraction of [^{11}C]PE2I is high, it can be expected that venous concentration of this tracer is considerably lower than arterial concentration during the initial blood peak. Therefore, only the arterial volume fraction, assumed to represent 1/3 of the total vascular volume, was considered. This was accomplished by constraining V_B to 1.5% in the compartment model fits.

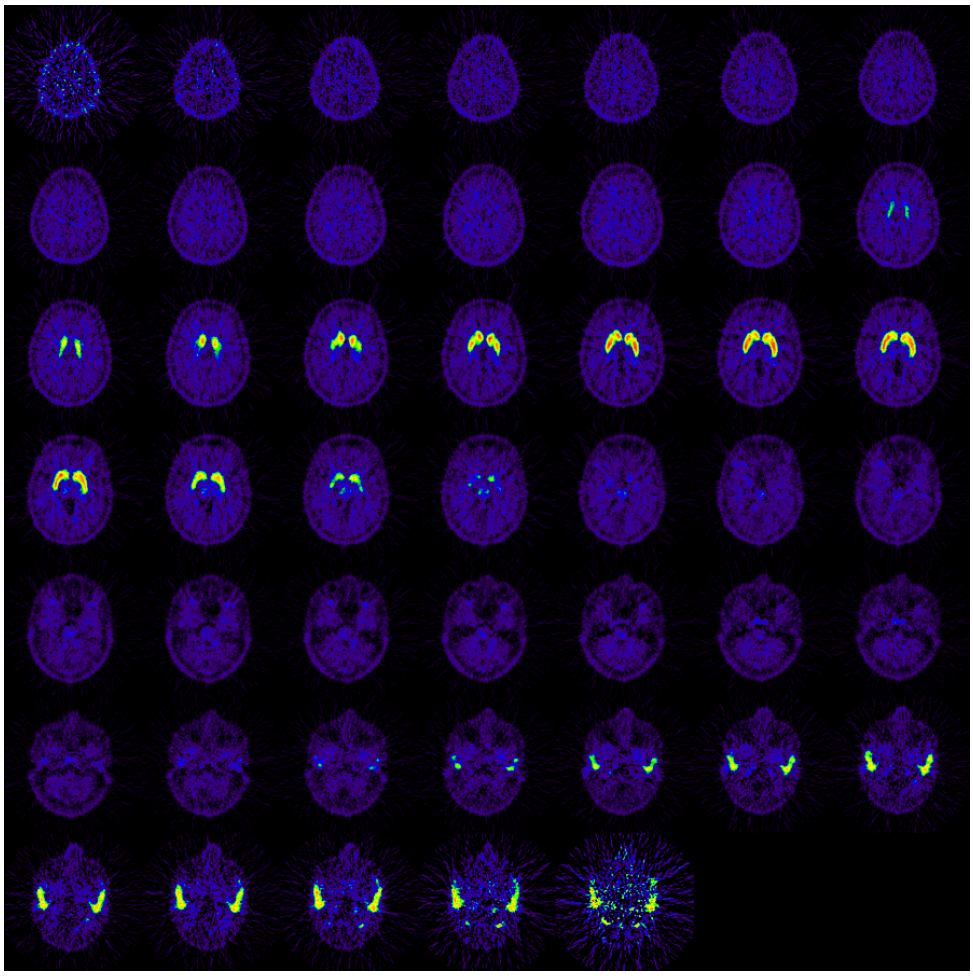
Images and graphs

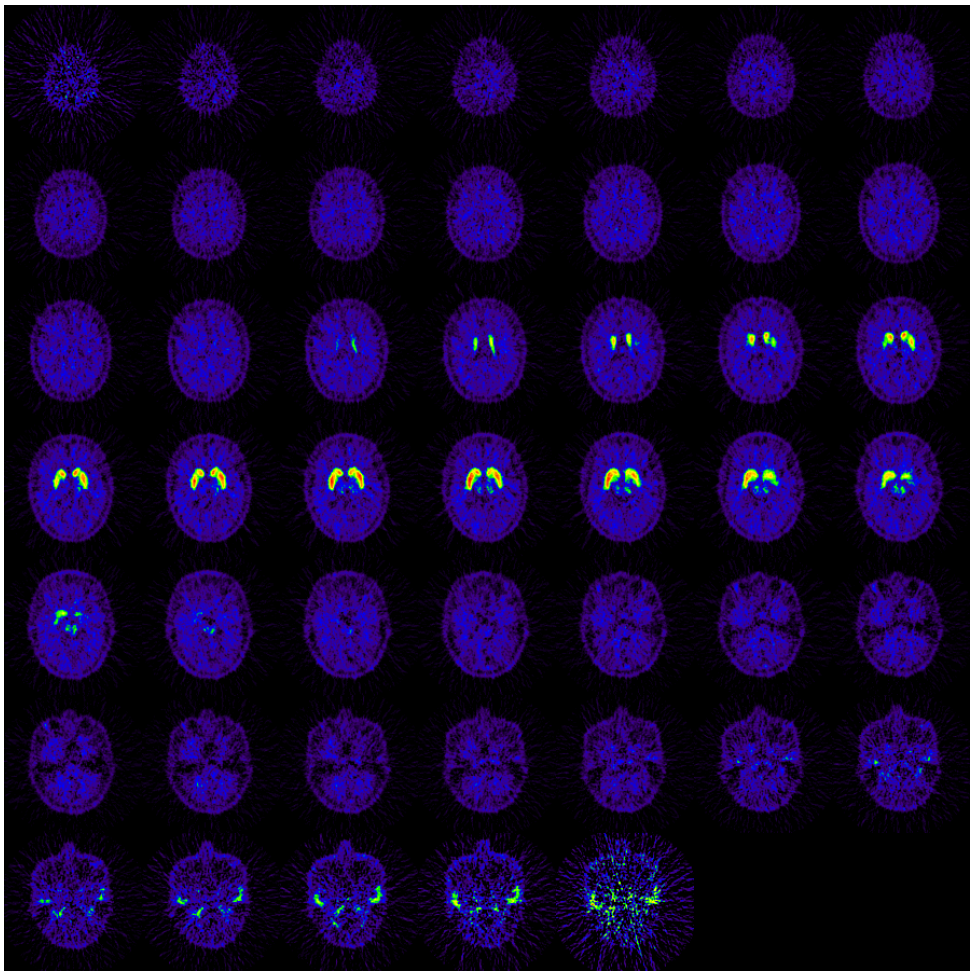
The next pages contain the following images:
- PET images from the three studies from all planes, as an average over the last eight frames (15-63 min)
- Regional time-activity curves
- Regional time-activity curves divided by metabolite corrected plasma
- Metabolite and delay-time corrected plasma curves.

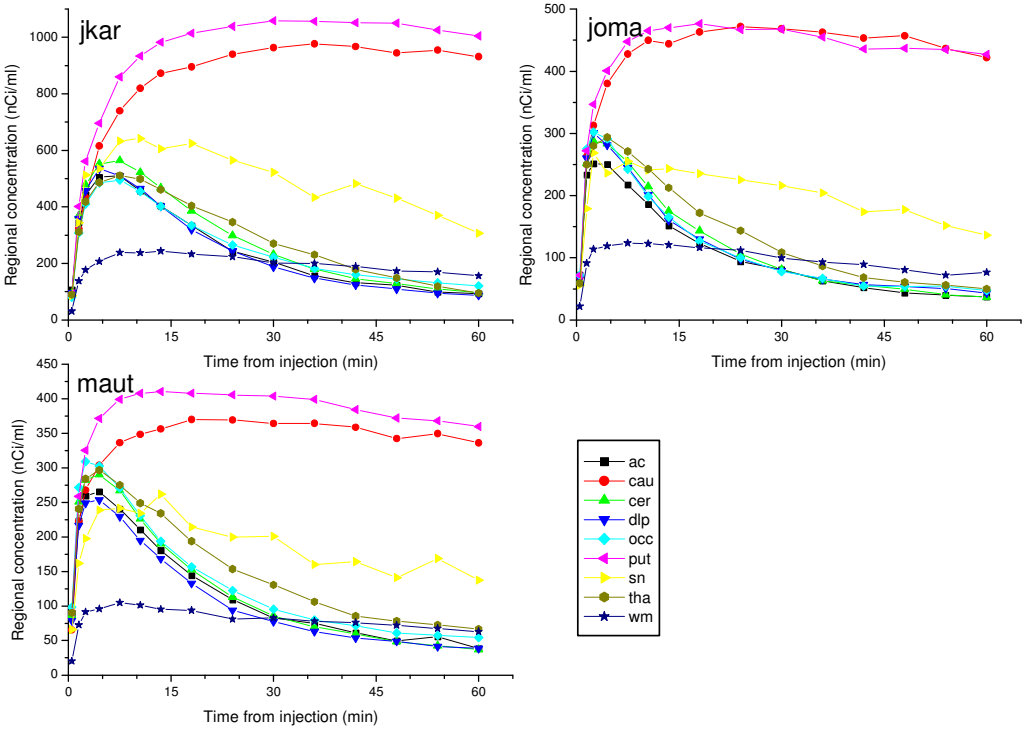
The regional curves of the first subject (jkar), are clearly higher (about 2x) than the two other; this is the case in striatal regions with high binding and in regions with low or nonexistent binding. The metabolite corrected plasma is also higher, but not in the same ratio, therefore the tissue-to-plasma –ratio is also higher in the first subject. This effect may be caused by different plasma protein binding.

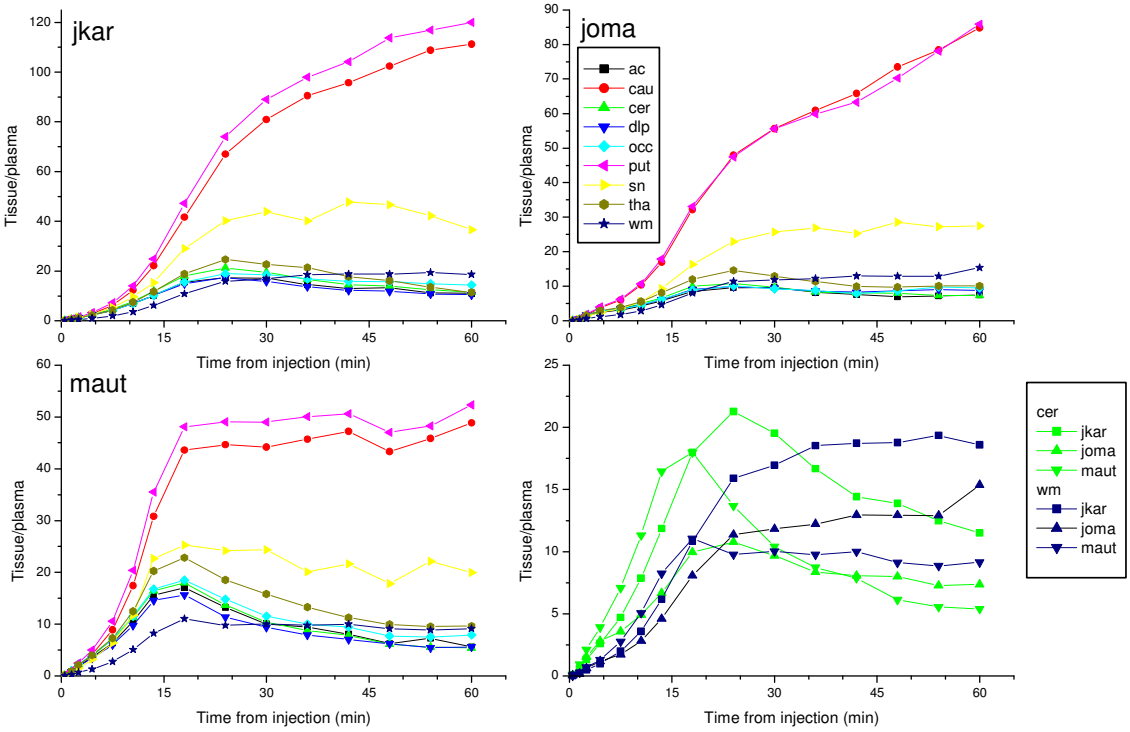
The shape tissue-to-plasma –ratio of 3rd subject (maut) looks different than the others. This may be caused by inaccuracies in plasma metabolite correction, because the end of metabolite corrected plasma curve of this subject is clearly not obeying exponential decline as the other two. Therefore the plasma-input model results are unreliable for this subject.

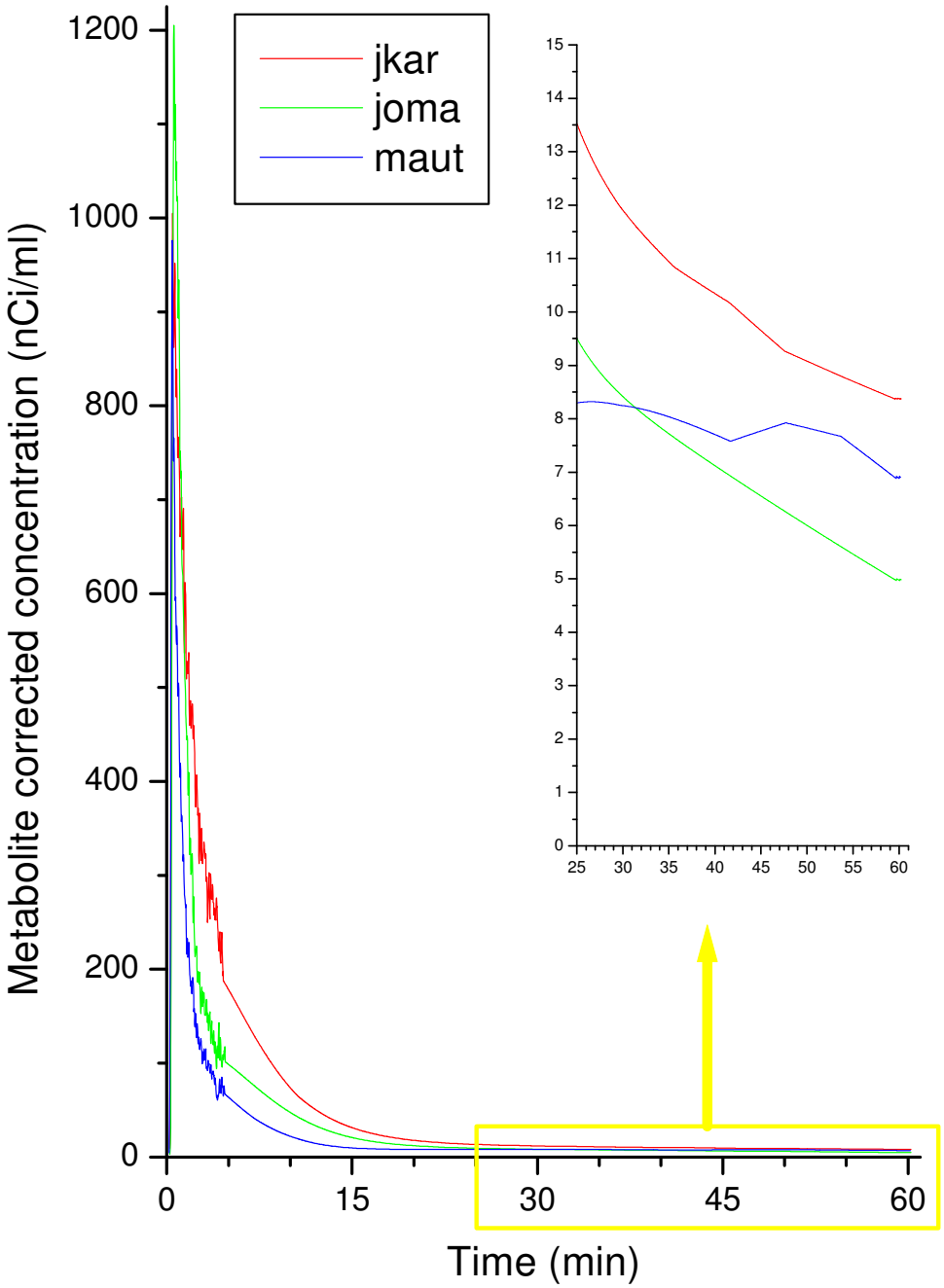







jkar
joma
maut
Regional concentration (nCi/ml)
Time from injection (min)
ac
cau
cer
dlp
occ
put
sn
tha
wm


jkar
joma
maut
Tissue/plasma
Time from injection (min)
ac
cau
cer
dlp
occ
put
sn
tha
wm
cer
jkar
joma
maut
wm
jkar
joma
maut


jkar
joma
maut
Metabolite corrected concentration (nCi/ml)
Time (min)
0
200
400
600
800
1000
1200
0
15
30
45
60
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
25
30
35
40
45
50
55
60