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 just 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

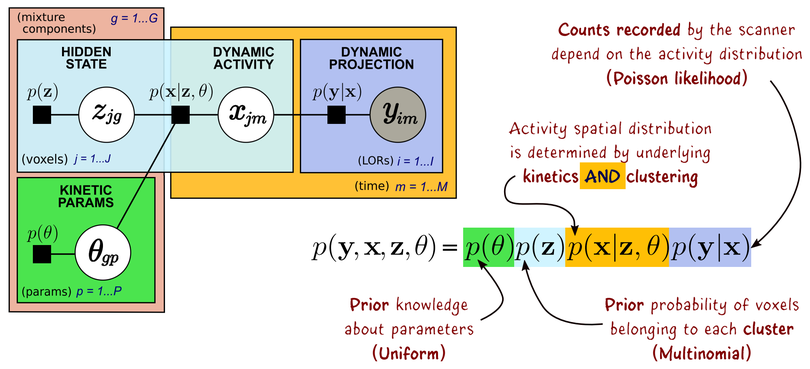
To evaluate how incorporating a time-series clustering step within the reconstruction may assist the estimate of images and maps.

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**: cluster-based regularization introduces a within-tissue, edge-preserving smoothing in both images and kinetic maps.
- **(Potential) details-recovering**: feasible to test different models for each tissue in reasonable time, and to choose the best one.

Theory

Probabilistic Graphical Model



$$p(\mathbf{y},\mathbf{x},\mathbf{z},\theta) = p(\theta)p(\mathbf{z})p(\mathbf{x}|\mathbf{z},\theta)p(\mathbf{y}|\mathbf{x})$$

Goal

Inferring the value of the three unknown, latent variables $\mathbf{x},\mathbf{z},\theta$ maximizing the joint distribution $p(\mathbf{y},\mathbf{x},\mathbf{z},\theta)$ 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 is updated at each iteration *(looking for redundancy/overlapping).*

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

Clusters with low variance *are formed by voxels with very similar kinetics:* ***stronger kinetic prior.***

Iterative inference

1) Updating the parameters of the Gaussian Mixture

$$\alpha_{jg}^{(n+1)} = \frac{\pi_{jg}^{(n)} \prod_m \mathcal{N}\left(x_{jm}^{(n)}, \mu_{gm}^{(n)}, \sigma_{gm}^{(n)}\right)}{\sum_{g'} \pi_{jg'}^{(n)} \prod_m \mathcal{N}\left(x_{jm}^{(n)}, \mu_{g'm}^{(n)}, \sigma_{g'm}^{(n)}\right)}$$

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

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

2) Updating the estimate of kinetic parameters

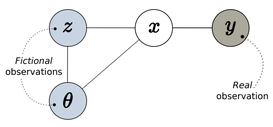
$$\theta_g^{(n+1)} = \arg\min_{\theta_g} \sum_m \|\hat{\mu}_{gm}^{(n+1)} - f(\theta_g; t_m)\|^2$$

$$\mu_{gm}^{(n+1)} = f(\theta_g^{(n+1)}; t_m)$$

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

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

3) Updating the estimate of activity time series



Final image update step

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

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

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

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**.

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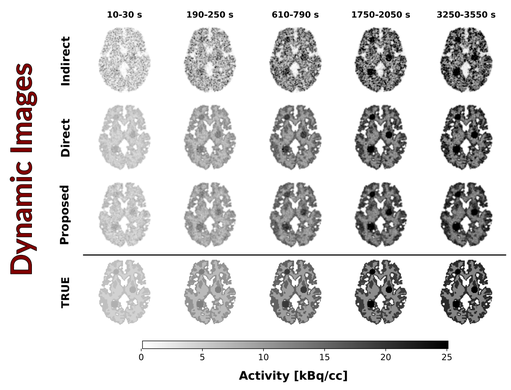
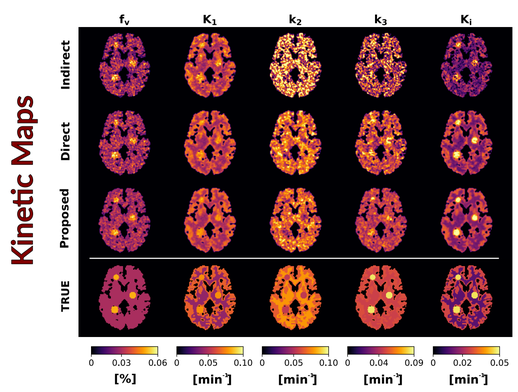
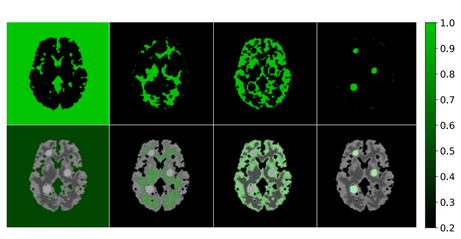
41st EMB CONFERENCE, Berlin (Germany), July 23-27, 2019

Simulation study







SIMULATION SETUP

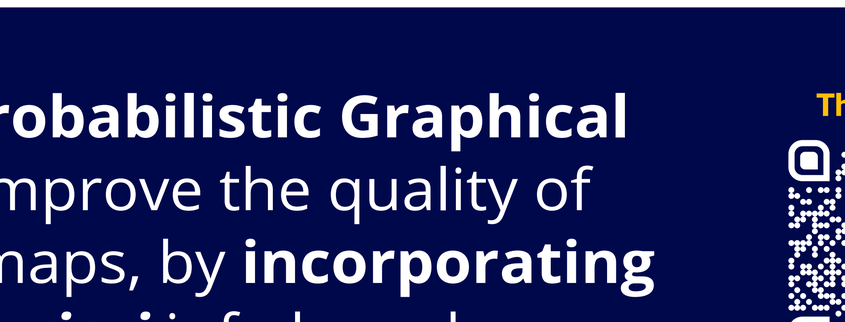
Dynamic [18F]FDG PET scans were simulated for a Siemens Biograph mMR scanner according to an irreversible bi-compartmental model. The scanning schedule consisted of 24 time frames, over 60 minutes: 4x20s, 4x40s, 4x60s, 4x180s, 8x300s.

INDIRECT
[OSEM recon followed by kinetic modeling]

DIRECT
[ICM-EM direct recon]

Scipioni et al., J Healthcare Eng, vol. 21, p. 14, 2018.

PROPOSED



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 correlates 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 [18F]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 correction matrices.