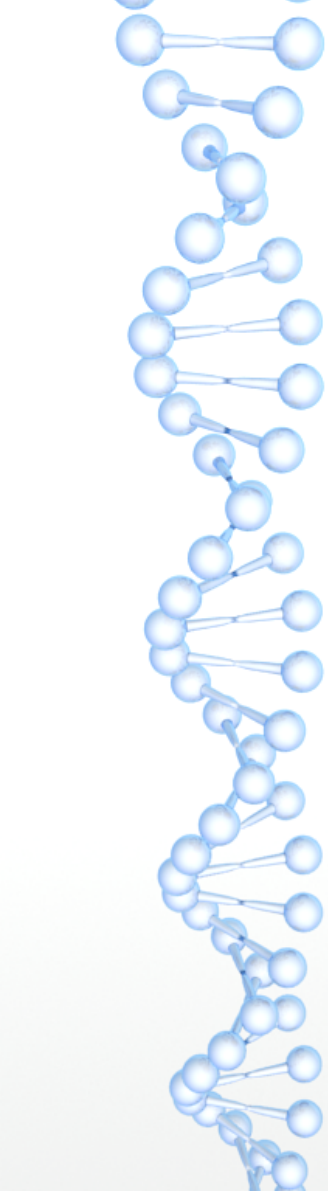


GenX

problem: we would like to predict the clinical response of immunotherapy, and identify the most relevant genetic pathways.

- Approaches (two 'pathways')
- Classification results
- Pathway visualisation?
- Suggestions

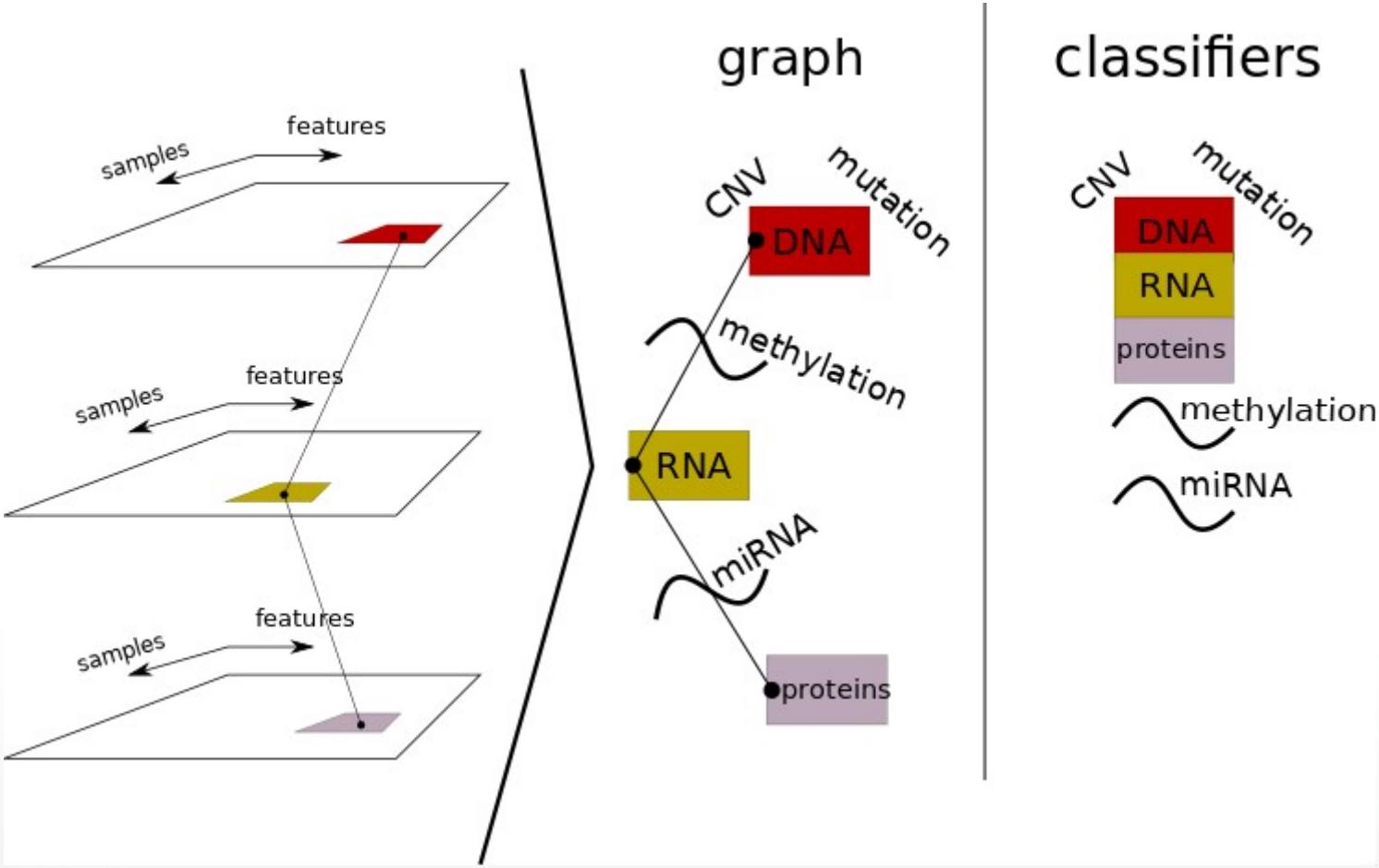
Approaches

In general: focus on immunotherapy response

- Pathway-focused: find graphs directly → aborted on day 2: need metabolic pathways to create intraset connections..
- Classification-focused: create classifiers per layer..**then**
  - Combo 1: meta-classifier on top of individual estimations
  - Combo 2: create classifier with the most important features per classifer

Caveat: we did **not** explictly introduce any first principles in the dataset connectivity..

Approaches


graph
classifiers
features
samples
features
samples
features
samples
CNV
mutation
DNA
methylation
RNA
miRNA
proteins
CNV
mutation
DNA
RNA
proteins
methylation
miRNA

Classification results

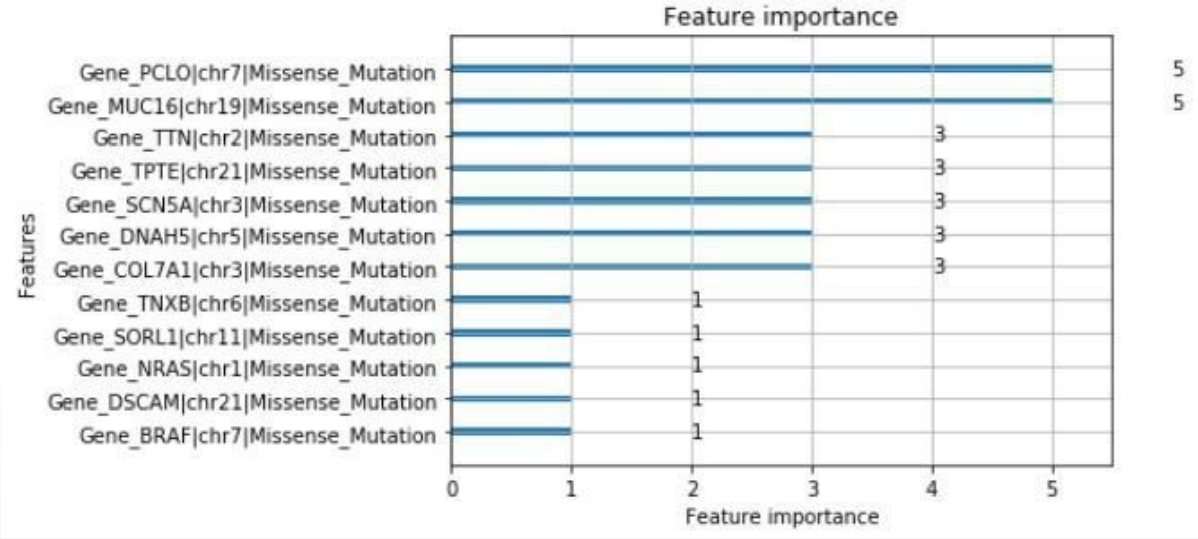
Per omics the predictors are **weak** (max 70% acc)

Combining the omic's based on the most important features **wins**. (does not include methylation data yet)

	precision	recall	f1-score	support
response	1	0.89	0.94	19
No response	0.9	1	0.95	19
avg / total	0.95	0.95	0.95	38

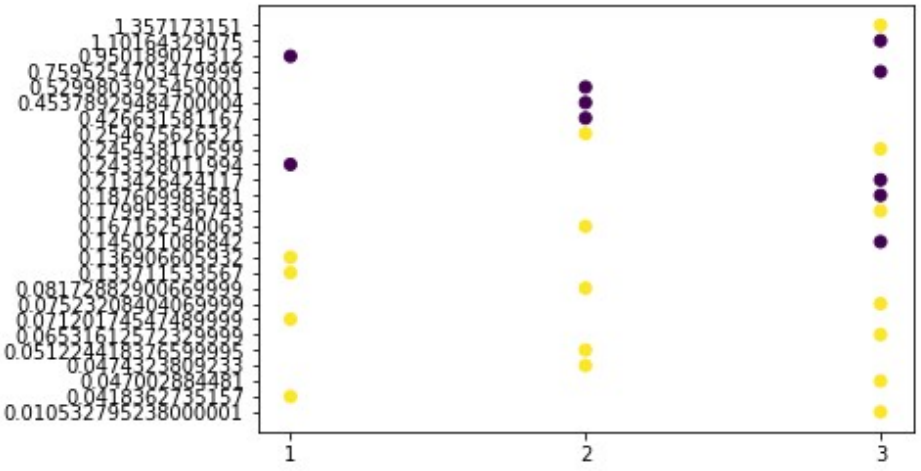
Classification results

- We find BRAF pv600e in the mutation classification as the single most important gene for the less important mutations
- miRNA and RNA data contributed the **most**, protein the **least**
- Strand matters

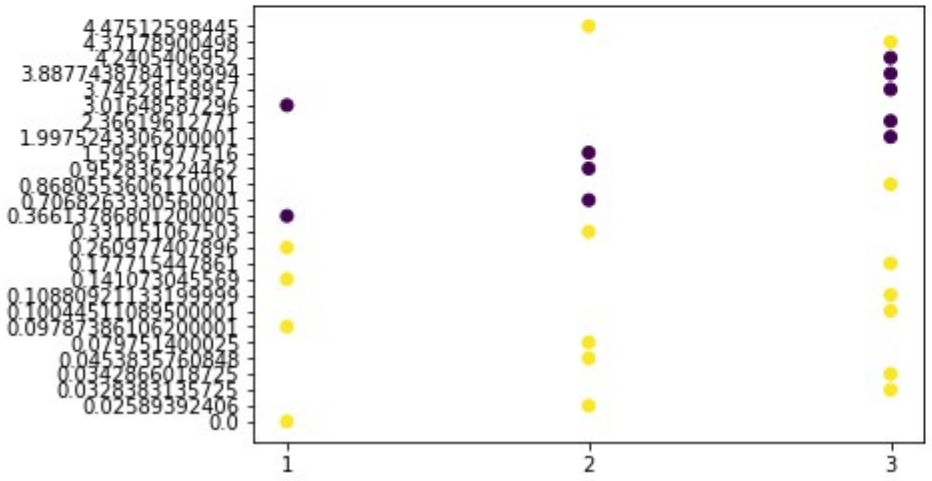


Classification results

MMRN1, +strand



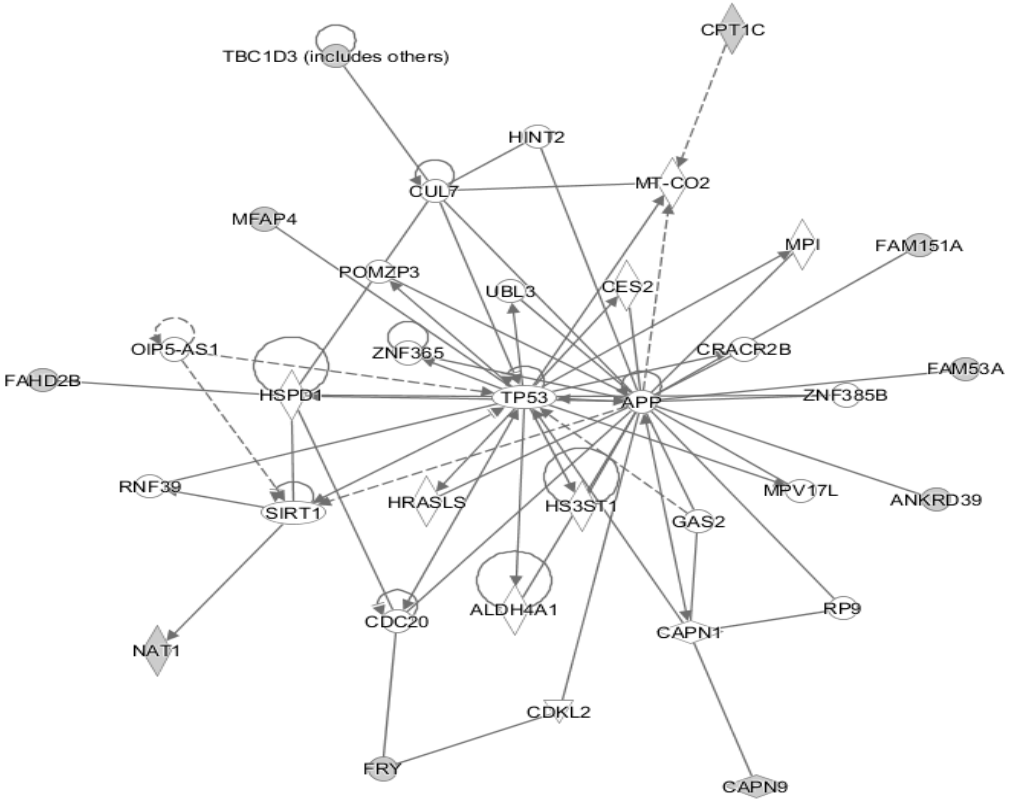
TFF3, -strand



Similar for: LRRC2, MFAP4, FAM151A

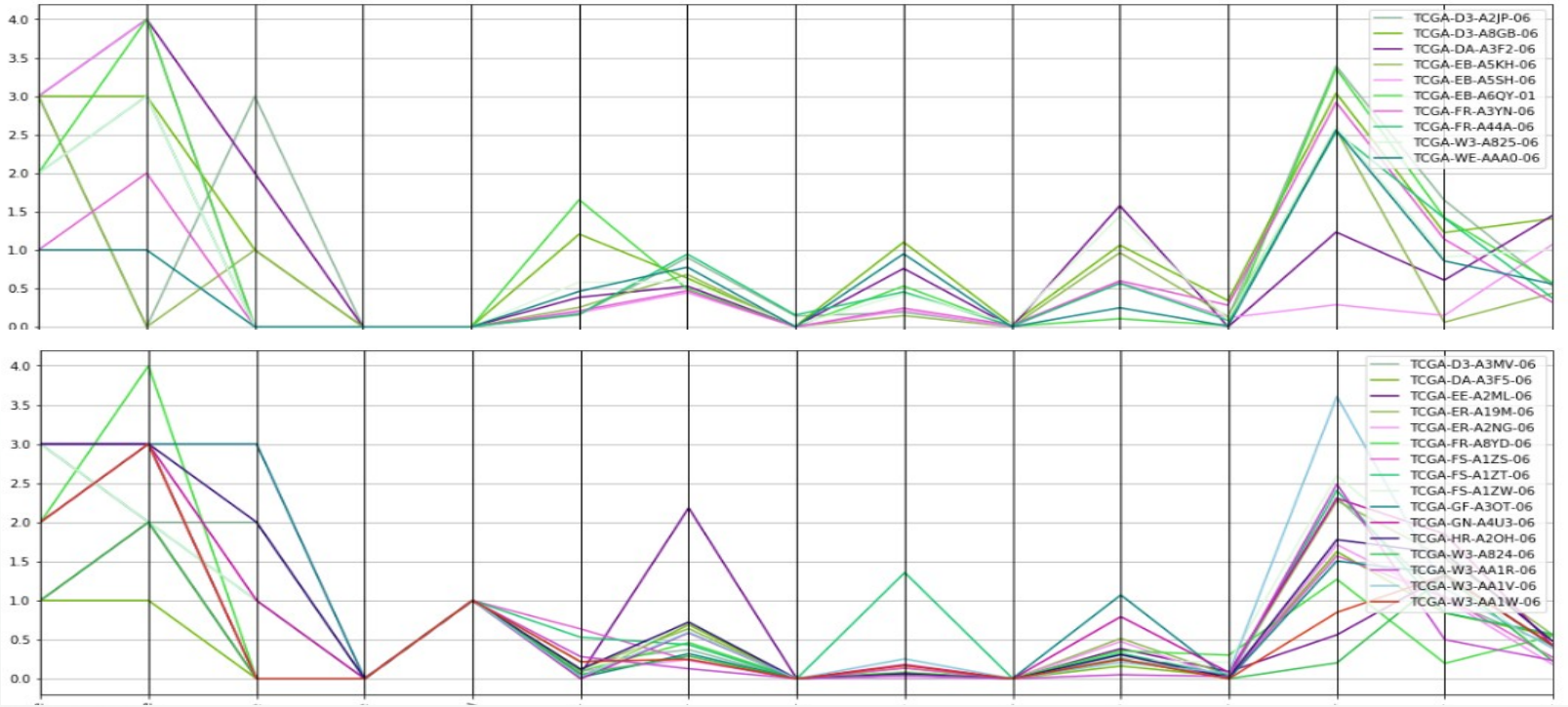
Classification results

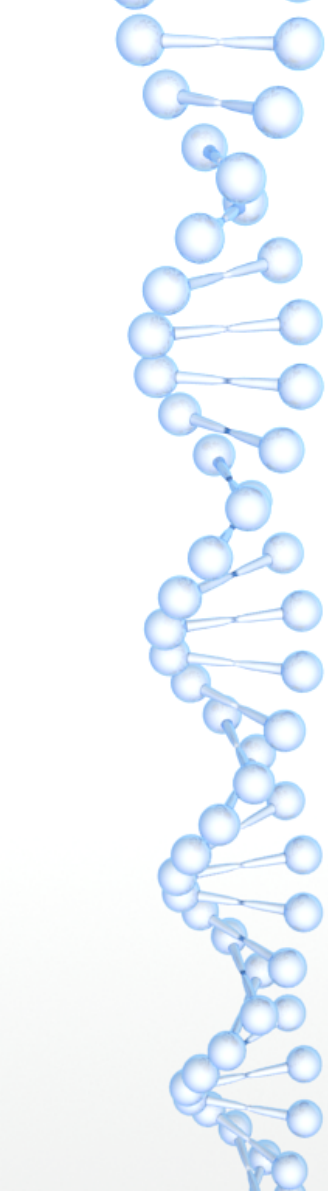
Confirmation of sorts with IPA tool..TP53 and APP were important in our final model



Pathway visualisation?

We take the most important features per omic, per patients and connect the omics per patient.





Suggestions

- Add metabolic pathway information: focus on pathways directly
- Specifically find the model that connects the omics
- In general: try to ‘prime’ the model with first principles
- Perform similarity analysis per omics over all features, per patient group
- Apply methylation and RNA expression to mutations, i.e. merge by element with a transformation function f(meth, rna)