



Working Student 16h/week (m/w/d)

MSAID is an innovative bioinformatics spin-off from the Technical University of Munich. Our interdisciplinary team specializes in the development of state-of-the-art deep learning and analytics pipelines for high-throughput protein analyses and we are looking for a strong candidate to support our development team.

The precise identification and quantification of proteins is a crucial step in the understanding, diagnosis, and treatment of diseases. Mass spectrometry-based proteomics is a powerful toolbox for the simultaneous analysis of thousands of proteins and represents the go-to technology for biomarker research and drug discovery. However, current data analysis solutions often rely on simple concepts that remained unchanged for decades - a challenge we aim to resolve.

Your contribution

- You will contribute to MSAID's research efforts for deep learning in molecular biology
- You will contribute to the creation of a deep learning-based protein analysis software to aid the understanding, diagnosis, and treatment of diseases
- You will evaluate and integrate the newest machine learning research findings into MSAID's internal machine learning pipelines

Your profile

- Studying Computer Science, Bioinformatics or a related field
- Demonstrated knowledge of scientific Python (numpy, pandas)
- Comfortable with Linux and bash
- Highly motivated, independent learner with curiosity to explore new fields
- Basic knowledge in machine learning, pattern recognition or data science are a plus

Our offer

- Opportunity to apply machine learning to biological and medical data making a real impact
- Environment for continuous professional development
- Young and highly motivated team with a flat hierarchy
- Relaxed startup atmosphere
- Student positions in Munich and Berlin

We look forward to receiving your comprehensive application as a single PDF file including your earliest starting date (to Dr. Martin Frejno): career@msaid.de

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