# Data Analysis

Jordan Lee - OHSU

- Ran on 12/15/20
- Based on V8 tarball, these results are before the miRNA correction to certain cancers
- If interest, will rerun once all v9 results from classifier groups in
- Process:
  - Select a cancer cohort
  - Select best model per team (overall weighted F1)
  - Pull corresponding feature set for each model
  - Map back to molecular values (in v8 tarball)
  - Cluster feature rows on molecular values (dendrogram not shown). No clustering on sample/subtype columns. Display molecular values in heatmap