

Tobias Rausch

Address

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Current Role

Oct 2009 - present

Bioinformatician, Genomics Core Facility / Genome Biology,
European Molecular Biology Laboratory (EMBL)

Education

11th May 2010

Doctor rer. nat. (PhD), Bioinformatics, Department of
Mathematics and Computer Science, Freie Universität Berlin
Thesis: "Dissecting multiple sequence alignment methods: the
analysis, design and development of generic multiple sequence
alignment components in SeqAn"

13th Sep 2006

M.Sc., Software Systems Engineering, University of Potsdam

10th May 2006

Certificate in BioMedical Informatics, University of Utah

31st Mar 2005

B.Sc., Software Systems Engineering, University of Potsdam

Selected Lecturing and Teaching Experiences

Cancer Genomics Course

Annually at EMBL-EBI, Lecturing Cancer Genomics, Course
Materials: <https://github.com/tobiasrausch/tutorial-delly>

Functional Genomics Course

Annually in Czech Republic, Lecturing WGS data analysis

Clinical Genomics & NGS

ESGM & ESHG course in Italy, Lecturing NGS Data Analysis

Festival of Genomics

NGS workshop in London 2016, Lecturing Cancer Genomics

AllBio Workshop

Swiss Institute of Bioinformatics 2014, Lecturing structural
variation (SV) calling

NGS Data Analysis

EMBL from 2012-2014, Lecturing Assembly, Variant Calling
and RNA-Seq

EMBO Metagenomics Course

EMBL 2013, Lecturing NGS Data Analysis Basics

EMBL PreDoc Course

Annually at EMBL, seminar on SV discovery or contribution
of course material

Other professional experiences

Thesis Advisor/Referee

Multi-Split-Mapping of NGS reads for variant detection
(M.Sc. Thesis, K. Trappe)

Implementing a Motif Finder based on STELLAR and
SeqAn::T-Coffee (B.Sc. Thesis, V. Vimalakanthan)

Train the Trainers

Training of delegates from Bioplatforms Australia at the EBI
Cancer Genomics Workshop in Hinxton

Scientific Visitors	Bioinformatics training for long-term and short-term scientific visitors. Among many others: Dr Philippe Ganot, Centre Scientifique de Monaco, Coral Genome Assembly Dr Andreas Untergasser, 1000 Genomes Data Analysis Stefan Mester, University Clinic Heidelberg, Structural Variant Calling for Heart Diseases Povilas Gibas, Undergraduate Intern from Lithuania, General Bioinformatics Training
Recruitment Panel Member	Member of several EMBL Recruitment Selection Panels for the following positions: Postdoctoral Fellow Heidelberg Human Bioinformatics (HD-HuB), de.NBI Postdoc Position with Georg Zeller, Bioinformatician with Bork, Huber and Korbel Group, Bioinformatician Genomics Core Facility

Research Interests

Algorithm Engineering NGS Technologies	Alignment, indexing, graph and SV detection algorithms Evaluation & comparison of DNA sequencing technologies & protocols
Pipeline Orchestration	Portable workflow and tool descriptions for pipeline management
Cancer Genomics Rare diseases	Mutation discovery & genotyping in WGS data Identification of genetic defects using WES

Scholarships

Oct 2006 to Oct 2009	Max Planck Research School Scholarship
Aug 2005 to May 2006	Fulbright Fellow, University of Utah, USA
May 2004 to Sep 2006	“Studienstiftung des Deutschen Volkes” Scholarship

Selected Shared First Author Publications

A full list of my publications is at Google Scholar:

<https://scholar.google.de/citations?user=fQ1VoZEAAAAJ>

ORCID: 0000-0001-5773-5620

1. Sudmant, P. H., **Rausch, T.** et al. An integrated map of structural variation in 2,504 human genomes. *Nature* 526, 75–81 (2015).
2. Kunz, J. B., **Rausch, T.** et al. Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. *Haematologica* 100, 1442–1450 (2015).
3. Bandapalli, O. R., Schuessele, S., Kunz, J. B., **Rausch, T.** et al. The activating STAT5B N642H mutation is a common abnormality in pediatric T-cell acute lymphoblastic leukemia and confers a higher risk of relapse. *Haematologica* 99, e188–192 (2014).
4. Greil, J., **Rausch, T.** et al. Whole-exome sequencing links caspase recruitment domain 11 (CARD11) inactivation to severe combined immunodeficiency. *J. Allergy Clin. Immunol.* 131, 1376–1383.e3 (2013).
5. **Rausch, T.** et al. Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. *Cell* 148, 59–71 (2012).
6. **Rausch, T.** et al. DELLY: structural variant discovery by integrated paired-end and split-read analysis. *Bioinforma. Oxf. Engl.* 28, i333–i339 (2012).

Selected Peer Reviewing

A full list of reviews is at Publons: <https://publons.com/author/1172942/tobias-rausch>

Main Peer Reviewer	Among other journals I acted as a main peer reviewer for Nucleic Acids Research, PLOS Computational Biology, Bioinformatics, Annals of Hematology and BMC Bioinformatics
Junior Co-Reviewer	Nature, Nature Genetics, Nature Biotechnology, Nature Biomedical Engineering, Genome Research

Selected Software Development Activities

A full list of my public Software Projects is at GitHub: <https://github.com/tobiasrausch>

Delly	Structural variant discovery & genotyping Downloaded >3000 times, >300 citations (Google Scholar)
Indigo	Web service to analyse Chromatogram traces http://gear.embl.de/indigo/
Alfred	NGS alignment statistics
ATAC-Seq	Analysis Pipeline to analyse open chromatic regions
nRex	Germline and somatic variant calling workflow
Repli-Seq	Normalization methods for replication sequencing data
tenX	Tools for 10X Genomics Data Sets
Strand-Seq	Strand-Seq pre-processing routines and inversion discovery methods
GeneCore Pipeline	Private Repository of the GeneCore QC and Alignment pipeline

IT Skills

Programming	C/C++, Bash, Python, Java, Perl
Software Libraries	Boost, HTSlib, sds-lite, SeqAn (former co-developer)
Debugging	gdb, valgrind
Performance	gprof, Google Performance Tools
Parallel Computing	OpenMP (used by Delly), Intel Threading Building Blocks
Statistics & Math	R, R Bioconductor, GNU Octave
HPC	Familiar with LSF, PBS and SLURM cluster management systems
Cloud Computing	Amazon Elastic Compute Cloud, Google Cloud Platform
Versioning Systems	git, subversion
Databases	MySQL, MongoDB
Text Processing	LaTeX, Sphinx, Markdown and Office
Operating Systems	Linux, Mac OS X, Windows
Web Technologies	Javascript, CSS, HTML, Bootstrap, JQuery, Flask, Unicorn, nginx

Language Skills

German	Native language
English	Fluent in written and spoken
French, Chinese	Basic knowledge

