

March 26, 2019

## PhD position – Functional Genomics and Computational Biology

A three-year Ph.D. position (65% E 13 TV-L) is immediately available at the Department of Biology (<http://www.bioinfo.nat.fau.de>) at the Friedrich-Alexander-Universität Erlangen-Nürnberg (Germany).

The focus of our research group is on understanding the dynamics of gene expression, which is central to evolution, development and disease. Gene expression is primarily controlled at the level of transcription, which is mediated by transcription factor activity and changes in the chromatin structure. Chromatin structure is largely determined by histone modifications and DNA methylation, collectively known as epigenetic marks. Large international efforts such as the ENCODE (<https://www.encodeproject.org/>) and FANTOM (<http://fantom.gsc.riken.jp/>) projects are now generating a wealth of transcriptomic and epigenomic data that should enable us to elucidate the mechanisms underlying health and disease. However, the analysis of these data is not trivial. In particular, repetitive regions in the genome pose an enormous challenge to current bioinformatics tools. It has been estimated that approximately two thirds of the human genome consists of repeats or repeat-derived sequences, and a predominant part of these sequences are transposable elements. This project aims at developing computational tools to aid the genome-wide characterization of sequences of transposon origin. Some of our related publications include:

Li L, Barth NKH, Hirth E, Taher L. Pairs of Adjacent Conserved Noncoding Elements Separated by Conserved Genomic Distances Act as Cis-Regulatory Units, *Genome Biol Evol.*, 2018 (<https://www.ncbi.nlm.nih.gov/pubmed/30184074>).

Taher *et al.*, Sequence signatures extracted from proximal promoters can be used to predict distal enhancers, *Genome Biology*, 2013 (<https://www.ncbi.nlm.nih.gov/pubmed/24156763>).

### Eligibility:

We are looking for talented, highly motivated applicants with:

1. A master's degree or equivalent within the field of computational biology, bioinformatics or related fields.
2. Familiarity with bash scripting, Perl (or Python) and R programming.
3. Experience with the analysis of Next-Generation Sequencing data (mainly from Illumina platforms).
4. Strong written and oral communication skills in English.

### How to Apply:

The position will remain open until filled. Please email applications to Leila Taher ([funcgenfau@gmail.com](mailto:funcgenfau@gmail.com)) with the subject "PhD Position". An application package must contain the following documents (please, send all in one PDF file):

1. A letter of interest.
2. A complete curriculum vitae.
3. A short (<3,000 characters) research proposal on the topic "regulatory functions of transposons". The following articles may be of some assistance:
  - An integrated encyclopedia of DNA elements in the human genome (<https://www.ncbi.nlm.nih.gov/pubmed/22955616>).
  - Chromatin-state discovery and genome annotation with ChromHMM (<https://www.ncbi.nlm.nih.gov/pubmed/29120462>).
  - A family of transposable elements co-opted into developmental enhancers in the mouse

neocortex (<https://www.ncbi.nlm.nih.gov/pubmed/25806706>).

4. Copies of transcripts.

5. Names and contact information for 2-3 references.

Only complete applications will be considered.