

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

- ▶ Most ML methods apply standardisation on both training and validation data
- ▶ But in clinical prediction, you might only have single samples to predict on

| X | Sample 1 | Sample 2 | Sample 3 |
|--------|----------|----------|----------|
| Gene 1 | 1.2 | 2.1 | 1.5 |
| Gene 2 | 5.6 | 4.6 | 7.1 |
| Gene 3 | 9.2 | 10.1 | 6.9 |
| Gene 4 | 4.1 | 3.6 | 2.7 |

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