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Project: Visualisation of the ASARI time-series data.   SS 2017

Two healthy participants took antibiotics over a 6 days therapy. They collected metagnomics samples one day prior to the therapy, in the first, third, sixth days of therapy, two days and 28 days after the therapy. Details of the project can be found in the publication `http://aac.asm.org/content/59/12/7335.long`.

The metagenomic profiles is defined as relative abundance of different bacterial taxa. Since that was whole-genome-sequencing not only taxonomic profile can be analysed, also functional, based on various classification systems.

Data comprise of the assignment of reads to the taxonomic and functional classifications in a MEGAN file. All assignments can be exported with MEGAN to the csv files to be used by the flask server.

Your job is to visualize the **change in time** of the taxonomic and functional profiles from sample to sample. You can derive data if you'd like. You can pick the most interesting functional classification.

Some hints on what would be interesting to see:

- General overview of all changes.

- What taxonomic or functional assignment class changes the most?

- What are the most variant assignment classes?

- Are there any common changes in both participants?

- Is there something that does not change?