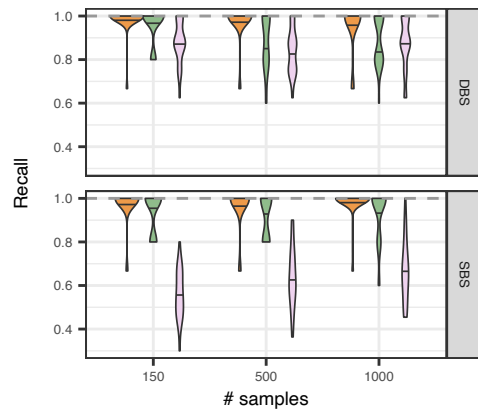


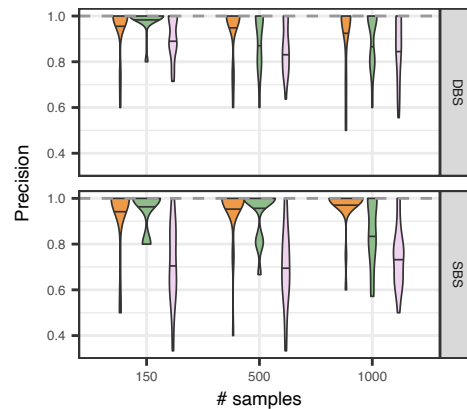
A

Recall of retrieved signatures



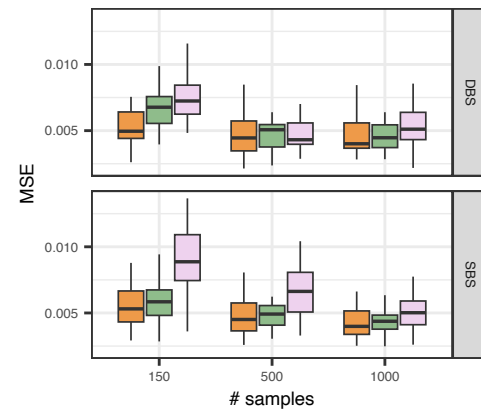
B

Precision of retrieved signatures



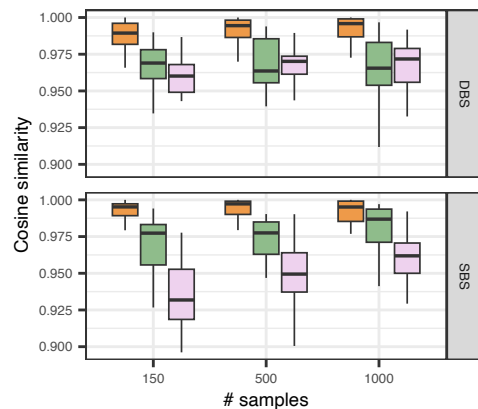
C

MSE of mutation counts



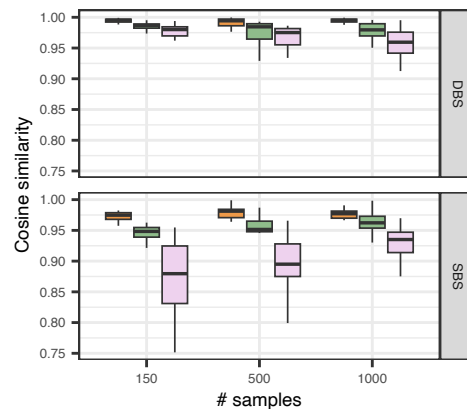
D

Cosine similarity of signatures



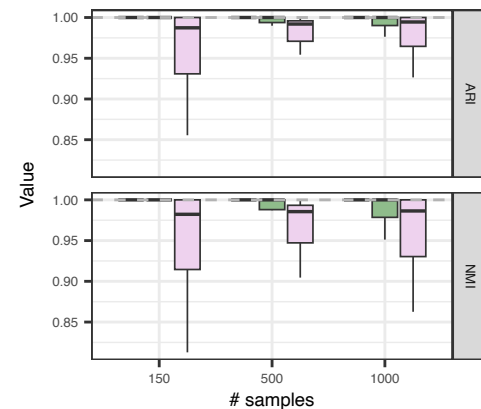
E

Cosine similarity of exposures



F

Clustering accuracy



signatures 0-3 4-5 6-13