Dr. Daniel Dörr

CONTACT	*Address*	Institute for Medical Biometry and Bioinformatics
		University Hospital Düsseldorf
		Moorenstr. 5
		40225 Düsseldorf
		Germany
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	Website	https://danieldoerr.de/
NATIONALITY	German	

SUMMARY

- Dr. rer. nat. in bioinformatics with excellent dissertation *(summa cum laude)*
- Interdisciplinary researcher in computational *omics, algorithms, and mathematical modeling with deep understanding of biological processes
- Experienced lecturer of graduate and undergraduate lectures and seminars
- Trained in leadership and management, experience in public speaking

PROFESSIONAL EXPERIENCE

09/2020 – now	*Bioinformatics Scientist*, Institute for Medical Biometry and Bioinformatics, Faculty of Medicine, Heinrich Heine University Düsseldorf, Germany
01/2020 – 08/2020	*Postdoctoral researcher*, Genome Data Science, Faculty of Technology, Bielefeld University, Germany
01/2017 – 12/2019	*Postdoctoral researcher*, Genome Informatics, Faculty of Technology, Bielefeld University, Germany
05/2015 – 12/2016	*Postdoctoral researcher*, Laboratory for Computational Biology and Bioinformatics, School of Computer and Communication Sciences, École Polytechnique Fédérale de Lausanne, Switzerland
09/2005 – 12/2010	*Software application engineer*, freelancer, Bielefeld, Germany

PROFESSIONAL ACTIVITIES

Member	*Editorial board of the Journal of Computational Biology, Mary Ann Liebert, Inc.*
Member	*Program Committee for the 22nd Workshop on Algorithms in Bioinformatics (WABI), Potsdam (Germany), 2022*
Member	*Program Committee for the 19th RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), La Jolla (US), 2022*
Member	*Program Committee for the 17th RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), Montpellier (France), 2019*
Member	*Program Committee for the 18th Workshop on Algorithms in Bioinformatics (WABI), Helsinki (Finland), 2018*
Member	*Program Committee for the 16th RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), Magog-Orford (Canada), 2018*

UNIVERSITY EDUCATION

12/2010 – 04/2015	Dr. rer. nat., Faculty of Technology, Bielefeld University, Germany

Thesis:	*Gene Family-free Genome Comparison*
Grade:	*excellent (summa cum laude)*
Graduate schools:	*CLIB Graduate Cluster Industrial Biotechnology, DFG Research Training Group (GRK 1906) "Computational Methods for the Analysis of the Diversity and Dynamics of Genomes", affiliated member*

10/2008 – 11/2010	M. Sc. in Bioinformatics and Genome Research, Bielefeld University, Germany

Thesis:	*Non-additive Substitution Rate Functions in Distance-Based Phylogenetic Reconstructions*
Grade:	*1.7 (good)*

10/2005 – 09/2008	B. Sc. in Bioinformatics and Genome Research, Bielefeld University, Germany

Thesis:	*A Feature-based Multiple Alignment Approach for Gas-chromatography-Mass Spectrometry Experiments*
Grade:	*1.6 (good)*

GRANTS, FELLOWSHIPS, AND AWARDS

08 – 19/01/2018	Erasmus+ Teaching Mobility Grant
03/2016	Nominated for the dissertation award of the German Informatics Society (GI)
02/2016	Dissertation award of the University Society Bielefeld
12/2010 – 06/2014	Doctoral scholarship of the CLIB Graduate Cluster Industrial Biotechnology
02/2014 – 04/2014	DAAD FITweltweit short term scholarship
10/2009 – 06/2010	Embassy scholarship, granted by the Israel Ministry of Foreign Affairs

VOLUNTARY SERVICE

09/2011 – 04/2015	Mentor in the program "*inter*Kontakt", Welcome Centre, Bielefeld University, Germany

INTERNSHIPS AND VISITS AT FOREIGN INSTITUTES

08 – 19/01/2018	Visiting lecturer, Department of Computer Science, University of Helsinki, Finland

Lecture:	*Intensive Course on Genome Rearrangements*
Host:	*Prof. Dr. Veli Mäkinen*

20 – 29/09/2017	Visiting scholar, Electrical Engineering & Computer Science School (EECS), Queensland University of Technology, Brisbane, Australia

Research topic:	*Methods for Large-scale Genome Segmentation*
Host:	*Prof. Dr. Jim Hogan*

02/2014 – 04/2014	Visiting scholar, Department of Mathematics, Simon Fraser University, BC, Canada

Research topic:	*Gene Family-free Median of Three*
Supervisor:	*Prof. Dr. Cedric Chauve*

06/2012 – 09/2012	Summer intern, Healthcare Informatics, IBM Research, Almaden, CA, United States

Research topic:	*Modeling Food-borne Disease Outbreaks*
Supervisor:	*Dr. James H. Kaufman*

08/2009 – 09/2010	Visiting scholar, Irwin and Joan Jacobs Graduate School, Technion, Haifa, Israel
	Research topic: *Optimal Distances in Stochastic Substitution Models*
	Supervisor: *Prof. Dr. Shlomo Moran*

FELLOWSHIPS, AND AWARDS

08 – 19/01/2018	Erasmus+ Teaching Mobility Grant
03/2016	Nominated for the dissertation award of the German Informatics Society (GI)
02/2016	Dissertation award of the University Society Bielefeld
12/2010 – 06/2014	Doctoral scholarship of the CLIB Graduate Cluster Industrial Biotechnology
02/2014 – 04/2014	DAAD FITweltweit short term scholarship
10/2009 – 06/2010	Embassy scholarship, granted by the Israel Ministry of Foreign Affairs

TEACHING EXPERIENCE

SS 2022	Substitute lecturer for two lectures, Heinrich Heine University Düsseldorf, *EMBuMI Lecture KDHDT*, lecture for medical students
WS 2020/2021	Co-Lecturer, Heinrich Heine University Düsseldorf, *Introduction to Medical Data Science*, lecture for medical students
WS 2020/2021	Co-Lecturer, Heinrich Heine University Düsseldorf, *Computational Multiomics*, graduate seminar for computer science students
SS 2020	Lecturer, Bielefeld University, *Programming*, graduate online course
WS 2019/2020	Lecturer, Bielefeld University, *Algorithms in Genome Research*, (under-) graduate lecture
SS 2019	Lecturer, Bielefeld University, *Sequence Analysis*, undergraduate lecture
WS 2018/2019	Lecturer, Bielefeld University, *Algorithms in Comparative Genomics*, (under-) graduate lecture
WS 2018/2019	Co-lecturer, Bielefeld University, *Bioinformatics Journal Club*, graduate seminar
SS 2018	Lecturer, Bielefeld University, *Sequence Analysis*, undergraduate lecture
SS 2018	Lecturer, Bielefeld University, *Bioinformatics Journal Club*, graduate seminar
Jan. 08-12, 2018	Lecturer, University of Helsinki, *Intensive Course on Genome Rearrangements*, graduate lecture
WS 2017/2018	Substitute lecturer for two lectures, Bielefeld University, *Algorithms in Genome Research*, graduate lecture
WS 2017/2018	Co-lecturer, Bielefeld University, *Sequence Analysis Practical Course*, undergraduate practical course
SS 2017	Lecturer, Bielefeld University, *Algorithms for Genome Rearrangement*, (under-) graduate lecture
SS 2017	Lecturer, Bielefeld University, *Bioinformatics Applications in Genome Research*, graduate practical course
WS 2016/2017	Co-lecturer, Bielefeld University, *Bioinformatics Journal Club*, graduate seminar
WS 2016/2017	Co-lecturer, Bielefeld University, *Genome Informatics Research Seminar*, graduate seminar
SS 2016	Substitute lecturer for two lectures, EPFL, *Computational Molecular Biology*, graduate lecture
WS 2014/2015	Lecturer, Bielefeld University, *Bioinformatics Journal Club*, graduate seminar
WS 2014/2015	Lecturer, Bielefeld University, *Genome Informatics Research Seminar*, graduate seminar
SS 2013	Co-lecturer, Bielefeld University, *Bioinformatics Applications in Genome Research*, graduate seminar
WS 2012/2013	Teaching assistant, Bielefeld University, *Phylogenetics*, undergraduate lecture

SS 2012	Co-lecturer, Bielefeld University, *ROSE – Random model of Simulated Evolution*, graduate project course
WS 2011/2012	Teaching assistant, Bielefeld University, *Phylogenetics*, undergraduate lecture
SS 2011	Teaching assistant (coordination of exercises), Bielefeld University, *Sequence Analysis II*, undergraduate lecture
SS 2010	Teaching assistant, Technion, *Project in Advanced Programming*, undergraduate project course
SS 2008	Teaching assistant, Bielefeld University, *Algorithms and Data Structures II*, undergraduate lecture
WS 2007/2008	Teaching assistant, Bielefeld University, *Algorithms and Data Structures I*, undergraduate lecture

COORDINATION OF SCIENTIFIC MEETINGS

07 – 08/11/2016	Colloquium on Algorithms in Molecular Biology (CLIMB), Lausanne, Switzerland
04 – 05/02/2013	Northwest German Bioinformatics Retreat, Paderborn, Germany

VOLUNTARY SERVICE

09/2011 – 04/2015	Mentor in the program "*inter*Kontakt", Welcome Centre, Bielefeld University, Germany

Last updated December 28, 2022

SCIENTIFIC PORTFOLIO

SCIENTIFIC PUBLICATIONS

Journal Articles

Liao, W., Asri, M., Ebler, J., Doerr, D. *et al.*, Marschall, T., Hall, I., Li, H., Paten, B., *A Draft Human Pangenome Reference*, Nature, Accepted; preprint available doi://10.1101/2022.07.09.499321, 2022

- Built a quality control pipeline for developing pangenome graphs of the consortium
- Developed a tool to reduce redundancy in pangenome graphs, now part of the construction piplines of HPRC graphs
- Developed a tool to asses pangenome growth statistics that are highlighted in the paper
- Co-writer of the manuscript

Bohnenkämper, L., Braga, M. D. V., Doerr, D., Stoye, J., *Computing the rearrangement distance of natural genomes*, Journal of Computational Bioloy, Vol 28:0, 2021

- Co-author of the integer linear program
- Co-writer of the manuscript

Nützmann, H-W., Doerr, D., Ramirez-Colmenero, A., Sotelo, J. E., Wegel, E., Di Stefano, M., Wingett, S. W., Fraser, P., Hurst, L., Fernandez-Valverde, S. L., Osbourn, A., *Active and repressed biosynthetic gene clusters have spatially distinct chromosome states*, Proceedings of the National Academy of Sciences, Vol. 117:24, 13800-13809, 2020

- Main author of bioinformatic analysis

Sevillya, G., Doerr, D., Lerner, Y., Stoye, J., Steel, M., Snir, S., *Horizontal Gene Transfer Phylogenetics: A Random Walk Approach*, Molecular Biology and Evolution, Vol. 37:5, 1470–1479, 2020

- Contribution to model design
- Design and execution of simulation study

Schulz, T., Stoye, J., Doerr, D., *GraphTeams: A Method for Discovering Spatial Gene Clusters in Hi-C Sequencing Data*, BMC Bioinformatics, Vol. 19:5, 308, 2018

- Coordination of the research
- Co-design of the computational model, development and implementation of the algorithm, design and major participation in the execution of the experiments
- Co-writer of the manuscript

Luhmann, N., Doerr, D., Chauve, C., *Comparative Scaffolding and Gap Filling of Ancient Bacterial Genomes Applied to Two Ancient Yersinia pestis Genomes*, Microbial Genomics, Vol. 3:9, e000123, 2017

- Analysis of the conservation of insertion sequence (IS) elements in ancient *Yersinia pestis* genomes

Doerr, D., Balaban, M., Feijão, P., Chauve, C., *The Gene Family-free Median of Three*, Algorithms in Molecular Biology, Vol. 12:14, 1, 2017

- Co-initiator and co-coordinator of the research
- Proof of computational complexity, development of the presented methods, major participation in the execution of the experiments
- Main writer of the manuscript
- Contains work established in Ph. D. thesis

Doerr, D., Kowada, L.A.B., Araujo, E., Deshpande, S., Dantas, S., Moret., B.M.E., Stoye, J., *New Genome Similarity Measures based on Conserved Gene Adjacencies*, Journal of Computational Biology, Vol. 26:6, 616-634, 2017

- Participation in the analysis of the computational complexities, implementation of the algorithms, design and major participation in the execution of the experiments
- Major writer of the manuscript

Lechner, M., Hernandez-Rosales, M., Doerr, D., Wieseke, N., Thévenin, A., Stoye, J., Hartmann, R.K., Prohaska, S.J., Stadler, P.F. *Orthology Detection Combining Clustering and Synteny for Very Large Datasets*, PLoS ONE, Vol. 9:8, p. e105015, 2014

- Development and implementation of the heuristic for synteny detection
- Participation in the execution of the simulations

Doerr, D., Stoye, J., Böcker, S., Jahn, K., *Identifying Gene Clusters by Discovering Common Intervals in Indeterminate Strings*, BMC Genomics, Vol. 15/Suppl 6, S2, 2014

- Design of the computational models, co-development and implementation of the algorithms, co-design and major participation in the execution of the experiments
- Major writer of the manuscript
- Work is part of Ph. D. thesis

Doerr, D., Gronau, I., Moran, S., Yavneh, I., *Stochastic Errors vs. Modeling Errors in Distance-based Phylogenetic Reconstructions.* Algorithms in Molecular Biology, Vol. 7, 22, 2012

- Execution of the simulations and experiments
- Co-writer of the manuscript
- Work is part of Master thesis

Proceedings

Bonnet, K., Marschall, T., Doerr, D., *Constructing founder sets under allelic and non-allelic homologous recombination*, Proceedings of WABI 2022, LIPIcs. Vol 6, 1-23, 2022

- Co-led of the research project
- Conceived and co-implemented the algorithms
- Main writer of the manuscript

Rubert, D.P., Doerr, D. Braga, M.D., *The potential of family-free rearrangements towards gene orthology inference*, Proceedings of RECOMB-CG 2021, Journal of bioinformatics and computational biology, Vol. 19 (06), 2140009, 2021

- Contributed computational experiments

Doerr, D., Chauve, C., *Small parsimony for natural genomes in the DCJ-indel model*, Proceedings of RECOMB-CG 2021, Journal of bioinformatics and computational biology, Vol. 19 (06), 2140009, 2021

- Conceived the computational model and algorithm
- Performed all computational experiments
- Main writer of the manuscript

Bohnenkämper, L., Braga, M. D. V., Doerr, D., Stoye, J., *Computing the rearrangement distance of natural genomes*, Proceedings of RECOMB 2020, LNCS, Vol. 12074, 3-18, 2020

- Co-author of the integer linear program
- Analysis of the genomic data
- Co-writer of the manuscript

Rubert, D., Martinez, F. H. V., Stoye, J., Doerr, D., *Analysis of local genome rearrangement improves resolution of ancestral genomic maps in plants*, Proceedings of RECOMB-CG 2019, BMC Genomics, Vol. 21/Suppl 2, 2020

- Coordination of the research
- Analysis of the genomic data and software development
- Main writer of the manuscript

Schulz, T., Stoye, J., Doerr, D., *Finding Teams in Graphs and its Application to Spatial Gene Cluster Discovery*, Proceedings of RECOMB-CG 2017, LNCS, Vol. 10562, 197-212, 2017

- Coordination of the research
- Co-design of the computational model, development and implementation of the algorithm, design and major participation in the execution of the experiments
- Co-writer of the manuscript

Doerr, D., Feijão, P., Balaban, M., Chauve, C., *The Gene Family-free Median of Three*, Proceedings of WABI 2016, Algorithms in Bioinformatics, LNCS, Vol. 9838, 102-120, 2016

- Co-initiator and co-coordinator the research
- Proof of computational complexity, development of the presented methods, major participation in the execution of the experiments
- Main writer of the manuscript
- Contains work established in Ph. D. thesis

Kowada, L.A.B., Doerr, D., Dantas, S., Stoye, J., *New Genome Similarity Measures based on Conserved Gene Adjacencies*, Proceedings of RECOMB 2016, LNBI, Vol. 9649, 204-224, 2016

- Co-analysis of the computational complexities, implementation of the algorithms, design and major participation in the execution of the experiments
- Major writer of the manuscript

Doerr, D., Hu, K., Renly, S., Edlund, S., Davis, M., Kaufman, J. H., Lessler, J., Filter, M., Käsbohrer, A., Appel, B., *Accelerating Investigation of Food-borne Disease Outbreaks using Pro-active Geospatial Modeling of Food Supply Chains*, Proceedings of HealthGIS 2012, ACM SIGSPATIAL, 2012

- Co-design of the computational model, implementation of the algorithms, design and execution of the experiments
- Major writer of the manuscript

Doerr, D., Thévenin, A., Stoye, J., *Gene Family Assignment-free Comparative Genomics*, Proceedings of RECOMB-CG 2012, BMC Bioinformatics, Vol. 13/Suppl 19, S3, 2012

- Co-design of the computational model, co-implementation of the algorithms and execution of the experiments, design of the analysis on real data
- Major writer of the manuscript
- Work is part of Ph. D. thesis

Doerr, D., Gronau, I., Moran, S., Yavneh, I., *Stochastic Errors vs. Modeling Errors in Distance-based Phylogenetic Reconstructions (Extended Abstract)*, Proceedings of WABI 2011, Algorithms in Bioinformatics, LNCS, Vol. 6833, 49-60, 2011

- Execution of the simulations and experiments
- Co-writer of the manuscript

Book Chapters

Doerr, D., Stoye, J., *A Perspective on Comparative and Functional Genomics.* Computational Biology, Bioinformatics and Phylogenetics, Vol. 29., pp. 361-372, 2019

- Design of the computational model, implementation of the algorithms and execution of the experiments, design of the analysis on real data
- Main writer of the manuscript

Doerr, D., Moret, B.M.E., *Sequence-Based Synteny Analysis of Multiple Large Genomes*, Comparative Genomics: Methods and Protocols, Methods in Molecular Biology, Springer, Ch. 11, Vol. 1704, 2018

- Design of the hands-on tutorial
- Co-writer of the manuscript

Doerr, D., Feijão, P., Stoye, J., *Family-Free Genome Comparison*, Comparative Genomics: Methods and Protocols, Methods in Molecular Biology, Springer, Ch. 12, Vol. 1704, 2018

- Implementation of the workflow
- Main writer of the manuscript

Dörr, D., *Genfamilienfreier Genomvergleich*, Ausgezeichnete Informatikdissertationen 2015, Lecture Notes in Informatics, Gesellschaft für Informatik, 91-100, 2016

- Extended abstract of Ph. D. thesis (german)

Braga, M.D.V., Chauve, C., Doerr, D., Jahn, K., Stoye, J., Thévenin, A., Wittler, R., *The Potential of Family-Free Genome Comparison*, Models and Algorithms for Genome Evolution, Springer, Ch. 13, 287-307, Vol. 19, 2013

- Participation in the formulation of the research direction
- Co-writer of the manuscript
- Work is part of Ph. D. thesis

PATENTS

Davis, M. A., Edlund, S. B., Kun, H., Kaufman, J. H., Renly, S. R., Dörr, D., *Proactive Simulation and Detection of Outbreaks based on Product Data*, patent number US2014/0365270A1, 2014

CONFERENCE AND INVITED TALKS

05/2022	International Genome Graph Symposium, Monte Verita, Ascona, Switzerland Title: *Founder set construction under allelic and non-allelic homologous recombination*
09/2021	18th Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG), virtually held Title: *Small Parsimony for Natural Genomes in the DCJ-Indel Model*
02/2020	Workshop "Data Structures in Bionformatics", National Institute for Research in Computer Science and Automation (INRIA), Rennes, France Title: *Hierarchical organization of syntenic blocks in large genomic datasets*
12/2019	Workshop "Comparative Genomics in Campo Grande", Federal University of Mato Grosso do Sul (UFMS), Campo Grande, MS, Brazil, **invited talk** Title: *Hierarchical organization of syntenic blocks in large genomic datasets*
10/2019	17th Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG), Montpellier, France Title: *Analysis of local genome rearrangement improves resolution of ancestral genomic maps in plants*
12/2018	Colloquium of the Centre for Mathematical Biology, University of Bath, UK, co-speaker Dr. Hans-Wilhelm Nützmann, **invited talk** Title: *Chromosome conformation and regulation of metabolic gene clusters in A. thaliana*
06/2018	Kolloquium für Bioinformatik und Systembiologie Mittelhessen (KoBIS), Technische Hochschule Mittelhessen, Gießen, Germany, **invited talk** Title: *GraphTeams: a method for discovering spatial gene clusters in Hi-C sequencing data*
09/2017	TN-IIS Meeting, Queensland University of Technology, Brisbane, Australia, **invited talk** Title: *Large-Scale Genome Comparison*
06/2017	Bernard Moret Festschrift, UC Berkeley, USA, **invited talk** Title: *Principled Synteny using Common intervals and Hierarchical Organization (PSyCHO)*
08/2016	16th Workshop on Algorithms in Bioinformatics (WABI), Aarhus, Denmark Title: *The Gene Family-free Median of Three*
06/2016	Mathematical and Computational Evolutionary Biology (MCEB), Hameau de l'Étoile, France Title: *Principled Synteny Analysis*
05/2016	Colloquium of the GI dissertation award 2015, Schloss Dagstuhl, Germany, **invited talk** Title: *Genfamilienfreier Genomvergleich* (German)
04/2016	20th International Conference on Research in Computational Molecular Biology (RE-COMB), Santa Monica, CA, United States Title: *New Genome Similarity Measures based on Conserved Gene Adjacencies*
10/2014	12th Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG), Cold Spring Harbor, NY, United States Title: *Identifying Gene Clusters by Discovering Common Intervals in Indeterminate Strings*

09/2012	10th Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG), Niterói, Brazil Title: *Gene Family Assignment-free Comparative Genomics*
09/2011	11th Workshop on Algorithms in Bioinformatics (WABI), Saarbrücken, Germany Title: *Stochastic Errors vs. Modeling Errors in Distance-based Phylogenetic Reconstructions*
06/2011	Phylogenetics: New Data, New Phylogenetic Challenges, Isaac Newton Institute for Mathematical Sciences, Cambridge, United Kingdom Title: *Stochastic Errors vs. Modeling Errors in Distance-based Phylogenetic Reconstructions*

Last updated December 28, 2022