

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 diseases. During my Ph.D., I developed SAFARI, a biomarker detection framework that revealed a sparse gene signature distinguishing early Mycosis Fungoides (MF) patients from those with benign inflammatory skin diseases. This work was patented and is leveraged by Dermagnostix in their emerging diagnostic tool "LymphX". Within the collaboration with the Chan Zuckerberg Initiative, I combine statistical genetics with multiple instance learning to pinpoint cellular contexts in which genes act as disease drivers, revealing mechanistic insights that inform therapeutic target identification.

Education

PhD Candidate in Computational Biology

HELMHOLTZ CENTER MUNICH | TECHNICAL UNIVERSITY MUNICH | LMU MUNICH | CHAN ZUCKERBERG INSTITUTE RESIDENCY

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

Munich, Germany

Oct 2021 - Present

M. Sc. in Data Engineering & Analytics

TECHNICAL UNIVERSITY OF MUNICH

- GPA: 1.7

Munich, Germany

Oct 2018 - Nov 2020

B. Sc. in Applied Computer Science

UNIVERSITY OF BAYREUTH

- GPA: 2.1

Bayreuth, Germany

Oct 2014 - Oct 2017

Research Experience

Development of a classifier for diagnosis of early Mycosis Fungoides

Helmholtz Center Munich

PHD STUDENT

Feb 2021 - Present

- Created SAFARI, a model-agnostic framework designed to identify a **sparse, robust** and **highly-expressed** gene signature for **rare** diseases, for clinical translation through direct application to gene expression data.
- Identified a minimal 6-gene biomarker panel consistently differentially expressed between early mycosis fungoides and benign inflammatory skin diseases across both bulk RNA-seq discovery and qPCR validation cohorts.
- Engineered data augmentation strategy to address measurement variability in housekeeping gene normalization, improving model robustness for clinical implementation.
- Demonstrated exceptional diagnostic performance with **90.4%** sensitivity and **92.2%** specificity using only two genes in qPCR validation, enabling cost-effective clinical deployment.
- Achieved superior early-stage mycosis fungoides detection compared to standard clinical methods (histopathology assessment and T-cell receptor clonality analysis) in a longitudinal patient cohort.

Leveraging single-cell RNA-seq to identify relevant cell contexts of putative causal genes in Eczema.

Helmholtz Center Munich, CZI
Residency

PHD STUDENT

October 2023- Present

- Applied single-cell Mendelian Randomization to eczema for the first time, identifying causal genes driving disease pathogenesis at unprecedented cellular resolution.
- Validated findings by demonstrating 78% ROC AUC overlap between identified causal genes and established therapeutic targets in Open Targets database, confirming clinical relevance.
- Integrated multiple-instance learning with statistical genetics to optimize cellular context identification, enabling more precise gene-disease association mapping than traditional approaches.
- Achieved superior performance in genetic association testing through learned cell-type weights, outperforming standard mean expression methods across cell populations.
- Identified disease-active cellular states with pathway characterization and biomarker profiles, providing mechanistic insights for targeted therapeutic intervention in immune diseases.

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 cardiovascular component and somatic mutations on ageing. *Aging Cell* <https://doi.org/10.1111/ace.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

Feb 2018 - 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 assess player fatigue after training and track performance during regular fitness checks, contributing to injury prevention.

REHAU Industries SE & Co. KG

Rehau, Germany

SOFTWARE ENGINEER INTERN

Nov 2017 - Jan 2018

- Developed a plugin for the open-source smart home system openHAB, enabling users to connect their automated sensor-based garden watering system with other IoT devices.

Skills

Programming	Python, R, Java, bash
Libraries / Frameworks	NumPy, Pandas, PyTorch, scikit-learn, scanpy, plink, DESeq2, edgeR, Spring
Tools / Platforms	AWS, Docker, Git, SQL, LaTeX, slurm, hydra
Languages	German, English

Honors & Awards

2025	Poster presentation at DKTK meeting , Presented classifier development and validation results for early MF diagnosis from psoriasis and eczema.	Freiburg, Germany
2025	Poster presentation at Helmholtz AI conference , Presented my work about single-cell Mendelian Randomization at the Helmholtz AI conference.	Karlsruhe, Germany
2025	Highlight poster at RECOMB Genetics , My work about single-cell Mendelian Randomization was awarded as a highlight poster with a presentation.	Seoul, KOR
2024	CZI Residency , Work on single-cell Mendelian Randomization was selected to be supported from Chan Zuckerberg Initiative.	Redwood, USA
2025	RECOMB Reviewer , Served as an invited external Reviewer for the field of Mendelian Randomization for the RECOMB Conference 2025.	Seoul, KOR
2024	ML4H Reviewer , Served as a reviewer for the “Machine Learning for Health” workshop 2024.	Vancouver, CA
2023	ML4H Workshop Presentation , Presented SAFARI framework for rare disease biomarker discovery at the “Machine Learning for Health” workshop.	New Orleans, US
2023	Inventor , Registered a patent titled “Differential Diagnosis of Mycosis Fungoides: Method and System” for discovering biomarkers distinguishing Eczema & Psoriasis from cutaneous T-cell lymphoma using SAFARI.	Munich, Germany
2023	Invited speaker , Delivered a presentation on “Biocomputational Analysis of Big Data” at the EADV-ESDR Summer Research Workshop: Big Data and Translation in Dermatology.	Freiburg, Germany
2023	Participant , Selected as a participant for the OxML - MLxHealth summer school.	Oxford, UK
2021	MuDS PhD candidate , Selected as a member of the Munich School for Data Science (MuDS).	Munich, Germany