

Job Title: Postdoctoral Researcher in Bioinformatics (50% Capacity)

Department: Department of Genetic Medicine and Development, Faculty of Medicine, University of Geneva

Location: Geneva, Switzerland

Duration: 2 Years (2024–2026)

Job Description:

The Wu Lab is seeking a motivated and skilled postdoctoral researcher in bioinformatics to join our small dynamic team at 50% capacity. The successful candidate will contribute to our exciting research on germline small non-coding RNAs using mouse genetics, customized and existing RNA sequencing methods, in-depth sequencing data analysis, and imaging. This part-time position offers a unique opportunity to work in a collaborative and interdisciplinary young lab in proximity to the Bioinformatic Support Platform at the Faculty of Medicine. The part-time position has the possibility to transition into a joint postdoctoral position with a higher working capacity with a second lab in the same department, provided that the candidate's expertise and interests align well with both labs and the work scope is clearly defined from the outset.

Key Responsibilities:

- Process, analyze, and interpret bulk RNA-seq, SMART-seq, and small RNA-seq data using existing and new tools.
- Develop and implement bioinformatics pipelines using mainly Python, Bash, and R scripts and codes.
- Collaborate with wet lab students and postdocs to integrate and visualize computational and experimental data.
- Collaborate with computational biologists in other groups and the Bioinformatic Support Platform to troubleshoot and learn new skills.
- Maintain reproducibility and transparency of analyses and manage scripts using version control systems (e.g., GitHub).
- Present research findings in meetings and publications.
- Participate in manuscript preparation.

- Stay informed with developments in relevant fields and contribute to lab meetings and discussions.

Qualifications:

- A Ph.D. in bioinformatics, computational biology, or a related field.
- Proficiency in English.
- Demonstrated experience with RNA sequencing data analysis and familiarity with common data processing steps (e.g., quality control, adaptor trimming, read mapping, etc.)
- Proficiency in common computational languages and tools for sequencing data analysis (i.e., Python, Bash, R, Bowtie, etc.).
- Knowledge of statistical methods for bioinformatics.
- Strong analytical and problem-solving skills.
- Excellent communication and teamwork abilities.
- Ability to work independently and manage time effectively.

Preferred Qualifications:

- Experience with and knowledge of small RNA-seq data.
- Experience in a collaborative research environment.
- Familiarity with methods to maintain reproducibility and version control systems (e.g., GitHub).

What We Offer:

- A stimulating research environment within the Faculty of Medicine with diverse research topics.
- Access to computational resources (HPC) and facilities (Genomics and Bioinformatics Support platforms).
- Opportunities for scientific growth and professional development.
- Opportunities to work closely with wet lab researchers and other bioinformaticians.
- A young, supportive, and collaborative team.

Application Process:

Please send the following documents to pei-hsuan.wu@unige.ch:

- Cover letter: detail your research experience and interest in the position.
- CV: include a list of publications.
- Contact information for three references.

Application Deadline:

Applications will be reviewed on a rolling basis until the position is filled.

Contact Information:

For inquiries regarding the position, please contact:

Prof. Pei-Hsuan Wu

Email: pei-hsuan.wu@unige.ch

Website: <https://www.unige.ch/medecine/gede/en/research-groups/wu-lab>

Google Scholar: <https://scholar.google.com/citations?user=JOqwP1IAAAAJ&hl=en>

About the lab:

We are fascinated by small RNAs. We are particularly interested in the function and mechanism of small RNAs in the germline and embryos, exploring regulation of RNA stability, RNA selection, paternal RNA function, and PIWI-interacting RNAs. To study these aspects of small RNAs, we use a combination of mouse genetics, high-throughput sequencing, and biochemical and imaging approaches. Successful candidates will analyze sequencing data and develop new tools to study RNA biology.

We encourage applications from all qualified individuals regardless of gender, race, ethnicity, disability, or any other characteristic protected by law.