

Markus Daniel Hoffmann, Ph.D.

Current position

2024 – present

Post-doctoral fellow
Section of Genetics and Physiology, LCMB/NIDDK/NIH,
Bethesda, Maryland 20892

Professional experience

2023 – 2024

Pre-doctoral fellow
Graduate Partnerships Program (GPP)
Host: Section of Genetics and Physiology,
LCMB/NIDDK/NIH, Bethesda, Maryland 20892
Partner: TUM School of Life Sciences, Technical University
of Munich, Munich, Germany

2020 – 2023

Pre-doctoral fellow
Department of Experimental Bioinformatics
Technical University of Munich
Freising, Germany
Completion of Doctoral degree: Nov., 27th, 2023

2018 – 2020

Student research assistant
Department of Experimental Bioinformatics
Technical University of Munich
Freising, Germany

2010 – 2013

Vocational trainee for applied informatics
[Professional Academy of Passau](#) and [msg-systems](#)
Passau, Germany

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Education

2020 – 2023	Lecturer and mentor certificate training for higher education PROLehre , Technical University of Munich Munich, Germany
2018 – 2020	Master of Science student in Bioinformatics Technical University of Munich Ludwig-Maximilians-Universität München Munich, Germany
2015 – 2018	Bachelor of Science student in Bioinformatics Technical University of Munich Ludwig-Maximilians-Universität München Munich, Germany
2013 – 2015	High school senior student Vocational High School of Passau Passau, Germany

Selection of scientific presentations

Oral presentations

2024	<i>TF-Prioritizer: a Java pipeline to prioritize condition-specific transcription factors</i> Systems Biology Georgetown University, Washington D.C., USA
2023	<i>Network medicine-based epistasis detection in complex diseases: ready for quantum computing</i> Bioinformatics Seminar Series Georgetown University, Washington D.C., USA
2023	<i>Exploring the exciting world of circRNAs</i> Bioinformatics Seminar Series Georgetown University, Washington D.C., USA
2022	<i>Network Medicine: Key Pathway Miner and BiCoN</i> Bioinformatics Seminar Series, Department of Biochemistry and Molecular Biology, Syddansk Universitet Odense, Denmark
2021	<i>Simulation, modeling, and network-guided detection of epistasis</i> ISMB/ECCB 2021 online conference

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Poster presentations

- 2024 *Immune deconvolution of data originating from various SARS-CoV-2 variants*
Food and Drug Administration (FDA) symposium
Rockville, Maryland, United States of America
- 2023 *circRNA-sponging: a pipeline for extensive analysis of circRNA expression and their role in miRNA sponging*
NIH Research Festival 2023
Bethesda, Maryland, United States of America
- 2023 *Immune deconvolution of data originating from various SARS-CoV-2 variants*
19TH ANNUAL NIH GRADUATE STUDENT RESEARCH SYMPOSIUM
Bethesda, Maryland, United States of America
- 2022 *spongEffects: ceRNA modules offer patient-specific insights into the miRNA regulatory landscape*
[ISCB Rocky 2022](#)
Aspen, Colorado, United States of America
- 2022 *spongEffects: ceRNA modules offer patient-specific insights into the miRNA regulatory landscape*
[ECCB2022](#)
Sitges, Spain
- 2022 *TF-Prioritizer: a Java pipeline to prioritize condition-specific transcription factors*
[TUM IAS](#) - General Assembly 2022
Munich, Germany

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Service to the scientific community

2024	Executive Chair-Elect NIDDK Fellowship Advisory Board (FAB) Bethesda, Maryland, United States of America
2024	19 th Annual NIDDK Scientific Conference 2024 Oral presentation judge Bethesda, Maryland, United States of America
2023	Member of the NIDDK Postdoctoral Recruitment Committee National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) Bethesda, Maryland, United States of America
2023	Co-chair of the speakers' committee NIDDK Fellowship Advisory Board (FAB) Bethesda, Maryland, United States of America
2023	18 th Annual NIDDK Scientific Conference 2023 Poster judge Bethesda, Maryland, United States of America
2023	FY2023 End of Year Postbac Procurement Poster judge Bethesda, Maryland, United States of America
2022 – 2024	Reviewer duty in the Journals BMC Genomics, Bioinformatics Advances, and Bioinformatics
2022 – 2023	Genetoberfest 2023 Head conference organizer Munich, Germany

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Teaching experience

2022	Introduction to Bioinformatics – Beginner level Lecturer at the Technical University of Munich Munich, Germany
2022	Introduction to Bioinformatics – Expert level Lecturer at the Technical University of Munich Munich, Germany
2022	Systems BioMedicine Lecturer at the Technical University of Munich Munich, Germany
2021	Introduction to Bioinformatics – Beginner level Lecturer at the Technical University of Munich Munich, Germany
2020	Bioinformatics for Ph.D. students Lecturer at the Technical University of Munich Munich, Germany
2020	Programming in R for Ph.D. students Lecturer at the Technical University of Munich Munich, Germany

Mentoring experience

- 1. Carmen Robinson (2023 – 2024; Technical University of Munich)**
Student research assistant: *Investigation of evolutionary conserved circRNAs*
- 2. Fabian Boehm (2023 – 2024; Technical University of Munich)**
Student research assistant: *Benchmarking of circRNAs detection tools*
- 3. Lisa Blankenhagen (2023 – 20234 Technical University of Munich)**
Bachelor's thesis: *Investigating the ENCODE database for active transcription Factors in human and mouse*
- 4. Sylvie Baier (2020 – 2024; Technical University of Munich)**
Bachelor's thesis: *An automatic and interactive platform for interpreting epistasis candidate SNP sets identified by NeEDL*
Student research assistant: *Network medicine-based epistasis detection in complex diseases: ready for quantum computing*
- 5. Julian Poschenrieder (2020 – 2024; Technical University of Munich)**
Bachelor's thesis: *Benchmarking of GenEpiSeeker against state-of-the-art tools for epistasis detection*
Student research assistant: *Network medicine-based epistasis detection in complex diseases: ready for quantum computing*
- 6. Nico Trummer (2021 – 2024; Technical University of Munich)**
Student research assistant: *TF-Prioritizer: a Java pipeline to prioritize condition-specific transcription factors*
Bachelor's thesis: *circRNAs in estrogen signaling and breast cancer biology*
- 7. Leon Schwartz (2021 – 2024; Technical University of Munich)**
Bachelor's thesis: *Analysis of circRNAs in Testicular Germ Cell Tumor*
Student research assistant: *Development of the circRNAs-sponging pipeline*
Master internship: *INSPECT: an automated pipeline to prioritize condition-relevant interactions of transcription factors and cis-regulatory elements to target genes*
Master internship: *Alternative splicing-aware analysis of competing endogenous RNA effects for SPONGEdb 2.0*
- 8. Lina-Liv Willruth (2021 – 2024; Technical University of Munich)**
Bachelor's thesis: *Immune deconvolution and BCR/TCR analysis of data originating from various SARS-Cov-2 variants*
Master internship: *Immune deconvolution and BCR/TCR analysis of data originating from various SARS-CoV-2 variants*
- 9. Norman Roggendorf (2021 – 2024; Technical University of Munich)**
Bachelor's thesis: *Investigating the IHEC Integrative Analysis collection for active transcription factors in specific cell or tissue types*
Student research assistant: *spongEffects: ceRNA modules offer patient-specific insights into the miRNA regulatory landscape*
- 10. Daniel Lochert (2022 – 2024; Technical University of Munich)**
Student research assistant: *Computationally analysis data from SETB1 knock out T-Cells*

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11. Leon Hafner (2022 – 2024; Technical University of Munich)

Master internship: *Alternative splicing-aware analysis of competing endogenous RNA effects for SPONGEdb 2.0*

Student research assistant: *INSPECT: an automated pipeline to prioritize condition-relevant interactions of transcription factors and cis-regulatory elements to target genes*

12. Lena Hackl (2022 – 2024; University of Hamburg)

Ph.D. candidate: *Mentoring of project leadership and student guidance skills*

13. Shreeti Chhatrala (2023; Georgetown University)

Summer Internship: *Identify SNPs that destroy GAS motifs*

14. Alexander Fastner (2022 – 2024; Technical University of Munich)

Master internship: *Alternative splicing-aware analysis of competing endogenous RNA effects for SPONGEdb 2.0*

15. Christian Hoffmann (2022 – 2024; Technical University of Munich)

Master internship: *Alternative splicing-aware analysis of competing endogenous RNA effects for SPONGEdb 2.0*

16. Vivienne Nahrstedt (2022 – 2024; Technical University of Munich)

Master internship: *Alternative splicing-aware analysis of competing endogenous RNA effects for SPONGEdb 2.0*

17. Korbinian Pürckhauer (2022 – 2024; Technical University of Munich)

Master internship: *Alternative splicing-aware analysis of competing endogenous RNA effects for SPONGEdb 2.0*

18. David Wagemann (2022 – 2024; Technical University of Munich)

Master internship: *Alternative splicing-aware analysis of competing endogenous RNA effects for SPONGEdb 2.0*

19. Johannes Veihelmann (2022; Technical University of Munich)

Bachelor's thesis: *Community detection methods for defining ceRNA modules*

20. Evelyn Scheibling (2020 – 2021; Technical University of Munich)

Master internship: *EpiJson - a tool for efficient input file format creation for the epistasis detection tool GenEpiSeeker*

Leadership experience

- 2020-2024 *Network medicine-based epistasis detection in complex diseases: ready for quantum computing*
Project leader of 50 team members
- 2023 [*Leading with Emotional Intelligence*](#) (FAES)
Bethesda, Maryland, United States of America
- 2023 [*Personal Leadership Development*](#) (FAES)
Bethesda, Maryland, United States of America
- 2021 [*Leadership and personality course*](#) (Technical University of Munich)
Munich, Germany

Bibliography

[ORCID](#)

[Google Scholar](#)

h-index	4	publications	8
citations	38	publications under review	5

† Corresponding author * Shared-first author
AI AI-based paper **DB** Database-based paper

1. **Hoffmann, M.**^{†,*,AI,DB}, Poschenrieder, J. M., Incudini, M., Baier, S., Fitz, A., Maier, A., Hartung, M., Hoffmann, C., Trummer, N., Adamowicz, K., Picciani, M., Scheibling, E., Harl, M. V., Lesch, I., Frey, H., Kayser, S., Wissenberg, P., Schwartz, L., Hafner, L., ... Blumenthal, D. B. (2023). Network medicine-based epistasis detection in complex diseases: ready for quantum computing. medRxiv : The Preprint Server for Health Sciences. <https://doi.org/10.1101/2023.11.07.23298205>
[PMCID: PMC10705612](#)
2. **Hoffmann, M.**^{†,*}, Willruth, L.-L., Dietrich, A., Lee, H. K., Knabl, L., Trummer, N., Baumbach, J., Furth, P. A., Hennighausen, L., & List, M. (2024). Blood transcriptomics analysis offers insights into variant-specific immune response to SARS-CoV-2. Scientific Reports, 14(1), 1–11. [PMCID: PMC10837437](#)
3. Hecker, D., Lauber, M., Behjati Ardakani, F., Ashrafiyan, S., Manz, Q., Kersting, J., **Hoffmann, M.**, Schulz, M. H., & List, M. (2023). Computational tools for inferring transcription factor activity. Proteomics, e2200462. [DOI:10.1002/pmic.202200462](https://doi.org/10.1002/pmic.202200462)
4. **Hoffmann, M.**^{†,*,AI}, Schwartz, L., Ciora, O.-A., Trummer, N., Willruth, L.-L., Jankowski, J., Lee, H. K., Baumbach, J., Furth, P. A., Hennighausen, L., & List, M. (2023). circRNA-sponging: a pipeline for extensive analysis of circRNA expression and their role in miRNA sponging. Bioinformatics Advances, 3(1), vbad093. [PMCID: PMC10359604](#)
5. **Hoffmann, M.**^{†,*,AI}, Trummer, N., Schwartz, L., Jankowski, J., Lee, H. K., Willruth, L.-L., Lazareva, O., Yuan, K., Baumgarten, N., Schmidt, F., Baumbach, J., Schulz, M. H., Blumenthal, D. B., Hennighausen, L., & List, M. (2023). TF-Prioritizer: a Java pipeline to prioritize condition-specific transcription factors. GigaScience, 12, giad026. [PMCID: PMC10155229](#)
6. **Boniolo, F., Hoffmann, M.**^{†,*,AI}, Roggendorf, N., Tercan, B., Baumbach, J., Castro, M. A. A., Robertson, A. G., Saur, D., & List, M. (2023). spongEffects: ceRNA modules offer patient-specific insights into the miRNA regulatory landscape. Bioinformatics, 39(5). <https://doi.org/10.1093/bioinformatics/btad276>. [PMCID: PMC10220456](#)
7. Hernández-Lorenzo, L., **Hoffmann, M.**^{AI}, Scheibling, E., List, M., Matías-Guiu, J. A., & Ayala, J. L. (2022). On the limits of graph neural networks for the early diagnosis of Alzheimer’s disease. Scientific Reports, 12(1), 17632. [PMCID: PMC9587223](#)
8. **Hoffmann, M.**^{*,DB}, Pachel, E., Hartung, M., Stiegler, V., Baumbach, J., Schulz, M. H., & List, M. (2021). SPONGEdb: a pan-cancer resource for competing endogenous RNA interactions. NAR Cancer, 3(1), zcaa042. [PMCID: PMC8210024](#)
9. Blumenthal, D. B., Baumbach, J., **Hoffmann, M.**, Kacprowski, T., & List, M. (2020). A framework for modeling epistatic interaction. Bioinformatics. <https://doi.org/10.1093/bioinformatics/btaa990>. [PubMed ID: 33252645](#)