Documentation:

Arman Rahmim, PhD; Nov 1, 2019

<http://www.qurit.ca/>

A C+Matlab-based PET simulation and reconstruction software, enabling realistic brain PET simulations, e.g. dynamic PiB PET imaging on the High Resolution Research Tomograph (HRRT).

You can download the folder here (~1.3GB):

<https://1drv.ms/u/s!AqTzxnxy6vxCi55J-7k7nRVLikodCQ?e=8edCeh>

There are two folders:

hrrt\_open\_2010-10-15\_r234B

HRRT\_PiB\_dynamic\_brain\_simulations

The first one contains HRRT recon code, that you can re-compile. Makefile is in there.

This code is also used for analytic simulation, with realistic noise that can also be added to it.

Next, please go to the second folder:

Start with this file:

HRRT\_simulate\_and\_recon.cmd

You will need large amount of space available for a single noise realization.

For more noise realizations, to save space, it will overwrite existing sinograms with new noise realizations, but will still create NEW/non-overwritten reconstructed images.

The program has seven steps, which you can turn on or off

create\_brain=1;

project\_atten=1;

create\_emission\_images=1;

project\_emission=1;

incorporate\_atten\_norm\_and\_noise=1;

perform\_reconstruction=1;

perform\_parametric\_estimation=1;

You probably don’t need the last one since it uses its own way of kinetic modeling to fit. You can do your own kind of kinetic modelling if you need to.

Kinetic parameters used to generate TACs for different regions are defined here:

generate\_images\_compartmental\_modeling\_256.m

This program uses Eq. 16 and 17 in this paper of ours:

"3.5D dynamic PET image reconstruction incorporating kinetics-based clusters"

Lijun Lu et al, Phys. Med. Biol., 2012.

<https://rahmimlab.files.wordpress.com/2015/06/lu_pmb12_3-5d_dynamic_pet_image_reconstruction.pdf>

which are standard compartmental modeling equations (2-tissue model).

dncat/ folder contains the code to create the brain regions, which are then fed to above .m matlab code to creates TACs.

NOTE: This uses our anthropomorphic brain phantom (also shared on our software page, but also included here).

The particular kinetic parameter numbers used in this code are for a PiB PET study.

For instance as you’ll see in there, for PiB, the k1, k2, k3, k4 and vB values are:

% For PiB (cingulate was based on Anterior Cingulate measurements, Brain

% Stem based on Pons, and white matter based on subcortical white matter)

% PiB -From the file: PiB ROI Matching - Julie.xlsx

values=[0.237 0.144 0.021 0.013 %Cingulate

0.310 0.172 0.015 0.011 %Occipital cortex (Cx)

0.278 0.147 0.018 0.016 %Anteroventral Striatum

0.252 0.147 0.020 0.013 %Brain Stem (including Pons)

0.288 0.151 0.010 0.012 %Cerebellum

0.235 0.114 0.040 0.030 %Parietal Cx

0.244 0.151 0.023 0.015 %Frontal Cx

0.282 0.163 0.020 0.013 %Precuneus

0.232 0.130 0.017 0.014 %Lateral Temporal Cx

0.251 0.150 0.017 0.013 %Somatosensory Cx

0.178 0.112 0.019 0.017 %Mesial Temporal Cx

0.104 0.087 0.067 0.020 %White matter

0.268 0.109 0.020 0.028 %Thalamus

0.278 0.155 0.018 0.014 %Occipital Pole

0.271 0.151 0.016 0.012];%Occipotemporal Cx (mean of

%lateral temporal and occipital)