



Postdoc Position in Comparative Genomics

The Hiller Lab at the LOEWE Center for Translational Biodiversity Genomics in Frankfurt, Germany is looking for an ambitious Postdoc to work on comparative genomic analysis of mammals and other taxonomic groups.

Description

The mission of our group is to discover genomic determinants of phenotypic differences between species, which is important to understand how nature's fascinating phenotypic diversity evolved and how it is encoded in the genome. Work in the lab ranges from genome assembly and alignment, annotating genes, developing and applying comparative genomic methods to discover key differences in genes (such as loss, gain, selection) and regulatory elements to using statistical approaches to associate genomic to phenotypic changes [1-8].

The postdoc will join our efforts to extend our methods repertoire to accurately detect additional types of genomic changes, to adopt them to other taxonomic groups, and to apply them on a large-scale to existing and numerous newly-sequenced genomes generated by us and our TBG collaborators.

Requirements

Applicants should have a strong publication record and a degree in bioinformatics / computational biology, genomics or a related area. Good programming skills in a Linux environment as well as 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/>

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 Senckenberg Gesellschaft für Naturforschung 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 **October 25th 2020**. 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