

Michael Scherer

Curriculum Vitae

Dr. Michael Scherer
Carrer Valencia 29, 5-3
08015 Barcelona, Catalunya, Spain
☎ +49 176 61 968 965
✉ michael.scherer@crg.eu



Personal Details

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

Professional Background

2021

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

2021

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 ABC² 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

Publications

Scientific articles *First-author publications*

- Bianchi, A.[†], Scherer, M.[†] 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.[†], Scherer, M.[†], Zeiner, K.[†], 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.[†], Schmidt, F.[†], Lazareva, O.[†], 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.[†], Scherer, M.[†], Assenov, Y.[†], Lutsik, P.[†], et al. (2019). RnBeads 2.0: comprehensive analysis of DNA methylation data. *Genome Biology*, 20(1), 55, doi: 10.1186/s13059-019-1664-9.

[†] Joint first authors

Contributing author publications

- 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.

Presentations

- Invited talks ○ 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
- 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

Teaching

- WS 17/18 The Elements of Statistical Learning, Prof. Dr. Dr. Thomas Lengauer, Saarland University
- WS 18/19 The Elements of Statistical Learning, Prof. Dr. Tobias Marschall and Dr. Jilles Vreeken, Saarland University
- WS 18/19 & WS 19/20 The Principles of Epigenetics and Epigenomics - a practical course on epigenomic data processing, Prof. Dr. Jörn Walter, Saarland University
- May 2019 German Network for Bioinformatics Infrastructure (de.NBI) course: DNA Methylation: From Design to Discovery

Awards

- 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

Languages

- German Native
- English Fluent
- Spanish, French Basic

Skills

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