Third meeting of Bio-brains, 160928

Participants: Ben, Domenico, Stephan, Johanna, Eva, Jo, Sigitas, Hanna F, Hanna B, Emelie

1. Discussing github, to keep track and share, and use as a forum. Everybody should set up an account and then email their username to Domenico.

2. We introduced our work, in brief:
-   Jo works on 16s data from bird poo. Uses uparse and explicit. Did PhD on microsatellites.
-   Sigitas will work on genomes from cyanobacteria viruses.
-   Hanna F works on amplicon sequencing datasets, both 16s and functional genes. Analyses with qiime. Has started with R.
-   Hanna B works on 16s data from fish bacteria. Uses uparse and explicit.
-   Emelie works with virus metagenomes, different tools. Wants to learn R.
-   Ben will work on metatranscriptomes, trancriptomes and 16s data. Will try diamond and Megan.
-   Domenico works with metatranscriptomics. Uses trinity. Also works with virus metagenomes. Interested in network of species in samples. Has worked with python and some R.
-   Stephan works with 16s on uparse and explicit. Also on transciptomics, and has used the Tuxedo-pipeline.
-   Johanna is planning extraction and analysing of pike genes/genomes. Wants to find genetic signals to compare.
-   Eva works with 16s data with uparse and explicit. Will also work on metatranscriptomics.

3. Brainstorming:
-   Journal club if someone finds something interesting
-   Presentation of scripts with tips and tricks
-   Tutorial presentations (e.g. on R or python)
-   Preprocessing from raw data
-   Basics on the command line
-   Understanding uparse pipeline and explicit
-   Finding stories in datasets
4. Next meeting: a doodle is sent out, but in week 43