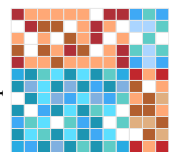


Data preprocessing

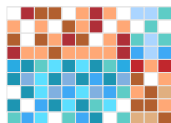
Reference signatures

Genes

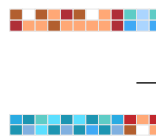
Compounds



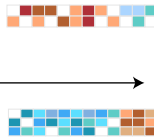
Quality control



Data splitting



Time point

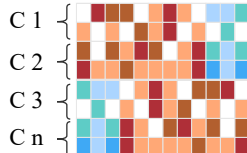


Cell type

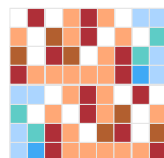
Model training

Subset reference signatures

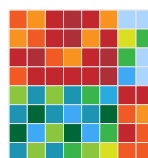
Genes



PCA

 P Dimension-reduced
signatures

LDA

 L TR Calculating
centroids TMR 

Similarity calculation

Query signatures

Dimension
reduction with P Transformation
with L TQ 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