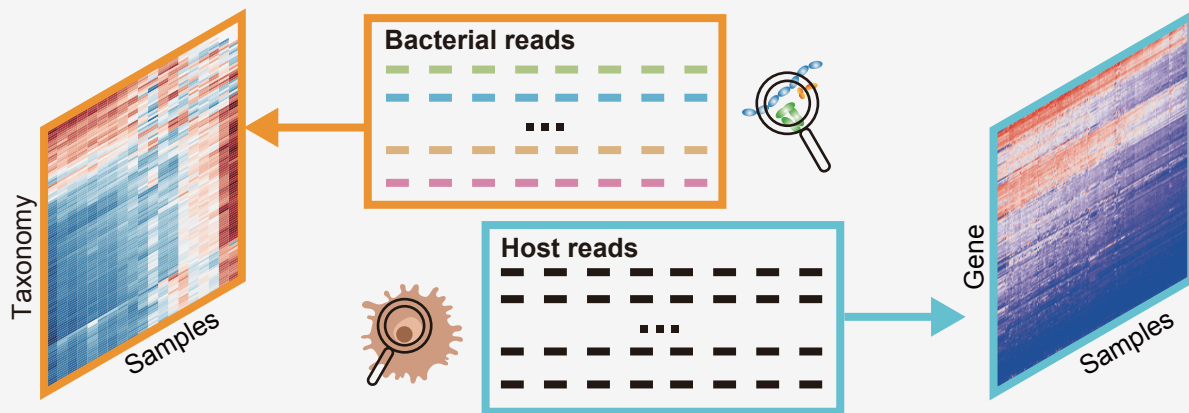


Input (meta-) transcriptome / (meta-) genome



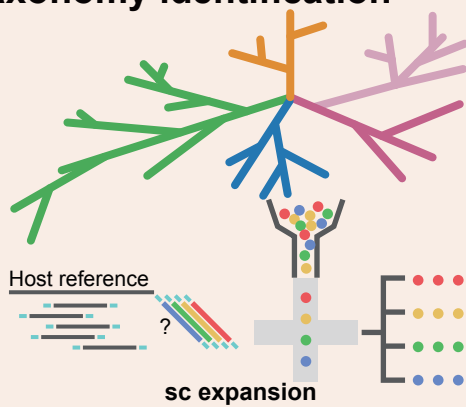
BACC

Bacterial taxonomy identification

Samtools:
Host reads removal

Kraken2: taxonomy
classification

Relative abundance /
CPM normalization

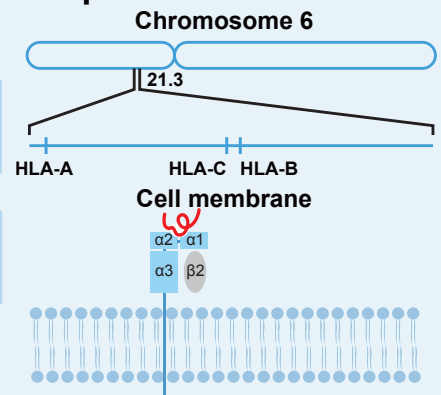


BACH

HLA allele prediction

Samtools:
Host chr6 extraction

HLAcan: HLA typing



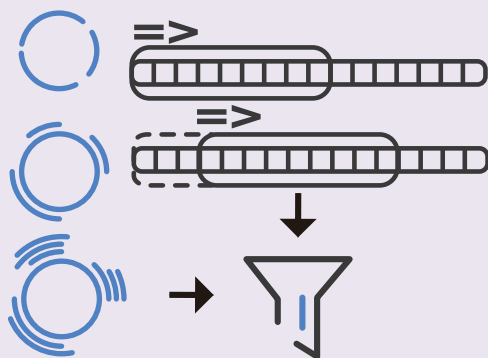
BACP

Bacterial peptide prediction

CheckM2: Bacterial
peptide inference
by NNs and GB

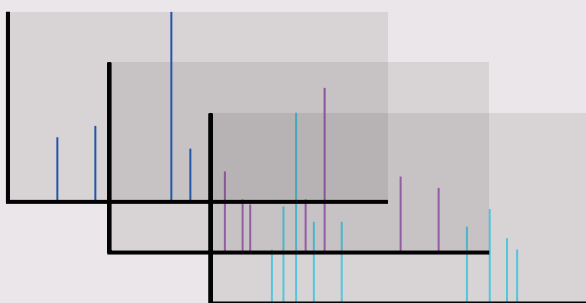
CD-HIT: Redundant
sequence filtering

Window sliding
(9-mer)



Proteome (optional)

Maxquant: MS
analysis



Prioritization

TAP efficiency
prediction

$$TAP_{logIC50} = s_0 + \sum_{i=1}^9 SMM_{i,a(i)}^{mat}$$

HLA-peptide affinity
prediction

$$BA_{rank} = \frac{\sum_{i=1}^{N_{total}} I(S_{random_i} \geq S_{peptide})}{N_{total}} \times 100\%$$

Bacterial neoantigen
candidates selection

$$SPARK = \log_2 \left(\frac{\text{Percentile}[TAP_{logIC50}, BA_{rank}]}{2} + 1 \right)$$

