

Bachelor/Master Thesis

Scientific Documentation of the Microbiome Analysis Pipeline SnoWMAⁿ

Taxonomic and phylogenetic fingerprinting based on sequence analysis of gene fragments from the small-subunit (SSU) 16S rRNA gene has become the standard technique in bacterial and archeal classification [1]. To facilitate bioinformatical analysis of microbial communities [2] originating from 16S amplicon studies, the analysis pipeline SnoWMAⁿ [3] was developed. It covers the entire analysis process, comprising data preprocessing, characterization, visualization and statistical analysis, as one easy to use straightforward web application. To guarantee getting started easily with the application as well as with result interpretation, a good user manual and documentation is absolutely mandatory.

The overall goal of this project is to establish a user documentation of the analysis pipeline as well as a tutorial which simplifies result interpretation. The following thesis objectives are specified:

1. General description of the analysis pipeline SnoWMAⁿ as well as its analysis fundamentals.
2. Detailed description of each single pipeline.
3. Development of walkthrough tutorials for each pipeline including result discussion and interpretation.
4. Establishment of FAQs and integration into the web-interface of SnoWMAⁿ.

References:

1. Halwachs B, Gorkiewicz G, Thallinger G: **High-Throughput Characterization and Comparison of Microbial Communities**. In *Computational Medicine*. Edited by Trajanoski Z. Springer Vienna; 2012:37-57.
2. Morgan XC, Huttenhower C: **Chapter 12: Human microbiome analysis**. *PLoS Comput Biol* 2012, **8**: e1002808.
3. Halwachs B, Hoffberger J, Stocker G, Snajder R, Gorkiewicz G, Thallinger GG: **High-Throughput Characterization and Comparison of Microbial Communities**. *Biomed Tech (Berl)* 2013.

ⁱ <http://snowman.genome.tugraz.at>