ADNI Biostatistics Conference call
3 March 2009

On call: John Kornak, David Shera, Fred Immerman, Kisook, Danielle Harvey, Laurel Beckett, Mike Weiner, Philip Insel??.

Mike introduced Philip Insel, a new MS person working at UCSF with Mike's lab; he has previous work with UCSD group. He will be working on the freesurfer data analysis for the next two months. He may get in touch with Laurel and Danielle. Laurel asked Philip to send us contact information so we can add him to the email list and know how to keep in touch.

Danielle updated us on the data available for analysis for the April meetings. Both the MRI and PET cores decided that we should do a two-tiered analysis in the spirit of the intent-to-treat analysis of clinical trials. The first analysis would include all data that passed the initial QC. The second tier would be restricted to various "clean" data sets based on further information. For example, there are a couple of scanners (one with PET, one for MRI) that have known issues. So one question would be how much data from those scanners affects the results. This is useful for ADNI II; we might put into protocol that those scanners would not be used. Another idea is that individual labs have their own QC approaches for their particular metrics; if they find problems that compromise specific metrics, they may flag certain results for exclusion. Since this is a second-tier analysis, we are starting on the analyses that make use of all data first.

Danielle wants to alert people, if they were not already aware, that the longitudinal biomarker data are now available for download. The biomarker data are now included as a separate table in the clinical data dump. The table is upennbiomk in the clinical set of tables. Right now we believe it is just baseline and 12 month data but they hope to add some 24 month. There are some issues right now on ptau data but the beta should be ok; you might want to hold off on ptau analysis (longitudinal, anyway) for now.

Danielle is checking on overlap tables to see if there is need for an update since last time in early February. If there are changes, she will rerun and circulate.

Based on tables from early February, MRI Core was concerned to make sure that all scans had been through all of Mayo's process (grad warp etc.). Mike Donohue and Danielle put together spreadsheets that identified scans with missing information or missing scan (acquired according to tracking but not on LONI), or scan at LONI but not corrected. They will be talking to Mayo this week to sort out spreadsheets. This may increase number of images available. Danielle will identify any additional scans.

For the 1.5T vs 3T comparison, the MRI core wanted to restrict analysis to those scans with highest quality, that is 1 or 2. Danielle provided lists to the labs of those. The majority of those subjects and scans are now processed. We will probably still do that comparison within lab, then summarize.

We are preparing for 3 talks at Seattle: Laurel will present summaries at the ISAB and SAB, and Danielle will present a talk on the comparison results for the big session on Sunday.

John added news on voxel-based analysis. Mike was worried about whether data-generated ROI's were being done correctly or whether there were biases being induced. John has exchanged many emails with the labs, especially Eric's lab, and he reports that for the most part they have been very careful to use training set and evaluate in the learning set. There was one small problem but that is being corrected. John believes we are actually ahead of the field on this. He did a journal club report on a paper that developed correlational analyses using data-driven selection and they are getting very inflated correlations because it is not training-test set approach. John did a little simulation of random noise data and showed beautiful correlations using their approach.

Danielle is writing the first of a series of papers on statistical methods for imaging; this one is on methods for comparison. One of the papers in our proposed series is in fact on the importance of cross validation and how to do; John might be a natural person to take the lead on this. The methods are well known in statistical literature but have not been thought about as much for imaging, and we may be able to adapt, with new ideas as needed.

Next call is Tuesday 7 April 2009, 10 AM Pacific time, to go over findings for presentation.