



Sunday, 22 September

Welcome Get Together: 19:00 „Treibhaus“ Angerzellgasse 8

<https://www.treibhaus.at/>

Monday, 23 September

General introduction: 09.00 – 10.00 *Seminar room (Ground floor)*

Lecture: 10.15 – 13.00 *Seminar room (Ground floor)*

Applications of HTS in trophic ecology

HTS technology

- Sequencing platforms
- Illumina's HTS sequencer models and their specifications

Computer Lab: 14.00 – 15.30 *Computer room #19*

- Getting started with UIBK IT systems, Linux and GenBank

Lecture: 16.00 – 17.30 *Seminar room (Ground floor)*

HTS study design and sample preparation

Key points for study design (gene selection and amplicon length, costs, sequencer choice)

What can commercial providers or HTS core facilities provide you?

Dinner: 19:00 Bierstindl Restaurant: Klostergasse 6 (www.bierstindl.eu/)

Tuesday, 24 September

Lecture: 08.00 – 12.00 *Seminar room (Ground floor)*

Library preparation

- tagging, controls, quantification, pooling, clean up

Illumina HTS runs – how does the run work?

- PCR and bridge amplification
- How does cluster density (template loading) affect your sequencing results?

Computer Lab: 13.00 – 15.30 *ZID, Computer room #19*

Data processing for targeted HTS

- File formats of the raw data
- Quality check of raw data

- Getting familiar with the example datasets
- Setting up a local database

Lecture: 16.00 – 17.00 *Seminar room (Ground floor)*

Computational needs

- Computational power for data processing
- Clusters for data processing
- Backup systems

Time for general questions

Wednesday, 25 September

Computer Lab: 08.00 – 12.00 and 13.00 – 16.00 *ZID, Computer room #19*

The MOTI Pipeline step by step (continued)

- Merging of paired-end data
- Data trimming
- How to generate a reference sequence data base
- Conducting local BLAST search

The MOTI Pipeline step-by-step on your own

Thursday, 26 September

Computer Lab: 08.00 – 12.00 and 13.00 – 16.00 *ZID, Computer room #19*

Data processing for targeted next generation sequencing (continued)

- Running the MOTI pipeline

Lecture: 16.30 – 17.30 *Seminar room (Ground floor)*

Sequence identification

- Reference data bases
- How does BLAST work?
- Alternatives to BLAST
- Using molecular operational taxonomic units (MOTUs)

Friday, 27 September

Computer Lab: 08.00 – 12.00 *ZID, Computer room #19*

Presentation of task-results

Summarizing the whole process

Data interpretation

- Do I have to set a cutoff?
- What was detected - contamination, environmental DNA, consumer or prey DNA?

Questions and feedback

Lunch buffet & MOTI certificates: 12:30 – 14.00