Broliden_5325

25 September, 2020

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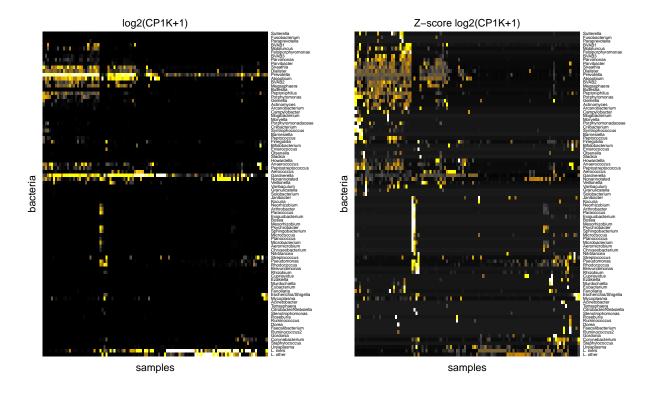
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#Load libraries and other scripts	
#Defining some variables for the analysis	

Loading data and metadata

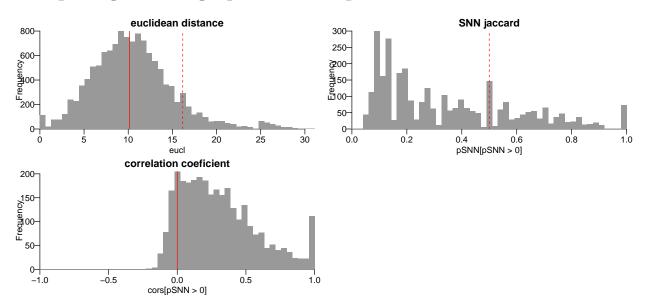
Merging microbiome datasets

Organise the datasets

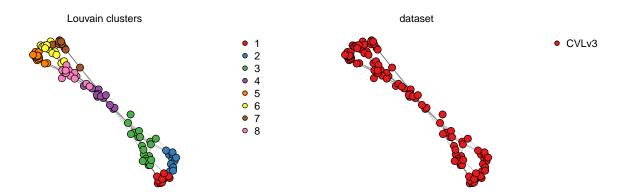
Organise the datasets



Computing a SNN graph from sample correlations



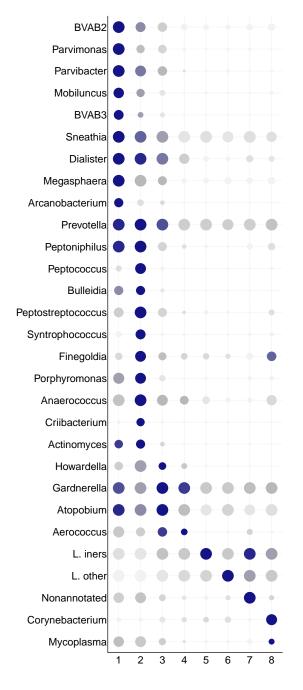
Visualise the data

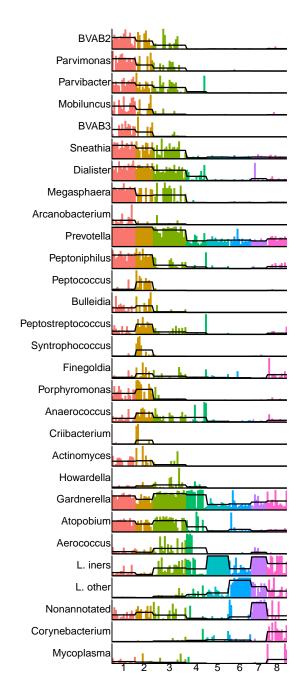


Computing differential expression across clusters

[1] 50 8

#Plotting the most significant bacteria across clusters

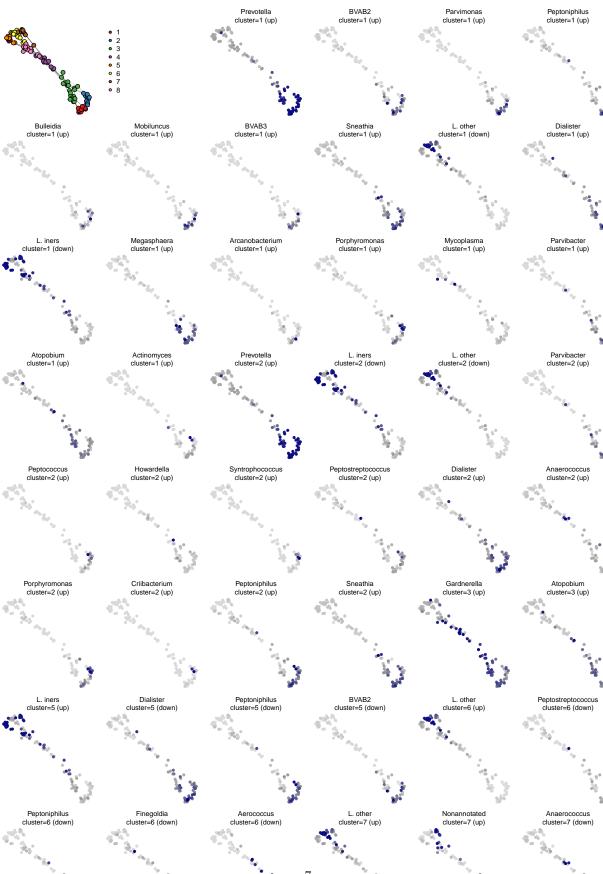




[1] "1"

[1] "2"

Plotting the most significant bacteria across clusters

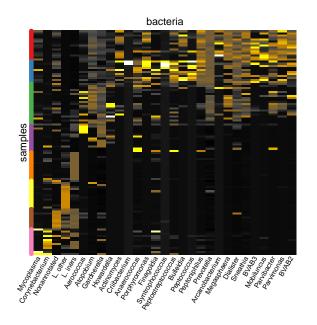


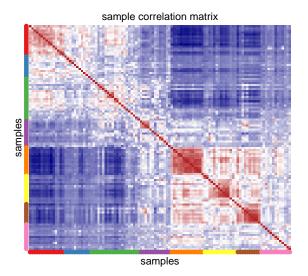
Corynebacterium

Peptostreptococcus

Dialister

#Plotting bacteria across clusters





[1] -0.01463636#Dataset integration