Curriculum Vitae Martin Treppner

Personal Details

Name:	Martin Treppner, PhD
Address:	Bernhardstr. 2,79098 Freiburg
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Day of Birth:	05. September 1990
Place of Birth:	Berlin, Germany
ORCID ID:	0000-0002-7284-2085

Education

since 04/2022	**Institute of Medical Biometry and Statistics, University of Freiburg, Germany** Postdoctoral Researcher - Machine learning
03/2018 - 03/2022	**Institute of Medical Biometry and Statistics, University of Freiburg, Germany** PhD - Machine learning; Grade: Summa cum laude ***Thesis title:*** *Deep Generative Models for Designing Single-Cell RNA-Sequencing Experiments*
10/2015 - 01/2016	**Exchange semester: Middle East Technical University, Ankara, Turkey** Master of Science
04/2015 - 10/2017	**Otto-von-Guericke-University, Magdeburg, Germany** Master of Science - Statistics; Grade: 1.7
09/2013 - 12/2013	**Exchange semester: Sookmyung Women's University, Seoul, South Korea** Bachelor of Science
10/2011 - 03/2015	**European-University Viadrina, Frankfurt (Oder), Germany** Bachelor of Science - Economics; Grade: 1.5

Experience

since 09/2022	**Head of the working group for single-cell data,** German Association for Medical Informatics, Biometry and Epidemiology (GMDS)
11/2021	**Co-Founder: Freiburg Young Scientist AI Network** https://freiburg-ai.github.io/
09/2021 - 08/2022	**Deputy head of the project group for single-cell data** German Association for Medical Informatics, Biometry and Epidemiology (GMDS)
04/2017 - 09/2017	**Master thesis: Max-Planck-Institute for evolutionary anthropology** Department of Genetics

08/2016 - 10/2016	**Internship: Max-Planck-Institute for evolutionary anthropology** Department of Genetics
08/2014 - 10/2014	**Internship: Federal Ministry of Finance Germany**
01/2014 - 03/2014	**Internship: Korea Economic Research Institute**

Teaching and Mentoring

09/2022	**Workshop: Interpretable Deep Learning for Single-Cell Data Analysis, German Conference on Bioinformatics 2022** https://github.com/ssehztirom/GCB-2022-WS1
04/2017 - 09/2017	**Head of Coordinators: Querschnittsbereich 1: Epidemiologie, Medizinische Biometrie und Medizinische Informatik**
since 2018	**Querschnittsbereich 1: Epidemiologie, Medizinische Biometrie und Medizinische Informatik** 9 tutorials
10/2016 - 02/2017	**Tutor: Institute for mathematical stochastics** Subject: Exploratory data analysis and probability
04/2016 - 07/2016	**Tutor: Institute for mathematical stochastics** Subject: Stochastics for engineers

IT Skills

Specialist	**R, Julia, macOS**
Advanced	**Shell, LaTeX, Microsoft Office, git**
Basic	**Python, Affinity Designer**

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Publications

- **Treppner, M.**, Haug, S., Köttgen, A., & Binder, H. (2022). Designing Single Cell RNA-Sequencing Experiments for Learning Latent Representations. bioRxiv. https://doi.org/10.1101/2022.07.08.499284.

- Brombacher, E., Hackenberg, M., Kreutz, C., Binder, H., & **Treppner, M.** (2022). The performance of deep generative models for learning joint embeddings of single-cell multi-omics data. bioRxiv. https://doi.org/10.1101/2022.06.06.494951.

- **Treppner, M.**, Binder, H. & Hess, M. (2022) Interpretable generative deep learning: an illustration with single cell gene expression data. Hum Genet, 1-18. https://doi.org/10.1007/s00439-021-02417-6.

- **Treppner, M.**, Salas-Bastos, A., Hess, M., Lenz, S., Vogel, T., & Binder, H. (2021). Synthetic single cell RNA sequencing data from small pilot studies using deep generative models. Sci Rep, 11(1), 1-11. https://doi.org/10.1038/s41598-021-88875-4.

- Appiah, B., Fullio, C., Haffner, C., Zeis, P., **Treppner, M.**, Bovio, PP., Cheffer, A., Bertani, I., Binder, H., Gruen, D., Kalebic, N., Taverna, E., & Vogel, T. (2022) DOT1L activity affects cell lineage progression in the developing brain by controlling metabolic programs. bioRxiv. https://doi.org/10.1101/2022.04.08.487591.

- Strecker, C., Krafft, A. J., Kaufhold, L., Hüllebrandt, M., **Treppner, M.**, Ludwig, U., Köber, G., Hennemuth, A., Hennig, J., & Harloff, A. (2021) Carotid geometry and wall shear stress independently predict increased wall thickness – a longitudinal 3D MRI study in high-risk patients. Frontiers in Cardiovascular Medicine, 1420. https://doi.org/10.3389/fcvm.2021.723860.

- Salas-Bastos, A., **Treppner, M.**, Herman, J. S., Koutsogiannis, D., Binder, H., Stadler, M. B., Grün, D., & Vogel, T. (2021). Single-cell transcriptomic resolution of stem cells and their developmental trajectories in the hippocampus reveals epigenetic control of cell state perseverance. bioRxiv. https://doi.org/10.1101/2021.07.21.452775.

- Frings, L., Henninger, F., **Treppner, M.**, Köber, G., Boeker, M., & Meyer, P. T. (2021). DAT SPECT Predicts Survival in Patients Assessed for Differential Diagnosis of Dementia. Journal of Alzheimer's Disease, 1-6. https://doi.org/10.3233/JAD-210062.

- Frings, L., Henninger, F., **Treppner, M.**, Köber, G., Boeker, M., Hellwig, S., Buchert, R., & Meyer, P. T. (2020). [123I] FP-CIT SPECT in Clinically Uncertain Parkinsonism Predicts Survival: A Data-Driven Analysis. Journal of Parkinson's Disease, 1-9. https://doi.org/10.3233/JPD-202214.

Scientific presentations

- **DAGStat Conference, 2022**: *Talk*
  Title: *scVIDE: Single-Cell Variational Inference for Designing Experiments*

- **42nd Annual Conference of the International Society for Clinical Biostatistics (ISCB), 2021**: *Talk*
  Title: *Statistical Power for Single Cell Representations*

- **67th Biometric Colloquium, 2021**: *Talk*
  Title: *Statistical power for cell identity detection in deep generative models*

- **Single Cell Biology, 2020**: *Poster*
  Title: *Generating Synthetic scRNA-Seq Data from Small Pilot Studies using Deep Learning*

- **German Conference on Bioinformatics (GCB), 2020**: *Talk*
  Title: *Determining Sample Size for Detection of Cell Identities in scRNA-seq Experiments*

- **Workshop on Computational Models in Biology and Medicine, 2020**: *Talk*
  Title: *Generating Synthetic scRNA-Seq Data from Small Pilot Studies using Deep Learning*

- **DAGStat Conference, 2019**: *Poster*
  Title: *Deep Boltzmann Machines for Simulating Single-Cell RNA-seq Data*

- **Workshop on Computational Models in Biology and Medicine, 2018**: *Talk*
  Title: *Simulating Single-Cell RNA-seq Data using Negative Binomial Deep Boltzmann Machines*

- **63. GMDS-Jahrestagung, 2018**: *Talk*
  Title: *Modeling Activity Tracker Data Using Deep Boltzmann Machines*

- **European Conference on Computational Biology (ECCB), 2018**: *Poster*
  Title: *Boltzmann Encoded Adversarial Machines for Simulating Single Cell RNA-seq Data*