Jan Gleixner

Curriculum Vitae

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EDUCATION

2018 – 2025	**Faculty of Biosciences** PHD (PENDING AWARD) – 1.0 *Heidelberg University*
2013 – 2018	**Molecular Biotechnology** **Major: Bioinformatics** MASTER OF SCIENCE – 1.1 *Heidelberg University*
2010 – 2013	**Molecular Biotechnology** **Major: Bioinformatics** BACHELOR OF SCIENCE – 1.9 *Heidelberg University*
2009	**Secondary School** **Major: Math & Informatics** ABITUR – 1.8 *Carl-Zeiss-Gymnasium, Jena*

WORK EXPERIENCE

MAR 2018 – JUL 2021, SEP 2021 – PRESENT

German Cancer Research Center (DKFZ) – Michael Boutros' lab and European Molecular Biology Laboratory (EMBL) – Oliver Stegle's group

Computational Biology

Development of experimental and computational methods to quantify causal effects on gene expression on different levels in high throughput:

- multimodal clonal barcoding strategies linking heterogeneous CRISPR editing outcomes to single-cell transcriptomes
- reproducible pipelines and statistical models for multi-omic perturbation analysis, including machine-learning–based quality control
- applications to investigate WNT signaling in colorectal cancer and aging in intestinal organoids derived from patients and mouse models[1]

JUN 2017 – FEB 2018

European molecular biology laboratory (EMBL) – Oliver Stegle's group

Causal Inference

Application of Invariant Causal Prediction (ICP) to single cell RNA expression CRISPR perturbation data[2]

OCTOBER 2015 – DECEMBER 2015

Max-Planck-Institute for Empirical Inference – Jonas Peters' group

Causal Inference

Development a likelihood score based bootstrap hypothesis test for the existence of a total causal effect in the framework of causal additive models

DECEMBER 2014 – JUNE 2015

Heidelberg University –
Labs of Barbara Di Ventura and Dirk Grimm

Synthetic Biology

Improving gene therapy by engineering a split Cas9 enzyme with improved expression from self-complementary Adeno-associated virus (scAAV)

FEBRUARY 2014 – NOVEMBER 2014

iGEM team Heidelberg 2014

Synthetic Biology

Development of a standard for cloning of Intein fusion proteins and use of Intein mediated circularization for stabilization of enzymes in a team of eleven students working full time with acquired funds over a hundred thousand euro[5]

FEBRUARY 2011 – OCTOBER 2013

Max Planck Institutes for Neurobiology and for Medical Research -- Moritz Helmstaedter's group

Biomedical Computer Vision

Programming of artificial neural networks to automatically segment 3D-electron microscope images of brain tissue and porting of those to GPUs; Development of features for and use of Random Forests for synapse detection

AUGUST & SEPTEMBER 2012

Duke University — Ute Hochgeschwender's lab

Neuro-optogenetics

Internship to learn cell culture, patch clamping and other neurobiology skills by analyzing and improving a Channelrhodopsin-Aequorin fusion protein[4]

MAY – JULY 2010

Leibniz Institute Natural Product Research and Infection Biology -- Hans Knoell Institute

Image Analysis Automation

Development of scripts in R and MATLAB for image analysis and statistical evaluation

JUNE 2009

Max Planck Institute for Biogeochemistry

Rustle Classifier Development

Literature search, preliminary experiments and their analysis by use of MATLAB and R

TECHNICAL SKILLS

PRIMARY	R (data.table, ggplot2), Python, Bash, LaTeX
ADDITIONAL	Git/GitHub/GitLab (VCS/CI/CD), Docker, Stan, PyTorch, TensorFlow, Theano, C++, Perl, MATLAB, Java, Haskell, JavaScript, Powershell, CUDA

AWARDS & SCHOLARSHIPS

2014	**iGEM – International Genetically Engineered Machines competition** *Winner team – “Ring of fire” (Heidelberg)*
2012	**DAAD’s (German academic exchange service) RISE worldwide program** *Full scholarship to carry out a research internship at Duke University (NC, USA)*
2011	**SYNtheSYS - Student competition on Synthetic & Systems Biology** *Winner team – “Faster than life”*
2009	**Jugend forscht** *State level, 2. award*

PUBLICATIONS

[1] MC Funk et al., *Aged intestinal stem cells propagate cell-intrinsic sources of inflammaging in mice*, Developmental Cell 58, 2914–2929.e7 (2023).

[2] CH Holland et al., *Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data*, Genome Biology 21, 36 (2020).

[3] M Goethe, J Gleixner, I Fita, and JM Rubi, *Prediction of Protein Configurational Entropy (Popcoen)*, J. Chem. Theory Comput. 14, 1811–1819 (2018).

[4] K Berglund et al., *Luminopsins integrate opto- and chemogenetics by using physical and biological light sources for opsin activation*, Proc Natl Acad Sci U S A 113, E358–367 (2016).

[5] MC Waldhauer et al., *Backbone circularization of Bacillus subtilis family 11 xylanase increases its thermostability and its resistance against aggregation.*, Mol. Biosyst. 11, 3231–43 (2015).