ADNI Biostatistics conference call: 1 May 2012
Present on call: Laurel Beckett, Danielle Harvey, Chun-Jung Huang, Naomi Saito, Mike Donohue, Nandini Raghavan, David Verbel, Pam Schwartz,

New Orleans: Our work was well received. John Trojanowski and Les Shaw presented new biomarker analyses (we do not have the data yet). Some labs presented new data on specialty sequences from the MRI core. Neither of these is submitted yet. Base and APP data is in the pipeline (from biomarker consortium). All presentations are online now and we encourage people to look at them (adniinfo.org, under scientist page, and try the steering committee.)

The data tracking committee meeting was important and quite helpful. The collaboration between ADCS and LONI has identified and diagramed the data flow and possible hold-ups, and they are going to prepare both overall and detailed reports that will be provided automatically, and will be available online as sort of a dashboard. The automation will be a huge help and (we hope) relieve the burden on Danielle, Naomi, and Mike's group. Data documentation requirements were also proposed for summary datasets. Each dataset would have to meet three criteria: completeness of the data (eg having visit id and patient id and date), a complete data dictionary at initial submission, and a methods paper at the initial submission. Data updates would have to be complete but would not require dictionary and methods paper unless the method has changed. Templates and examples for dictionary and methods document were suggested.

Nandini asked about documentation for PiB methods; Danielle thinks it is available and will send a note. Also, she asked about the cross-validation, which is available on the "scientist" portion of the web site. Both training/ test and k-fold cross-validation sets are available there. We will try to set up our example code for both, in SAS and R, and will try to put this on the ADNI data site and include a methods document. The main reason we set up a specific cross-validation scheme was to ensure that when labs develop new data-driven regions of interest or other predictive schemes, they use the same training set, leaving a common test set available for comparison across models.

Mike, Anthony, Laurel and Danielle are going to develop a document/ guideline on how to operationalize the IOM guidelines for biomarker discovery to ADNI data. We think this would be helpful to get people to conform more to the steps.

Nandini reported on the ADNI PPSB data mining session. (Laurel was there, too.) There were 4 presentations and a good discussion and exchange. Nandini thinks it was a good thing to share the work that people were doing separately.

Laurel suggested organizing a session at JSM 2013 on data mining in early-stage AD (MCI, NC) for people using ADNI data, the placebo group, and others doing this. We will pursue this idea over the next few months.

The next call is June 5. There will not be a call in August because of JSM; we are not sure yet about July.