**Universität Bielefeld**
**Technische Fakultät**

**AG Genominformatik**
**Prof. Dr. Jens Stoye**
**Dr. Marília D. V. Braga**

# Algorithms in Genome Research
## Winter 2018/2019

## Exercises

**Number 7, Discussion: 2018 December 14**

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.