

# Michael Scherer

## Curriculum Vitae

Dr. Michael Scherer  
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### Personal Details

Date of Birth 01/October/1992  
Place of Birth St. Wendel, Germany

### Professional Background

2024

**Group Leader in Computational Biology**, German Cancer Research Center DKFZ - Division of Cancer Epigenomics, Heidelberg, Germany.

2021

2024

**DFG Postdoctoral Fellow (since 01.04.2022)**, Centre for Genomic Regulation - Department of Bioinformatics and Genomics, Barcelona, Spain.

2021

2024

**Postdoctoral Researcher (since 12.04.2021)**, Centre for Genomic Regulation - Department of Bioinformatics and Genomics, Barcelona, Spain.

2021

2021

**Research Technician (01.02.2021-11.04.2021)**, Centre for Genomic Regulation - Department of Bioinformatics and Genomics, Barcelona, Spain.

### Educational Background

2016

2020

**PhD Candidate Computational Biology**, Max-Planck-Institute for Informatics - Department of Computational Biology & Applied Algorithmics and Department of Genetic/Epigenetics - Saarland University, Saarbrücken, Germany.

2014

2016

**Master Studies Computational Biology**, Saarland University, Germany.

2011

2014

2011

**Bachelor Studies Computational Biology**, Saarland University, Germany.

2011

**Abitur**, Cusanus Gymnasium, St. Wendel, Germany.

### Theses

**PhD Thesis** Computational Solutions for Addressing Heterogeneity in DNA Methylation Data, Supervisors: Prof. Dr. Dr. Thomas Lengauer and Prof. Dr. Jörn Walter, Date of Colloquium: March 30th, 2021, Final grade: Magna cum laude

**MSc Thesis** Dissecting DNA Methylation in Human Aging, Supervisor: Prof. Dr. Dr. Thomas Lengauer, Final Grade: 1.3

**BSc Thesis** Extension of the ABC<sup>2</sup> database by DNA-protein interactions, Supervisor: Prof. Dr. Volkhard Helms, Final Grade: 1.6

### Research Interests

Bioinformatics & Computational Biology

- Computational Epigenomics
- Single-Cell Data Analysis
- Statistical Learning
- Cancer Epigenomics

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## Publications

- Scherer, M.<sup>†</sup>, Singh, I.<sup>†</sup>, Braun, M.<sup>†</sup>, Szu-Tu, C.<sup>†</sup>, et al. (2025). Clonal tracing with somatic epimutations reveals dynamics of blood ageing. *Nature*, 643, 478-487. doi: 10.1038/s41586-025-09041-8
- Bianchi, A.<sup>†</sup>, Scherer, M.<sup>†</sup> et al. (2022). scTAM-seq enables targeted high-confidence analysis of DNA methylation in single cells. *Genome Biology*, 23, 229 doi: 10.1186/s13059-022-02796-7
- Scherer, M. et al. (2021). Identification of tissue-specific and common methylation quantitative trait loci in healthy individuals using MAGAR. *Epigenetics and Chromatin*, 14, 44 doi: 10.1186/s13072-021-00415-6
- Filipinski, K.<sup>†</sup>, Scherer, M.<sup>†</sup>, Zeiner, K.<sup>†</sup>, et al. (2021). DNA methylation-based prediction of response to immune checkpoint inhibition in metastatic melanoma. *Journal For ImmunoTherapy of Cancer*, 9, 7, doi: 10.1136/jitc-2020-002226.
- Scherer, M.<sup>†</sup>, Schmidt, F.<sup>†</sup>, Lazareva, O.<sup>†</sup>, et al. (2021). Machine learning for deciphering cell heterogeneity and gene regulation. *Nature Computational Science*, 1, 183-191, doi: 10.1038/s43588-021-00038-7. (Review article)
- Scherer, M., et al. (2020). Reference-free deconvolution, visualization and interpretation of complex DNA methylation data using DecompPipeline, MeDeCom and FactorViz. *Nature Protocols*, 15, 3240-3263, doi: 10.1038/s41596-020-0369-6.
- Scherer, M., et al. (2020). Quantitative Comparison of Within-Sample Heterogeneity Scores for DNA Methylation Data. *Nucleic Acids Research*, 48(8), e46, doi: 10.1093/nar/gkaa120.
- Müller, F.<sup>†</sup>, Scherer, M.<sup>†</sup>, Assenov, Y.<sup>†</sup>, Lutsik, P.<sup>†</sup>, et al. (2019). RnBeads 2.0: comprehensive analysis of DNA methylation data. *Genome Biology*, 20(1), 55, doi: 10.1186/s13059-019-1664-9.

<sup>†</sup> Joint first authors

### Contributing author publications

- Sollier, E., Riedel, A., ..., Scherer, M., ..., Plass, C. (2025). Enhancer hijacking discovery in acute myeloid leukemia by pyjacker identifies MNX1 activation via deletion 7q. *Blood Cancer Discovery*. <https://doi.org/10.1158/2643-3230.BCD-24-0278>
- Karpova, D., Huerga Enabo, H., ..., Scherer, M., et al. (2025) Clonal Hematopoiesis Landscape in Frequent Blood Donors. *Blood*. doi: 10.1182/blood.2024027999
- Kelly, K., Scherer, M., et al. (2024) EpiCHAOS: a metric to quantify epigenomic heterogeneity in single-cell data. *Genome Biology*, 25, 305. doi: 10.1186/s13059-024-03446-w
- Sollier, E., Heilmann, J., Gerhauser, C., Scherer, M., Plass, C., Lutsik, P. (2024). Figeno: multi-region genomic figures with long-read support. *Bioinformatics*, 40(6), 2024.04.22.590500. <https://doi.org/10.1093/bioinformatics/btad120>
- Jaramillo, S., Scherer, M., et al. (2024). Late-onset NPM1 mutation in a MYC-amplified relapsed / refractory acute myeloid leukemia patient treated with gemtuzumab ozogamicin and glasdegib. *Haematologica*. doi: 10.3324/haematol.2023.284922
- Maji, R., ... Scherer, M., et al. (2023). Alterations in the hepatocyte epigenetic landscape in steatosis. *Epigenetics and Chromatin*, 16, 30, doi: 10.1186/s13072-023-00504-8
- Beneyto-Calabuig, S., ... Scherer, M., et al. (2023). Clonally resolved single-cell multi-omics identifies routes of cellular differentiation in acute myeloid leukemia. *Cell Stem Cell*, 30, 5, doi: 10.1016/j.stem.2023.04.001
- Mishra, N., ... Scherer, M., et al. (2022). Longitudinal multi-omics analysis identifies early blood-based predictors of anti-TNF therapy response in inflammatory bowel disease. *Genome medicine*, 14, 110. doi: 10.1186/s13073-022-01112-z
- Mattonet, K., ... Scherer, M., et al. (2022). Prenatal exposure to endocrine disrupting chemicals is associated with altered DNA methylation in cord blood. *Epigenetics*, 17, 9. doi: 10.1080/15592294.2021.1975917
- Tierling, S., ... Scherer, M., et al. (2022). Bisulfite profiling of the MGMT promoter and comparison with routine testing in glioblastoma diagnostics. *Clinical epigenetics*, 14, 26. doi: 10.1186/s13148-022-01244-4
- Decamps, C., ... Scherer, M., et al. (2020). Guidelines for cell-type heterogeneity quantification based on a comparative analysis of reference-free DNA methylation deconvolution software. *BMC Bioinformatics*, 21(1), 16. doi: 10.1186/s12859-019-3307-2
- Handl, L., Jalali, A., Scherer, M., et al. (2019). Weighted elastic net for unsupervised domain adaptation with application to age prediction from DNA methylation data. *Bioinformatics*, 35(14), doi: 10.1093/bioinformatics/btz338.

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## Presentations

- Invited talks
- Somatic epimutations enable single-cell lineage tracing in native human cells, *Single Cell Genomics Day*, Virtual, 2025
  - Reference-free deconvolution of complex DNA methylation data - a detailed protocol, *Health Data Challenge (2nd edition)*, Aussois, France, 2019
- Conference talks
- Quantitative comparison of within-sample heterogeneity scores for DNA methylation data, *German Conference on Bioinformatics (GCB)*, Frankfurt, Germany, 2020
  - DNA methylation jointly encodes clonal identity and cell state in single cells, *Innovations in Single-Cell Omics (ISCO)*, Barcelona, Spain, 2024
- Conference flash talks
- RnBeads 2018 - comprehensive analysis of DNA methylation data, *Conference on Intelligent Systems in Molecular Biology (ISMB)*, Chicago, USA, 2018
  - Comprehensive pipeline for processing, deconvolution and visualization of complex DNA methylation data, *Student Council Symposium at ISMB*, Basel, Switzerland, 2019

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## Teaching

- ST24 & ST25 Data Analysis Course, Molecular Biotechnology, Heidelberg University
- ST24 & ST25 Seminar Vortragstechniken, Molecular Biotechnology, Heidelberg University
- ST24 & ST25 Introduction into DNA methylation data analysis, Major "Cancer Biology", Heidelberg University
- May 2019 German Network for Bioinformatics Infrastructure (de.NBI) course: DNA Methylation: From Design to Discovery
- WT 18/19 & WT 19/20 The Principles of Epigenetics and Epigenomics - a practical course on epigenomic data processing, Prof. Dr. Jörn Walter, Saarland University
- WT 18/19 The Elements of Statistical Learning, Prof. Dr. Tobias Marschall and Dr. Jilles Vreeken, Saarland University
- WT 17/18 The Elements of Statistical Learning, Prof. Dr. Dr. Thomas Lengauer, Saarland University

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## Awards

- Fellowship DKFZ Dr. Rurainski Fellowship awarded from 2024-2026
- Fellowship DFG Walter Benjamin Postdoctoral Fellowship awarded from 2022-2024
- Honor's Degree Master's Studies, Final Grade: 1.3
- Outstanding poster award Student Council Symposium at ISMB, July 2018

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## Languages

- German Native
- English Fluent
- Spanish, French Basic

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## Skills

- Programming R,  $\LaTeX$ , Python, Bash
- Tools GitHub, Inkscape/GIMP, Overleaf
- Other skills Communication, Organization, Writing, Teaching