

CB-C2: 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	Block – 3x 6h / 3 days
Time	The exact date incl. time will be announced separately
Place	Online. Dial-in data are sent separately
Prerequisite for the course	The students should already have attended the accompanying lecture.
Aim of the course	<ul style="list-style-type: none">• During the practical course, the student will use public example data sets to conduct a full phylogenetic analysis. This includes retrieving sequence information from databases, aligning the sequences, reconstructing phylogenies, quantifying the support for branching points in a phylogeny and estimating the temporal signal contained in viral phylogenies.• The students will learn how to use the tools Seaview, Muscle, ClustalW, PhyML and TempEst. The students will also learn some basics how to retrieve data from some of the NCBI databases.• It is recommended that the participants are attending the accompanying lecture that runs in parallel.