

	08.03.10 (LH I)	09.03.10 (LH I)	10.03.10 (LH I)	11.03.10 (4020)
9.15-10.45 Lecture	Introduction Linux Sequence databases rRNA databases Phylogenetic programs, ARB & SILVA	Phylogeny, Part I Alignment Models of evolution Methods for tree reconstruction	Phylogeny, Part II Methods for tree reconstruction Confidence tests Filters Phylogenetic markers	Phylogeny, Part III Molecular probes Design, Pitfalls Solutions
	Break	Break	Break	Break
11.15-13.00 Demo	Demonstration Introduction cont. Accounts Installation of Linux Installation of ARB	Demonstration Import of sequences Aligner + Alignment Fast addition of new sequences to a phylogenetic tree	Demonstration Phylogenetic tree reconstruction Bootstrapping Construction and use of filters	Demonstration Probe design, Probe Match ML Bootstrapping, RAxML Miscellaneous (e.g. MOTHUR)
13.00 – 14.00	Lunch break	Lunch break	Lunch break	Lunch break
14.00 – 17.00 Course Break 15.30-15.45	Demo/work Basic commands Linux/KDE Data retrieval from public databases First steps in ARB	Computer work Import of sequences Alignment Phylogenetic addition of sequences	Computer work Phylogenetic tree reconstruction Construction and use of filters	Computer work Probe design Finish own work