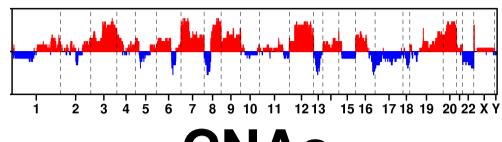
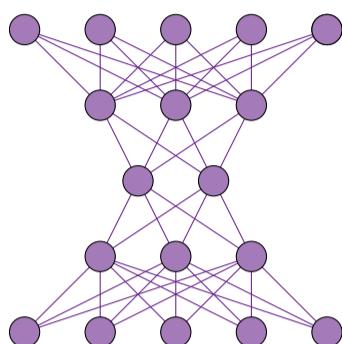


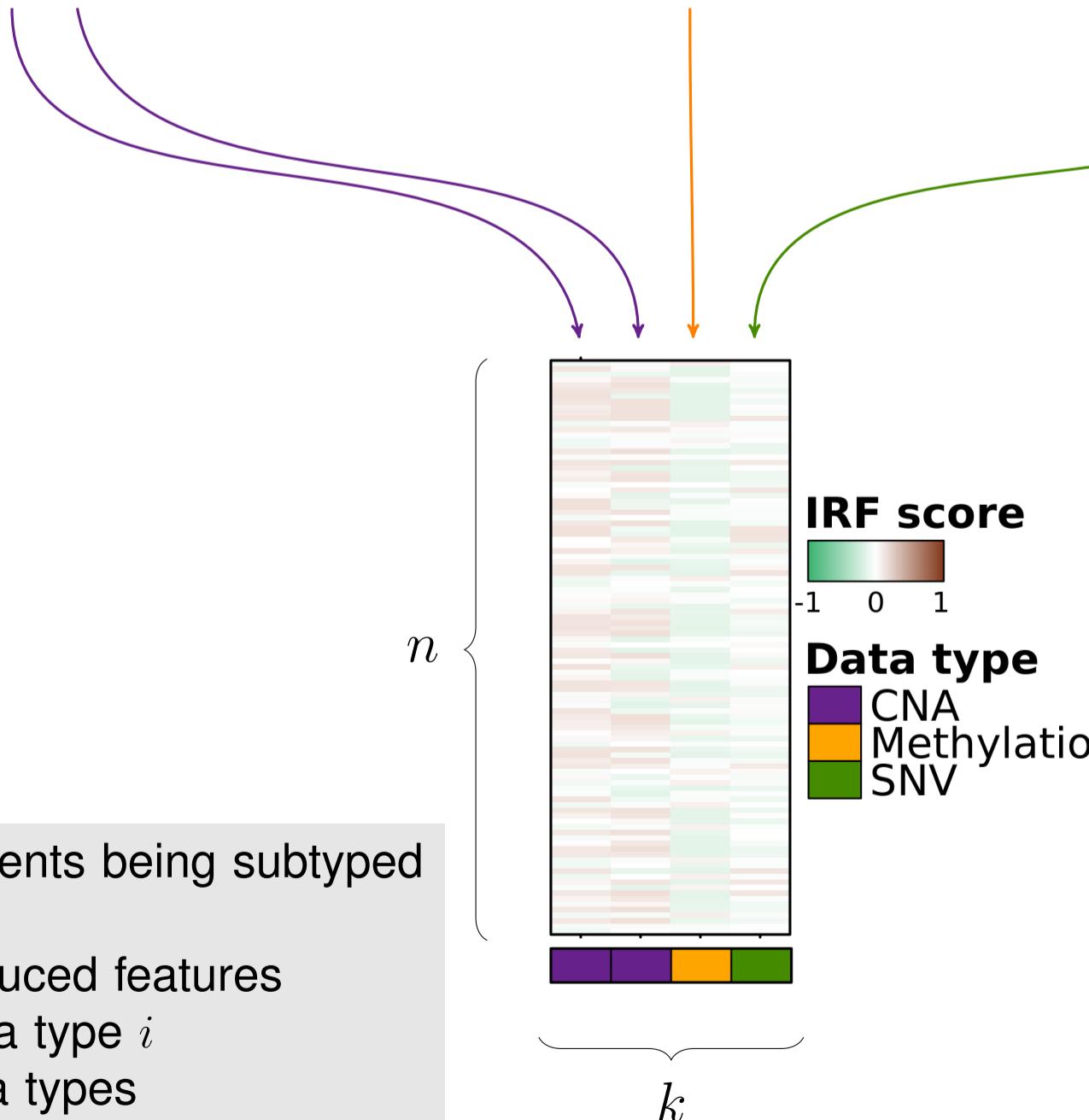
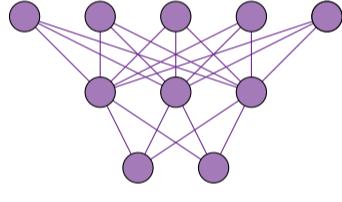
Data type 1



Train
autoencoder



Extract
bottleneck
layer



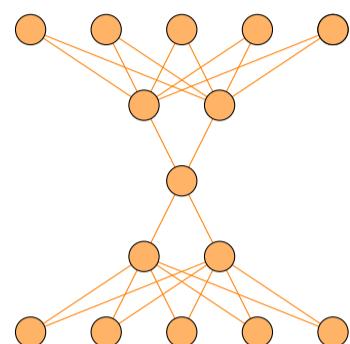
n = # patients being subtyped
 k = $\sum_{i=1}^d f_i$
 f_i = # reduced features
 for data type i
 d = # data types

Data type 2

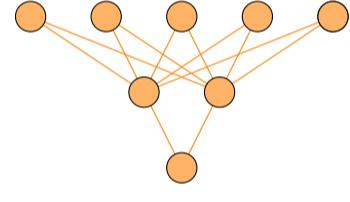


Methylation

Train
autoencoder



Extract
bottleneck
layer

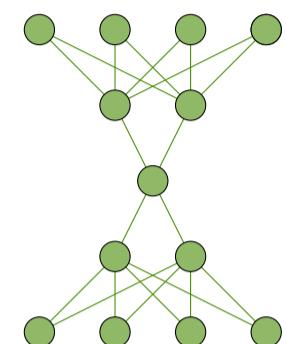


Data type 3

ACAGCA**G**GCTTAC

SNVs

Train
autoencoder



Extract
bottleneck
layer

