- We will continue with "Phylogenetics" (Chapter 7 and Chapter 8 of Understanding Bioinformatics, 2008 by Marketa Zvelebil and Jeremy O. Baum).

- Small hint for mandatory assignment 2: The black squares in the boxplots (like used in the article "A parameter-adaptive dynamic programming approach for inferring cophylogenies") can be plotted using `stripchart(X,add=TRUE,at=Y,pch=15,cex=2)`, where X and Y are the position of the square. Example:

  `stripchart(1,add=TRUE,at=0.00762,pch=15,cex=2)`

- Details regarding the oral exam are made available online immediately after the last lecture.