



The newly funded research unit ***Beyond the exome*** aims to identify, analyze, and predict the disease potential of non-coding DNA variants in patients with rare genetic diseases. The unit is shared between three different Institutions in Berlin that are the Charite University Hospital, the Humboldt University, and the Max Delbrueck Center (MDC) for Molecular Medicine. Our research is centered around the question of how non-coding regulatory mutations and structural variants in the human genome cause disease. For that we have put together a team of 12 Principal Investigators from such diverse fields as Clinical Medicine, Genetics, Biophysics, Cell and Molecular Biology, Bioinformatics, and Machine Learning.

## PhD candidate in BIOINFORMATICS / COMPUTATIONAL GENOMICS

Within the framework of this research unit, a fully funded PhD position in computational genomics is available in our Genome Informatics research group at the Berlin Institute of Health/Charité. The group specializes in **algorithm development for the analysis of high-throughput sequencing data** with a focus on human structural variation. Our aim is to advance the abilities to reliably detect and accurately genotype all types of genomic variation by exploring new types of data and combining algorithmic and statistical approaches. *Beyond the exome* provides the ideal environment to ultimately apply our methods to clinical data. For more information on the project, research unit and Genome Informatics group, please visit our websites at [www.beyond-the-exome.org](http://www.beyond-the-exome.org) and <https://kehrlab.github.io>

### Your area of responsibility:

- Develop and implement novel computational methods for the identification of germline structural variation
- Explore linked read sequencing data for these methods
- Apply your methods to whole-genome sequencing data sets of rare disease patients
- Collaborate with internal and external partners

### Your profile:

- Master's degree in computational biology, bioinformatics, computer science, statistics, or a related field
- Knowledge of sequence analysis algorithms
- Proficiency in a programming language such as C++, Java or Python
- Strong interest in working with genomic data
- Ability to communicate ideas across classic subject boundaries in spoken and written English

**Start date:** November 15<sup>th</sup>, 2019

**Length of employment:** 3 years

**Working time:** 39 hrs per week

**Pay Scale:** E13 (100%) according to collective agreement TVöD VKA-K

Employees are grouped into pay scales according to their qualifications and personal requirements. You can find our collective bargaining agreements (Tarifverträge) here: <https://www.charite.de/en/careers/>

Applications including the application form found at [www.beyond-the-exome.org](http://www.beyond-the-exome.org), a 1-page letter of motivation, CV, reference letters and certificates should be submitted by email to [beyondtheexome@charite.de](mailto:beyondtheexome@charite.de) on August 31<sup>st</sup>, 2019 the latest. For questions about the project and position, please contact [birte.kehr@bihealth.de](mailto:birte.kehr@bihealth.de)