Job Announcement ref. #12-22014

PostDoc Position in Gene Annotation

The Hiller Lab at the LOEWE Center for Translational Biodiversity Genomics (TBG) in Frankfurt, Germany is looking for an ambitious PostDoc (m/f/d) to apply and develop new gene annotation approaches.

The Project

Comprehensively annotating genes in newly-sequenced genomes remains a challenging task. Our lab recently developed TOGA [1], the first method that integrates gene annotation and orthology inference, and used it to provide comparative annotations for >1000 mammals and birds (http://genome.senckenberg.de/). The project aims at developing a new automated strategy to integrate TOGA annotations with transcriptomics (short read RNA-seq and long read Iso-seq) data to produce comprehensive, high-quality gene annotations. We also aim at further improving TOGA by incorporating deep learning predictions into the annotation process. The new strategy will be applied to assemblies of numerous species, including bats, cetaceans, birds, snakes and fish, sequenced by us and collaborators. This will form the basis to uncover key differences in genes and link phenotypic adaptations of these species to differences in their genomes. The postdoc is expected to work closely with other lab members and capitalize on a wealth of existing methods and comparative genomic data.

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 gene 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 [1-10].

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 and a leave of 30 days per year. Frankfurt is a vibrant and highly-international city at the heart of Europe that combines a skyscraper skyline with ample park and green areas. The Economist index recently ranked Frankfurt among the top 10 most livable cities worldwide.

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 gene annotation, comparative genomics or methods development is an advantage.

Place of employment:	**Frankfurt am Main**
Working hours:	**full time (40 hours/week), optional: part-time (80%)**
Type of contract:	**initially limited for 2 years with the possibility of an extension**
Salary and benefits:	**according to the collective agreement of the State of Hesse (pay grade E 13 100%)**

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.#12-22014**), 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 application deadline is **December 15th, 2022**.

Zertifikat seit 2012
audit berufundfamilie

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

Recent publications

[1] Kirilenko BM, *et al.* Integrating gene annotation with orthology inference at scale. Science, in press, 2022

[2] Blumer *et al.* Gene losses in the common vampire bat illuminate molecular adaptations to blood feeding. Science Advances, 2022

[3] Roscito *et al.* Convergent and lineage-specific genomic differences in limb regulatory elements in limbless reptile lineages. Cell Reports, 38(3):110280, 2022

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

[5] 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

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

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

[8] Lee *et al.* Molecular parallelism in fast-twitch muscle proteins in echolocating mammals. Science Advances, 4(9), eaat9660, 2018

[9] Sharma *et al.* A genomics approach reveals insights into the importance of gene losses for mammalian adaptations. Nature Communications, 9(1), 1215, 2018

[10] Nowoshilow *et al.* The axolotl genome and the evolution of key tissue formation regulators. Nature, 554(7690), 50-55, 2018