



Job Announcement ref. #12-22006

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 apply and develop new comparative genomic methods.

The Project

The project combines the development of new comparative genomic methods to uncover key genomic differences with large-scale analyses to link phenotypic adaptations to genomic differences, which is a central goal in the genomics era. Powerful computational methods are fundamental to gain novel insights through comparative genomics and our lab has developed several approaches to address the phenotype – genotype question (<https://github.com/hillerlab/>). We aim at expanding our methods repertoire by detecting new “types” of relevant differences, such as genomic changes in non-coding RNAs and gene duplication events. New and existing approaches will then be applied to vertebrate genomes, including new assemblies generated in our lab, to reveal the genomic underpinnings of phenotypic differences. The postdoc is expected to work closely with other lab members and to capitalize on a wealth of comparative data for several hundred vertebrate genomes (<http://genome.senckenberg.de/>).

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 sequencing and assembly of reference-quality genomes, 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 [1-9].

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. TBG provides access to cutting-edge computational (HPC clusters, genome browser) and lab infrastructure to sequence genomes. English is the working language in our lab. Senckenberg and TBG provide flexible working hours, an annual special payment, a company pension scheme, the Senckenberg badge for free entry in museums, the zoo, botanical garden and Palmengarten, a leave of 30 days per year, and a subsidy job ticket for public transport. 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 PhD degree in bioinformatics/computational biology, computer science, 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 comparative genomics is an advantage.

Place of employment: Frankfurt am Main
Working hours: full time (40 hours/week)
Type of contract: initially for 2 years, but funding is available to extend it further
Salary and benefits: according to the collective agreement of the State of Hesse (pay grade E13 100%)

The position is fully funded and should ideally start as soon as possible.

The employer is the Senckenberg Gesellschaft für Naturforschung who supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference.

How to apply

Please send your application, mentioning the reference of this job announcement (**ref.#12-22006**), by e-mail to Michael Hiller (michael.hiller@senckenberg.de) and recruiting@senckenberg.de.

The application should include the reference number of this job announcement, a CV with publication list and contact information for at least two references, a summary of previous research experience (max 1 page), and copies of certificates, transcripts and grades.

The initial application deadline is **April 5th, 2022**.



For more information please contact Prof. Dr. Michael Hiller, michael.hiller@senckenberg.de or visit <https://tbg.senckenberg.de/personen/hiller/>.

Recent publications

- [1] Blumer *et al.* Gene losses in the common vampire bat illuminate molecular adaptations to blood feeding. *Science Advances*, 2022
- [2] Roscito *et al.* Convergent and lineage-specific genomic differences in limb regulatory elements in limbless reptile lineages. *Cell Reports*, 38(3):110280, 2022
- [3] Jebb *et al.* Six reference-quality genomes reveal evolution of bat adaptations. *Nature*, 583, 578–584, 2020
- [4] Huelsmann *et al.* Genes lost during the transition from land to water in cetaceans highlight genomic changes associated with aquatic adaptations. *Science Advances*, 5(9), eaaw6671, 2019
- [5] Hecker *et al.* Convergent gene losses illuminate metabolic and physiological changes in herbivores and carnivores. *PNAS*, 116(8), 3036-3041, 2019
- [6] Roscito *et al.* Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. *Nature Communications*, 9:4737, 2018
- [7] Lee *et al.* Molecular parallelism in fast-twitch muscle proteins in echolocating mammals. *Science Advances*, 4(9), eaat9660, 2018
- [8] Sharma *et al.* A genomics approach reveals insights into the importance of gene losses for mammalian adaptations. *Nature Communications*, 9(1), 1215, 2018
- [9] Nowoshilow *et al.* The axolotl genome and the evolution of key tissue formation regulators. *Nature*, 554(7690), 50-55, 2018