

Maren Hackenberg

Postdoctoral researcher

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Research profile

I develop statistical and machine learning methods for biomedical data, particularly for omics and small, heterogeneous, or longitudinal datasets. My work bridges statistical modeling, deep learning, and biomedical applications and I aim for approaches that are mathematically principled and practically useful. I enjoy collaborating across disciplines and have experience spanning single-cell omics, deep generative models, dynamic modeling, and computational software. My current postdoctoral project extends these ideas to spatial omics, where I work on landmark-informed modelling of tissue structure.

Positions and education

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| Since 05/2026 | Postdoctoral researcher , European Molecular Biology Laboratory (EMBL), Heidelberg, in the Huber group , funded by an EIPOD-LinC Postdoctoral Fellowship. |
| 07/2025-04/2026 | Postdoctoral researcher , Institute of Medical Biometry and Statistics, University of Freiburg, within the DFG-funded Collaborative Research Center SmallData . |
| 05/2020-07/2025 | PhD (Dr. rer. nat.) in Biostatistics awarded by the Faculty of Mathematics and Physics, University of Freiburg. Research conducted at the Institute of Medical Biometry and Statistics, University of Freiburg, within the DFG-funded Research Training Group MeInBio .
Supervisor: Prof. Dr. Harald Binder.
Thesis: <i>Capturing dynamics under misspecification and potential transformation.</i> (Link) |
| 01/2024-08/2024 | Parental leave (child born January 2024). |
| 04/2023-06/2023 | Visiting researcher at the Oslo Centre for Biostatistics and Epidemiology, University of Oslo, Norway. DAAD-funded.
Supervisor: Prof. Dr. Manuela Zucknick. |
| 04/2018-04/2020 | M. Sc. in Mathematics , University of Freiburg, Germany.
Thesis: <i>Temporal dynamics in generative models.</i> (Link) |
| 10/2012-03/2018 | State Examination in Mathematics and Latin (Erstes Staatsexamen fürs Lehramt an Gymnasien), University of Freiburg, Germany.
Thesis: <i>From compact groups to algebra.</i> |

Selected publications

Full list of 20 peer-reviewed papers and six preprints available on my [ORCID record](#) and in the appendix.

*: Equal contribution.

Menger J, Krissmer SM, Kreutz C, Binder H, **Hackenberg M**. mmContext: an open framework for multi-modal contrastive learning of omics and text data. *Bioinformatics*, 2026, published online ahead of issue. doi:10.1093/bioinformatics/btag338  [mengerj/mmcontext](https://github.com/mengerj/mmcontext)

Hackenberg M, Pechmann A, Kreutz C, Kirschner J, Binder H. A statistical approach to latent dynamic modeling with differential equations. *The American Statistician* **80**(1), 89–99, 2026. doi:10.1080/00031305.2025.2539999
 [maren-ha/LatentDynamics.jl](https://github.com/maren-ha/LatentDynamics.jl)

Hackenberg M*, Canal Guitart L*, Backofen R, Binder H. Evaluating discrepancies in dimensionality reduction for time-series single-cell RNA-sequencing data. *Briefings in Bioinformatics* **26**(3), 2025. doi:10.1093/bib/bbaf287
 [laia-cg/scManifoldDynamics](https://github.com/laia-cg/scManifoldDynamics)

Hackenberg M*, Brunn N*, Vogel T, Binder H. Infusing structural assumptions into dimension reduction for single-cell RNA sequencing data to identify small gene sets. *Communications Biology* **8**, 414, 2025. doi:10.1038/s42003-025-07872-9  [NiklasBrunn/BoostingAutoencoder](https://github.com/NiklasBrunn/BoostingAutoencoder)

Hackenberg M, Grodd M, Kreutz C, Fischer M, Esins J, Grabenhenrich L, Karagiannidis C, Binder H. Using differentiable programming for flexible statistical modeling. *The American Statistician* **76**(3), 270-279, 2022. doi:10.1080/00031305.2021.2002189 [maren-ha/DifferentiableProgrammingForStatisticalModeling](#)

Lenz S, **Hackenberg M**, Binder H. The JuliaConnectoR: a functionally-oriented interface for integrating Julia in R. *Journal of Statistical Software* **101**(6), 1-24, 2022. doi:10.18637/jss.v101.i06 [stefan-m-lenz/JuliaConnectoR](#)

Funding and awards

2026-2029	EIPOD-LinC Postdoctoral Fellowship , European Molecular Biology Laboratory. Competitive postdoctoral fellowship for a self-designed interdisciplinary research project, funded by Horizon Europe Marie Skłodowska-Curie Actions COFUND. Project title: <i>Towards quantitative histology and micro-anatomy using mathematical modelling and machine learning on spatial omics</i> .
2026	Dissertation Award of the German Association for Medical Informatics, Biometry and Epidemiology (GMDS) e. V., Section Medical Bioinformatics and Systems Biology
2026	Gustav Adolf Lienert Award of the International Biometric Society, German Region, for an excellent biometric publication.
2026	Outstanding Women in Small Data Award of the CRC <i>SmallData</i> , University of Freiburg
2024-2025	Internal seed funding grant by the CRC <i>SmallData</i> , 50,000€, Co-Project Leader. Project title: <i>Prediction of cell lineage trajectories by integration of small scRNA-seq datasets into a large reference dataset</i> .
2023	Scholarship of the German Academic Exchange Service (Deutscher Akademischer Austauschdienst) for research stay at the University of Oslo with a self-designed project.
2021	Bernd Streitberg Award of the International Biometric Society, German Region, for an excellent master's thesis.
2020	Young Statisticians Award of the International Biometric Society, German Region, for an outstanding conference contribution.
2015-2020	Scholarship of the German Academic Scholarship Foundation (Studienstiftung des deutschen Volkes) for outstanding academic achievements.

Teaching, mentoring and outreach

Since 2021	Mentoring and (co)-supervision of two B.Sc. Mathematics theses, five M.Sc. Mathematics theses and one M.Sc. Epidemiology thesis , as well as internship, research assistant, and PhD projects across biomedical data science. Topics range from single-cell representation learning, foundation models for omics, and spatial transcript localisation to electrophysiological neuron recordings, rare-disease trajectories, neural differential equations, and deep generative models. Several student projects led to student first-author or co-author publications (4) and preprints (2).
Since 02/2021	Regular statistical consulting for members of the Medical Faculty (> 20 projects), contributing to ongoing collaborations and publications in neuropediatrics and immunology.
Since 10/2020	Regular tutorials in medical biometry, epidemiology and statistics (8 tutorials).
2021, 2023	Seminar assistant for the M.Sc. Mathematics seminar "Medical Data Science".
2025	Girls' Day with CRC <i>SmallData</i> : co-designed and co-led a full-day interactive program introducing data-driven biomedicine to local secondary school girls. GitHub
2025	Science Days with CRC <i>SmallData</i> : interactive demonstrations on data science and artificial intelligence.
2015-2018	Teaching assistant at the Mathematical Institute, University of Freiburg, for undergraduate Mathematics lectures in linear algebra and complex analysis (5 tutorials).

Activities in the research system

Since 04/2025	Speaker of the Early Career Working Group of the International Biometric Society, German Region.
11/2022-04/2026	Ombudsperson of the Institute of Medical Biometry and Statistics, University of Freiburg.
10/2021-09/2023	Secretary to the board of the German Association for Medical Informatics, Biometry and Epidemiology (GMDS) e. V.
Since 2022	Peer review for <i>Genome medicine</i> , <i>Scientific reports</i> , <i>BMC Bioinformatics</i> , <i>BMC Medical informatics and decision making</i> .

Selected scientific presentations

Regular presentations at national and international conferences, seminars, summer schools and workshops since 2019. A full list is included in the appendix.

09/2026	ISCB/GMDS 2026 , Freiburg, Germany Award talk: Capturing dynamics under misspecification and potential transformation.
07/2026	EMBL Lautenschläger Summer School , Heidelberg, Germany Summer school talk: How AI is reshaping computational biology.
05/2026	Conference of the Central European Network , Warsaw, Poland Talk: A statistical approach to latent dynamic modeling with differential equations.
12/2025	Advances in Single-Cell Technologies Symposium , Freiburg, Germany Talk: Alignment of single-cell transcriptomics and electrophysiology with foundation model representations across modalities and cells.
09/2024	Conference of the German Association for Medical Informatics, Biometry and Epidemiology (GMDS) , Dresden, Germany Talk: Integrating different measurement instruments in a longitudinal clinical registry using a domain adaptation approach.
11/2022	Seminar of the Dutch region of the International Biometric Society , virtual Invited talk: From dynamic modeling of disease trajectories to single-cell omics: state-of-the-art methods development in Julia.
10/2022	Annual NORBIS Conference , Rosendal, Norway Invited workshop: Differentiable programming for flexible modelling with small data.
11/2021	Young Statisticians Lecture Series , virtual Invited talk: The best of both worlds: combining deep learning and modelling for time-series single-cell RNA-sequencing data.

Open-source software

scVI.jl	Julia package for fitting variational autoencoders to single-cell data using count distributions, based on the Python <code>scvi-tools</code> ecosystem. maren-ha/scVI.jl
Latent Dynamics.jl	Julia package for learning dynamics using a statistical approach based on ODEs in the latent space of a deep learning model. maren-ha/LatentDynamics.jl

Appendix

Full list of peer-reviewed publications

- Menger J, Krissmer SM, Kreutz C, Binder H, **Hackenberg M**. mmContext: an open framework for multi-modal contrastive learning of omics and text data. *Bioinformatics*, 2026, published online ahead of issue. doi:10.1093/bioinformatics/btag338  mengerj/mmcontext
- Brunn N, **Hackenberg M**, Vogel T, Binder H. Sparse dimensionality reduction for analyzing single-cell-resolved interactions. *Bioinformatics Advances* **6**, 1, 2026. doi:10.1093/bioadv/vbag047
 NiklasBrunn/Sparse-dimension-reduction
- Kaufmann MM, **Hackenberg M**, Pargeter WJ, Backofen R, Binder H, Cathomen T. Systematic benchmarking of CRISPR-Cas9 off-target prediction tools reveals limitations and implications for preclinical assessment. *Human Gene Therapy*, 2026, published online ahead of issue. doi:10.1177/10430342261466407
- Herrmann A, Kuhn A, **Hackenberg M**, Matilainen J, Mayer S, Groeschel S, Uhl M, Krägeloh-Mann I, Janzarik WG. Diagnostic clues and pitfalls in pontocerebellar hypoplasia type 2A. *Pediatric Neurology* **178**, 186-194, 2026. doi:10.1016/j.pediatrneurol.2026.02.019
- Meyer T, Meyer R, **Hackenberg M**, Oelke D, Gengenbach L, Rummelt C, Wilcken H, Maas-Bauer K, Wäsch R, Duyster J, Bertz H, Duque-Afonso J, Finke J, Zeiser R, Wehr C. Machine learning-based prediction of one-year mortality after alloHCT identifies the impact of pre-transplant immunity and inflammation. *Frontiers in Immunology* **16**, 2026. doi:10.3389/fimmu.2025.1745873
- Schächter C, **Hackenberg M**, Pfaffenlehner M, Tambe-Ndonfack FB, Schmidt T, Pechmann A, Kirschner J, Hasenauer J, Binder H. Using latent representations to link disjoint longitudinal data for mixed-effects regression. *Statistics in Medicine* **45**(18–19), e70701, 2026. doi:10.1002/sim.70701 [arXiv:2510.25531](https://arxiv.org/abs/2510.25531)
- Hackenberg M***, Canal Guitart L*, Backofen R, Binder H. Evaluating discrepancies in dimensionality reduction for time-series single-cell RNA-sequencing data. *Briefings in Bioinformatics* **26**(3), 2025. doi:10.1093/bib/bbaf287
- Hackenberg M***, Brunn N*, Vogel T, Binder H. Infusing structural assumptions into dimension reduction for single-cell RNA sequencing data to identify small gene sets. *Communications Biology* **8**, 414, 2025. doi:10.1038/s42003-025-07872-9  NiklasBrunn/BoostingAutoencoder
- Schächter C, **Hackenberg M**, Treppner M, Raum H, Bödecker J, Binder H. scSpecies: enhancement of network architecture alignment in comparative single-cell studies. *Genome Biology* **26**, 397. doi:10.1186/s13059-025-03866-2, 2025.  cschaech/scspecies_package
- Hackenberg M**, Pechmann A, Kreutz C, Kirschner J, Binder H. A statistical approach to latent dynamic modeling with differential equations. *The American Statistician* **80**(1), 89–99, 2026. doi:10.1080/00031305.2025.2539999
 maren-ha/LatentDynamics.jl
- Kuhn A, **Hackenberg M**, Klauser AL, Herrmann A, Matilainen J, Mayer S, Frölich S, Krägeloh-Mann I, Groeschel S, Janzarik WG. Constructed growth charts and nutrition for pontocerebellar hypoplasia type 2A. *Developmental Medicine & Child Neurology* **68**, 82–90, 2026. doi:10.1111/dmcn.16394
- Pretzel P, Herrmann A, Kuhn A, Klauser AL, Matilainen J, Kellner J, **Hackenberg M**, Mayer S, Laugwitz L, Uhl M, Groeschel S, Janzarik W. Brain morphometry and psychomotor development in children with PCH2A. *European Journal of Pediatric Neurology*, 2025. doi:10.1016/j.ejpn.2025.04.004
- Hackenberg M**, Pfaffenlehner M, Behrens M, Pechmann A, Kirschner J, Binder H. Investigating a domain adaptation approach for integrating different measurement instruments in a longitudinal clinical registry. *Biometrical Journal*, 2024. doi:10.1002/bimj.70023  maren-ha/IntegratingMeasurementInstruments
- Farhadyar K, Bonofiglio F, **Hackenberg M**, Zöller D, Binder H. Combining propensity score methods with variational autoencoders for generating synthetic data in presence of latent subgroups. *BMC Medical Research Methodology* **24**(1), 198, 2024. doi:10.1186/s12874-024-02327-x.

Brombacher E*, **Hackenberg M***, Kreutz C, Binder H, Treppner M. The performance of deep generative models for learning joint embeddings of single-cell multi-omics data. *Frontiers in Molecular Biosciences* **9**, 2022. doi:10.3389/fmolb.2022.962644  [maren-ha/multiomics_dgms](#)

Hackenberg M, Harms P, Pfaffenlehner M, Pechmann A, Kirschner JB, Schmidt T, Binder H. Deep dynamic modeling with just two time points: Can we still allow for individual trajectories?, *Biometrical Journal* **64**(8), 1426-1445, 2022. doi:10.1002/bimj.202000366  [maren-ha/DeepDynamicModelingWithJust2TimePoints](#)

Lenz S, **Hackenberg M**, Binder H. The JuliaConnectoR: a functionally-oriented interface for integrating Julia in R. *Journal of Statistical Software* **101**(6), 1-24, 2022. doi:10.18637/jss.v101.i06  [stefan-m-lenz/JuliaConnectoR](#)

Grodd M, Refisch L, Lorenz F, Fischer M, Lottes M, **Hackenberg M**, Kreutz C, Grabenhenrich L, Binder H, Wolkewitz M. Prognosemodelle zur Steuerung von intensivmedizinischen COVID-19-Kapazitäten in Deutschland (*Forecasting models to guide intensive care COVID-19 capacities in Germany*). *Medizinische Klinik - Intensivmedizin und Notfallmedizin*, 2022. doi:10.1007/s00063-022-00903-x

Hackenberg M, Grodd M, Kreutz C, Fischer M, Esins J, Grabenhenrich L, Karagiannidis C, Binder H. Using differentiable programming for flexible statistical modeling. *The American Statistician* **76**(3), 270-279, 2022. doi:10.1080/00031305.2021.2002189  [maren-ha/DifferentiableProgrammingForStatisticalModeling](#)

Hess M, **Hackenberg M**, Binder H. Exploring generative deep learning for omics data using log-linear models. *Bioinformatics* **36**(20), 5045-5053, 2020. doi:10.1093/bioinformatics/btaa623  [ssehztrom/Exploring-generative-deep-learning-for-omics-data-by-using-log-linear-models](#)

Full list of preprints

Brunn N, Guitart LC, Farhadyar K, Fullio CL, Kailer J, Vogel T, **Hackenberg M**, Binder H. Mapping spatial cell-cell communication programs by tailoring chains of cells for transformer neural networks. [bioRxiv:2026.03.18.712664](#), 2026. *Under revision*.  [NiklasBrunn/ScCChain.jl](#)

Kabus F, **Hackenberg M**, Hindel J, Cholvin T, Kilias A, Brox T, Valada A, Bartos M, Binder H. Embedding interpretable ℓ_1 -regression into neural networks for uncovering temporal structure in cell imaging. [arXiv:2603.02899](#), 2026. *Under review*.

Farhadyar K, **Hackenberg M**, Ahrens K, Schenk C, Kollmann B, Tüscher O, Lieb K, Plichta MM, Reif A, Kalisch R, Wolkewitz M, Hess M, Binder H. A statistical perspective on transformers for small longitudinal cohort data. [arXiv:2602.16914](#), 2026. *Revision submitted*.  [kianaf/MiniTransformer](#)

Krissmer SM, Menger J, Rollin J, Vogel TM, Binder H, **Hackenberg M**. Adding layers of information to scRNA-seq data using pre-trained language models. [bioRxiv:2025.08.23.671699](#), 2025. *Under revision*.  [MariaKrissmer/alias](#)

Hackenberg M, Connor SG, Kabus F, Brawner J, Markham E, Hardalupas M, Chowdhury A, Backofen R, Köttgen A, Rohde A, Binder N, Binder H, the Collaborative Research Center 1597 Small Data. Small Data Explainer - The impact of small data methods in everyday life. [arXiv:2507.11773](#), 2025. *Revision submitted*. *In collaboration with the Royal Society; contributing to the [Disability Technology report](#)*.

Eichin F*, **Hackenberg M***, Broichhagen C, Kilias A, Schmoranz J, Bartos M, Binder H. Incorporating structural knowledge into unsupervised deep learning for two-photon imaging data. 2021. [bioRxiv:2021.05.18.443587v2](#)  [incorporating-structural-knowledge-into-unsupervised-deep-learning-for-two-photon-imaging-data](#)

Full list of conference presentations and workshops

09/2026	ISCB/GMDS 2026 , Freiburg, Germany Award talk: Capturing dynamics under misspecification and potential transformation.
07/2026	EMBL Lautenschlager Summer School , Heidelberg, Germany Summer school talk: How AI is reshaping computational biology.
05/2026	Conference of the Central European Network , Warsaw, Poland Talk: A statistical approach to latent dynamic modeling with differential equations.
12/2025	Advances in Single-Cell Technologies Symposium , Freiburg, Germany Talk: Alignment of single-cell transcriptomics and electrophysiology with foundation model representations across modalities and cells.
03/2025	DAGStat Conference , Berlin, Germany Talk: A statistical approach to latent dynamic modeling with differential equations.
09/2024	Conference of the German Association for Medical Informatics, Biometry and Epidemiology (GMDS) , Dresden, Germany Talk: Integrating different measurement instruments in a longitudinal clinical registry using a domain adaptation approach.
06/2024	Summer school of the Data2Health research college , Koblenz, Germany Talk: Deep learning with small data in biomedicine.
09/2023	Conference of the GMDS , Heilbronn, Germany Talk: Dimension reduction for temporal patterns in time-series single-cell RNA-seq data.
09/2023	Conference of the Central European Network and the International Biometric Society, German Region (IBS-DR) , Basel, Switzerland Talk: Dimension reduction for temporal patterns in time-series single-cell RNA-seq data.
08/2023	Conference of the International Society for Clinical Biostatistics (ISCB) , Milan, Italy Talk: Latent dynamic modeling with differential equations for individual disease trajectories.
07/2023	Workshop Statistical Computing , Guenzburg, Germany Talk: Combining componentwise boosting with neural networks for structuring latent representations of single-cell RNA-sequencing data.
11/2022	Seminar of the Dutch region of the International Biometric Society , virtual Invited talk: From dynamic modelling of disease trajectories to single-cell omics: state-of-the-art methods development in Julia.
10/2022	Annual NORBIS Conference , Rosendal, Norway (GitHub) Invited workshop: Differentiable programming for flexible modelling with small data.
09/2022	German Conference on Bioinformatics , Halle an der Saale, Germany Workshop: Interpretable deep learning for single-cell data analysis. (GitHub)
08/2022	Conference of the ISCB , Newcastle, UK Talk: Julia – a pragmatic approach to scientific computing. Poster: Combining deep learning and dynamic modelling to infer disease trajectories of patients with SMA.
07/2022	Workshop Statistical Computing , Guenzburg, Germany Talk: Differentiable programming for flexible gradient-based optimisation of statistical models: an exemplary modelling challenge.
03/2022	Conference of the Deutsche Arbeitsgemeinschaft Statistik , Hamburg, Germany Talk: Combining deep learning and dynamic modelling for time-series single-cell RNA-sequencing data.
11/2021	Young Statisticians Lecture Series , virtual Invited talk: The best of both worlds: combining deep learning and modelling for time-series single-cell RNA-sequencing data.

- 10/2021 **Workshop Biometrical Aspects of Genome Analysis**, virtual
Talk: Using variational autoencoders to identify metabolite interactions and their genetic associations.
- 09/2021 **Conference of the GMDS**, virtual
Talk: Inferring developmental trajectories and optimised dimension reduction from time-series single-cell RNA-seq data.
- 07/2021 **European Conference on Computational Biology**, virtual
Poster: Inferring developmental trajectories and optimised dimension reduction from time-series single-cell RNA-seq data.
- 05/2021 **Stuttgart Julia Meetup**, virtual
Talk: DiffEqFlux.jl: combining deep learning and dynamic modelling in Julia.
- 03/2021 **Biometric Colloquium**, virtual
Talks: Temporal dynamics in generative models (*Bernd-Streitberg Award*); Differentiable programming for flexible statistical modelling.
- 09/2020 **Conference of the GMDS and the Central European Network of the International Biometrical Society (CEN-IBS)**, virtual
Talk: Temporal dynamics in generative models (*Young Statisticians Award*).
- 08/2020 **Conference of the International Society for Clinical Biostatistics (ISCB)**, virtual
Talk: Latent dynamic modelling with just two time points: can we still get individual trajectories?
- 03/2019 **Conference of the Deutsche Arbeitsgemeinschaft Statistik**, Munich, Germany
Poster: Julia as a data scientist's working environment: a deep learning case study.