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

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 **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 **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^2 database by DNA-protein interactions, Supervisor: Prof. Dr. Volkhard Helms, Final Grade: 1.6

Research Interests

Bioinformatics & Computational Biology	○ Single-Cell Data Analysis ○ Statistical Learning ○ Gene Regulation
Others	○ Aging ○ Development & Disease

Publications

Articles published by outlets with scientific quality assurance, book publications, and works accepted for publication but not yet published

First-author publications

○ 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

○ 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). Quantiative 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

○ 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.

○ 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

Other publications, both peer-reviewed and non-peer-reviewed

○ Bianchi, A., Scherer, M. et al. (2021). scTAM-seq enables targeted high-confidence analysis of DNA methylation in single cells. *bioRxiv*, doi: 10.1101/2022.04.11.487648 (Preprint)

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	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

Skills

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