Michael Jahn

Curriculum vitae

Personal information

Name	Dr. rer. nat. Michael Jahn
Date of birth	Dec 31, 1985
Born in	Dresden, Germany
Address	Street name, number, ZIP code City, Country
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Current position

Postdoctoral scientist, Bioinformatics Platform, Laboratory of Emmanuelle Charpentier, Max-Planck-Unit for the Science of Pathogens (MPUSP), Berlin.

Education

July 10, 2015	**Graduated *Doctor rerum naturalium***, at the University of Leipzig, Germany, with *summa cum laude* (1.0).
2011–2015	**PhD studies**, Group of Prof Susann Müller, Dept. Environmental Microbiology, Helmholtz-Centre for Environmental Research, Leipzig. Thesis: 'Characterization of population heterogeneity in a model biotechnological process using *Pseudomonas putida*'.
2005–2011	**Diploma studies, biology**, Dresden University of Technology (TUD), main subjects: genetics, biochemistry, immunology. Diploma thesis: 'Dynamic mating pheromone gradients for induction of mating projection and fluorescence in yeast', group of Prof Gerhard Rödel, grade 1.2.
1996–2004	**High school**, Romain-Rolland-Gymnasium, Dresden, Abitur with grade 1.6.
1992–1996	**Elementary school**, Dresden.

Work experience

8/2022–now	**Postdoctoral scientist**, Bioinformatics Platform, Laboratory of Emmanuelle Charpentier, Max-Planck-Unit for the Science of Pathogens (MPUSP), Berlin.
5/2016–5/2022	**Postdoctoral scientist**, System-wide analysis and metabolic engineering of autotrophic bacteria in the group of Prof Paul Hudson, Science For Life Laboratory - Royal Institute of Technology, Stockholm.
8–12/2009	**Erasmus internship**, Center of Excellence in Evolutionary Genetics and Physiology at the group of Prof Mikko Nikinmaa, Dept. of Biology, University of Turku, Finland.
2008–2009	**Student assistant**, Institute of Genetics, group of Prof Gerhard Rödel, Dept. of Biology, Dresden University of Technology (TUD).
2007–2008	**Student assistant**, Mitteldeutscher Praxisverbund Humangenetik, Dresden.
2004–2005	**Voluntary service 'Freiwilliges Ökologisches Jahr'**, national park 'Sächsische Schweiz', tour guide and education.

Leaves

11/2019–3/2020	Parental leave with 2nd child Sophie
9/2015–4/2016	Parental leave with 1st child Simon

Awards

Nov 25, 2015	**PhD-Award** 2015 by the Helmholtz-Centre for Environmental Research, Leipzig. Awarded annually for excellent dissertations.

Awarded grants

Nov 11, 2019	**Investigation of protein resource allocation in the model CO_2 fixing bacterium *Ralstonia eutropha*** (Swedish: Undersökning av proteiners resursfördelning i en modell för CO_2-fixerande bakterier, *Ralstonia eutropha*). Funding agency: FORMAS. Project number: 2019-01491. Project leader: Dr. Michael Jahn. Awarded funding for period 2020-01-01-2021-12-31. Total funds: 2,000,000 SEK (200,000 Euro).

Teaching and supervision

Teaching	**Lecture for course KE2130 'Renewable fuels'**, at KTH Stockholm, 2020-2022. Topics: Metabolic engineering, whole cell biocatalysis, genome-scale models, flux balance analysis.
	Lecture for course 'Introduction to the programming language R' and its application for flow cytometry data, at the Helmholtz Centre for Environmental Research, Leipzig, 2015.
PhD council	Member of the PhD council and the Environmental Board of the Helmholtz Centre for Environmental Research, Leipzig, 2011-2015. Tasks: Improving environmental footprint of the center, providing guidance for starting PhD students, organizing events.

Qualifications and skills

Expertise	Analytical thinking, understanding complex phenomena, Project managing, supervision, leadership, Scientific writing of papers, funding proposals, reports, Design of experimental strategies to solve a problem, Explorative analysis and visualization of complex (biological) data, Creation of pipelines for automated data processing, Application of clustering and machine learning algorithms, High-throughput lab methods (NGS, protein mass spectrometry)
Programming languages	R (expert), Python (advanced), Linux bash, Markdown, Latex, Git
Authored software	WeightedTreemaps, ShinyTreemaps – visualizing gene expression with treemaps, CRAN package ShinyProt, ShinyLib, ShinyMC – interactive apps to visualize proteomics, gene knockout library, and bioreactor cultivation data fluctuator – interface to overlay flux data on metabolic maps in R lattice-tools – panel functions to extend R lattice snakemake-crispr-guides, nf-core-crispriscreen – pipelines to create CRISPRi libraries and process resulting NGS data
Metabolic models	*Synechocystis* resource allocation model, for GAMS, and ported to python. Genome scale metabolic model (python) for *Cupriavidus necator* a.k.a. *Ralstonia eutropha*. Resource balance analysis model (python) for *Cupriavidus necator*.
Certificates	Approved project manager for genetic works, according to German laws (§ 14,15 GenTSV), 2015.

Peer review and outreach

Peer review	Active reviewer for several journals including Microbial Cell Factories, Frontiers in Microbiology, Photosynthesis Research, and others. The full list of my review contributions is available on Publons or ORCID.
Outreach	All software and computational pipelines available on GitHub. Research communicated to the public *via* home page, ResearchGate, and Twitter.

Languages

German	Native language
English	Proficient user, CEF level C1
Swedish	Vantage user, CEF level B2

Publications

- Miao R, **Jahn M**, Shabestary K, Peltier G, Hudson EP. *CRISPR interference screens reveal growth−robustness tradeoffs in Synechocystis sp. PCC 6803 across growth conditions*. The Plant Cell, **2023**. Link.

- Grätz L, Kowalski-Jahn M, Scharf MM, Kozielewicz P, **Jahn M**, Bous J, Lambert NA, Gloriam DE, Schulte G. *Pathway selectivity in Frizzleds is achieved by conserved micro-switches defining pathway-determining, active conformations*. Nature Communications, **2023**. Link.

- Janasch M, Crang N, Asplund-Samuelsson J, Sporre E, Bruch M, Gynnå A, **Jahn M**, Hudson EP. *Thermodynamic limitations of PHB production from formate and fructose in Cupriavidus necator*. Metabolic engineering, **2022**. Link.

- **Jahn M**, Crang N, Janasch M, Hober A, Forsström B, Kimler K, Mattausch A, Chen Q, Asplund-Samuelsson J, Hudson EP. *Protein allocation and utilization in the versatile chemolithoautotroph Cupriavidus necator*, eLife, 10, **2021**. Link.

- Karlsen J, Asplund-Samuelsson J, **Jahn M**, Vitay D, Hudson EP. *Slow Protein Turnover Explains Limited Protein-Level Response to Diurnal Transcriptional Oscillations in Cyanobacteria*. Frontiers in Microbiology, 12, 820, **2021**. Link.

- Yao L, Shabestary K, Björk SM, Asplund-Samuelsson J, Joensson HN, **Jahn M**, Hudson EP. *Pooled CRISPRi screening of the cyanobacterium Synechocystis sp PCC 6803 for enhanced industrial phenotypes*. Nature Communications, **2020**. Link.

- Karlsen J, Asplund-Samuelsson J, Thomas Q, **Jahn M**, Hudson EP. *Ribosome Profiling of Synechocystis Reveals Altered Ribosome Allocation at Carbon Starvation*. MSystems 3, e00126-18, **2018**. Link.

- **Jahn M**, Vialas V, Karlsen J, Maddalo G, Edfors F, Forsström B, Uhlén M, Käll L, Hudson EP. *Growth of Cyanobacteria Is Constrained by the Abundance of Light and Carbon Assimilation Proteins*. Cell Reports 25, 478−486.e8., **2018**. Link.

- Shabestary K, Anfelt J, Ljungqvist E, **Jahn M**, Yao L, Hudson EP. *Targeted Repression of Essential Genes To Arrest Growth and Increase Carbon Partitioning and Biofuel Titers in Cyanobacteria*. ACS Synthetic Biology, 7, 1669−1675, **2018**. Link.

- **Jahn M**, Vorpahl C, Hübschmann T, Harms H, Müller S. *Copy number variability of expression plasmids determined by cell sorting and Droplet Digital PCR*. Microbial Cell Factories, **2016**. Link.

- Lindmeyer M, **Jahn M**, Vorpahl C, Müller S, Schmid A, Bühler B. *Variability in subpopulation formation propagates into biocatalytic variability of engineered Pseudomonas putida strains*. Frontiers in microbiology 6, **2015**. Link.

- Lieder S, **Jahn M**, Koepff J, Müller S, Takors Ralf. *Environmental stress speeds up DNA replication in Pseudomonas putida in chemostat cultivations*. Biotechnology journal, **2015**. Link.

- **Jahn M**, Günther S, Müller S. *Non-random distribution of macromolecules as driving forces for phenotypic variation*. Current Opinion in Microbiology. 25:49-55, **2015**. Link.

- Rödiger S, Burdukiewicz M, Blagodatskikh K, **Jahn M**, Schierack P. *R as an environment for reproducible analysis of DNA amplification experiments*. R Journal 7/1:127-150, **2015**. Link.

- **Jahn M**, Vorpahl C, Türkowsky D, Lindmeyer M, Bühler B, Harms H, Müller S. *Accurate determination of plasmid copy number of flow-sorted cells using droplet digital PCR*. Analytical Chemistry 86:5969-76, **2014**. Link.

- Lieder S, **Jahn M**, Seifert J, von Bergen M, Müller S, Takors R. *Subpopulation-proteomics reveal growth rate, but not cell cycling, as a major impact on protein composition in* Pseudomonas putida *KT2440*. AMB Express 4:71, **2014**. Link.

- **Jahn M**, Seifert J, von Bergen M, Schmid A, Bühler B, Müller S. *Subpopulation-proteomics in prokaryotic populations*. Current Opinion in Biotechnology 24:79-87, **2013**. Link.

- **Jahn M**, Seifert J, Hübschmann T, von Bergen M, Harms H, Müller S. *Comparison of preservation methods for bacterial cells in cytomics and proteomics*. Journal Of Integrated Omics 3:1-9, **2013**. Link.

- **Jahn M**, Mölle A, Rödel G, Ostermann K. *Temporal and spatial properties of a yeast multi-cellular amplification system based on signal molecule diffusion*. Sensors 13:14511-22, **2013**. Link.