Job Announcement ref. #12-21009

PhD Position in Comparative Genomics

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

The Project

We offer several projects that range from the development of new comparative genomic methods to accurately detect relevant genomic changes in big datasets to applying existing and new approaches to link phenotypic adaptations to genomic differences, which is a central goal in the genomics era. The PhD student is expected to capitalize on a powerful repertoire of Forward Genomics and other methods such as TOGA ((Tool to infer Orthologs from Genome Alignments) as well as available genome alignments and comparative data for hundreds of mammals and birds. 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 PhD student.

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 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.

Place of employment:	**Frankfurt am Main**
Working hours:	**part-time (30 hours/week)**
Type of contract:	**initially for 3 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 TV-H, 75%)**

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 offer (**ref.#12-21009**), by e-mail to Michael Hiller (michael.hiller@senckenberg.de) and recruiting@senckenberg.de. Alternatively use our online application form on https://www.senckenberg.de/en/career/apply-online/. The application should include a CV with publication list and contact information for at least two references, and a summary of previous research experience (max 1 page), and copies of certificates, transcripts and grades.

The initial application deadline is **December 12th, 2021**, but the search will continue until the position has been filled.

For more information please contact Prof. Dr. Michael Hiller, michael.hiller@senckenberg.de or use the following link: 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. bioRxiv, 2021.2010.2018.462363 (2021).

[2] Jebb *et al.* Six reference-quality genomes reveal evolution of bat adaptations. Nature, 583, 578–584, 2020

[3] 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

[4] Hecker *et al.* Convergent gene losses illuminate metabolic and physiological changes in herbivores and carnivores. PNAS, 116(8), 3036-3041, 2019

[5] Roscito *et al.* Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. Nature Communications, 9:4737, 2018

[6] Langer *et al.* REforge associates transcription factor binding site divergence in regulatory elements with phenotypic differences between species. MBE, 35(12), 3027–3040, 2018

[7] Lee *et al.* Molecular parallelism in fast-twitch muscle proteins in echolocating mammals. Science Adv, 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