Universität Greifswald Institute für Mathematik and Informatik Marc Hellmuth

# 1. ÜBUNG "BIOINFORMATIK", SS 16

## Aufgabe 1: (2 Credits)

Titin is a muscle protein whose gene has the largest known coding sequence - 80,781 DNA bases. How many amino acids long is titin?

### Aufgabe 2: (18 Credits)

Recall the *Nirenberg-Matthaei-Experiment*: We introduced the technique of transcribing synthetic mRNA in order to solve some of the genetic code. The synthetic mRNA was periodic in nature: XXXX..., XXYXXY..., XYYXYY..., etc. Derive all the information you can about the genetic code using only two letters A and C. Clearly define the synthetic mRNA and their protein products. Recall that only the presence of amino acids could be detected, not the sequence.

### **Aufgabe 3:** (2.5+5+2.5 = 10 Credits)

Consider a gene as a subsequence of the DNA that encodes one protein and let S be a the protein (sequence of aminoacids) CRICK.

- (a) Which aminoacids are encoded?
- (b) How many different genes g can theoretically code for this sequence S?
- (c) Write down one possible gene q encoding S.

#### Aufgabe 4: (10 Credits)

Let us consider a protein simply as a sequence of aminoacids. Consider the set R of DNA sequences of length 3n with  $n \in \mathbb{N}$ . Let  $R' \subseteq R$  be the set of sequences  $r \in R$  that can theoretically code for proteins. In particular, assume that each sequence  $r = r_1 r_2 \dots r_{3n} \in R'$  begins with the startcodon coding for Met, ends with a stopcodon and none of the codons  $r_i r_{i+1} r_{i+2}$  with  $i \mod 3 = 1$  and 3 < i < 3n-2 corresponds to a start- or stopcodon.

Determine the cardinality |R'| for n = 1, n = 2 and n > 3.

Deadline: Monday - April 11, 2016 - 2.15pm