Microbiome Bioinformatics
2017 Spring Lecture Series for High School Students
Bioinformatics and Research Computing, Whitehead Institute

Gut microbiome: comparing geographical locations and related individuals

*In the study by Yatsunenko, T., et al.[*], they compared **gut** microbiomes among human populations. Here, we'll briefly look at how gut microbiomes compares between populations from Amazonas of Venezuela and US metropolitan areas.*

We'll use the tool MetaCoMET (probes.pw.usda.gov/MetaCoMET : click on "Start"). The tool makes visualization tools typically used in bioinformatics such as a heatmap and PCA to examine large/complex datasets.

A pre-loaded dataset comprised of four United States citizens and four Amazonas of Venezuela is here,
http://probes.pw.usda.gov/MetaCoMET/MetaCoMET_result.php?ID=0010194eb59eb50c954dd994b8f43f2e

1. Comparing the two groups: USA and Venezuela, how many enterotypes, or OTUs, are similar and different between the two populations? [Click on the numbers in the Venn diagram to see more details]
2. In the Taxonomy tab you'll see a Krona figure (multi-layered pie chart). What enterotypes are abundant? [Click on "Click Me!" to get a stacked bar graph that's easier to visualize]
3. Click on the heatmap tab and examine the clustering. Examine how the two groups are clustered and how members (ie. samples) are clustered. Is there anything unexpected?
4. Under the PCoA tab, examine how the two groups are plotted. Is this similar to the clustering?
5. Based on these data what conclusions can you draw between the microbiomes of these two populations?

[*]Yatsunenko, T., et al. *Human gut microbiome viewed across age and geography*. Nature (2012)

Data is available from https://github.com/biocore/American-Gut/tree/master/data/GG
you can upload the GG_100nt.biom file and the metadata (description) is in GG_100nt.txt
(Select a few samples of AMZ and US of your choice when prompted)