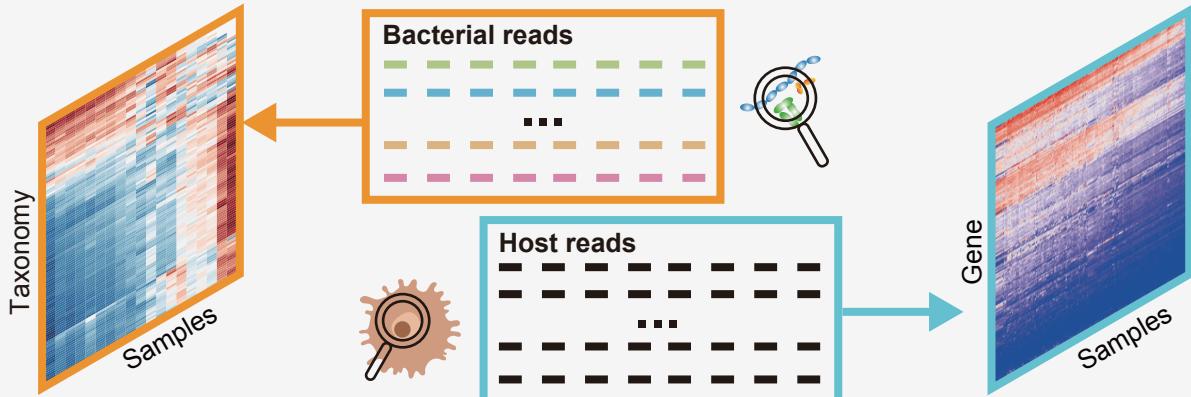


Input (meta-) transcriptome / (meta-) genome

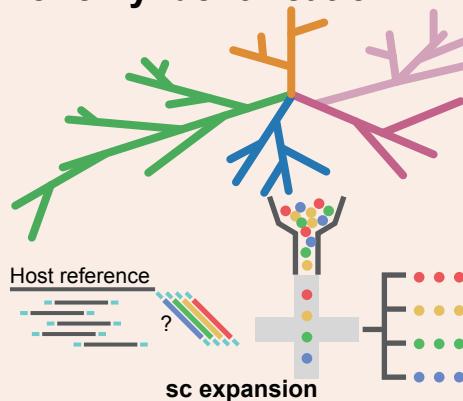


BACC Bacterial taxonomy identification

Samtools:
Host reads removal

Kraken2: taxonomy classification

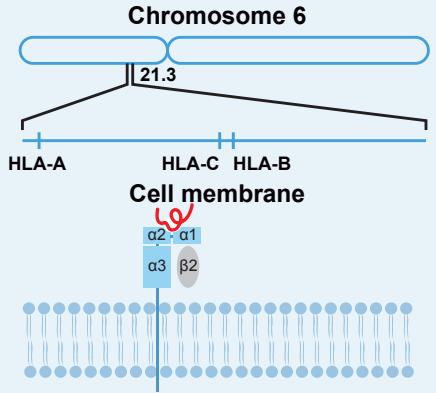
Relative abundance / CPM normalization



BACH HLA allele prediction

Samtools:
Host chr6 extraction

HLAscan: HLA typing



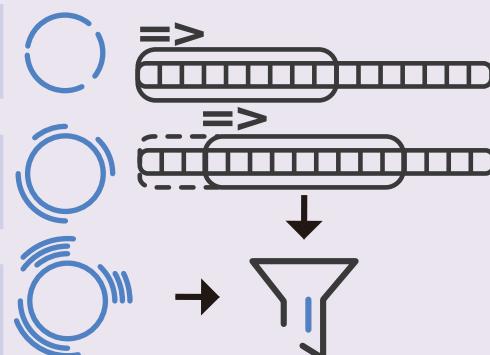
BACP

Bacterial peptide prediction

CheckM2: Bacterial peptide inference by NNs and GB

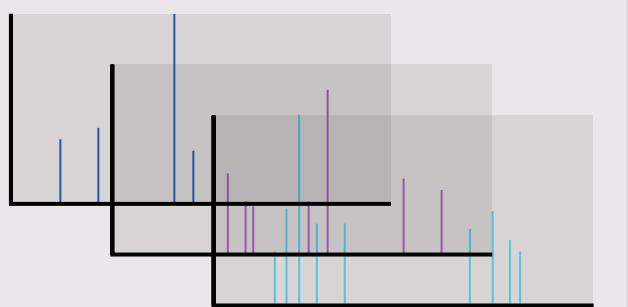
CD-HIT: Redundant sequence filtering

Window sliding (9-mer)



Proteome (optional)

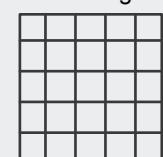
Maxquant: MS analysis



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

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