

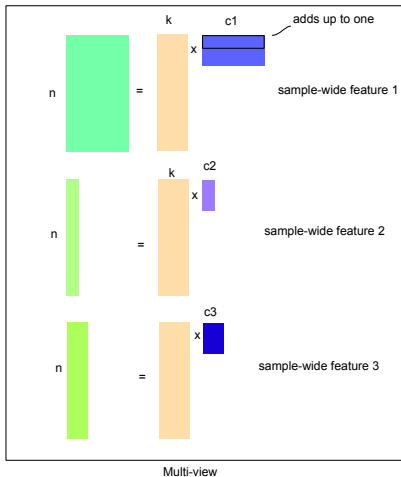
# Signatures for CN: how do embed CN in matrix form

- Each sample contains several features (independent of each other), each feature can be categorised into multiple components
  - Geoff's signatures: features are concatenated
  - \*Multi-View Clustering via Joint Nonnegative Matrix Factorization\*
- Each sample contains many segments, each segment has multiple characteristics which can be categorised as compartments of features (Shiraishi)
  - Equivalent to SNV, but for multiple features (instead of the single trinucleotide change)
  - You can potentially get inspired by \*Mutational signatures of complex genomic rearrangements in human cancer\*

# To do (?)

- ① Run Geoff's signature extraction, Shiraishi's minimal example
- ② For Shiraishi's method: define segment-specific features, and categorise each feature in each segment to get the input matrix for pmsignature
- ③ Create github repo if you think it'd be useful

# To do (?)



Benefits over method on the right:

- you do not have signatures that are defined by a single component
- the exposures can be absolute exposures, the units being "number of segment-equivalents", "number of change-points-equivalents", etc.

the weights, or exposures (shared)

$n$ : number of samples

$k$ : number of signatures

$c1$ : number of components of feature 1

Geoff

