

Student Info – Bioinformatik Praktikum I

13.01.2014 – 31.01.2014

Goal Characterization of bacterial trans-encoded small anti-sense RNAs in *Stenotrophomonas maltophilia*.

Educational objective:

- Work with a wide range of bioinformatic programs in a Linux environment
- Properly document the work flow and the results
- Present the own results in front of the class

Background Bacteria use different RNA based systems to adjust their gene expression to different environmental conditions. One of them are the so called trans-encoded small anti-sense RNA (sRNA). These sRNA are transcribed and can base pair (therefore anti-sense) with different mRNA which are encoded elsewhere in the genome (therefore trans-encoded). Thereby, the sRNA can modulate the translation rate of its target.

Tasks During the course the students are guided to predict sRNA genes in the genome of *Stenotrophomonas maltophilia*. This is done with in-silico tools and by analyzing publicly available data from a deep sequencing experiment devoted to annotated transcription start sites (dRNA-seq). In a second step this putative sRNA annotation is tested for differential gene expression between the wild type and a Hfq mutant. Hfq is an RNA chaperon which plays an important role in the establishment of the sRNA - mRNA interaction. Finally targets for the best sRNA candidates are predicted.

Methods

- Deep sequencing quality control
- Deep sequencing read mapping
- Statistical analysis of dRNA-seq data
- In-silico prediction of ncRNA
- Gene annotation format handling
- Differential gene expression analysis of RNA-seq data
- sRNA target prediction

Tools

• FastQC	• RNAz
• segemehl	• BEDtools
• TSSAR	• HTseq-count
• NAPP	• DESeq
• SIPHT	• CopraRNA
• multiz, tba	