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Assessment of input function distortions on kinetic model parameters in simulated dynamic 82Rb PET perfusion studies

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Objectives: The determination of the exact shape of the input function is a particular challenge in dynamic cardiac 82Rb PET perfusion studies. The dynamic range of the activity in these studies easily covers two orders of magnitude. Additionally, the injection bolus has a very sharp peak. The measurement of the input function depends on both experimental errors (e.g. random noise, limited spatial resolution) and data processing (e.g. frame durations). These issues are a source of error in the assessment of the input function, especially regarding the peak value and the decaying slope. Thus, the goal of our study is to address the influence of such distortions of the input function on the model parameter K1, which is linked to myocardial perfusion [1].

Methods: Using a one-compartment kinetic model [2,3,4], noise-free myocardium TACs representing dynamic PET datasets were simulated with model parameters covering a range of physiologic interest [3]. The TAC simulations are based on different input functions computed with a generic analytical function. The parameters of this function have been derived by numerical fits of various Rubidium PET measurements of the left ventricular bloodpool.
The simulated input function and myocardium TACs have then been applied in a kinetic analysis in the following way: the analytical input function has been distorted by parameter variation, leading to different peak values and decaying slopes. Then, the kinetic parameters have been re-estimated, using the respective (unmodified) myocardium TAC as reference data. The (relative) bias of the K1 estimation was calculated and analyzed as a function of the input TAC variation, and compared across the investigated range of kinetic model parameters.

Results: Underestimating (overestimating) the input peak value causes an overestimation (underestimation) of K1, respectively. The magnitude of this effect depends strongly on the blood volume fraction, and the FWHM of the input function. This is because the wider the input peak, the stronger is the coupling of the input function to the observed myocardium TAC. For reasonable values of the model parameters, the relative bias in K1 is easily ±(10-30)% for a ±10% error in the input peak. This causes an even larger bias in the blood flow values, due to its nonlinear coupling to K1 [5].

Conclusion: Even with noise-free data, moderate errors in the estimation of the input peak value lead to significant errors in the estimated K1 parameter. Therefore, an accurate estimation of the input peak, e.g. by appropriate frame durations, is necessary for a reliable kinetic analysis and blood flow estimation.

References:

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