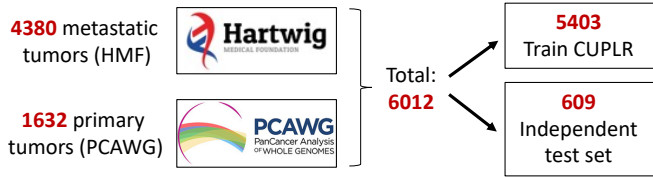


Introduction

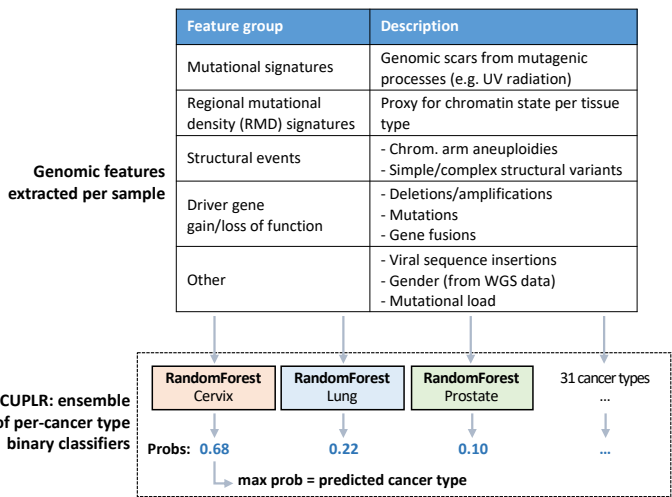
- Primary tumor tissue of origin (TOO) guides treatment decisions
- ... typically determined by histopathology
- ... cannot be determined for 3-5% of metastatic tumors
- A whole genome sequencing (WGS) based machine learning classifier can aid pathologists with clarifying TOO

CUPLR (Cancer of Unknown Primary Location Resolver)

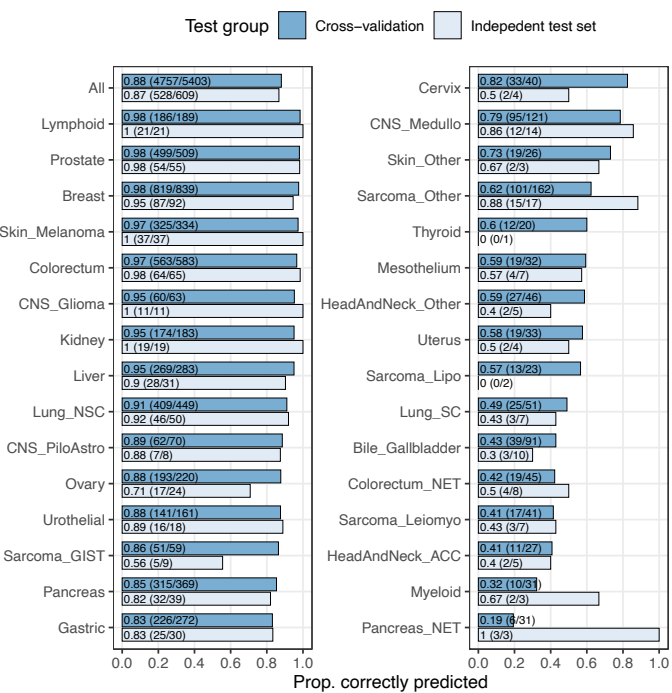
Samples and training



Features and model

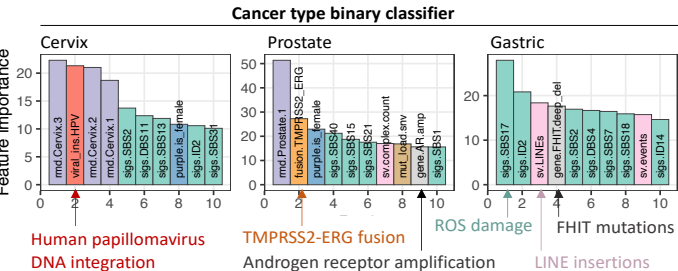


CUPLR predicts TOO with 87% overall accuracy



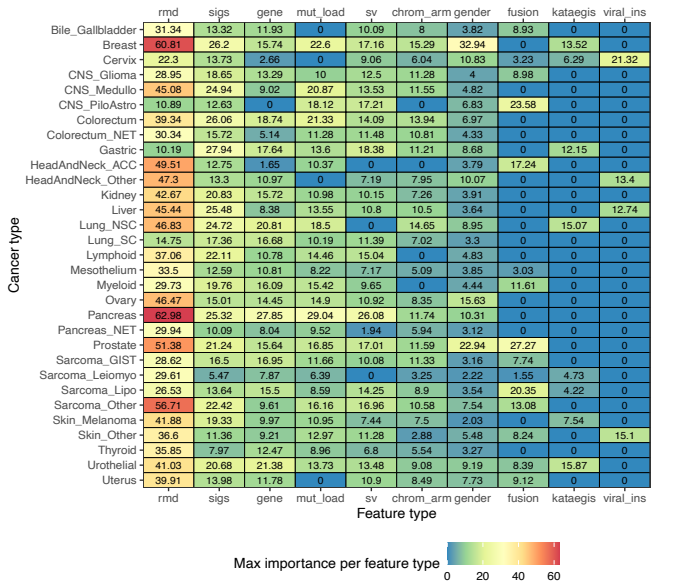
Features predictive of TOO

Certain features used by CUPLR are known to be associated with the respective cancer types



Overall, the most predictive feature types are:

- Chromatin state (RMD signatures)
- Mutational scars from mutagenic processes (mutational signatures)



Patient report

For a patient, the top predicted cancer types are shown. In cases with no clear top prediction, info on the features supporting a prediction still allows a pathologist to make an informed decision on the TOO of a patient

HMF002928A (actual cancer type: Unknown)

