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Vesa Oikonen

Analysis of renal perfusion from [^{15}O]H_2O PET studies: Dispersion correction

Aim

To investigate how large impact the correction for physiological dispersion has on the perfusion model estimates and on the goodness of fits. Dispersion in blood collection system is not considered here, because this has been measured and corrected.

Materials and methods

PET studies: us0568, us0569, us0570, us0571 (subject #1); us0550, us0551, us0552, us0553 (subject #3); and us0490, us0494, us0495, us0496 (subject #3). All studies of one subject are scanned during one session.

Input curve: Arterial blood TACs measured using on-line blood sampler (pump). TACs are calibrated, corrected for physical decay and for the dispersion in collection system.

Renal data: ROIs were drawn on renal cortex in single image planes and pixel average TACs for left and right kidney were calculated.

Procedure and software: Batch file for processing blood TAC is modified to take physiological dispersion constant as a parameter. The dispersion constants 0, 2.5, 5, and 7.5 s are tested. The modified batch file name is water_input_disp.bat. The selected dispersion constant may thus have an effect also on the result of time delay estimate. Batch file makes time delay fitting using fitdelay 1.9.0 against regional renal TACs. Perfusion is estimated using fit_h2o 1.1.1, fitting also Va at the same time, but allowing no further change in time delay. This whole procedure is done using batch file app_b.bat.

Results and discussion

Results are shown in table B1. Correcting for physiological dispersion lead into a bit smaller estimates of time delay, i.e. blood TAC was moved less to the left. RBF increased and RBV decreased clearly with increased dispersion correction; in other words, if there is physiological dispersion which is not taken into account, then RBF is underestimated and RBV overestimated. There was no clear difference in the goodness of fits between dispersion constants in the population level, and by visual inspection, in single studies the model fits to data were also similar with all dispersion constants. This suggests that no common dispersion time constant can be defined that could be applied to all studies.

Table B1. The effect of biological dispersion correction (in addition to correction of dispersion in blood collection system) on the delay time estimate and on the parameters of the perfusion model. The mean of absolute differences (delay time) or relative percentage differences (others) to estimates achieved without setting any additional dispersion correction is presented with standard deviations.

	Dispersion 2.5 s	Dispersion 5.0 s	Dispersion 7.5 s
Delay time (s)	1.1 ± 1.2	1.3 ± 1.6	1.7 ± 1.7
RBF (%)	12 ± 17	28 ± 27	32 ± 36
RBV (%)	-25 ± 25	-57 ± 35	-70 ± 31
Sum-of-Squares (%)	0 ± 23	3 ± 32	11 ± 58

Conclusion

Based on the measured blood and PET data it is not possible to recommend a single dispersion constant that could be applied to all studies. Omitting dispersion correction may lead to considerable underestimation of RBF and overestimation of RBV.