

## Gut microbiome: comparing geographical locations and related individuals

In the study by Yatsunenکو, T., et al.<sup>\*</sup>, 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](http://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](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]  
*Venezuela and USA have 2693 OTUs shared, and 2667 and 963 OTUs unique, respectively. Clicking on the numbers and then showing as stacked bar chart will show the composition (eg. in the shared, Firmicutes is the most abundant).*
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]  
*Firmicutes is the most abundant enterotype followed by Bacteroidetes.*
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?  
*The two populations, Venezuela and USA, form two major clusters showing the importance of geographic location on the gut microbiome. Within each cluster, family members are more closely related (eg. USchp18 child/mom). USchp35Child clusters separately, from other US samples, it might be due to the gut microbiome in the child is not well established yet. Also, the two elderly individuals (Amz6/7 elderly) are closely clustered indicating influence of age on the gut microbiome.*
4. Under the PCoA tab, examine how the two groups are plotted. Is this similar to the clustering?  
*The PCA plot shows the separation (ie. larger variation) between USA and Venezuela samples (on PC1).*
5. Based on these data what conclusions can you draw between the microbiomes of these two populations?  
*Geographic location, age, un/related family members (ie. genetics) all have an effect or influence on the gut microbiome of an individual.*

<sup>\*</sup>Yatsunenکو, 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)