

Gene sequences

Multiple sequence alignments

Pairwise distance matrices

Imputed pairwise distance matrices

Pre-processing  
(e.g. filtering, trimming, ...)

Calculate pairwise distances (e.g. normal, dN, dS, dN/dS)

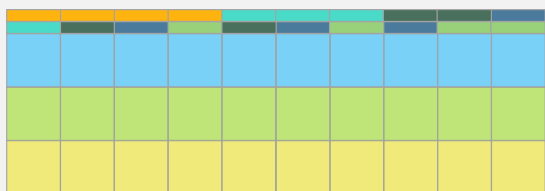
Impute missing taxon pairs, impute diagonals

Test of genes

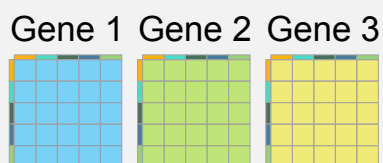


Collapse

Gene 1  
Gene 2  
Gene 3

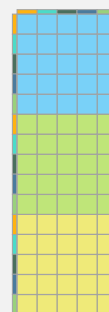


Test of taxa across outlier genes

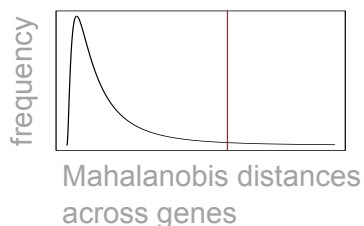


Stack

Gene 1  
Gene 2  
Gene 3

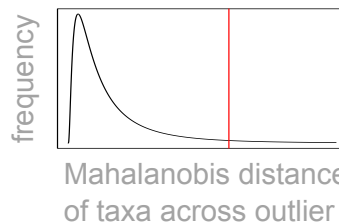


Mahalanobis distances



Extract outliers  
(quantile)

Outlier genes



Mahalanobis distances

Outlier genes +  
outlier species

Extract outliers  
(Chisq test)