

# DIRECT 4D PET RECONSTRUCTION WITH DISCRETE TISSUE TYPES

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## Summary

**Dynamic Positron Emission Tomography** is known for its ability to extract spatio-temporal information of a radiotracer in tissue. We present a **novel direct reconstruction framework** performing concurrent clustering as a potential aid in addressing high levels of noise typical of voxel-wise kinetic modeling.

**Probabilistic Graphical Modeling (PGM)** theory is used to describe the problem, and to derive an iterative inference strategy, which provides **concurrent estimate of kinetic parameter maps, activity images, and segmented clusters**.

## Key-concepts

### CORE ASSUMPTIONS

- Imaged volume contains a **finite number of different functional regions**, each with a unique kinetic behavior.
- **Voxel-wise time courses** are determined by the functional cluster they belong to and they are modeled as a **mixture of Normal distributions** with as many components as clusters.

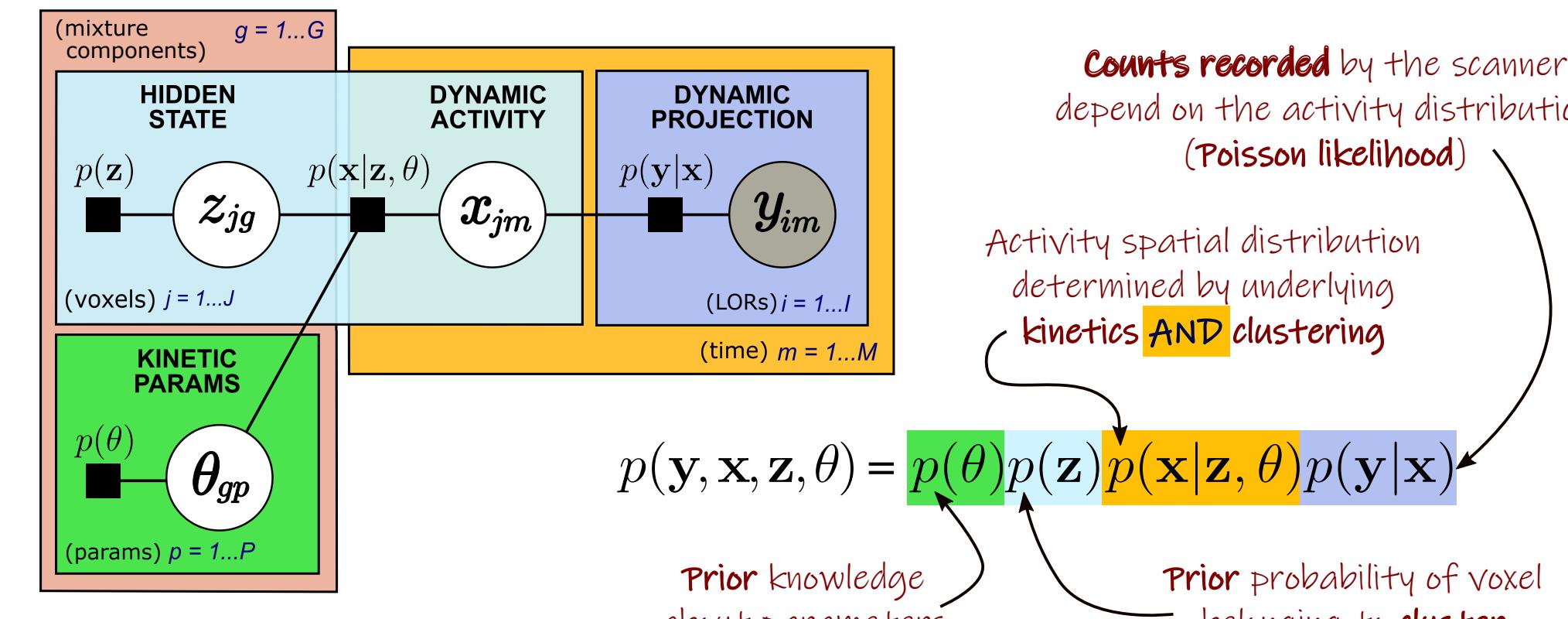
### AIM OF THE WORK

To evaluate how incorporating a clustering step within the reconstruction may assist the estimate of images and maps.

## Is it worth the effort?

- **Lower computational cost and easier implementation:** we need to apply kinetic modeling just to a few cluster means.
- **Noise reduction:** clustering introduces a within-tissue edge-preserving smoothing in both dynamic images and kinetic maps.
- **(Potential) details-recovering:** feasible to test different models for each tissue and to choose the best one.

## Probabilistic Graphical Model



### Goal

Inferring the value of the three unknown, latent variables  $x, z, \theta$  maximizing the joint distribution  $p(y, x, z, \theta)$  associated with the graph.

### Strategy

The joint optimization can be performed by alternating the optimization of the marginal posterior of each variable, conditioned to the provisional estimates of all the others (**Iterated Conditional Modes** approach).

### Number of clusters updated at each iteration (looking for redundancy).

**Voxels guided to resemble the cluster mean** with higher posterior membership probability (extending the idea of voxels' neighborhoods).

**Cluster with low variance**, formed by voxels with very similar kinetics: **stronger kinetic prior**.

## Theory

### Iterative inference

#### 1) Updating the parameters of the Gaussian Mixture

$$\alpha_{jg}^{(n+1)} = \frac{\pi_{jg}^{(n)} \prod_m \mathcal{N}(x_{jm}^{(n)}, \mu_{gm}^{(n)}, \sigma_{gm}^{(n)})}{\sum_g \pi_{jg}^{(n)} \prod_m \mathcal{N}(x_{jm}^{(n)}, \mu_{gm}^{(n)}, \sigma_{gm}^{(n)})}$$

$$\pi_{jg}^{(n+1)} = \frac{1}{\text{size}(C_j)} \sum_{k \in C_j} \alpha_{kg}^{(n+1)}$$

$$z^{(n+1)} = \arg \max_z p(z|x, \theta, y)|_{x^{(n)}, \theta^{(n)}}$$

#### 2) Updating the estimate of kinetic parameters

$$\theta_g^{(n+1)} = \arg \min_{\theta_g} \sum_m \|\mu_{gm}^{(n+1)} - f(\theta_g; t_m)\|^2$$

$$\mu_{gm}^{(n+1)} = \frac{\sum_j [\alpha_{jg}^{(n+1)} (x_{jm}^{(n)} - \mu_{gm}^{(n+1)})^2]}{\sum_j \alpha_{jg}^{(n+1)}}$$

$$\theta^{(n+1)} = \arg \max_{\theta} p(\theta|x, z, y)|_{x^{(n)}, z^{(n+1)}}$$

#### 3) updating the estimate of activity time series

$$x_{jm}^{(n+1)} = \frac{x_{jm}^{(n)}}{\sum_i p_{ij} + \frac{\partial \log p(x|z, \theta)}{\partial x_{jm}^{(n)}} \sum_i p_{ij} \sum_j p_{ij} x_{jm}^{(n)}} \sum_i p_{ij} \frac{y_{im}}{\sum_j p_{ij} x_{jm}^{(n)}}$$

$$\log p(x|z, \theta) = \sum_{j,m,g} \alpha_{jg}^{(n+1)} \frac{(x_{jm}^{(n)} - \mu_{gm}^{(n+1)})^2}{\sigma_{gm}^{(n+1)}}$$

Final image update step

We can apply concepts of **Probabilistic Graphical Modeling (PGM)** theory to improve the quality of **4D PET** images and kinetic maps, by **incorporating** within the reconstruction **a priori info** based on **kinetic modeling and functional clustering**.

This poster!

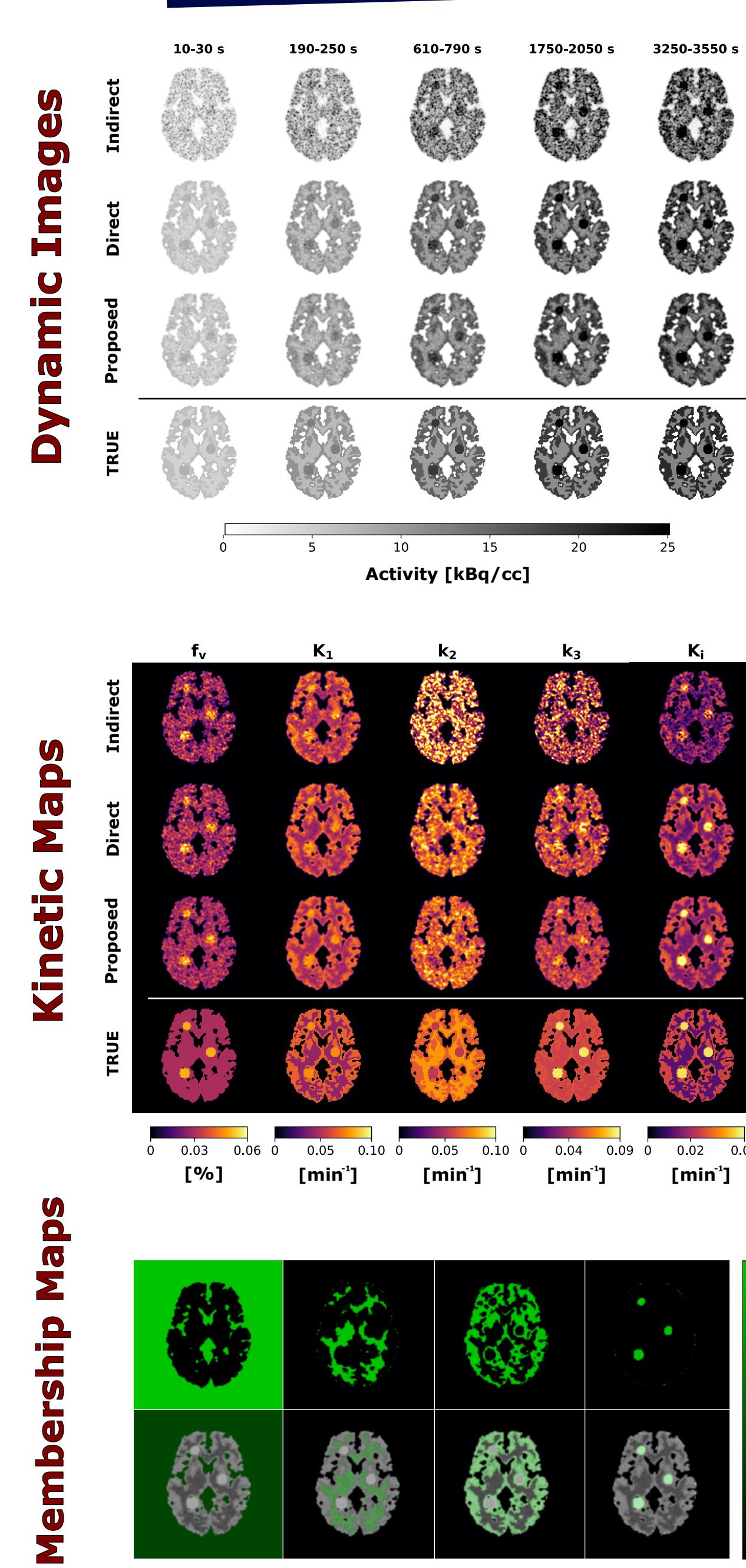
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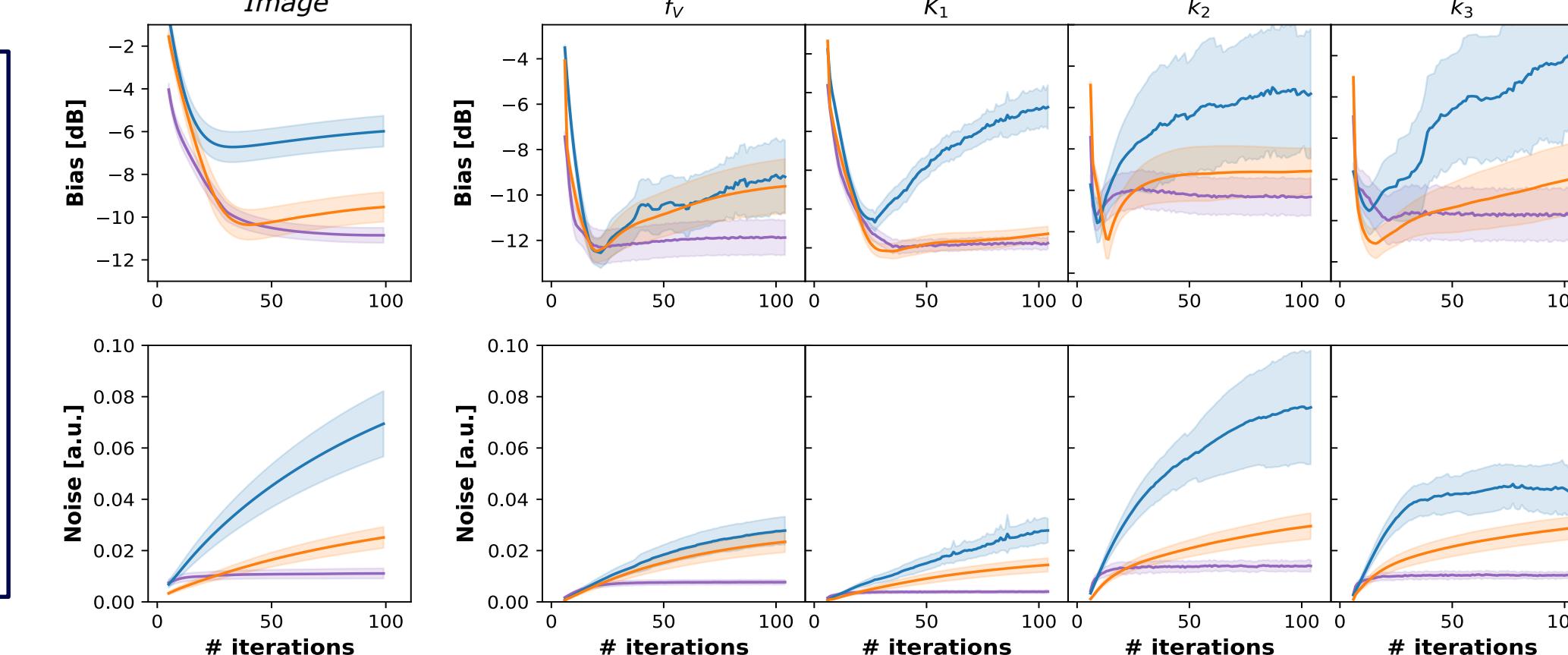
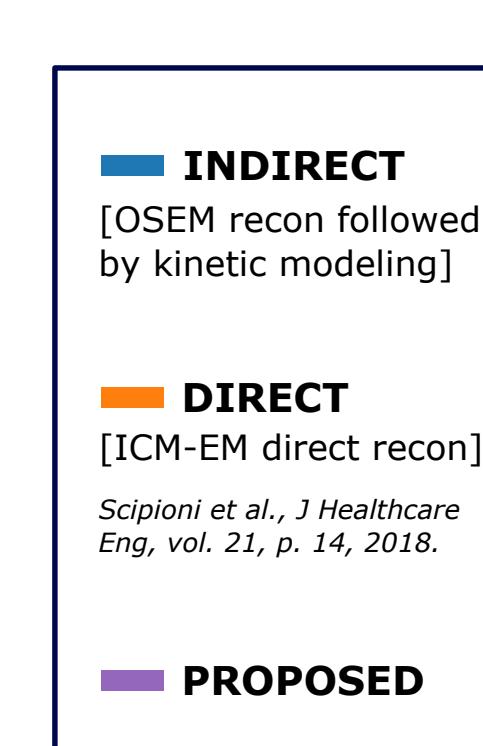
41st **EMB** CONFERENCE, Berlin (Germany), July 23-27, 2019

## Simulation study



### SIMULATION SETUP

Dynamic [<sup>18</sup>F]FDG PET scans were simulated for a Siemens Biograph mMR scanner according to an irreversible bi-compartmental model. The scanning schedule consisted of 24 time frames over 60 minutes: 4x20s, 4x40s, 4x60s, 4x180s, 8x300s.



## RESULTS

### Bias and noise trends as function of the number of iterations

- both kinetic-informed methods improve bias and noise w.r.t. indirect method
- when the proposed method identifies the optimal number of clusters and their means (after ~30 iterations), noise stops increasing, while bias keeps decreasing.

### Simulation's images (left column)

- improved overall quality of estimated kinetic maps

- interesting greater capability of recovering edges between different tissues

### Real data's image (right column)

- constraints that correlate the activity of successive time points allow recovering details in early frames

- higher SNR thanks to within-cluster spatial regularization

### Estimate of posterior membership probability maps

- they play active role in reconstruction and kinetic modeling

- we anticipate them being of help in understanding tissue kinetic behavior

## Real human data study

A dynamic [<sup>18</sup>F]FDG PET scan was performed on the Siemens Biograph mMR. First 40 minutes of listmode raw data were binned into 24 time frames: 12x10s, 2x30s, 3x60s, 2x120s, 4x300s, 1x600s. Vendor software was used to compute corrections.

