Martin **Meinel**

PHD CANDIDATE · MACHINE LEARNING FOR HEALTH

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Profile

Computational biologist passionate about advancing precision medicine through machine learning and statistical genetics, with particular expertise in inflammatory skin diseases. During my Ph.D., I developed SAFARI, a biomarker detection framework that identified a sparse gene signature distinguishing early Mycosis Fungoides (MF) patients from those with benign inflammatory skin diseases. This work was patented and is currently being leveraged by Dermagnostix GmbH in their emerging diagnostic tool "LymphX". Furthermore, through collaboration with the Chan Zuckerberg Initiative, I combine statistical genetics with multiple instance learning to pinpoint cellular contexts where genes act as disease drivers, revealing mechanistic insights that inform therapeutic target discovery.

Education

PhD Candidate in Computational Biology
Munich, Germany

HELMHOLTZ CENTER MUNICH | TECHNICAL UNIVERSITY MUNICH | LMU MUNICH | CHAN ZUCKERBERG INITIATIVE RESIDENCY
Oct 2021 - Present

- Supervised by Dr. Michael Menden, Dr. Natalie Garzorz-Stark & Dr. Francesco Paolo Casale

M. Sc. in Data Engineering & Analytics
Munich, Germany

TECHNICAL UNIVERSITY OF MUNICH
Oct 2018 - Nov 2020

B. Sc. in Applied Computer Science
Bayreuth, Germany

UNIVERSITY OF BAYREUTH
Oct 2014 - Oct 2017

Research Experience

Patented work on diagnostic biomarkers for Mycosis Fungoides
Helmholtz Center Munich

PHD STUDENT
Feb 2021 - Present

- Developed SAFARI, a **model-agnostic computational framework** for sparse, robust biomarker extraction for **underrepresented conditions**, specifically designed to resolve the diagnostic ambiguity of early Mycosis Fungoides (MF).
- Identified a minimal 6-gene biomarker panel concordantly differentially expressed between early MF and benign inflammatory skin diseases across both **bulk RNA-seq discovery and qPCR development cohorts**.
- Optimized the biomarker panel down to a **2-gene classifier** to maximize cost-effectiveness and clinical utility, achieving an exceptional diagnostic performance (**Sensitivity = 91%, Specificity = 94%**) in the qPCR development cohort.
- Proved clinical generalizability and robustness by validating the classifier across **7 independent international medical centers**, essential for real-world applications.
- Demonstrated superior predictive value for early MF detection compared to standard-of-care clinical methods (histopathology assessment and clinical view) in longitudinal patient cohorts.

Revealing cellular contexts for early-stage target discovery via attention-based single-cell Mendelian Randomization
Helmholtz Center Munich, CZI Residency

PHD STUDENT
October 2023- Present

- Leveraged single-cell Mendelian randomization (scMR) on Eczema to identify **disease-driving genes at cell-type resolution**.
- Validated translational relevance by using scMR-derived scores to predict established therapeutic targets (Open Targets), achieving a **78% ROC AUC**.
- Conceptualized and integrated multiple instance learning within single-cell genetics to **pinpoint cellular contexts beyond cell-type level**, maximizing genotype-expression associations.
- Demonstrated that the identified cellular contexts capture key immune mechanisms, including **PD1-signaling** and **Costimulation by the CD28 family**, validating mechanistic relevance for **targeted therapeutic intervention**.
- Designed and implemented a rigorous Bayesian model comparison (Wakefield ABFs), providing the strongest evidence (posterior probability, PP, > 0.70) that the sub-cell-state model is the most plausible causal mechanism for the *IL18RAP* locus.

Efficient implementation of deep convolutional Gaussian Processes
TU Munich

RESEARCHER
Jan 2020 - Nov 2020

- Implemented deep convolutional Gaussian processes as an alternative to convolutional neural networks (CNNs), to obtain uncertainty estimations for predictions on the MNIST dataset, aimed at enhancing computation speed (thesis available [here]).
- Conducted a thorough evaluation of multiple imputation algorithms to determine their efficiency in approximating the kernel matrix and achieving optimal performance on test data.
- Accomplished a substantial **40% reduction in training time** by using only 20% of the original training data while maintaining a high classification accuracy of **86%** on the MNIST dataset (compared to 98% accuracy with the entire training set).

Publications

- Garger, D., **Meinel, M.**, Dietl, T., Hillig, C., Garzorz-Stark, N., Eyerich, K., de Angelis, M., Eyerich, S., Menden M.P. (2023).The impact of the cardio-vascular component and somatic mutations on ageing. *Aging Cell,* https://doi.org/10.1111/acel.13957.
- Fischer, F., Doll, A., Uereyener, D., Roenneberg, S., Hillig, C., Weber, L., Hackert, V., **Meinel, M.**, Farnoud, A., Seiringer, P., et al. (2023). Gene expression based molecular test as diagnostic aid for the differential diagnosis of psoriasis and eczema in formalin fixed and paraffin embedded tissue, microbiopsies and tape strips. *The Journal of Investigative Dermatology*, S0022-202X(23)00156-2. https://doi.org/10.1016/j.jid.2023.02.015.
- Farnoud, A., Ohnmacht, A. J., **Meinel, M.**, & Menden, M. P. (2022). Can artificial intelligence accelerate preclinical drug discovery and precision medicine?. *Expert opinion on drug discovery*, 17(7), 661–665. https://www.tandfonline.com/doi/epdf/10.1080/17460441.2022.2090540.

Working experience

Opitz Consulting GmbH
Munich, Germany

SOFTWARE ENGINEER WORKING STUDENT   *Oct 2019 - Oct 2020*

- Built a docker skeleton for Apache Zeppelin, enabling users to start a docker container running Apache Zeppelin on openShift with one click.
- Created a web application for Allianz IDS GmbH, allowing employees to track, assign, and rate investment orders within the department.

REHAU Industries SE & Co. KG
Bayreuth, Germany

SOFTWARE ENGINEER WORKING STUDENT   *Nov 2017 - Mar 2019*

- Developed ALEXA skill for the 2018 FRONTALE window exhibition, demonstrating several features of the smart window.
- Implemented a web app for Medi Bayreuth to track player performance and fatigue for injury prevention.
- Developed an openHAB plugin to connect sensor-based garden watering systems with other IoT devices.

Skills

Genomic Technologies	Bulk RNA-sequencing analysis (DESeq2, edgeR, fgsea, clusterProfiler)
	Single-Cell RNA-seq analysis & integration (scanpy, Harmony, scCODA)
	Statistical Genetics (Mendelian Randomization, GWAS, HEIDI, Colocalization, PLINK)
Programming & Data Analysis	Python (NumPy, Pandas, scikit-learn, pyTorch), R, Bash
High-Performance & Cloud Computing	hydra, Slurm, Docker, Git, AWS
Languages	English (Fluent), German (Native)

Honors & Awards

Patents

2023	Registered patent "Differential Diagnosis of Mycosis Fungoides: Method and System" leveraging SAFARI to discover biomarkers distinguishing early MF from Eczema & Psoriasis.	*Munich, Germany*

Invited speaker session

2023	Presented "Biocomputational Analysis of Big Data" to researchers in dermatology at the EADV-ESDR Summer Research Workshop: Big Data and Translation in Dermatology.	*Freiburg, Germany*

Oral presentations

2025	Oral presentation at **Neurips AI4D3 workshop** of how modeling intra-celltype heterogeneity in single-cell MR enhances early-stage drug target discovery.	*San Diego, USA*
2025	Oral presentation at **EORTC CLTG** about the identification and clinical translation of biomarkers in early MF.	*Athens, Greece*

Poster presentations

2025	Highlight poster with oral presentation on cell-state-aware single-cell Mendelian Randomization at **RECOMB Genetics**.	*Seoul, KOR*
2023	Presented the SAFARI framework for rare disease biomarker discovery at the **ML for Health** workshop.	*New Orleans, USA*
2025	Presented work on cell-state-aware single-cell Mendelian Randomization at the Helmholtz AI conference.	*Karlsruhe, Germany*
2025	Presented classifier development and validation results for early MF diagnosis from psoriasis and eczema.	*Freiburg, Germany*

Academic services

2025	External reviewer for the field of Mendelian Randomization for the **RECOMB** Conference.	*Seoul, KOR*
2024	Reviewer for the **Machine Learning for Health** workshop.	*Vancouver, CA*
2025	Supervisor of three students for their master's theses and internships.	*Munich, Germany*
2024	Teaching assistant for Computational Modeling for System Genetics.	*TU Munich*