

	30.11.10 (LH I)	01.12.10 (LH I)	02.12.10 (LH I)	03.12.10 (4020)
9.15-10.45 Lecture	<b>Introduction</b> Linux Sequence databases rRNA databases Phylogenetic programs, ARB & SILVA	<b>Phylogeny, Part I</b> Alignment Models of evolution Methods for tree reconstruction	<b>Phylogeny, Part II</b> Methods for tree reconstruction Confidence tests Filters Phylogenetic markers	<b>Phylogeny, Part III</b> Molecular probes Design, pitfalls, and solutions
	Break	Break	Break	Break
11.15-13.00 Demo	<b>Demonstration</b> Introduction cont.  Accounts Installation of Linux Installation of ARB	<b>Demonstration</b> Import of sequences/ the ARB name server  ARB database management Aligner + Alignment/ The ARB pt-server Fast addition of new sequences to a phylogenetic tree	<b>Demonstration</b> Phylogenetic tree reconstruction  Bootstrapping Construction and use of filters Tree optimizations/export	<b>Demonstration</b> Probe design, probe match Additional features of ARB ML Bootstrapping, RAXML Miscellaneous (e.g. mothur) Remaining questions
13.00 – 14.00	Lunch break	Lunch break	Lunch break	Lunch break
14.00 – 17.00 Course Break 15.30-15.45	<b>Demo/work</b> Basic commands Linux/KDE Databases and data retrieval First steps in ARB	<b>Computer work</b> Import of sequences Alignment Phylogenetic addition of sequences	<b>Computer work</b> Phylogenetic tree reconstruction Construction and use of filters	<b>Computer work</b> Probe design Finish own work