

- We will cover with “Indexing Techniques and Algorithmic Approximation” (Chapter 5.3 of “Understanding Bioinformatics”). You will get an introduction to BLAST and FASTA.
- We will start with the topic “Coevolution”. Mandatory reading (available via Blackboard):
  - Chapter 1 from “Tangled Trees - Phylogeny, Cospeciation, and Coevolution”, 2003, edited by Roderic D. M. Page. ISBN-13: 978-0226644677 (21 pages)
  - A parameter-adaptive dynamic programming approach for inferring cophylogenies. Daniel Merkle, Martin Middendorf, Nicolas Wieseke, BMC Bioinformatics, 2009, to be published, (17 pages)

Optional reading (available via Blackboard):

- Jungles: A new solution to the host/parasite phylogeny reconciliation problem. Charleston, M. A. Mathematical Biosciences 149:191-223, 1998.
- Reconstruction of the Cophylogenetic History of Related Phylogenetic Trees with Divergence Timing Information, D. Merkle, M. Middendorf, Theory in Biosciences 123(4): 277-299, 2005