

Prof. Dr. Harald Binder

Institution: Institute of Medical Biometry and Statistics (IMBI)
Faculty of Medicine and Medical Center, University of Freiburg

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Position: Full Professor (W3) and Director of the Institute

Academic education including academic degrees

Scientific graduation

2011 Habilitation, Medical Biometry and Statistics, University of Freiburg,
Advisor: Prof. Dr. Martin Schumacher

2006 Promotion/Ph.D., Statistics, Ludwig-Maximilians-Universität München,
Supervisor: Prof. Dr. Gerhard Tutz

2001 – 2006 Ph.D. studies, Statistics, Ludwig-Maximilians-Universität München

2000 – 2001 M.A., Mathematical Behavioral Sciences, University of California Irvine

1996 – 2000 Diploma, Psychology, University of Regensburg

Employment

2017 – now Professor for Medical Biometry and Director, Institute of Medical Biometry and
Statistics, University of Freiburg, Germany

2011 – 2017 Professor for Medical Biometry, University Medical Center Mainz, Germany

2006 – 2011 Research Associate, Institute for Medical Biometry and Medical Informatics,
Medical Center, University of Freiburg, Germany

2001 – 2006 Researcher, Department of Psychiatry, University of Regensburg, Germany

Other activities, awards and honours

2021 – now President of the German Association for Medical Informatics, Biometry and
Epidemiology (GMDS) e.V.

2019 – now Co-Speaker of the Profile Field “Data Analysis and Artificial Intelligence” of the
University of Freiburg

2018 – 2019 Area Head Medical Bioinformatics and Systems Biology of the GMDS e.V.

2017 – now Member of the Directorate of the Freiburg Center for Data Analysis and Modeling

Most important publications

1. 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* 2022;962644.
2. 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* 2022;76(3):270–9.
3. Kuruc F, Binder H, Hess M. Stratified neural networks in a time-to-event setting. *Brief Bioinform* 2022;23(1):1–11.
4. Treppner M, Binder H, Hess M. Interpretable generative deep learning: an illustration with single cell gene expression data. *Human Genetics* 2022;141:1481–98.
5. Nußberger J, Boesel F, Lenz S, Binder H, Hess M. Synthetic observations from deep generative models and binary omics data with limited sample size. *Brief Bioinform* 2021;22(4):1–12.
6. Treppner M, Salas-Bastos A, Hess M, Lenz S, Vogel T, and Binder H. Synthetic single cell RNA sequencing data from small pilot studies using deep generative models. *Scientific Reports* 2021;11:9403.
7. Hess M, Hackenberg M, and Binder H. Exploring generative deep learning for omics data by using log-linear models. *Bioinformatics* 2020;36:5045–53.
8. Marini F, Linke J, and Binder H. ideal: an R/Bioconductor package for interactive differential expression analysis. *BMC Bioinformatics* 2020;21:565.
9. Hess M, Lenz S, Blätte TJ, Bullinger L, and Binder H. Partitioned learning of deep Boltzmann machines for SNP data. *Bioinformatics* 2017;33:3173–80.
10. Poplawski A and Binder H. Feasibility of sample size calculation for RNA-seq studies. *Briefings in Bioinformatics* 2017;19:713–20.