Masterarbeit:
Discovering new non-coding RNAs in Bacteria

Dr. Zasha Weinberg (zasha@bioinf.uni-leipzig.de)

November 2, 2016

Background: During the last 15 years, science has truly begun to appreciate the biological significance of RNAs that do not code for proteins. Bacteria have a diverse range of RNAs that push the boundaries of RNA versatility and reveal new aspects of biology. For example, riboswitches bind small molecules, and are able to reject other small molecules that may differ by only one atom. Ribozymes are able to catalyze chemical reactions, requiring an intricate arrangement of nucleotides.

RNAs such as these can be detected by comparing many homologous nucleotide sequences in order to find covarying mutations. Using a system based on this idea, my colleagues and I at Yale University discovered 12 novel riboswitch classes (out of 26 known) and 4 ribozyme classes that cut themselves (out of 9 known)—and many more RNAs whose functions remain a mystery. As large amounts of sequence data have recently become available, there is a clear possibility to find RNAs that were previously too rare to find.

Project: This project involves analyzing multiple-sequence alignments predicted by a computer to find the most promising and interesting candidates. This analysis requires integrating predictions from multiple computer programs, and preparing high-quality data that will interest experimental biologists. Some scripts will become important to focus searches on the most promising targets, and to fully evaluate the predictions.

Basic knowledge of Linux is essential. Knowledge of a scripting language like Perl or Python is helpful.

If interested: please e-mail Dr. Zasha Weinberg at zasha@bioinf.uni-leipzig.de.