Pharmacokinetic analysis of dynamic PET data: comparison between *direct* parametric reconstruction and conventional *indirect* voxel-based estimation

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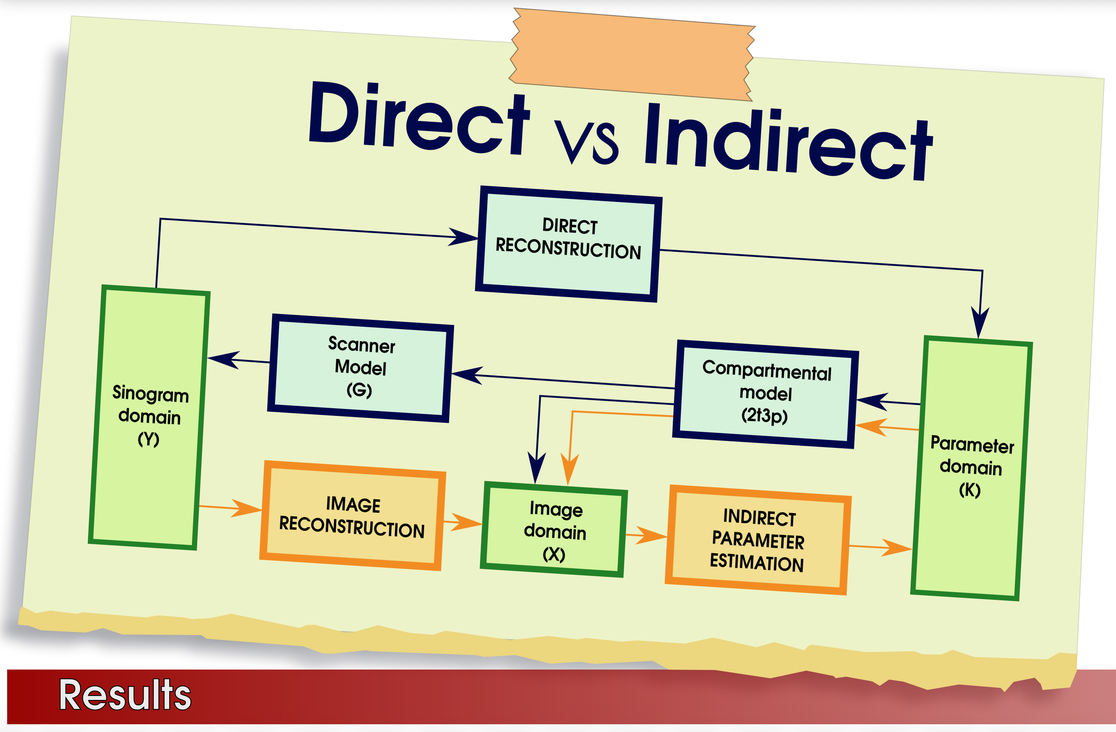
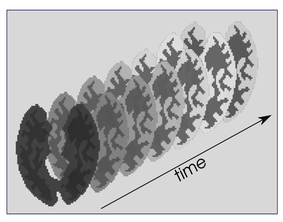
Background

Dynamic positron emission tomography (PET) studies allow to quantify tissue-specific biochemical properties. *Conventional pharmacokinetic analysis* requires the *voxel-wise time activity curve fitting* performed on a sequence of independently reconstructed PET images. Direct parametric reconstruction methods **combine emission image reconstruction and kinetic modeling into a single formula**, estimating parametric images directly from raw data. In the present work a comparison between the two pharmacokinetic analysis methods is performed on *simulated and clinical brain18F(FDG) PET data*.

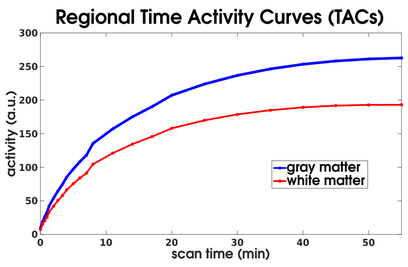


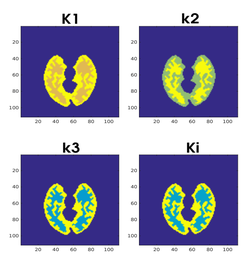
Simulation

Monte Carlo simulation includes **2D dynamic raw data** generation of a **brain phantom** (gray and white matter) based on realistic kinetic parameter's values.
Attenuation and random counts effect are included. The Feng's model is used to generate the input function. 20 realizations are analyzed, each including **24 time samples** ranged from 10s to 600s.



Dynamic scan simulation





Kinetic map simulation

Clinical data

Clinical 2D 18F(FDG) dynamic PET data relevant to the brain of a patient (**24 time frames**) are acquired by **GE PET/CT DRX scanner**.
The time series have been sampled using *different frame duration times*: 12x10sec, 2x30sec, 3x60sec, 2x120sec, 4x300sec e 1x600sec.
The raw data were acquired using **315 angular positions** and **367 lines of response** (LORs).
The same *ROI-based input function* (covering the carotid) is used for both methods.

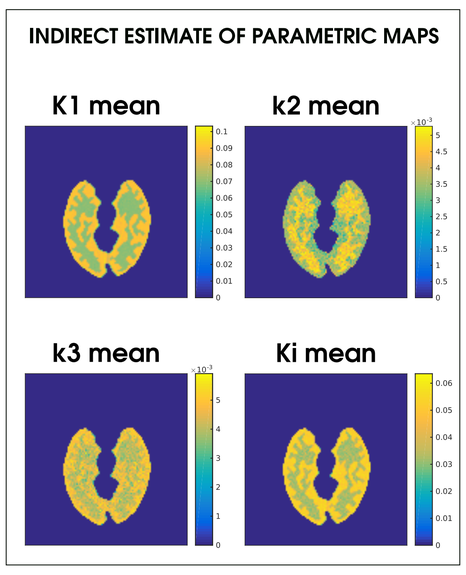
Results

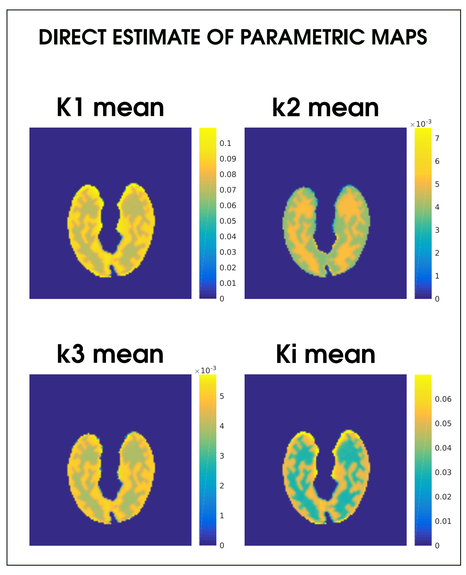
SIMULATION

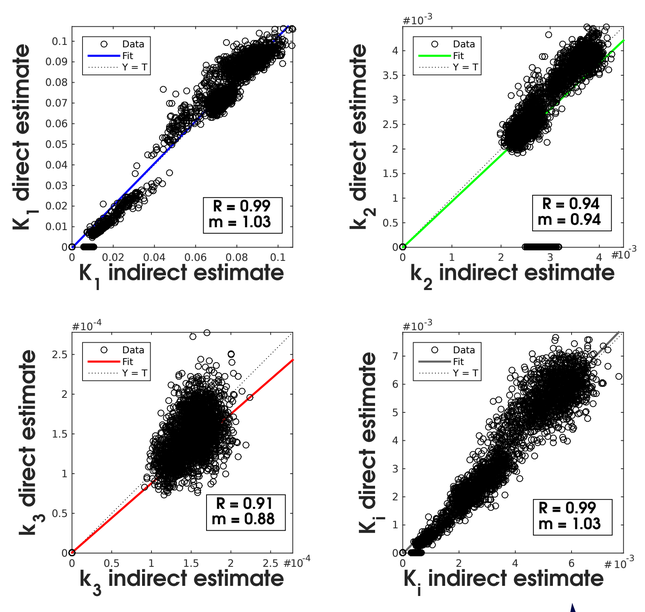
We analyzed *50 realizations of a Montecarlo simulation* of both approaches. In the figures on the right you can see the mean kinetic maps over those iterations, for both direct and indirect reconstruction methods.

The **conventional estimation** consists of *a full OSEM reconstruction* and one step of *voxel-wise non linear least square parametric fitting* with a 2 compartments-3k kinetic model.

The **direct algorithm** is based on *optimization transfer framework* and performs, at each iteration, an EM-like dynamic image update and a pixel-wise penalized likelihood kinetic fitting using the same model as in conventional kinetic analysis.







On simulated data **we assessed the goodness of direct method with nRMSE**, normalizing the error on direct estimate with the one relevant to conventional estimate.

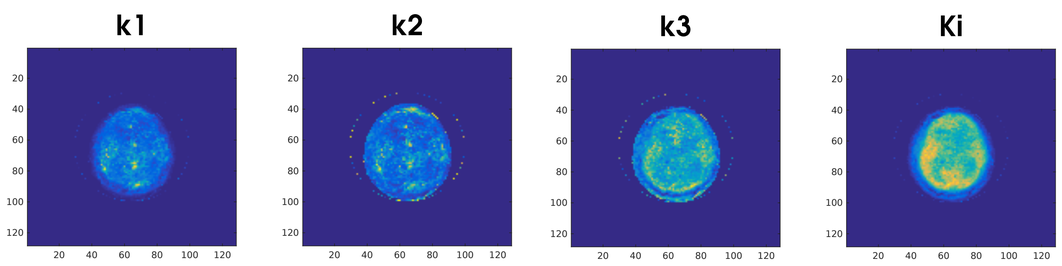
NORMALIZED ROOT MEAN SQUARE (nRMSE)

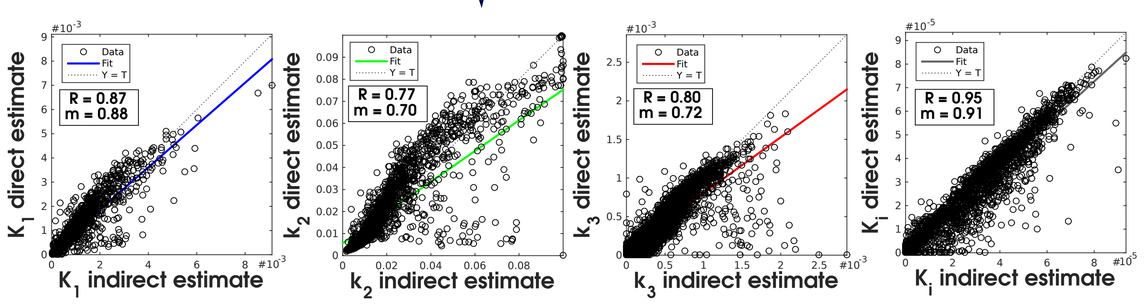
$$\text{normalized RMSE}(k_i) = \frac{\sqrt{\frac{1}{|\mathcal{S}|}\sum_{s\in\mathcal{S}}\left(k_{i,s}^{\text{true}} - k_{i,s}^{\text{DIRECT}}\right)^2}}{\sqrt{\frac{1}{|\mathcal{S}|}\sum_{s\in\mathcal{S}}\left(k_{i,s}^{\text{true}} - k_{i,s}^{\text{INDIRECT}}\right)^2}}$$

K1 = 0.7722 ± 0.0024
k2 = 0.7847 ± 0.0077
k3 = 1.0003 ± 5.16e-05
Ki = 0.9960 ± 1.3e-04

Linear regression analysis has been performed for each of the kinetic constants to compare both methods, on simulated and clinical data.

CLINICAL DATA





Conclusions

nRMSE analysis on simulated data shows a smaller error for directly estimated parameters. This could be due to a slight overestimation of k-values in conventional approach, particularly evident onclinical data, as it results from regression analysis. Further studies have been planned to asses the feasibility of direct kinetic estimation on real clinical dataset and the goodness of the estimated parametric maps.

References

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