

Exam

Time and Location

The exam date is Friday, January 8th, 2010 (in U49B). Note that you cannot calculate an examination time from your slot in the sequence, since students before you may not show up. Thus, if you want to be certain to be examined, show up early.

Procedure

When it is your turn for examination, you will first have to defend the two mandatory assignments. You should start by presenting material related to the first mandatory assignment (Dynamic Programming and Sequence Alignment, approx. 5 minutes), and then present what you did in the second mandatory assignment (Cophylogenetics, approx. 10 minutes). For the presentation of the second mandatory assignment you might prepare (but you don't have to) up to 5 slides (transparencies or PDF on USB stick) that you can use in your presentation (different group members are welcome to use the same slide set). Expect me to interrupt you and to ask specific questions when appropriate.

After your presentation I will ask you question related to the complete curriculum (including mandatory assignment 1 and 2). An incomplete list of topics that I might use for asking is given on the next page. Note that the complete examination will last approximately 25-30 minutes, so do not count on more than 15 minutes for your own presentation.

Curriculum:

The curriculum in the course consists of all the literature referenced on the weekly notes. You can rely on that you will only be examined in the parts of the material that was discussed at lectures. Note that the mandatory assignments are part of the curriculum, too.

An incomplete list of questions that you might be asked:

- Central Dogma
- Local and Global Sequence Alignment
 - Smith-Watermann
 - Needleman-Wunsch
 - Scoring Model
- Substitution and scoring matrices
 - PAM
 - BLOSUM
 - Log-Odds Ratio
- BLAST and FASTA (incl. suffix trees, hashing, chaining)
- Coevolution
 - Co-evolutionary events
 - Costs
 - DP approach
 - Statistical Tests
 - Tanglegram Layout Problem (including ILP formulation)
- Genome Rearrangements
 - (Strong) Common Intervals
 - PQ-Trees
 - Sorting
 - Reversal Median Problem
- Phylogenetics
 - Species and Gene Trees, Homology
 - Distance Correction
 - Distance based methods
 - UPGMA
 - Fitch-Margoliash
 - Neighbor Joining
 - Maximum Parsimony
 - Fitch's algorithm