PhD Position — Computational Genomics Research Group, Institute of Genetic Epidemiology

We are looking for a talented PhD student to join the **Computational Genomics** research group at the Institute of Genetic Epidemiology, Medical University of Innsbruck. This is a fully funded, 4-year position under a FWF-funded project at the intersection of genomics and computational medicine.

Our Research

The Institute of Genetic Epidemiology is a **leading center for Lp(a) research**, bringing together computational genomics, wet-lab, and clinical expertise.

Lipoprotein(a) [Lp(a)] is one of the strongest known genetic risk factors for cardiovascular disease. A large fraction of Lp(a)'s heritability is encoded in a massive variable number tandem repeat (VNTR) region that standard sequencing and analysis methods cannot resolve.

Our group develops **computational tools and statistical methods** to decode these complex genomic regions at scale. We work with large population cohorts, and cloud/HPC infrastructure. We translate computational findings into biological and clinical insights in close collaboration with wet-lab and clinical partners within the institute.

This project will advance the state of the art in VNTR analysis, with direct implications for cardiovascular risk prediction and precision medicine.

Selected publication:

- Di Maio S, Zöscher P, Weissensteiner H, Forer L, Schachtl-Riess JF, Amstler S, Streiter G, Pfurtscheller C, Paulweber B, Kronenberg F, Coassin S, Schönherr S. Resolving intra-repeat variation in medically relevant VNTRs from short-read sequencing data using the cardiovascular risk gene *LPA* as a model. *Genome Biology*, 25:167 (2024). https://doi.org/10.1186/s13059-024-03316-5

What You Will Do

As a PhD student in our group, you will contribute to:

- Develop and apply computational methods to resolve complex VNTR regions in the *LPA* gene and structurally similar loci
- Perform large-scale statistical genetics analyses linking Lp(a) genomics to cardiovascular disease risk across biobank-scale cohorts
- Build, benchmark, and release open-source bioinformatics tools and reproducible analysis pipelines
- Collaborate with wet-lab partners to validate computational findings (wet-lab involvement is flexible and based on your interests)

- Present your work at national and international conferences and contribute to peer-reviewed publications

Candidate Profile

Required:

- Master's degree in molecular medicine, computer science, bioinformatics, computational biology, or a closely related field
- A strong interest in, or ideally prior programming experience with, one or more of the following: command line tools, Python, R, or equivalent.

Advantageous:

- Experience with genomic or multi-omics data analysis
- Familiarity with statistical genetics (GWAS, population genetics)
- Familiarity with cloud or HPC computing environments
- Experience with PCR and/or sequencing in a DNA lab

We value curiosity over a perfect checklist of qualifications.

What We Offer

- **Fully funded 4-year position** (gross salary: €39.649/year, 30 h/week, FWF/MUI scale)
- High-impact research problem with clear clinical relevance
- Active mentorship and structured support toward your PhD milestones
- Access to large-scale genomic datasets and modern HPC and GPU infrastructure
- Budget for conferences
- A collaborative, international lab culture. **English is the working language**
- Supported by the AISCM faculty at MUI, with opportunities to extend your research into AI
- **Innsbruck**, an alpine city with outstanding quality of life and direct rail connections to Munich, Milan, and Zurich

How to Apply

Applications are reviewed on a rolling basis; start date is flexible.

Please send the following documents to Sebastian Schönherr at sebastian.schoenherr@i-med.ac.at:

All application materials should be submitted in English.

1. Cover letter (1 page max) describing your research interests, relevant experience, and why this project excites you
2. CV
3. Contact details of 1–2 referees

Contact

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