

CB-L2: Comparative genomics, phylogenetics and other sequence-based analyses

Person in charge and Representative	Lauber
Contact person	BIOMEDAS Office
Semester	3
Topic cluster	Computational biology
Duration/Credit	4-7 lectures of 1.5 hours
Time	The exact date incl. time will be announced separately
Place	Online. Dial-in data are sent separately
Prerequisite for the lecture	The students should already have attended the Introduction lectures, in particular the "Introduction to bioinformatics and computational biology" lecture.
Aim of the lecture	<p>The lecture will cover</p> <ul style="list-style-type: none"> • the following topics: <ol style="list-style-type: none"> 1. Sequence analysis <ol style="list-style-type: none"> 1.1 Gene finding 1.2 TF binding motif analysis 1.3 UCSC genome browser 2. Comparative genomics <ol style="list-style-type: none"> 2.1 Ortholog vs. Paralog vs. Analog 2.2 Alignment building and curating 2.3 Interactive alignment viewing 2.4 Homology search (Blast, HMMer) 3. Molecular phylogenetics <ol style="list-style-type: none"> 3.1 Evolutionary model selection 3.2 Tree reconstruction methods 3.3 Time-calibration of phylogenies 4. Advanced evolutionary analyses <ol style="list-style-type: none"> 4.1 Natural selection inference 4.2 Ancestral state reconstruction 4.3 Gene sharing networks 4.4 Phylogenetic networks