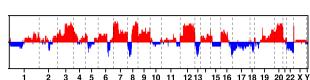


Patient profiles



CNAs



Methylation



SNVs

Step 1:

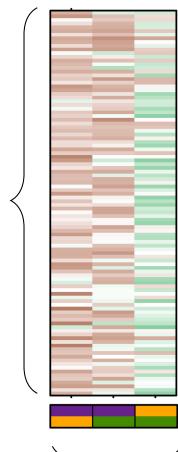
Consensus pairwise similarity

ex. Concensus integrative similarity (CIS)

CIS score

Data type

- CNA
- Methylation
- SNV



m

Step 2:

Step 2:

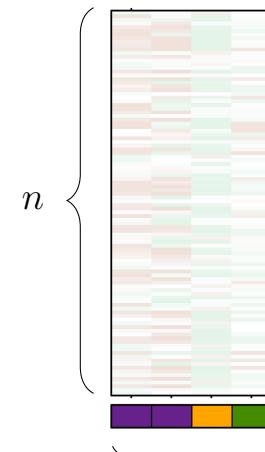
Independent feature reduction

ex. using autoencoders

IRF score

Data type

- CNA
- Methylation
- SNV



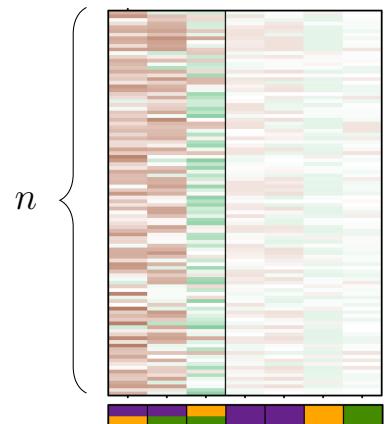
k

Weight & merge

feature score

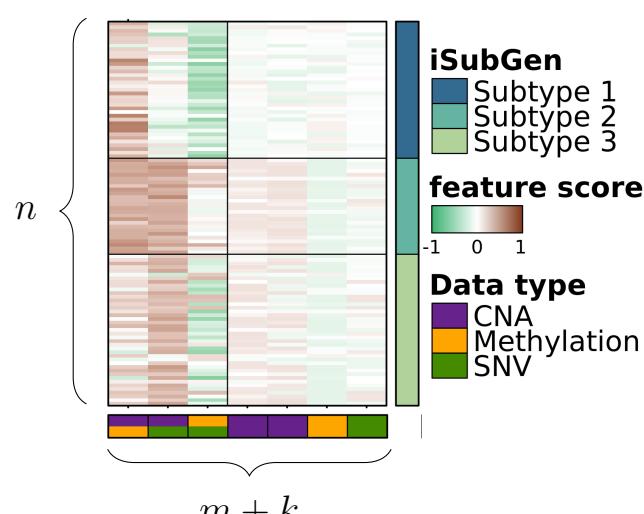
Data type

- CNA
- Methylation
- SNV



m + k

Pattern discovery



m + k

$n = \# \text{ of patients being subtyped}$
 $k = \sum_{i=1}^d f_i$
 $f_i = \# \text{ of reduced features for data type } i$
 $m = \frac{d(d-1)}{2}$
 $d = \# \text{ of data types}$