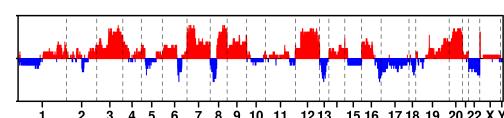


## B. Creating the similarity measures matrix for an example

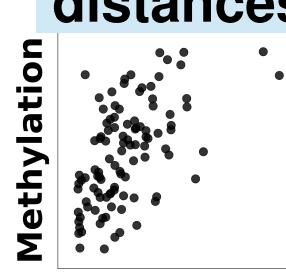
### Aberration type 1



CNAs  
↓  
Calculate pairwise distances

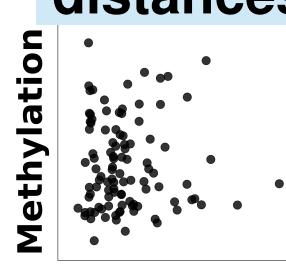
Distance matrix  
patients →  
patients ↓

Correlate distances



CNA

Correlate distances



CNA

Correlate distances



CNA

### Aberration type 2

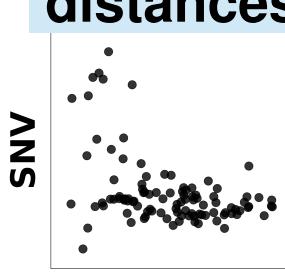


Methylation  
↓

Calculate pairwise distances

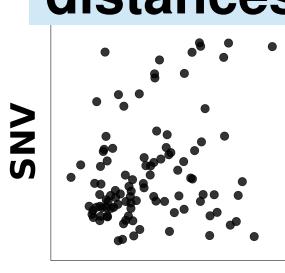
Distance matrix  
patients →  
patients ↓

Correlate distances



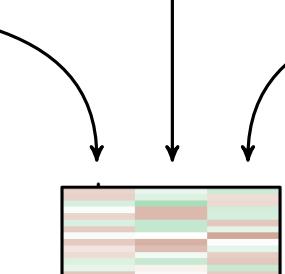
CNA

Correlate distances



CNA

Correlate distances



CNA

### Aberration type 3

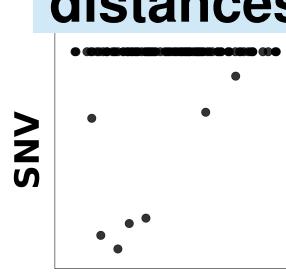


SNVs  
↓

Calculate pairwise distances

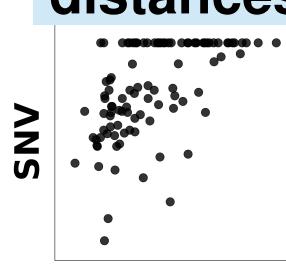
Distance matrix  
patients →  
patients ↓

Correlate distances



Methylation

Correlate distances

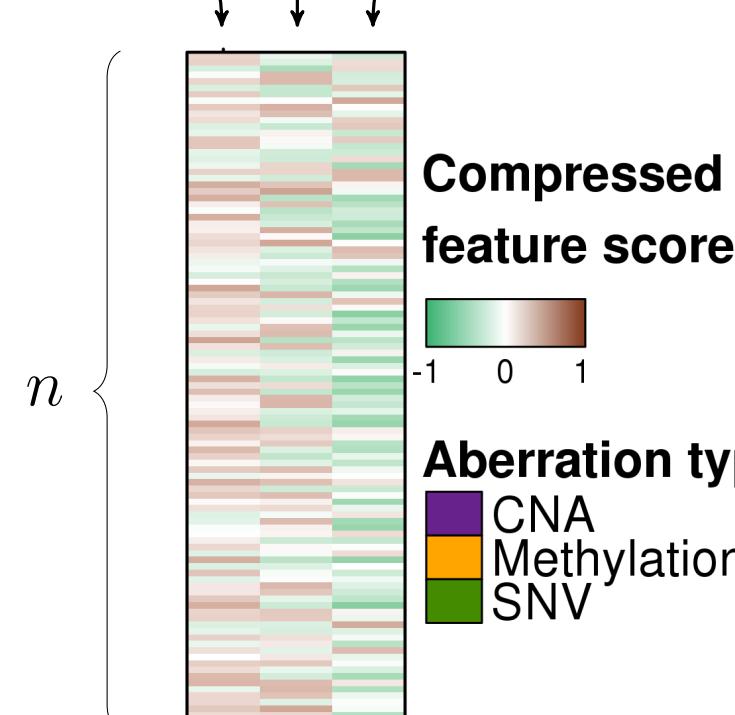


Methylation

Correlate distances



Methylation



$$n = \# \text{ of patients being subtyped}$$

$$m = \frac{d(d-1)}{2}$$

$$d = \# \text{ of aberration types}$$