LUKAS HEUMOS

RESEARCH SOFTWARE ENGINEER & POSTDOC

Munich, Germany · Orchid· CV · Github · Google Scholar · LinkedIn · Email

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Research software engineer and data scientist focused on user friendly and scalable solutions for single-cell multiomics, biological data management, and electronic health records. Co-founder of the scverse consortium for foundational tools for single-cell omics data.

PROFESSIONAL EXPERIENCE

Research Software Engineer February 2023 – Present

LaminLabs, Munich, Germany | full-time since July 2024

- Working on API and UX of the core open source products including biological data management & data curation (lamindb) and ontologies & knowledge graphs (bionty)
- Leading ontology support, Nextflow integration, ML experiment tracking, and spatial omics support

PhD student & Postdoc January 2021 – present

Helmholtz Munich (Fabian Theis), Munich, Germany | part-time since July 2024

- Focus on single-cell analysis tooling, analysis best practices, and electronic health records.
- 6 first/first shared high impact papers and 10+ co-authorships
    - Led the best practices in single-cell consortium which led to a widely used online book and a publication in *Nature Reviews Genetics*
    - Led the development of the open source framework for exploratory electronic health record analysis termed *ehrapy* was published in *Nature Medicine*
    - Led the development of the scverse framework for perturbation data analysis termed *pertpy*. It is currently in press in *Nature Methods*
- Mentoring 4 PhD students and leading 10 individual students that contribute to my projects.

Co-founder & steering council January 2021 - present

scverse

- Co-founded the scverse consortium that hosts some of the most widely used tools in single-cell analysis such as scanpy and scvi-tools. Grew the core team to > 20 people and the community to more than 1000 members
- Led the successful application into NumFOCUS as a fiscally sponsored project
- Co-organized > 10 hackathons and conferences in Europe and the US
- Leading operations and partnerships with major pharma and hardware companies

Intern November 2020 - December 2020

Boehringer Ingelheim, Biberach, Germany

- Contributed open source code to MegaQC with a focus on usability and security
- Developed internal tooling to validate sample sheets

EDUCATION

Technical University of Munich, Germany 2021 – 2024

PhD in Bioinformatics and machine learning (accepted - defense expected in late 2025)

- Thesis title: “Scalable computational methods for biomedical data analysis”

University of Tübingen, Germany 2015 – 2020

BSc and MSc in Bioinformatics

- Focus on machine learning and omics data analysis

Selected Awards & Honors

WORLD.MINDS member	since 2023
Winner (scverse) of SIB Bioinformatics Innovative Resource Award (10000CHF)	2025
Lindau Nobel Laureate Meetings young scientist	2020 & 2023
Winner of CampusSource open-source software award (10000€)	2022
Bronze, silver, and gold medal in iGEM competitions	2018 – 2020
Invited by NEB to meet Nobel Laureate Richard J. Roberts in Ipswich, USA	2019
Award for exceptional student commitment by the University of Tübingen	2019
9th place among 1000+ teams, German Founders' Prize for Students	2015

Skills & Contributions (Symbol (*) indicates maintainer status)

Technical skills: Python (primary), Nextflow, R, AWS, DevOps, Machine learning
Domain knowledge: Single-cell multiomics, Perturbations, EHR
Open source: scverse (scanpy*, pertpy*), theislab (single-cell-best-practices*, ehrapy*, ehrdata*, hadge*), nf-core (mhcquant), laminlabs (lamindb, bionty*)

Selected Publications (Symbols (*, #) indicate equal contribution)

A full list of publications is available on my Google Scholar profile.

1. **Heumos, L.***, Ehmele, P., Treis, T. *et al.* An open-source framework for end-to-end analysis of electronic health record data. *Nat Med* 30, 3369–3380 (2024). https://doi.org/10.1038/s41591-024-03214-0
2. **Heumos, L.**, Ji Y., May L., et al.: Pertpy: an end-to-end framework for perturbation analysis, bioRxiv (2024), https://doi.org/10.1101/2024.08.04.606516 in press in *Nature Methods*
3. **Heumos, L***., Schaar, A.C*., Lance, C. *et al.* Best practices for single-cell analysis across modalities. *Nat Rev Genet* 24, 550–572 (2023). https://doi.org/10.1038/s41576-023-00586-w
4. Virshup, I*., Bredikhin, D*., **Heumos, L*.** *et al.* The scverse project provides a computational ecosystem for single-cell omics data analysis. *Nat Biotechnol* 41, 604–606 (2023). https://doi.org/10.1038/s41587-023-01733-8