

Data Analysis

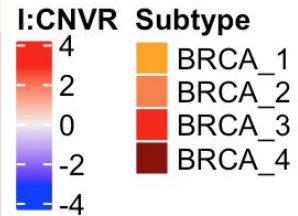
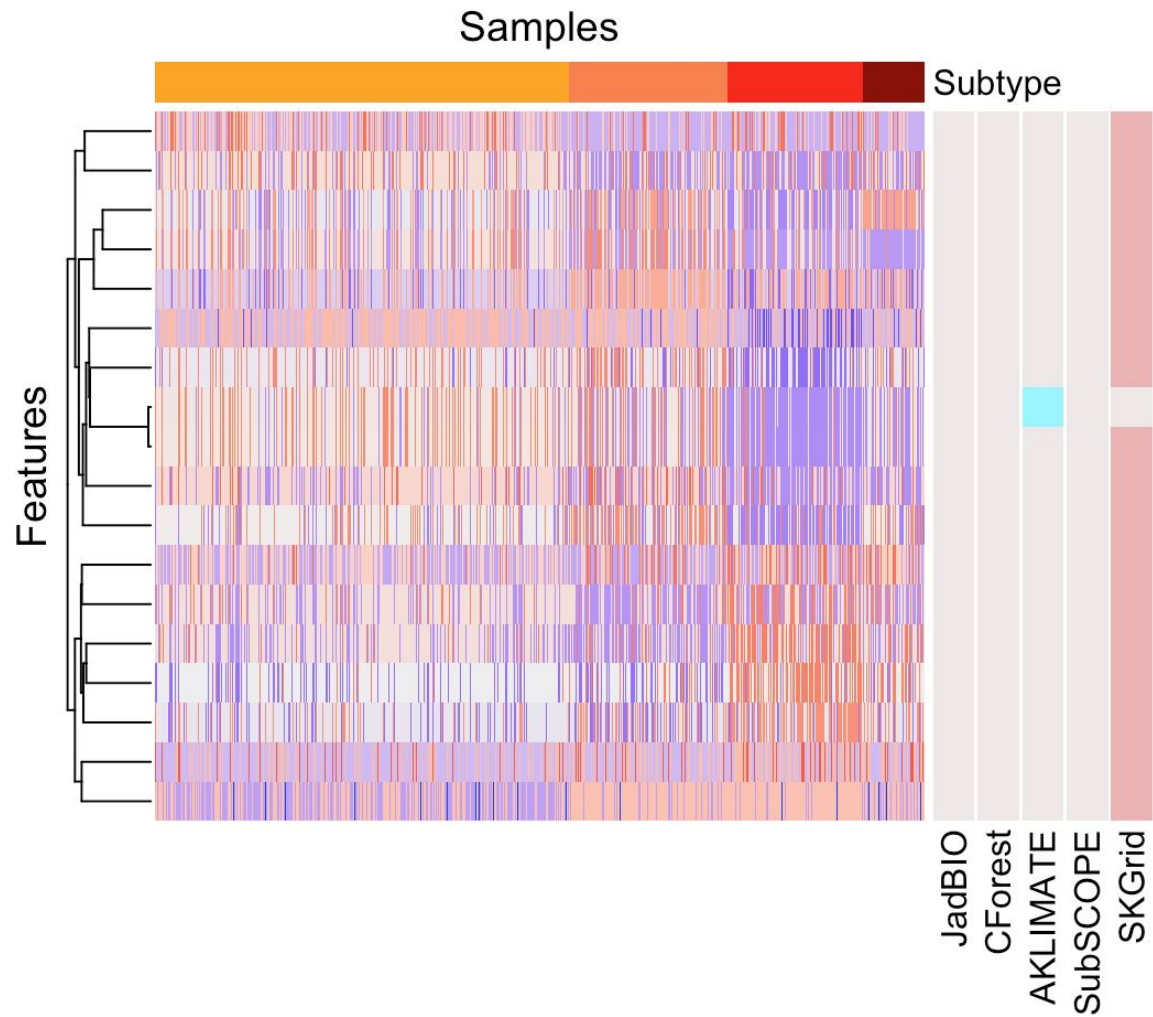
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- Ran on 12/15/20 - 12/16/20
- Based on V8 tarball, these results are before the miRNA correction to certain cancers
- If interest, will rerun once all v9 results from classifier groups in
- Process:
 - Select a cancer cohort
 - Select best model per team (overall weighted F1)
 - Pull corresponding feature set for each model
 - Map back to molecular values (in v8 tarball)
 - Heatmap 1: scaled molecular data
 - Cluster feature rows on z-scores of molecular values (sd=1, zero centered). No clustering on sample/subtype columns. Display z-scores on heatmap
 - Heatmap 2: raw molecular data
 - Cluster feature rows on molecular values. No clustering on sample/subtype columns. Display molecular values on heatmap

All heatmaps clustered using complete linkage method (max dist between clusters before merging) and euclidean distance

Heatmaps Part 1

Scaled Data



Ordered feature rows	
## [1] "I:CNVR"	
## [1] 18	
## [1] "I:CNVR::LZTS1:11178:"	"I:CNVR::DOHH:83475:"
## [3] "I:CNVR::MIR4728:100616132:"	"I:CNVR::SLC4A1:6521:"
## [5] "I:CNVR::PSMD12:5718:"	"I:CNVR::BRICD5:283870:"
## [7] "I:CNVR::OR6C1:390321:"	"I:CNVR::LOC644936:644936:"
## [9] "I:CNVR::CRSP8P:441089:"	"I:CNVR::RFC1:5981:"
## [11] "I:CNVR::FOXA1:3169:"	"I:CNVR::ZNRF3:84133:"
## [13] "I:CNVR::TTC39B:158219:"	"I:CNVR::CYP4A22:284541:"
## [15] "I:CNVR::ACTR2:10097:"	"I:CNVR::TREM1:54210:"
## [17] "I:CNVR::GOT2:2806:"	"I:CNVR::hsa-mir-548d-1:-1533:"

