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