Master’s Thesis

High throughput full-length SSU rRNA sequencing

Method evaluation and comparison with 16S rRNA short amplicon sequencing

Project description

The aim of this study is to analyse stool samples using full-length SSU rRNA, similar to Karst et al. (2018). This will allow a deeper insight into species and strains present. Sequencing of full-length SSU rRNA is possible when using adapters containing unique molecular barcodes, which are ligated to the 16S-rRNA molecules. The library is split and either processed using the Illumina Nextera Kit (to sequence full-length 16S rRNA) or circularized to physically link both adapters allowing assignment of reads to a given full-length rRNA.


Methods

• Performing RNA/DNA extraction & purification
• NGS sample preparation including: molecular tagging, reverse transcription, tagmentation, etc.
• Next generation sequencing on Illumina MiSeq
• Data analysis using IMNGS, Rhea, etc.

Requirements

• Student in Master program: Biochemistry, MBT, Biology or equivalent
• Student who is interested in microbiology & molecular biology
• Previous experience with standard molecular biology methods, preferably RNA work and NGS methodology

Interested?

If you are interested please contact: isabel.abellan-schneyder@tum.de
Starting date: as soon as possible
Core Facility Microbiome/NGS & Microbial Bioinformatics

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The Gut and its Microbes

Human and animal guts contain uncounted number of bacteria providing different functions: Digestion, vitamin production, health conditions and immune functions, etc. The interaction between the microbiome (all microbes) and the host is largely unknown. Different compositions of bacteria can cause illness, like intestinal bowel disease. We aim in understanding the function of the microbiome by composition and gene regulation. Knowledge about the microbiome enables interventions for better health.

16s rRNA Amplicon Sequencing

Storage and extraction → Amplification (440 bp, V3/V4, 15+10s) → Purification → Sequencing (MiSeq) → Analysis

RNA Seq & RIBO Seq – Gene Finding and Regulation

Isolate RNA → Remove rRNA → Fragment RNA → Transcription → Translation

Isolate ribosomes → Digest mRNA → Isolate footprints

Bacteria Isolation and Identification / Sequencing

Fermenter → Anaerobic chambers → Sequencing → Annotation

What we offer...

... as Core Facility Microbiome/NGS
- 16s rRNA Amplicon Seq for gut, fermenter, leaves, skin, ...
- Custom amplicon sequencing
- RNA Seq
- Ribo Seq
- Whole Genome (Bacteria) Seq
- Metagenome sequencing of microbiomes
- Analysis of strains (e.g., annotation)
- Culturing of anaerobic bacteria
- Wheelerstephan Strain Collection (>12,000 bacteria & yeasts)
- Complete pipeline for 16s rRNA analysis
- Courses in how to use the pipeline
... ask us...

... for Students (Lab & Bioinformatics)
- Bachelor thesis
- Master thesis
- Lab work
- Lab courses

about NGS / microbiome / method development / PCR improvements / implementing new methods / bioinformatics methods, etc.