

# Assessment #1 – Analysis of Human Gut Microbiome Community Structure

[https://github.com/inna-tsyb/metagenomics/tree/main/lecture\\_01](https://github.com/inna-tsyb/metagenomics/tree/main/lecture_01)

## Inna Kucheroval

A total of 400 samples were analyzed, and found 30 unique bacterial species.

- Data quality:

The graphs and coverage index show that we looked deeply enough to find all the species present.

- Sample adequacy:

The Accumulation Curve levels off after the 30th sample, indicating which means that the 400 participants provide a representative sample of this microbial community.

A few main groups make up most of the microbiome, which is normal in people:

- Bacillota (about 52%) and Bacteroidota (27.3%) are the most common phyla.
- Among genera, Bacteroides (12%) and Bifidobacterium (8%) are the most common.
- Lactobacillus acidophilus is the most common species, found in 19% of samples.

The analysis shows that no single species is found in most samples. Even the most common species appear in less than 20% of participants. No universal set of bacterial species is present across all individuals in this group, signaling considerable inter-individual variability.

### Alpha diversity

- Richness: Most samples have only 3 to 6 species, which is much lower than usual. This is because the study only looked at 30 species, while the normal human microbiome has hundreds.
- Shannon Index: An average value of 1.33 demonstrates limited community complexity.
- Evenness: A high value (0.9) indicates that species are generally balanced within each sample, with no single species predominating. Rare exceptions, such as sample MB-6097, exhibit dominance by one species.

### Beta diversity (Variability between individuals)

The PCA graph shows no clear groups. The samples form a single, mixed cloud, which confirms high differences between people. Each person's microbiome is unique, and the first two main factors explain only 10% of the differences.

The primary finding is that bacterial community composition differs markedly between men and women.

- Lactobacillus acidophilus and Escherichia coli are most common in women, Phocaeicola\_A sp900765575 and Merdibacter merdipullorum are most common and dominant in men.
- Common core: There are no shared species among the top five most abundant taxa in men and women.
- Age: Age does not have a significant effect on most species. There is only a slight trend for Prevotella copri with advancing age.
- Dysbiosis: Samples with a Shannon index of 0 exhibit a complete loss of diversity. This may be a medical sign of strong effects like antibiotics or disease.

- Representativeness: The findings only partly apply to everyone. The low number of species and the fact that most participants were women (73.5%) .

- Limitations: 1. Diet: Lack of dietary information precludes explanation for the high prevalence of Bacteroides. 2. BMI and health status: These data would provide insight into the recorded low diversity. 3. Geography: Microbiome composition is strongly influenced by geographic and demographic background.