

Martin Meinel

PHD CANDIDATE · MACHINE LEARNING FOR HEALTH

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Profile

Computational biologist with expertise in statistical genetics, single-cell RNA-seq analysis, and diagnostic biomarker discovery. Developed SAFARI, a biomarker discovery framework that identified gene signatures distinguishing early Mycosis Fungoides from benign inflammatory diseases. This work was **patented** and is now integrated into the RUO diagnostic tool **"Erysk"** by **Dermagnostix GmbH**. As a **Chan Zuckerberg Initiative resident**, developed attention-based methods integrating machine learning with statistical genetics to identify cell subgroups where genetic regulation is strongest, advancing precision therapeutic targeting. This work was selected for **oral presentation** at the NeurIPS 2025 AI4D3 workshop on virtual cells and drug discovery.

Education

PhD Candidate in Computational Biology

HELMHOLTZ CENTER MUNICH | LMU MUNICH | CHAN ZUCKERBERG INITIATIVE 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

Munich, Germany

Oct 2018 - Nov 2020

B. Sc. in Applied Computer Science

UNIVERSITY OF BAYREUTH

Bayreuth, Germany

Oct 2014 - Oct 2017

Research Experience

Patented work on diagnostic biomarkers for Mycosis Fungoides

PHD STUDENT

Helmholtz Munich

Oct 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 a strong diagnostic performance (**Sensitivity = 91%, Specificity = 94%**) in the qPCR development cohort.
- Proved clinical generalizability and robustness by validating the classifier across **8 independent international medical centers**.
- Demonstrated superior predictive value for early MF detection compared to standard-of-care clinical methods (histopathology assessment and clinical view) in longitudinal patient cohorts.
- Integration of single-cell expression data sets revealed disease-specific elevated expression: **LCK in T cells (MF) vs. HOMER1 in keratinocytes (eczema, psoriasis)**.
- Integrated spatial transcriptomic data sets (10X Visium) **confirmed disease-specific marker expression** in the skin.

Causal Inference for early-stage target discovery (FocusMR)

PHD STUDENT

Helmholtz Munich, CZI Residency

Oct 2023 - Present

- Built **FocusMR**, an attention-based single-cell Mendelian Randomization framework to resolve causal disease genes and the cellular context where their regulation is strongest.
- Applied to eczema GWAS and OneK1K single-cell genetics data, prioritized 34 candidate causal genes at cell-type level with **four loci mapping to fine-grained sub-cell-states**.
- Recovered known biology as validation with *PRKCQ-AS1* in naive/central memory CD8⁺ T cells, enriched for PD-1 signaling and CD28 costimulation.
- Discovered a *TAPBPL*-defined CD4⁺ T cell state undetectable by standard subtype annotation, revealing a distributed Th17/Th22-polarized program via FocusMR's learned cell weights.
- Developed **Bayesian validation strategy** to assess robustness of identified cell states across independent data.

Efficient implementation of deep convolutional Gaussian Processes

RESEARCHER

TU Munich

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/acer.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>.

[†] symbolizes shared first authorship.

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 assess investment orders within the department.

REHAU Industries SE & Co. KG

Bayreuth, Germany

SOFTWARE ENGINEER WORKING STUDENT

Nov 2017 - Mar 2019

- Developed an 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	Single-Cell RNA-seq analysis & integration (scanpy, Harmony, scVI, scANVI, scCODA)
	Spatial transcriptomics analysis & integration (scanpy, scANVI, 10X Visium)
	Statistical Genetics (Mendelian Randomization, GWAS, HEIDI, Colocalization, PLINK)
	Bulk RNA-sequencing analysis (DESeq2, edgeR, fgsea, clusterProfiler)
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

Patent

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

2025	Oral presentation at NeurIPS AI4D3 workshop on how to identify cellular contexts of causal genes enhancing 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

Chan Zuckerberg Initiative Residency

2024	Selected for CZI residency for developing cell-context-aware target discovery methods to identify cellular contexts of causal genes for precise therapeutic targeting.	Redwood, USA
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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
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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 at DKTK meeting.	Freiburg, Germany