

**Algorithms in Genome Research
Winter 2020/2021**

Exercises

Number 4, Discussion: 2020 December 04

1. What is the mRNA Codon used in the incorporation of Selenocysteine? Does this codon also code for something else? How is this possible?
2. Describe the general idea of a covariance model. Can you imagine any other application in bioinformatics in which covariance models could be used?
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.