Bachelor project 2024/2025

HPI Hasso Plattner Institut
Digital Engineering • Universität Potsdam

MAX-PLANCK-INSTITUT
FÜR MOLEKULARE GENETIK

MethylWiz - magically making epigenetic analysis accessible and engaging for experimental scientists

This bachelor project aims to develop MethylWiz, an interactive DNA methylation data analysis platform that transforms complex DNA methylation data into stunning, interactive visualizations. This tool will empower experimental scientists to uncover the mysteries of epigenetic changes with ease and precision.

Vision

DNA methylation is an essential epigenetic modification that plays a significant role in regulating gene expression, cellular differentiation, and development. Due to its cell-type specific pattern and disease-specific alterations, DNA methylation is becoming increasingly relevant in biomedical research. However, with an estimated 28 million CpGs scattered throughout the human genome, analyzing and visualizing DNA methylation data presents substantial challenges for experimentalists due to its complexity and the sheer volume of data. This intricate process requires tools to interpret and depict methylation patterns accurately.

A dedicated data analysis platform would immensely aid experimental researchers with little or no computational knowledge by providing intuitive and interactive visualization capabilities and robust analytical tools. Therefore, the aim of this project is to create a user-friendly, no-code data analysis platform for DNA methylation. The primary focus is the statistical representation and quantification of distributions and changes across multiple samples and genomic regions. The application should be interactive and scalable to produce publication-ready figures, report reproducible code, and be flexible enough to allow for interfaces with various specialized tools like the Integrative Genome Viewer or differential-methylation callers.

Magic powers we are looking for

- Knowledge in programming in python/R or strong software development knowledge and ability to transfer to python/R;
- Interest or experience in software implementation using agile development methodology;
- Willingness to interact directly with the project partner;
- Interest in the biological application field (no prior knowledge required);
- Experience statistics and/or machine learning is desirable but not required.

Project partner

Research at the Max Planck Institute for Molecular Genetics (MPIMG) is dedicated to decoding the genome of human beings and other organisms - specifically those layers that trigger diseases when they malfunction. The director and head of the Department of Genome Regulation, Alexander Meissner, and his group aim to decipher why and to which end the epigenetic signature of malignant tumor cells bears remarkable similarities to that of the developing embryo's placenta. They utilize various forms of state-of-the-art sequencing devices, which can decode the entire epigenetic material of a human being within a few days and thereby create terra-bytes of DNA methylation data, which need to be analyzed and visualized to expand our knowledge on how and when cancer arises.

Supervisors from the new chair of Computational Genomics

Zhihan Zhu (zzhu@molgen.mpg.de)
Dr. Sara Hetzel (hetzel@molgen.mpg.de)
Dr. Helene Kretzmer (kretzmer@molgen.mpg.de)

We are at the MPI for Molecular Genetics in Berlin and will join the HPI in October. Please don’t hesitate to email us or set up a meeting!