

Date	Topic	Sections	Speaker
07-Feb	Intro		
09-Feb	No Class		
14-Feb	Basic alignment of string sequences	1.1.-2.3.	Roel Wijgers
16-Feb	Heuristic alignment algorithms, cost matrices	2.5.-2.9	Thomas van Dijk
21-Feb	Markov chains, Hidden Markov , Viterbi algorithm	3-3.2.	Wouter Duivesteijn
23-Feb	Parameter estimation for HMMs, Baum-Welch algorithm, Model topology, Numerical stability	3.3-3.7	Elze de Groot
28-Feb	Alignment using HMMs	4-4.6.	Wouter Slob
02-Mar	Profile HMMs for sequence families, Viterbi equations	5-5.5.	Roderick Jansen
07-Mar	Probability estimation, weights	5.6.-5.9.	Jan-Pieter van den Heuvel
09-Mar	Multiple sequence alignment methods	6-6.4.	Pavla Sehnalova'
14-Mar	Multiple alignment by HMM training, Phylogenetic trees	6.5.-7.2.	Ron de Bruijn
28-Mar	Phylogenetic trees II	7.3.-7.7.	Shriprakash Sinha
30-Mar	Probabilistic models of evolution	8-8.4.	Jevgenijs Ivanovs
04-Apr	More extensive probability models of evolution	8.5 - 8.6	Ting
06-Apr	Transformational Grammars	9.1 - 9.6	Adriano Galati
11-Apr	Large scale evaluation of profile HMMs	<i>Paper</i>	Gerben Oostra