Specialty area: Single Subject Neuroimaging
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Highlights:

- Comparing group analyses to single subject analyses
- Considerations when seeking out biomarkers
- Importance of the interpretation of modeling results

Title: From Group Analysis to Individual Studies: Statistical Considerations

Target audience: Neuroimagers seeking out brain-based biomarkers. Some basic knowledge of the general linear model will be assumed.

Outcome/Objectives: The purpose of this talk is to compare typical models that we use in group analyses for different imaging modalities and think about how these models would be applied in a single subject setting.

Purpose: The most common group analyses used in imaging, and often the first step in identifying a potential biomarker, is to see whether this potential biomarker is statistically different in one group compared to another (two sample t-test) or whether this indicator correlates with level of disease. As the future goal is to be able to take the biomarker's value for a single subject and use this to direct their treatment or outcome, it is important to take a close look at what the group models achieve and how useful these models will be in the single subject setting. To bolster power in a group analysis, large sample sizes are often accrued, whereas single subject analyses require a finer tuned data preprocessing pipeline in order to reduce within-subject variability. Not properly preprocessing data can have different impacts on the analysis, depending on the analysis that is being conducted. For example, with motion artifact if a patient suffers more motion than a control group (or different patient groups), in a test comparing means (single subject to group or group to group) variance differences will not inflate the risk of false positives. On the other hand, in a correlation-based analysis (e.g. the correlation between two regions of the brain using resting state fMRI) differences in variability can induce false positive differences between groups.

For a new subject, to determine whether or not their mean activation is more like that of a patient or a control subject effectively requires proving the null (that the subject is *not* different than some group), which is not possible using Frequentist statistics (i.e. p-values). Thus the interpretation of our standard group models and how well it suits the future use of that statistic in a single subject model should be considered.

Methods: Most of the discussion will involve the general linear model as it is used across a wide variety of imaging modalities. Additionally the use of intraclass correlation coefficient (ICC) and related measures to assess reproducibility will be discussed.

Results/Discussion/Conclusions: Understanding how some of the more traditional models we use in our group analyses behave in single subject analyses sheds light on the search for a biomarker. It is likely that the standard GLM models we tend to use will need to be used in a different way and that we will need to consider different types of analyses to evaluate our potential biomarkers.