



MAX-PLANCK-GESELLSCHAFT



Postdoc Position in Evolutionary Genomics

The Hiller Lab at the Max Planck Institute in Dresden, Germany, is looking for an ambitious Postdoc to work on comparative genomic analysis of bats and other mammals.

Project description

The postdoc will utilize publicly-available genomes of numerous mammals as well as newly-sequenced genomes of several bats to discover the genomic basis of interesting phenotypic differences between these species. The postdoc will apply and further develop our genomics methods, and analyze results by integrating biomedical knowledge and generated functional genomics data. Promising candidate genes will be tested experimentally, either by the Postdoc or in collaboration. Funding is according to the German TVöD scale and available for at least 3 years.

Our Lab

We combine computational biology, comparative genomics and experiments to investigate how nature's fascinating phenotypic diversity evolved and how it is encoded in the genome. On the computational side, we align and annotate genome assemblies [1-3], develop and apply comparative genomic methods to discover key differences in genes and regulatory elements [4-9], and use statistical approaches to associate genomic to phenotypic differences [10,11]. On the experimental side, we use RNA-seq, ATAC-seq, functional assays and CRISPR-Cas9 to reveal the molecular function of genomic regions and to test causality between genomic and phenotypic differences [12,13]. Our group is part of the [Bat1K](#) project that aims at generating reference-quality genomes of all bats.

The lab is based at the Max Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG) and we are jointly affiliated with the Max Planck Institute for the Physics of Complex Systems, both in Dresden. Both institutes are highly interactive and interdisciplinary workplaces, provide an international atmosphere with English as working language and access to cutting-edge computational and experimental infrastructure and facilities. The MPI-CBG was awarded one of the "Best Places To Work for Postdocs" in 2011.

Requirements

Applicants should have a strong publication record and a degree in bioinformatics / computational biology, genomics or a related area. Excellent 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 (hiller@mpi-cbg.de). Further information: <https://www.mpi-cbg.de/hiller>

The Max Planck Society strives for gender and diversity equality. We welcome applications from all backgrounds.

Application deadline is November 30th 2019. The position is available immediately and the search continues until the position has been filled.

Recent publications

1. Nowoshilow S, et al. (2018). The axolotl genome and the evolution of key tissue formation regulators. *Nature* 554: 50-55.
2. Roscito JG, et al. (2018). The genome of the tegu lizard *Salvator merianae*: combining Illumina, PacBio, and optical mapping data to generate a highly contiguous assembly. *Gigascience* 7.
3. Sharma V, Hiller M (2017). Increased alignment sensitivity improves the usage of genome alignments for comparative gene annotation. *Nucleic Acids Res* 45: 8369-8377.
4. Sharma V, et al. (2018). A genomics approach reveals insights into the importance of gene losses for mammalian adaptations. *Nat Commun* 9: 1215.
5. Sharma V, et al. (2018). Loss of RXFP2 and INSL3 genes in Afrotheria shows that testicular descent is the ancestral condition in placental mammals. *PLoS Biol* 16: e2005293.
6. Jebb D, Hiller M (2018). Recurrent loss of HMGCS2 shows that ketogenesis is not essential for the evolution of large mammalian brains. *Elife* 7: e38906.
7. Florio M, et al. (2018). Evolution and cell-type specificity of human-specific genes preferentially expressed in progenitors of fetal neocortex. *Elife* 7: e32332.
8. Huelsmann M, et al. (2019). Genes lost during the transition from land to water in cetaceans highlight genomic changes associated with aquatic adaptations. *Science Adv* 5: eaaw6671.
9. Hecker N, et al. (2019). Convergent gene losses illuminate metabolic and physiological changes in herbivores and carnivores. *PNAS* 116: 3036-3041.
10. Prudent X, et al. (2016). Controlling for Phylogenetic Relatedness and Evolutionary Rates Improves the Discovery of Associations Between Species' Phenotypic and Genomic Differences. *Mol Biol Evol* 33: 2135-2150.
11. Langer BE, et al. (2018). REforge Associates Transcription Factor Binding Site Divergence in Regulatory Elements with Phenotypic Differences between Species. *Mol Biol Evol* 35: 3027-3040.
12. Roscito JG, et al. (2018). Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. *Nat Commun* 9: 4737.
13. Lee JH, et al. (2018). Molecular parallelism in fast-twitch muscle proteins in echolocating mammals. *Science Adv* 4: eaat9660.