

**Algorithms in Genome Research
Winter 2011/2012**

Exercises

Number 3, Discussion: 2011 November 25

1. Describe the general idea of a covariance model. Can you imagine any other application in bioinformatics in which covariance models could be used?
2. What is the mRNA-Codon used in the incorporation of Selenocysteine? Does this codon also code for something else? How is this possible?
3. Which types of information may be used by a prokaryotic gene finder?
What are the algorithmic/computational techniques that are employed?
4. What are the main issues why eukaryotic gene finding is more difficult than prokaryotic gene finding?
What are the algorithmic/computational techniques that are used in order to account for this increased difficulty?
5. Discuss the issue of obtaining test data sets for HMM training in gene finding.