Data Studio

1:30–3:00pm, Wednesday, 11 May 2022
Conference Room X393, Medical School Office Building, 1265 Welch Road, Stanford, CA
Videoconference: https://stanford.zoom.us/j/92154339367?pwd=T2ZpSXlGdWxFTHNKZ1ptclF1ZFErUT09
Password: 761452

Investigator: **Elizabeth Mayne** Neurology

Title: **Of Mice and Strokes**

Summary:

The Data Studio Workshop brings together a biomedical investigator with a group of experts for an in-depth session to solicit advice about statistical and study design issues that arise while planning or conducting a research project. This week, the investigator(s) will discuss the following project with the group.

The hippocampus is a vital part of the brain for learning and memory. In adult mice, ischemic stroke induces neurogenesis in the hippocampus even when the hippocampus isn't directly injured by the stroke. However, the newborn neurons are structurally abnormal. The increase in neurogenesis after stroke causes cognitive impairment when these neurons mature and integrate into the hippocampus. We do not know what causes the increase in neurogenesis after stroke. We hypothesize that the acute inflammatory response to stroke is a likely cause. This inflammatory response peaks within the first three days after stroke. We hypothesize that inflammatory mediators induce signaling cascades within neuronal precursor stem cells (NPCs) that result in the increase in neurogenesis. The peak of neurogenesis is usually about 7-14 days after stroke. Furthermore, we do not know whether this increase in neurogenesis after stroke occurs in "pediatric" mice.

We plan to perform experimental stroke or sham surgery on "pediatric" and adult transgenic mice. We will sacrifice a cohort at 3 and 10 days after stroke, respectively, to perform cell-specific RNA sequencing on NPCs. The day 3 time point is when inflammatory response is maximal. We hypothesize that we will identify the transcriptional changes in NPCs in response to stroke that may cause the increase in neurogenesis. The day 10 time point is when neurogenesis is maximal. We hypothesize that we will identify transcriptional changes present in the stroke group that is absent in the sham group and that these transcriptional changes will identify the mechanisms that contribute to abnormal growth and maturation in the post-stroke-born neurons.

We want to test whether the inflammatory response to experimental ischemic stroke differs between "pediatric" and adult mice. We are also interested in identifying transcriptional changes that might reflect differences in post-stroke neurogenesis between the "pediatric" and adult mice. We would like to include both male and female mice, but based on data from cell-specific RNA-sequencing in astrocytes and microglia after stroke using RiboTag, we do not predict that there will be sex differences. This would entail an experimental design with two time points (3, 10 days) and 8 groups at each time point [2 Ages ("pediatric", adult) times 2 Genders (female, male) times 2 Surgeries (stroke, sham)]. Based on time, budget, and surgical capacity, we could do 4-6 animals per group (for a total of 48-64 animals).

Questions:

Our pilot immunohistochemical data have shown that "pediatric" mice have a 25% increase in neurogenesis after stroke (sham mean 0.24 cells per square micrometer with SD 0.05 versus stroke mean 0.30 cells per square micrometer with SD 0.06).

1. Is this a reasonable experimental design with that number of biological replicates?
2. I would like to make multiple comparisons as listed below. How will this affect the number of biological replicates?
   (a) "pediatric" stroke vs "pediatric" sham at 3 days
   (b) "pediatric" female vs "pediatric" male at 3 days
   (c) "pediatric" stroke vs "pediatric" sham at 10 days
   (d) "pediatric" stroke vs adult stroke at 10 days

Zoom Meeting Information

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Join from PC, Mac, Linux, iOS or Android:
  https://stanford.zoom.us/j/92154339367?pwd=T2ZpSXlGdWxFTHNKZ1ptclF1ZFErUT09
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For more information about Data Studio:

http://med.stanford.edu/dbds/resources/data-studio.html