From: **Lee, John** leej@mir.wustl.edu
Subject: Re: pet aif project matlab code attached
Date: March 26, 2014 at 7:00 PM
To: Shimony Josh shimonyj@mir.wustl.edu

Josh:

The version of wrapper bayes_petmri that you sent uses a function handle to logprob_petmri which I do not yet have.   I'll assume that substituting a function handle to logprob_exp, which I have and which calls calc_mriaif as well as calc_petaif, will be reasonable and continue exploring the code.

Thanks,
John

On Mar 25, 2014, at 2:48 PM, Shimony, Joshua <shimonyj@mir.wustl.edu> wrote:

> John
>
> Here is the code.
>
> the .mat file is the pet data from one subject. it has AIF, whole brain (WB), white matter (WM), gray matter (GM) but I don't use all that info.
>
> bayes_petmri is the wrapper and it now estimates too many parameters. I can explain in person.
> calc_mriaif creates a fake mri AIF so this can be replaced by the real thing
> calc_petaif get the pet aif from the mri aif using a convolution.
> logprob_exp checks how good the estimate is. it currently uses both the aif and the WB curve, but i think it is a cheating version now since it tries to optimize the fake mri aif, which normally it would not do. This has to be changed and it may be best if I show you how.
> mcmc is the hard core piece of the code that does the markov chain stuff. Best to not change this.
>
> we likely need to meet to get you going.
> thanks
> Josh
> <p7861ho1AS.mat><bayes_petmri.m><calc_mriaif.m><calc_petaif.m><logprob_exp.m><mcmc.m>