

# Master's position in Bioinformatics

The **URPP Evolution in Action: From Genomes to Ecosystems** ([evolution.uzh.ch](http://evolution.uzh.ch)) is seeking Masters students for projects in bioinformatics. The URPP Evolution in Action involves multiple research groups in biology, and it plays an important integrative role for the diverse biological disciplines at UZH.

We have several projects available at the interface between computation and biology, which aim to gain insight into biological mechanisms by mining data from labs and literature. These projects involve the analysis of multi-omics data, including DNA methylation, transcriptome, chromatin modifications, and chromatin accessibility in plants. Some projects also involve software development.

We are looking for candidates with programming experience in **R/ Python/ Julia/ Rust** and knowledge of **UNIX**-like platforms. Familiarity with **git** and experience in analyzing high-throughput sequencing data and tool development is advantageous, but not necessary. Applicants with research experience are particularly encouraged to apply. We welcome applicants from a variety of backgrounds, including biology, bioinformatics, mathematics, computer science, physics, or any relevant interdisciplinary field.

The position will be hosted in the research group of **Prof. Ueli Grossniklaus** at the Botanical Garden of the University of Zurich. The student will be directly supervised by **Dr. Deepak Tanwar**, and will join a team of bioinformaticians and biologists who work together on the generation and analysis of experimental data, and tools development. Through this position, students will have the opportunity to learn or improve their skills in version-controlled genomic/epigenomic data analysis, writing efficient code, making publication-ready figures, cluster computing, scientific writing, and presentation skills.

To apply, please send a CV to Deepak Tanwar at [deepak.tanwar@evolution.uzh.ch](mailto:deepak.tanwar@evolution.uzh.ch)

## Projects (non-exhaustive list)

1. **Decoding the Genomic Tapestry:** Pangenome Unveiling with Cutting-edge Visualization Techniques for *Arabidopsis thaliana*
2. Predicting RNA-seq coverage from DNA sequence as a unifying model of gene regulation in *Arabidopsis thaliana*
3. Development of **Methylator** for **Galaxy** platform to analyze DNA methylation data generated from bulk and single-cell protocols