

# PhD student positions in bioinformatics

Job opening from January 26, 2016.

<http://www.rna.uni-jena.de/>

The Research Group **RNA Bioinformatics and High Throughput Analysis** in Jena has multiple openings for PhD positions. We are looking for talented and motivated PhD students who are interested in (at least) one of the following topics:

- **High throughput sequencing analysis**

We are specialized to analyze huge amounts of RNA-Seq data produced by current high-throughput sequencing methods. We are looking for a bioinformatician to process data based on state-of-the-art techniques (quality control, reference mapping, *de novo* assembly, quantification, visualization) as well as to develop own scripts and tools to find genes differential expressed between certain conditions. Based on RNA-Seq data of a host and its pathogen we try to find out more about the ecology and species barriers in emerging viral diseases by detecting protein- and non-coding genes differential expressed between different combinations of species, tissues and time points post infection.

- **Virus bioinformatics**

Since the last emerging viral epidemics/pandemics, caused by SARS, MERS and Ebola, viruses are extensively studied in wet lab, however specific bioinformatic tools are still missing. We develop new tools to find conserved RNA secondary structures and RNA-RNA interactions in viral genomes to understand the viral replication. Furthermore we want to facilitate the viral genome assembly. It is a challenging task to assemble viral sequences out of samples, including millions of host sequences. A new challenge is also the design of synthetic viruses with weak clinical symptoms along with still viable viruses. A successful design can be used to produce cheap vaccinations within decent time.

- **Monitoring antibody profiles**

To rapidly monitor the specific antibody profile of a patient and decide on vaccination, currently used methods of serological analysis need to be improved. We are looking for a bioinformatician to develop better tools for identification of immunodominant domains (epitopes, antigenic determinants) on bacterial, viral and other microbial proteins. In a four-party project, the results of this *in silico* study will be verified in the diagnostic lab by testing patient sera, and the feedback will be used to refine the epitope identification software.

- **Epigenetic regulation by long non-coding RNAs**

The project will focus on elucidating lncRNA-genome interactions and their impact on gene regulation in mammalian cells. The candidate will be involved in developing tools and techniques to detect novel lncRNA/DNA structures genome-wide, to identify the associated binding proteins and to unravel the underlying regulatory mechanisms. The work will include state-of-the-art laboratory techniques (e.g. ChIP, ChRIP, high throughput sequencing, proteomics) and bioinformatical analysis of the data.

- **Combined metabolome and transcriptome analysis**

In this project we analyse transcriptomics and metabolomics data of cyanobacteria to analyse their fitness regarding the circadian clock. On transcriptomic level we want to identify unknown genes and differentially analyse different time points of the circadian rhythm. On metabolomic level we want to fill the gaps in the metabolic networks. In particular, we want to combine the analysis of both data types to compensate for incompleteness in one of the data sources.

Applicants should have:

- a Master in bioinformatics, computational biology or a related area,
- a passion for developing and using computational tools and algorithms to analyze large biological data sets,
- good programming skills in a unix environment,
- high motivation and the ability to work both independently and in a team.

**Application Deadline:** ASAP

Candidates are encouraged to send their application including CV and a short description of research experience and interests to:

[franziska.hufsky@uni-jena.de](mailto:franziska.hufsky@uni-jena.de)