PhD project: Cross-species gut microbiota comparison with a focus on naked mole-rat longevity

In this project, I analyse fecal microbiota from different rodents. Data from naked mole-rats (Heterocephalus glaber, NMR; n=19) and Specific-Pathogen-Free mice (Mus musculus, SPF mouse, n=4) were newly obtained at Kumamoto University. Data from MSM/Ms and FVB/N mice were obtained at Chiba Cancer Center. Reads from Damaraland mole-rats (Fukomys damarensis, DMR; n=20) [Bensch et al. 2022 PeerJ], European brown hares (Lepus europaeus, hare; n=9) and European rabbits (Oryctolagus cuniculus, rabbit; n=12) [Shanmuganandam et al. 2020 PeerJ], Lesser blind mole-rat (Nannospalax leucodon, spalax; n=15) [Sibai et al. 2020 OMICS J Integr Biol], and Siberian flying squirrel (Pteromys volans orii, PVO; n=19) [Liu et al. 2020 Sci Rep] were downloaded from previous studies.

The repository is organised in four directories:

1. `code`: the folder with all scripts, such as bash and R scripts

- r-scripts:
- bash-scripts

2. data: data

- fastq
- metadata
- qiime

3. images

- barplots
- diversity
- taxaboxplots

4. output

- diffabund
- picrust
- rdafiles
- rtables