TRON

Bioinformatics Software Developer (m/f/d)

Fulltime - Mainz

We are seeking a motivated **Bioinformatics Software Developer (m/f/d)** to join our **Computational Genomics** unit. We are an interdisciplinary team of scientists, PhD students, and software engineers who develop bioinformatics tools, predictive models, and data analysis pipelines to identify biomarkers and therapeutic targets for personalized immunotherapies against cancer. In close collaboration with multiple teams at TRON, as well as with partners from academia, clinics, and industry, we apply and validate our computational approaches and translate them into clinical practice.

The successful candidate will develop and maintain bioinformatics software and fully reproducible, end-to-end workflows to analyze diverse biological datasets, including genomics and transcriptomics sequencing data from large cohorts of tumor samples.

Your tasks and responsibilities:

- Design, implement, and maintain computational analysis tools and pipelines for high-throughput sequencing data, including WGS, WES, RNA-seq, scRNA-seq, spatial transcriptomics and long-read sequencing.
- Improve in-house bioinformatics pipelines to enhance accuracy, reproducibility, and development lifecycle automation.
- Benchmark and systematically test in-house and public methods with experimental confirmation data
- Build database and predictive AI systems for the discovery of novel therapy targets and biomarkers
- Provide guidance and support to PhD students and scientists on best practices in reproducible data science and high performance compute workflows
- Collaborate closely with multidisciplinary teams of developers, technicians, scientists, and PhD students across multiple projects

What you bring:

- MSc in Bioinformatics, Computer Science, or a related field
- At least two years of professional experience in bioinformatics software development
- Advanced programming skills in Python and Nextflow; experience with R and Snakemake or other workflow languages is a plus
- Proficiency in structured software development practices, including version control, testing, containerization, and CI/CD systems
- Hands-on experience with Linux-based compute clusters, job schedulers, and cloud computing
- Familiarity with next-generation sequencing (NGS) data and related bioinformatics tools is advantageous
- Knowledge of databases and machine learning libraries is a plus

Enthusiasm and curiosity for the diverse activities of our research institute complete your profile.

We offer:

- A dynamic, innovative, and creative research environment
- An open, collegial, and supportive working atmosphere in a respectful organizational culture
- A highly diverse and inclusive workforce
- Access to our GPU-accelerated HPC cluster and laboratories with cutting-edge sequencing technologies
- Performance-based remuneration and other benefits
- Opportunities for personalized professional development
- Convenient access via public transport and car as well as bicycle parking spaces
- The possibility of hybrid working arrangements

TRON is an internationally recognised institute for application-oriented research. We combine the strengths of academic research with the requirements of quality-controlled industrial developments. At TRON, we share a common mission to develop innovative solutions for the immunotherapeutic treatment of cancer, infectious diseases and other serious diseases with high medicinal need for development.

TRON was founded in Mainz in 2010 and works in close cooperation with universities and hospitals as well as with regional, national and international research institutions and pharmaceutical companies.

As part of our team, you will have the opportunity to work at the cutting edge of translational science.

If all this appeals to you, we look forward to getting to know you.

Please send us your complete and informative application documents (cover letter, CV, references) in a single document of max. 5 MB by e-mail to Human Resources at **jobs (at) tron-mainz.de**, Job-ID: 43104-25-01-WAMSC.

For more information, visit our homepage at www.tron-mainz.de and our GitHub page: https://github.com/TRON-Bioinformatics