QIBA fMRI Biomarker Committee (BC) Call

Wednesday, August 19, 2020 at 11 a.m. (CT) Call Summary

In attendance

Feroze Mohamed, PhD (Co-chair) Jay J. Pillai, MD (Co-chair) David Soltysik, PhD (Co-chair)

Shruti Agarwal, PhD Ping Hou, PhD Ichiro Ikuta, MD, MMSc Andrew Kalnin, MD David Scott, PhD James Voyvodic, PhD **RSNA staff** Joe Koudelik Susan Stanfa

Moderator: Dr. Soltysik

Review of Previous Call Summary

• The 08.05.2020 call summary was approved as presented

Dr. Voyvodic's Round-1 DRO Project: Comparing clinical fMRI analyses

- Collaborators and sites included:
 - David Soltysik, PhD US FDA
 - Jerry Wang, PhD Southwest Texas University
 - Jay Pillai, MD Johns Hopkins University
 - Feroze Mohamed, PhD Jefferson University

- Kirk Welker, MD Mayo Clinic
- o Yuxiang Zhou, PhD, DABR Beaumont Hospital
- Ted DeYoe, PhD Medical College of Wisconsin
- Jim Voyvodic, PhD Duke University
- Dr. Voyvodic noted that Francisco Zamorono, PhD Universidad del Desarrollo (Santiago, Chile), is interested in analyzing the data; anyone is welcome to request the link from Dr. Voyvodic
- Main categories of sources of signal variance included: head motion, physiological noise, scanner noise, and task dependent noise
- Sources of variance affecting fMRI included scanner, task design, training procedures, stimulus presentation system, physiology, pathology, patient movement, task performance, and analysis procedures
- In this DRO study, eight groups analyzed the same bilateral hand motion and language scan data within the context of neurosurgical planning; another sentence task was also analyzed
- All sites were sent a survey re: their methodology; seven returned analysis results and descriptive information
- Dr. Pillai asked that Dr. Agarwal, his post-doctorate assistant at the time of the study, with whom he worked to compile site data, be given author credit on the publication
 - Dr. Voyvodic asked to be notified re: anyone else who should be included
- There were ten different sets of Round-1 DRO motor maps across all eight sites
- Each DRO set contained whole brain T1, bilateral hand motion EPI scan and sentence-completion EPI scan
- Sites varied in how they aligned their EPI images with T1 images
- It was noted that variability resulted from how data were analyzed and was not inherent in the data itself
- Analysis issues were related to imaging registration, not thresholding, and can be reconciled using AMPLE normalization
- With four of the analysis methods, registrations were correct and agreed with the original maps
- Conclusions:
 - Most sites use the General Linear Model (GLM) approach
 - One site routinely uses correlation analysis (does not have a concept of standard thresholding)
 - One site also uses t-test analysis for near-real-time results

- Raw maps are generally similar across sites; different software produces similar spatial patterns, however, there were some unexplained exceptions
- Sites differ significantly in thresholding
- AMPLE normalization reduces threshold variability
- Some sites differ significantly in anatomical registration
- Sites differ in use of slide orientation information
- o Need to explain issues encountered (i.e., sources of variation) and how to mitigate
- fMRI BC members were asked for their feedback
 - It was recommended that this analysis of DRO data from multiple sites be submitted for publication as soon as possible, as it is very important overall for the QIBA effort – specifically with clinical sites conducting routine processing
 - o It was also noted that this type of study has not been published before
 - Most sites were willing to work with Dr. Voyvodic to correct some of the issues, but help is needed to obtain missing information from two of the unresponsive sites, so that remaining issues can be resolved

Action Items

• Dr. Voyvodic to reach out to project PIs at the various study sites for specific approach details; Dr. Pillai volunteered to help with this as well

Next call: Wednesday, September 2, 2020 at 11 a.m. CT (1st & 3rd weeks of each month)

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