



Job Announcement ref. #12-24001

ERC-funded Bioinformatician Position

The Hiller Lab at the LOEWE Center for Translational Biodiversity Genomics (TBG) in Frankfurt, Germany is looking for a Bioinformatician to work on the BATPROTECT project to investigate the genomic basis of long healthspans, disease resistance and viral tolerance in bats.

BATPROTECT

is a 6-year funded ERC synergy grant project that will use bats as natural models of healthy aging and disease tolerance to elucidate the molecular mechanisms behind bat's exceptional longevity and resistance to viral and age-related diseases. BATPROTECT brings together a team of global leaders in bat biology and ageing (Emma Teeling, Dublin), bat immunology and virology (Linfa Wang, Singapore), evolution and genomics (Michael Hiller, Frankfurt), and ageing model organisms (Bjoern Schumacher, Cologne) that will jointly investigate aging and immune responses in bats from the wild and captive colonies, discover genes with evolutionary importance for longevity and disease resistance, and functionally validate longevity and immune regulators in stem and differentiated cells of bats and model organisms, with the ultimate goal to uncover new directions to improve human healthspan and disease outcome.

The Project

The Bioinformatician will be responsible for the assembly of reference-quality genomes of more than one hundred bat species, for which we are generating PacBio HiFi and HiC data. For a few focal species, we also aim at generating a T2T assembly. The Bioinformatician will also work on analyzing transcriptomics data that we are sequencing in parallel for all target bat species, using this data and our homology-based methods (TOGA) to annotate the new genomes, generating whole genome alignments of bats and other mammals, and supporting the BATPROTECT project with other data processing and analysis tasks.

The Bioinformatician will work closely with other Bioinformaticians at TBG, other members of the BATPROTECT team and the Hiller lab. We offer exchanges with the other BATPROTECT labs as well as yearly retreats with all project members.

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 gene expression, 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 (large 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 2022 index ranked Frankfurt among the top 10 most livable cities worldwide.

Your profile

- A Master-level degree in bioinformatics / computational biology, genomics or a related area. A PhD degree is an advantage, but not strictly required.
- Excellent programming skills in a Linux environment as well as experience with shell scripting and Unix tools.
- Previous experience in genome assembly and ideally genome annotation.

Place of employment: Frankfurt am Main
Working hours: full time (40 hours/week) / part-time options are available
Type of contract: initially limited for 2 years, but ERC funding is available for a total of 4 years
Start date: flexible but should ideally be in late spring 2024.
Salary and benefits: according to the collective agreement of the State of Hesse (pay grade E13)

Senckenberg is committed to diversity. We benefit from the different expertise, perspectives and personalities of our staff and welcome every application from qualified candidates, irrespective of age, gender, ethnic or cultural origin, religion and ideology, sexual orientation and identity or disability. Women are particularly encouraged to apply, as they are underrepresented in the field of this position; in the case of equal qualifications and suitability they will be given preference. Applicants with disabilities (“Schwerbehinderung”) will be given preferential consideration in case of equal suitability. Senckenberg actively supports the compatibility of work and family and places great emphasis on an equal and inclusive work culture.

How to apply

Please send us your application documents containing

- 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)

in electronic form (as a coherent PDF file) by **March 22, 2024** to recruiting@senckenberg.de quoting **the reference number #12-24001**, or apply through the online application form on our homepage.

Senckenberg Gesellschaft für Naturforschung
Senckenberganlage 25
60325 Frankfurt a.M.
E-Mail: recruiting@senckenberg.de



For more information please contact Prof. Dr. Michael Hiller, michael.hiller@senckenberg.de or visit the lab webpage <https://tbg.senckenberg.de/hillerlab/>. For more information about the Senckenberg Gesellschaft für Naturforschung, please visit www.senckenberg.de.

Recent publications

- [1] Kirilenko BM, *et al.* Integrating gene annotation with orthology inference at scale. *Science*, 380(6643), 2023
- [2] Osipova E, *et al.* Loss of a gluconeogenic muscle enzyme contributed to adaptive metabolic traits in hummingbirds. *Science*, 379(6628), 185-190, 2023
- [3] Blumer *et al.* Gene losses in the common vampire bat illuminate molecular adaptations to blood feeding. *Science Advances*, 8(12), 2022
- [4] Roscito *et al.* Convergent and lineage-specific genomic differences in limb regulatory elements in limbless reptile lineages. *Cell Reports*, 38(3):110280, 2022
- [5] Jebb *et al.* Six reference-quality genomes reveal evolution of bat adaptations. *Nature*, 583, 578–584, 2020

- [6] 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), 2019
- [7] Hecker *et al.* Convergent gene losses illuminate metabolic and physiological changes in herbivores and carnivores. *PNAS*, 116(8), 3036-3041, 2019
- [8] Roscito *et al.* Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. *Nature Communications*, 9:4737, 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