

Workshops der GfBS Tagung 2015 im Museum A. Koenig Bonn,  
Termin Samstag 21. März, Start 9.30Uhr, (soweit nicht anders vereinbart)

### **Workshop I**

**Oliver Niehuis (1), Malte Petersen (1), Christoph Mayer (1), Vera Batista (1),  
Manuela Sann (2): Target DNA Enrichment – Methodology, Software, Practical  
Experience Report**

1 Center for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig  
Bonn, Adenauerallee 160, 53113 Bonn

2 Leibniz Institute for Evolution and Biodiversity Science at the Humboldt University in Berlin,  
Invalidenstraße 43, 10115 Berlin, Germany

In this workshop, we will outline the method of target DNA enrichment (a.k.a. exome capture, hybrid enrichment) as a method of obtaining nucleotide sequence data for phylogenomics. Topics covered will include probe design, software to use for bait design, laboratory procedures, and we will demonstrate how enriched DNA sequences can be reliably assigned to target genes.

### **Workshop II**

**Matthias Bernt (1), Alexander Donath (2): “MITOS” Mitogenom-Annotation**

1 Professur für Parallelverarbeitung und Komplexe Systeme Fakultät für Mathematik und  
Informatik Universität Leipzig

2 Zentrum für Molekulare Biodiversitätsforschung /  
Zoologisches Forschungsmuseum Alexander Koenig

The analysis of mitochondrial genomes is a standard method in phylogenetic and phylogeographic studies. Manual annotation of mitochondrial genes, however, is often time consuming and cumbersome. MITOS (MITOchondrial genome annotation Server) is a free web server for the automated annotation of metazoan mitochondrial genomes. It uses state-of-the-art methods for a consistent annotation of protein and non-protein-coding genes.

We will give an insight in the methodology behind MITOS and present the latest improvements that lead to MITOS v2.

Participants are given the chance to analyze a metazoan mitochondrial genome of their choice and to discuss the results and their interpretation together with the workshop lecturers.

## **Workshop III**

### **Alexander Blanke: High quality 3D reconstruction for everyone: open-source solutions and their workflow to analyze and publish microCT data.**

Zentrum für Molekulare Biodiversitätsforschung /  
Zoologisches Forschungsmuseum Alexander Koenig

3D reconstruction of morphologic structures is an increasingly used method. Correct specimen preparation and data handling presupposed, it delivers precise information about the spatial distribution of structures, volumetric information, functional characteristics etc.

At the same time figures can be generated in an easy way and 3D models deposited as electronic supplements in addition to the raw data.

The majority of scientists use expensive programs and workstations to access this methodological field. The aim of this workshop is to introduce several method pipelines which are completely open source and do not need workstations.

Participants will learn:

- how to segment (manually and semi-automatic and fully automatic) microCT data with various levels of detail
- export them into rendering software
- create 3D models ready for publication
- create figures with open source desktop publishing

Pros and cons of 3D reconstruction will be discussed.

If time permits, some post-processing options for 3D reconstructions will be presented.

For example:

- generating 3D PDFs
- generating videos / animations
- prospects for functional analyses (only in brief)

Participants are invited to use their own datasets. Of course example data sets will be provided, if needed.

Prerequisites for this workshop:

- bring your own laptop (WITH a mouse!), preferably a Windows machine (use WINE in case you are an Apple user, but don't expect too much)
- if you have your own dataset, contact the organizers WELL IN ADVANCE (meaning several weeks before the workshop starts!)