



Postdoc Position in Comparative Genomics

The Hiller Lab at the LOEWE Center for Translational Biodiversity Genomics (TBG) in Frankfurt, Germany is looking for an ambitious Postdoc to investigate the genomic basis of phenotypic differences between vertebrates.

Project

The project aims at linking phenotypic adaptations to genomic differences, which is a central goal in the genomics era. The postdoc is expected to capitalize on a powerful repertoire of Forward Genomics and other methods as well as genome alignments and comparative data for several hundred mammals and birds that the lab has generated. A large list of interesting adaptations including metabolic, physiological and morphological traits in bats, dolphins, other mammals and vertebrates is available to be studied, and choices can be influenced by the preference of the postdoc.

Our lab

The mission of our group is to understand how nature's fascinating phenotypic diversity has evolved and how it is encoded in the genome. Work in the lab includes genome sequencing and assembly, genome alignment and annotation, development and application of comparative genomic methods to discover differences in genes and *cis*-regulatory elements, and the use of statistical approaches to link phenotypic to genomic changes [1-8].

Our lab is part of TBG (<https://tbg.senckenberg.de/>) and Senckenberg Research Society, and is based near the city center of Frankfurt am Main, Germany. The TBG provides access to cutting-edge computational infrastructure (HPC, genome browser) and lab facilities to sequence genomes of diverse creatures. English is the working language in our lab. Frankfurt is a vibrant and highly-international city at the heart of Europe that combines a skyscraper skyline with ample park and green areas.

Requirements

Applicants should have a degree in bioinformatics/computational biology, genomics or a related area, and a strong publication record. Solid programming skills in a Linux environment and experience with shell scripting and Unix tools are required. Previous experience in large-scale comparative genomic data analysis is an advantage.

How to apply

If interested, please email (i) your CV including publication list and contact information for at least two references and (ii) a summary of previous research experience (max 1 page) to Michael Hiller (Michael.Hiller@senckenberg.de). Further information: <https://tbg.senckenberg.de/personen/hiller/>

The position is fully-funded. Salary and benefits are according to TV-H E13 100%. The position will be initially for 2 years, but funding is available to extend it further. The employer is the Senckenberg Society for Nature Research in Frankfurt am Main. Senckenberg supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference.

Application deadline is **February 26th 2021**. The position is available immediately and the search continues until the position has been filled.

Recent publications

- [1] Jebb *et al.* Six reference-quality genomes reveal evolution of bat adaptations. *Nature*, 583, 578–584, 2020
- [2] Huelsmann *et al.* Genes lost during the transition from land to water in cetaceans highlight genomic changes associated with aquatic adaptations. *Science Adv*, 5(9), eaaw6671, 2019
- [3] Hecker *et al.* Convergent gene losses illuminate metabolic and physiological changes in herbivores and carnivores. *PNAS*, 116(8), 3036-3041, 2019
- [4] Roscito *et al.* Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. *Nature Communications*, 9:4737, 2018
- [5] Langer *et al.* REforge associates transcription factor binding site divergence in regulatory elements with phenotypic differences between species. *MBE*, 35(12), 3027–3040, 2018
- [6] Lee *et al.* Molecular parallelism in fast-twitch muscle proteins in echolocating mammals. *Science Adv*, 4(9), eaat9660, 2018
- [7] Sharma *et al.* A genomics approach reveals insights into the importance of gene losses for mammalian adaptations. *Nature Communications*, 9(1), 1215, 2018
- [8] Nowoshilow *et al.* The axolotl genome and the evolution of key tissue formation regulators. *Nature*, 554(7690), 50-55, 2018