

Why we do not have an omics-based clinical risk score?

- ▶ Most ML methods applies standardisation to resolve this
- ▶ But in clinical prediction, you might only have single samples to predict on

New X	Sample 4
Gene 1	4.2
Gene 2	3.8
Gene 3	8.4
Gene 4	3.1

Statistical challenges

- ▶ Different scaling on genes leads to differences in predicted values
- ▶ Variable selection due to differences in correlation
- ▶ Single-patient prediction

Transferability

The prediction on one gene expression platform should be equivalent to another platform

