Matthias Meyer-Bender

Computational Biologist

Blumenstr. 3
69115 Heidelberg
(+49) 176 3221 5730
matthias.meyerbender@embl.de

WORK EXPERIENCE

European Molecular Biology Laboratory (EMBL) & Heidelberg University, Heidelberg — *PhD Candidate*

OCTOBER 2022 – TODAY

Method development for spatial omics data preprocessing and analysis. Analysis of large data sets to gain insights into hematological malignancies.

Helmholtz Center, Munich — *Student Research Assistant*

FEBRUARY 2021 – AUGUST 2022

Researched drug repositioning approaches for combating tuberculosis by applying statistical and machine learning methods. Applied network inference and node embedding methods to elucidate molecular mechanisms underlying acute-on-chronic liver failure.

Gene Center, Munich — *Student Research Assistant*

APRIL 2019 - APRIL 2022

Developed a pipeline to process high-throughput loss-of-function screens and established an interactive platform enabling downstream analyses. Contributed to the discovery of a novel cellular pathway involving the protein DELE1.

EDUCATION

Technical University of Munich & Ludwig-Maximilians-University, Munich — *MSc, Bioinformatics*

2020 - 2022

Thesis: “Modeling Acute-On-Chronic Liver Failure in Mice Using Multi-Modal Data”

Supervised by: Dr. Christoph Ogris, Prof. Dr. Dr. Fabian Theis

University of Copenhagen, Copenhagen

2020–2021

Exchange Semester during Master’s Studies

Technical University of Munich & Ludwig-Maximilians-University, Munich — *BSc, Bioinformatics*

2017 - 2020

Thesis: “Machine Learning Prediction of Longitudinal Antibiotics Impact on Tuberculosis Quantified with Mass Spectrometry Data”

Supervised by: Dr. Michael Menden, Prof. Dr. Dr. Fabian Theis

TECHNICAL SKILLS

Python

Snakemake

Slurm

R

Bash

Java

SQL

LANGUAGES

German – *Native*

English – *Fluent*

French – *Basic*

PUBLICATIONS

Meyer-Bender, M., Voehringer, H., Schniederjohann, C., Koziel, S., Chung, E., Popova, E., ... & Huber, W. (2025). Spatialproteomics: an interoperable toolbox for analyzing highly multiplexed fluorescence image data. Accepted in Nature Methods, 2025-12.

Fitzgerald, D., Roider, T., Baertsch, M. A., Kibler, A., Horlova, A., Chung, E., …, **Meyer-Bender, M.**, … & Huber, W. (2023). A single-cell multi-omic and spatial atlas of b-cell lymphomas reveals differentiation drives intratumor heterogeneity. bioRxiv, 2023-11.

Fessler, E., Eckl, E. M., Schmitt, S., Mancilla, I. A., **Meyer-Bender, M. F.**, Hanf, M., ... & Jae, L. T. (2020). A pathway coordinated by DELE1 relays mitochondrial stress to the cytosol. Nature, 579(7799), 433-437.

CONFERENCE PRESENTATIONS AND POSTERS

Poster: Spatialproteomics: an interoperable toolbox for analyzing highly multiplexed fluorescence image data. Presented at ISMB/ECCB 2025 (Liverpool, England), German Conference on Computational Biology (GCB) 2025 (Düsseldorf, Germany), Spatial Biology: The Melting Pot (ESSB) 2025 (Heidelberg, Germany), AI in One Health 2025 (Heidelberg, Germany), EMBL PhD Symposium 2024 (Heidelberg, Germany)

Flash Talk: Spatialproteomics: an interoperable toolbox for analyzing highly multiplexed fluorescence image data. Presented at scverse Conference 2024

SOFTWARE, TRAINING AND COMMUNITY ENGAGEMENT

Lead developer: SegTraQ
Python toolkit for quantitative and visual quality control of segmentation and transcript assignment in spatial omics.
GitHub: github.com/LazDaria/SegTraQ

Lead developer: Spatialproteomics
Interoperable toolbox for analyzing highly multiplexed fluorescence image data.
GitHub: github.com/sagar87/spatialproteomics

Contributor: scverse ecosystem
Spatial Proteomics Working Group, spatialdata, spatialdata_plot
GitHub: https://github.com/scverse/spatialdata-plot

Workshop instructor: Ukrainian Biological Data Science School (2024, 2025) (Uzhhorod, Ukraine)
2024: Skin cancer detection with convolutional neural networks
2025: Predicting protein localization from images with transfer learning

Workshop instructor: ECCB 2024 (Turku, Finland)
Spatialproteomics hands-on workshop

Hackathon contributor: Scverse Hackathon 2025 (Paris, France)
Developed multi-sample comparison features for spatial data

Hackathon contributor: CytoData 2025 (Berlin, Germany)
Explored Cell Painting profiles for scientific discovery