

## Research Software for DNA Methylation Analyses

DNA methylation analyses represent one of the most prevalent techniques for genome-wide epigenetic characterizations e.g., for diagnoses of brain tumors. Only few companies offer the techniques and services to perform these analyses and they typically store the results in proprietary file formats, opaque to researchers. Despite significant efforts in reverse-engineering the structure of these files, there is no library for compiled languages that offers read/write access for all relevant sections.

We are looking for a summer student who will contribute to our toolkit for efficient analysis of DNA methylation data by pursuing one or multiple of the following goals:

- refactoring our Rust-based idat-crate for read/write operations to support further organisms (especially mouse-genome)
- extending our CI/CD pipeline (adding integration tests, integration with crates.io)
- writing and extending the documentation of the considered file formats

### Group

IT

### Project Category

B5. Computing

### Special Qualifications

The successful applicant should have at least beginner's experience with a statically typed programming language (e.g., C, C++, Rust, Java...) and should be interested in interdisciplinary work.

### DESY Site

Hamburg

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