

Dr. Julia Helmecke

Bioinformatician



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10. Mai 1990 in Starnberg



read more ▶

or visit julia-helmecke.de 



Work Experience

09/2019
- today

POSTDOC IN BIOINFORMATICS

at TU Braunschweig, BRENDA Enzymes

- Update and development of the comparative annotation tool *EnzymeDetector*
- Development of the tool for sharing pathway maps and visualization of omics-data *MetaboMAPS*
- Further development of the BRENDA pathway maps
- Development of the web-based toolbox for metabolic modeling MMTB

06/2016
- 10/2019

DOCTORAL STUDENT IN BIOINFORMATICS

at TU Braunschweig

- Metabolic modeling and in silico metabolic engineering of *Sulfolobus acidocaldarius*
- Development of interactive web-tools for the curation and analysis of metabolic networks
- Development of web-based tools for integration and visualization of systems biology data

Graduated with *magna cum laude*

09/2014
- 06/2015

RESEARCH ASSISTANT

at Helmholtz Centre for Infection Research

- Phenotyping, qPCR, ELISA
- Data analysis



Education

10/2014
- 05/2016

MASTER OF SCIENCE IN BIOLOGY

at TU Braunschweig

Thesis degree: 1,3
Final degree: 1,4

10/2009
- 10/2014

BACHELOR OF SCIENCE IN BIOLOGY

at University of Bayreuth/ TU Braunschweig

Thesis degree: 1,3
Final degree: 2,4

06/2009

ABITUR

at Gymnasium Julianum Helmstedt

Final degree: 1,9

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Expertise

Data Integration & Visualization
Software & Web Development
Systems Biology

Soft Skills

Creativity
Analytical Thinking
Communication

Interest

Soccer5
Graphics Design & Typography
Writing Books
Landscape Photography



Portfolio

METANO TOOLBOX

Open-Source Toolbox for metabolic modeling

Implemented in Python 3, Solver: GLPK

pypi.org/project/metano

MMTB

Web-Interface for Metano and data base for reactions and metabolites

Backend in Python via Flask

mmtb.brenda-enzymes.org

METABOMAPS

Platform for the visualization of multi-omics data on metabolic pathway maps

Backend in PHP, Frontend in JavaScript

metabomaps.brenda-enzymes.org

BRENDA PATHWAY MAPS

Reimplementation and Development of the BRENDA pathway map: zoom-based rendering, data visualization

SVG-manipulation via D3.js

brenda-enzymes.org/pathway_index.php



Publications

- 2020 ● Helmecke, J., Schomburg, D. & Neumann-Schaal, M. (2019). MetaboMAPS: Pathway Sharing and Multi-omics Data Visualization in Metabolic Context. *under review*.
- 2019 ● Helmecke, J. *Vom Genom zum systemweiten Verständnis des Stoffwechsels thermoacidodophiler Sulfolobales* Dissertation (Technische Universität Braunschweig, 2019), 1–188.
- 2019 ● Vetter, A. M., Helmecke, J., Schomburg, D. & Neumann-Schaal, M. (2019). The Impact of Pyroglutamate: *Sulfolobus acidocaldarius* Has a Growth Advantage over *Saccharolobus solfataricus* in Glutamate-Containing Media. *Archaea*, 2019, 1–9.
- 2018 ● Steglich, M., Hofmann, J. D., Helmecke, J., Sikorski, J., Spröer, C., Riedel, T., ... Nübel, U. (2018). Convergent Loss of ABC Transporter Genes from *Clostridioides difficile* Genomes is Associated with Impaired Tyrosine Uptake and p-Cresol Production. *Frontiers in Microbiology*, 9, 901.

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Hard Skills

Python 3	● ● ● ● ●
Web Development	● ● ● ● ●
> HTML 5, CSS, ...	● ● ● ● ●
> Bootstrap 4	● ● ● ● ●
> JavaScript	● ● ● ● ●
> PHP	● ● ● ● ●
> Flask Framework	● ● ● ● ●
R	● ● ● ● ●
MySQL	● ● ● ● ●
LaTeX	● ● ● ● ●

Microsoft Word	● ● ● ● ●
Microsoft Excel	● ● ● ● ●
Adobe Illustrator	● ● ● ● ●
Adobe InDesign	● ● ● ● ●
Adobe Photoshop	● ● ● ● ●

Linux	● ● ● ● ●
Windows	● ● ● ● ●

Languages

German	● ● ● ● ●
English	● ● ● ● ●
Spanish	● ● ● ● ●

ZUSAMMENFASSUNG DER DOKTORARBEIT

Archaea are globally distributed and can even be found in harsh environments, including high salt concentrations, acidic or alkaline pH, as well as temperatures close to the boiling or freezing point of water. Archaea evolved unique metabolic strategies to adapt to these hostile conditions and are therefore of high interest to biotechnology.

In this study, the metabolism of thermoacidophilic Sulfolobales was investigated. In order to establish a basis for metabolic modeling and systems biology, the genomes of four members of Sulfolobales were reannotated. As a result, the amount of uncharacterized proteins was reduced from 32 % to 18 %.

MMTB, a web-based tool, was developed for generating and analyzing metabolic models. Generating models is accomplished by associating biochemical reactions to genome annotations. Analyzing models is accomplished via visualizations and an interface to the open source toolbox Metano.


On the basis of the reannotation and with help of MMTB, a genome-wide metabolic model of *Sulfolobus acidocaldarius* was developed. The generated metabolic model is able to predict quantitative growth of *S. acidocaldarius* and was evaluated and used in two use cases. First, investigating the catabolism of amino acids revealed that the valine degradation pathway depends on availability of other amino acids. Second, investigating targets for metabolic engineering to produce ethanol from lignocellulosic biomass revealed that inserting a phosphofructokinase is essential for ethanol production in *S. acidocaldarius*.

Further, the reannotation was used to draw metabolic maps for the four Sulfolobales. To enhance those maps and allow integrating systems biological data, the web-based MetaboMAPS was developed. MetaboMAPS directly visualizes large-scale datasets on the metabolic maps. This innovative visualization technique was made available to an international audience by integrating it into BRENDA metabolic pathway maps.

This study contributes to the systems understanding of Sulfolobales, by providing reannotation of four species, genome-wide metabolic modeling, and development of MetaboMAPS. The value of these contributions was demonstrated in several examples from the disciplines of systems biology and biotechnology. Additionally, this work contributes to the community of systems biology by providing the MMTB and new data integration tools in BRENDA metabolic pathway maps.


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