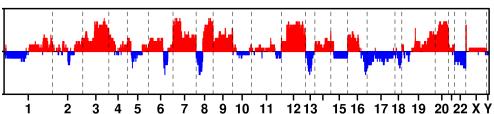


Aberration type 1

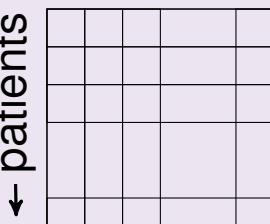


CNAs

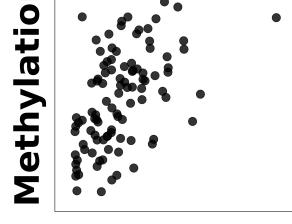
Calculate pairwise distances

Distance matrix

patients →

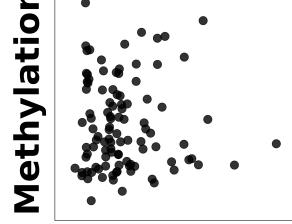


Correlate distances



CNA

Correlate distances



CNA

Aberration type 2

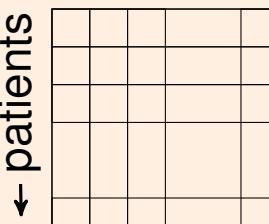


Methylation

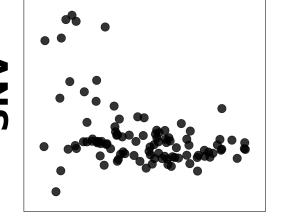
Calculate pairwise distances

Distance matrix

patients →

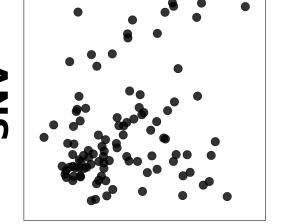


Correlate distances

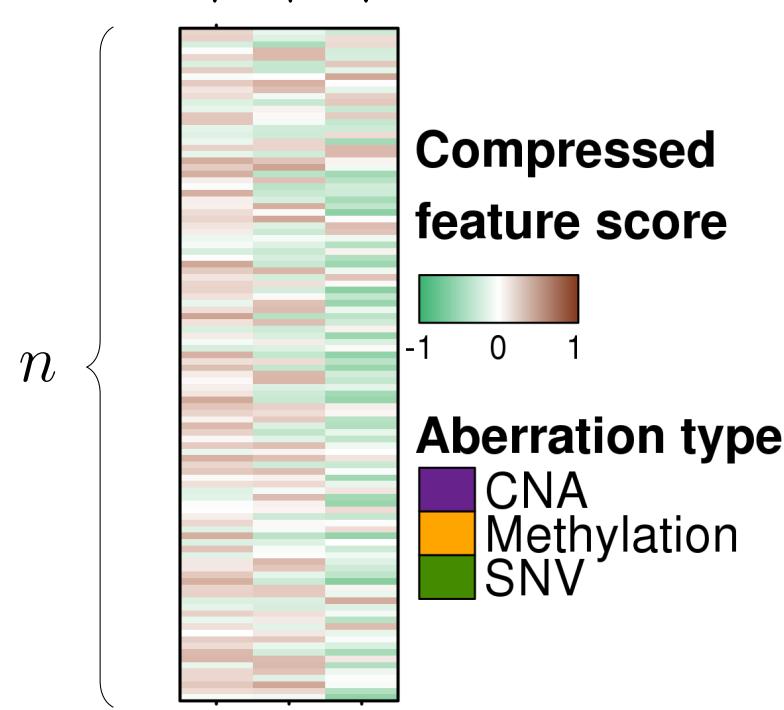


CNA

Correlate distances



CNA



Aberration type 3

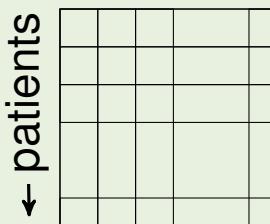


SNVs

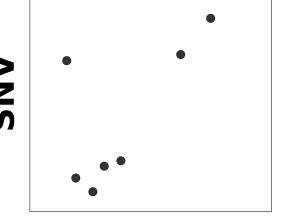
Calculate pairwise distances

Distance matrix

patients →

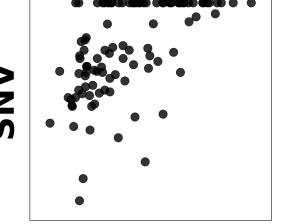


Correlate distances



Methylation

Correlate distances



Methylation

$n = \#$ of patients being subtyped
 $m = \frac{d(d-1)}{2}$
 $d = \#$ of aberration types