

# andreasbremges

computational biology of infection research

## personal

born May 10th, 1985  
2 children aged 2 and 5

## contact

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## languages

native German  
fluent English  
basic Finnish

## programming

C, Java, Perl, R  
Unix, Grid Engine  
Git, Travis CI  
L<sup>A</sup>T<sub>E</sub>X

## education

2003–2005	<b>Associate Engineer</b> in Automation Technology Average: <b>1.6</b> , Practical: <b>1.0</b>	Siemens AG, Düsseldorf
2005–2008	<b>Bachelor</b> of Science, <b>Bioinformatics and Genome Research</b> Average: <b>1.6</b> , Thesis: <b>1.0</b>	Bielefeld University
2008–2011	<b>Master</b> of Science, <b>Bioinformatics and Genome Research</b> Average: <b>1.4</b> , Thesis: <b>1.0</b>	Bielefeld University
2010	<b>Erasmus Programme</b> Master's Degree Programme in Bioinformatics	University of Helsinki
2011–Now	<b>Ph.D. Candidate</b> , <b>Bioinformatics</b> Alex Sczyrba's group: Computational Metagenomics	Bielefeld University
2015–Now	<b>DZIF Software Developer</b> Alice McHardy's group: Computational Biology of Infection Research	Helmholtz Centre for Infection Research
2016–	<b>Postdoctoral Researcher</b> Alice McHardy's group: Computational Biology of Infection Research	Helmholtz Centre for Infection Research

## experience

2005	<b>Software Developer</b> 6 months internship, programming in C and Assembly language	Siemens Rail Systems, Krefeld
2007–2009	<b>Teaching Assistant</b> Algorithms & Data Structures, Programming in Java, Project Development	Bielefeld University
2009–2010	<b>Research Assistant</b> Member of Robert Giegerich's group (Practical Computer Science)	Bielefeld University
2012–Now	<b>Affiliate Scientist</b> Hosted by Zhong Wang (Genome Analysis), visited twice for ~3 weeks each	DOE Joint Genome Institute, Walnut Creek

## awards

2011	<b>Ph.D. Scholarship</b> CLIB Graduate Cluster Industrial Biotechnology	Bielefeld University
2012	<b>Best Talk Award</b> Bioinformatics Research and Education Workshop	University of Bergen

## interests

**professional:** sequencing technologies, data analysis, software development, bioinformatics best practices, information visualization **personal:** quality time with family and friends, audio & hi-fi, bodyweight exercises, single malt scotch whisky

## communication skills

2008–2009	<b>Moderation International</b> 3 semesters of moderation training in English	Bielefeld University
2012	<b>Bioinformatics Research and Education Workshop</b> Talk and “paper”	University of Bergen
2012–2014	<b>Annual Retreats</b> within the CLIB Graduate Cluster 3 poster presentations, 1 talk	Bielefeld, Dortmund, Düsseldorf
2014	<b>Presenting Data and Information &amp; See, Think, Design, Produce</b> Edward Tufte with Jonathan Corum, Maria Popova, Randall Munroe	Seattle
	<b>Wellcome Trust Genome Informatics 2014</b> Poster presentation	Churchill College, Cambridge
	<b>German Conference on Bioinformatics</b> Poster presentation	Bielefeld University
2015	<b>Bioinformatics for amplicon and shotgun metagenome analysis</b> Workshop co-organizer & lecturer	HZI Braunschweig
	<b>NGS data processing and variant calling with GATK</b> Workshop organizer & lecturer	HZI Braunschweig

## publications

2010	<b>Fine-tuning structural RNA alignments in the twilight zone</b> <b>Bremges, A</b> , Schirmer, S, Giegerich, R	BMC Bioinformatics
2013	<b>A silent exonic SNP in kdm3a affects nucleic acids structure but does not regulate experimental autoimmune encephalomyelitis</b> Gillett, A, Bergman, P, Parsa, R, <b>Bremges, A</b> , Giegerich, R, Jagodic, M	PLOS ONE
2014	<b>Complete genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT5344</b> Wibberg, D, Luque-Almagro, VM, Igeño, MI, <b>Bremges, A</b> , Roldán, MD, Merchán, F, Sáez, LP, Guijo, MI, Manso, MI, Macías, D, Cabello, P, Becerra, G, Ibáñez, MI, Carmona, MI, Escibano, MM, Castillo, F, Sczyrba, A, Moreno-Vivián, C, Blasco, R, Pühler, A, Schlüter, A	Journal of Biotechnology
2015	<b>Fractionation of biogas plant sludge material improves metaproteomic characterization to investigate metabolic activity of microbial communities</b> Kohrs, F, Wolter, S, Benndorf, D, Heyer, R, Hoffmann, M, Rapp, E, <b>Bremges, A</b> , Sczyrba, A, Schlüter, A, Reichl, U	Proteomics
	<b>Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant</b> <b>Bremges, A</b> , Maus, I, Belmann, P, Eikmeyer, FG, Winkler, A, Albersmeier, A, Pühler, A, Schlüter, A, Sczyrba, A	GigaScience
In press	<b>Bioboxes: standardised containers for interchangeable bioinformatics software</b> Belmann, P, Dröge, J, <b>Bremges, A</b> , McHardy, AC, Sczyrba, A, Barton, MD	
Submitted	<b>Genomic characterization of <i>DeFluviitoga tunisiensis</i> L3, a key hydrolytic bacterium originating from a thermophilic production-scale biogas plant</b> Maus, I, Cibis KG, <b>Bremges, A</b> , Stolze, Y, Wibberg, D, Tomazetto, G, Blom, J, Sczyrba, A, König, H, Pühler, A, Schlüter, A	
In preparation	<b>Metagenomic proxy assemblies of single cell genomes</b> <b>Bremges, A</b> , Jarett, J, Woyke, T, Sczyrba, A <b>corsage: Metagenome-enabled error correction of single cell sequencing reads</b> <b>Bremges, A</b> , Singer, E, Woyke, T, Sczyrba, A	