

Grundlagen der Bioinformatik

SoSe 2018

Assignment 01

Submit electronically in Ilias by 23.4.2016, 10h

1 IntelliJ (2 points)

Download and install the Community Edition of IntelliJ (Java IDE). Make sure that you are using the latest version of Java 8. (The use of IntelliJ and Java 8 will make it easier for the tutors to help you with any Java questions that you might have.)

2 Java FastA class (3 points)

Implement a Java class called **FastA** that you can use to read, write and maintain a list of DNA or amino acid sequences (as strings). Your class should provide the following methods:

- `void read (Reader r)` - read sequences in FastA format
- `void write (Writer w)` - write sequences in FastA format
- `int size ()` - the number of sequences
- `String getHeader (int i)` - get the *i*-th header
- `String getSequence (int i)` - get the *i*-th sequence
- `void add (String header,String sequence)` - add a new header and sequence

3 Translator (5 points)

To demonstrate your FastA class, write a Java program *Translator* that takes as input a FastA file of DNA sequences and produces as output a FastA file of all six-frame translations (into amino acid sequences) of each of the input DNA sequences. To identify a translated sequence, report its input header and add +1, +2, +3, -1, -2 or -3 to indicate its frame.

The program should take the names of the input and output files as command-line options.

This program should use all the methods implemented in your FastA class.

Apply it to the file `dna_01.fasta.gz` available from the Ilias page.