[Screencast Script]
Italics are instructions about what to show on the screen.

Introduction

Welcome to our metagenomic data visualization tool.

This tool was designed to help researchers explore metagenomic data, which gives information on the microorganisms that are present in a biological sample, and the abundances of all genes and gene pathways that are present.

Our tool allows the user to explore different aspects of this dataset such as the evolutionary relationship between the species found in all samples, species abundance per sample, and information on gene pathways and function.

The tree

Scroll to show full tree in view

In the phylogenetic tree view, the user is able to see the evolutionary relationship between the species found in all the samples.

The user is first presented with all phyla classified across the samples.

Expand and collapse a branch

Clicking on a node will expand a branch, revealing further taxonomic divisions, and clicking again will collapse it.

Stacked bar chart
On the right, the user can see a stacked bar chart displaying abundances, according to a specific level of classification across all samples.

Expand tree

As the tree expands its depth, the stacked bar chart will update abundances according to the deepest level of classification that the user is in.

Nodes at the deepest level are colored to match the corresponding bars in the stacked barchart.

Mouse over a bar

Mousing over a bar highlights that species in every sample so that you can easily see the differences.

Mouse over a legend

Mousing over a species in the legend fades that species on the bar chart.

Click on legend species

Clicking on the species will remove it,

Click again

and clicking again will make it reappear.

The sunburst

Select sunburst radio button

Selecting the sunburst view allows the user to see the different species present within one selected host sample.

Click on MONARCH_WILD_249

You can choose which sample to look at by clicking on a sample name in the bar chart labels.

[take a few seconds to show this functionality]

You can see that the Monarch condition has much more diversity than the NoMonarch samples.

Click on non-monarch sample

Hover over ring

You can also mouseover the rings(which represent a taxonomic level) and click for more information.

Click on sunburst to show zoom

Heatmap, violin plot, and gene detail

Scroll down to lower half of webpage

The lower section of the visualization shows a subset of the genes in the samples.

The bottom left side has a heatmap which offers the user two options, either to look at the genes in the samples or the gene pathways.

Click on radio buttons

The heatmap contains information about the top differentially expressed genes between the two conditions.

Heatmap mouseover demo

If you are interested in more information about a gene, you can click on it and it will update the violin plot.

Click on a square/rectangle within the heatmap
Move to violin plot

You can see the differential expression between the two groups of interest and more detail on mouseover
Show violin plot mouseover

Clicking on the save button

Click on save button, then click on link

Creates a link that will take the user to an online reference database containing more information about the selected gene.