

Data Analysis

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- 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 subtype columns. Display molecular values in heatmap









