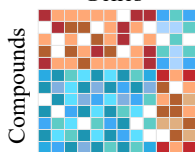


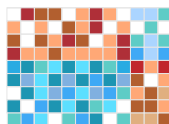
Data preprocessing

Reference signatures

Genes



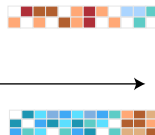
Quality control



Data splitting



Time-point



Cell type

Model training

Subset reference signatures

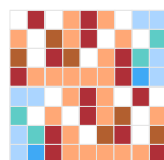
Genes



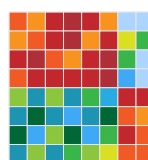
PCA

 P

Dimension reduced signatures



LDA

 L TR 

Calculating centroids

 TMR 

Similarity calculation

Query signatures

Dimension reduction with P Transforming with A Calculating similarity against the TRM TQ TMR

0.4	0.3	0.2	-0.3	-0.8
0.7	0.2	0.1	-0.2	-0.3

Similarity matrix