

ADNI Biostat conference call
20 June 2006

Present on call: Danielle Harvey, John Kornak

John updated us on the discussion from the MR call that took place a little over a week ago. The voxel-based calls have now been merged with the MR calls, so any voxel-based issues will be discussed at the beginning of the usual MR conference calls. The big topics of discussion on the last call were a common template to be used by the voxel based groups for both MR and PET and the idea of a split half analysis. The MR labs seemed to think that a common template, such as the Colin Holmes high resolution/high contrast average brain, would be a good idea. Bill Jagust was also on the call and said he would bring the idea back to the PET group (although on the PET call on June 7, there was discussion of coming up with a template that identified “functional regions” as opposed to “anatomical regions”). He thought they could try to come up with regions that at least somewhat corresponded to the anatomical regions being used for MR. This topic will be discussed more on the next PET call which will happen in early July.

The second topic of the split half analysis was something that had come up on the PET call and was discussed further on the MR call. The idea behind this method would be to a priori define half of the data to be used for “training” purposes or to identify potential regions of interest and then use the second half of the data to validate those findings. Mike was less enthusiastic about this idea, because he thought that there is plenty of information in the literature on regions of interest and that there is no need to re-invent the wheel. He thought the MR and PET groups could easily identify ROIs based on experience and literature without having to set aside half of the data for those purposes. This topic will come up further on the PET calls, as many of the PET labs are still interested in this idea.

An open question that is being investigated by Gene Alexander is when to normalize the images to a standard template (i.e. do analyses using favorite template, but then do final analysis using the standard template or start by normalizing to the standard template and then do the analysis in that space). The idea here is that VBM works better when normalized to an average brain generated by the data whereas TBM works better if you normalize to a single scan. Gene will be looking into these two options to see which will be the best approach.

Multivariate approaches like PLS were something that had come up on the PET call (and would also potentially make the split sample approach more reasonable) and so discussion came up on the MR call about these methods. These methods may end up being done as secondary analyses, but not the primary analyses for ADNI (mainly because it may be hard to convince the FDA that such approaches are reasonable to use for clinical trials).

The next call will be on July 18, since two weeks from now is July 4. If issues come up before then, we will discuss them by email.