



Input

mapping files (BAM)
(one per investigated genome)

structural annotation of the
reference sequence (GFF)



Calculate read coverage per position (I)



Calculate read coverage per gene (II)



Discard genomes with an average coverage below a given cutoff (default=10) (III)



Construct input matrix (IV)



Determine dispensability score for each gene (V)

$$\text{dispensability score (gene } g) = 1 / \left[\frac{\sum_{n=1}^N \left(\frac{\text{average cov. of gene } g \text{ in genome } n}{\text{average cov. over all genes in genome } n} \right)}{\text{total number of genomes (N)}} \right]$$



Visualize the score distribution (VI)