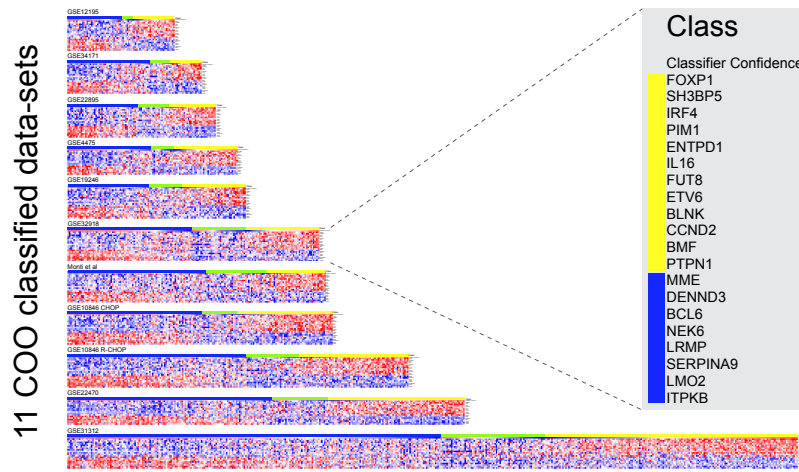
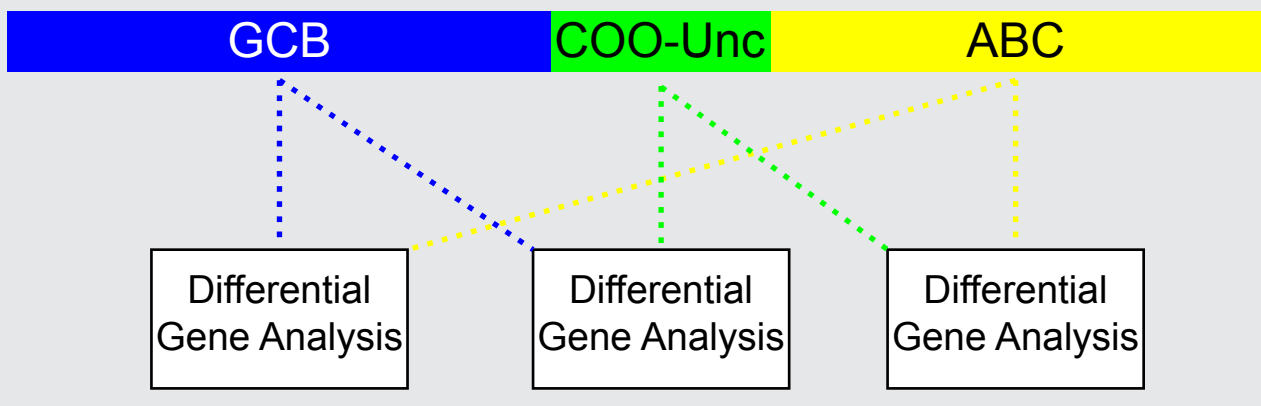


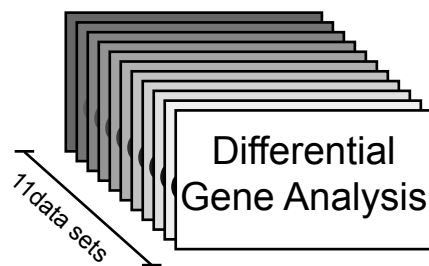
Outline: Meta-profile generation



Per data-set



Across data sets / per comparison



Merge results:

- Consider genes with adjusted p-val < 0.05
- Normalise fold changes per data set (NormFC)
- Find number of data sets each gene is differentially expressed in (NumDataSets)
- Rank genes by NumDataSets then NormFC

Enriched >= 6 Data sets

