Dependence Testing for Phenotypic Attributes in Connectomes

Team Captain: Sambit Panda

Sandhya Ramachandran, Bear Xiong, Richard Guo, Satish Palaniappan

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Opportunities

- Healthy Brain Network
- Well-supported statistical inference packages (MGC, energy, dHSIC, kernlab)

Significance

- Anxiety disorders are the most common mental illness in the U.S., affecting 18.1% of the population every year.[1]
- Anxiety disorders are highly treatable, yet only 36.9% of those suffering receive treatment.[1]
- Current diagnoses of psychiatric disorders vary from doctor to doctor and are based primarily on checklists and self reports, lacking quantitative support.
- Certain and early diagnosis allows early treatment.

[1]https://adaa.org/about-adaa/press-room/facts-statistics

Gaps

- No comprehensive analysis on whether measured phenotypes correlate with a connectome

Challenges

- Need to merge similar stat repositories for a more comprehensive tool
- No *standard* method for measuring correlation between connectomes and phenotypes

Action

- Sprint 1: Improve the energy package by merging in relevant tests from MGC and other sources.
- Sprint 2: Analyze whether functional connectomes are dependent on targeted phenotypic attributes (i.e. anxiety) using improved energy package.
- Sprint 3: Replace functional connectomes with MGC connectomes and repeat experiments from sprint 2.

Aim 1: Improve functionality of energy and MGC packages

- Actions
    - Port fastMGC (Matlab) into MGC (R)
    - Incorporate MGC into the R package energy
    - Add random forest based independence testing into MGC
- Expected outcome
    - A modified energy package incorporating MGC with more features and more efficient implementation
- Potential Pitfalls
    - We break MGC or energy :(
    - Need permission to commit to energy

Aim 2: Discover whether connectomes are dependent on targeted phenotype

- Actions:
    - Use energy statistical package to find correlation statistics between connectomes related to the targeted phenotype (i.e. anxiety)
    - Analyze statistical significance of correlations
- Expected outcome
    - P-value measuring significance of any correlations found
- Potential Pitfalls
    - No strong correlations found to analyze

Aim 3: Replace functional connectomes with MGC connectomes

- Actions:
  - Replace functional connectomes with MGC connectomes by using MGC as a correlation statistic between nodes.
  - See whether new insights can be made using MGC connectomes by repeating experiments from Sprint 2.
- Expected Outcomes:
  - MGC connectomes
  - P-value measuring significance of any correlations found between MGC connectomes and phenotypes

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Possible Team Names

- DIGLETT (Dependence In Graphs by Leveraging Energy TesTs)
- LUGIA (Leveraging Undergrads for Graph Independence Analysis)