

DR. DANIEL DÖRR

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| CONTACT | <i>Address</i> | Institute for Medical Biometry and Bioinformatics University Hospital Düsseldorf Moorenstr. 5 40225 Düsseldorf Germany |
| | <i>Phone</i> | +49 (0) 211 81-06562 |
| | <i>Email</i> | mail@danieldoerr.de |
| | <i>Website</i> | https://danieldoerr.de/ |
| NATIONALITY | German | |

SUMMARY

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

PROFESSIONAL EXPERIENCE

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

PROFESSIONAL ACTIVITIES

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| Member | <i>Program Committee for the 17th RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), Montpellier (France), 2019</i> |
| Member | <i>Program Committee for the 18th Workshop on Algorithms in Bioinformatics (WABI), Helsinki (Finland), 2018</i> |
| Member | <i>Program Committee for the 16th RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), Magog-Orford (Canada), 2018</i> |

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 “*interKontakt*”, 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*

GRANTS (MAJOR CONTRIBUTIONS)

- Horizon 2020 project, European Training Network “*Algorithms for Pangenome Computational Analysis (AL-PACA)*”, 2020, funding: 3.7M €

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

WS 2020/2021 Co-Lecturer, Heinrich Heine University Düsseldorf, *Medical Data Science*, graduate lecture f. medical students
WS 2020/2021 Co-Lecturer, Heinrich Heine University Düsseldorf, *Computational Multi-omics*, seminar f. 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 Lecturer for two dates, 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 Lecturer for two dates, 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

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| SS 2013 | Co-lecturer, Bielefeld University, <i>Bioinformatics Applications in Genome Research</i> , graduate seminar |
| WS 2012/2013 | Teaching assistant, Bielefeld University, <i>Phylogenetics</i> , undergraduate lecture |
| SS 2012 | Co-lecturer, Bielefeld University, <i>ROSE – Random model of Simulated Evolution</i> , graduate project course |
| WS 2011/2012 | Teaching assistant, Bielefeld University, <i>Phylogenetics</i> , undergraduate lecture |
| SS 2011 | Teaching assistant (coordination of exercises), Bielefeld University, <i>Sequence Analysis II</i> , undergraduate lecture |
| SS 2010 | Teaching assistant, Technion, <i>Project in Advanced Programming</i> , undergraduate project course |
| SS 2008 | Teaching assistant, Bielefeld University, <i>Algorithms and Data Structures II</i> , undergraduate lecture |
| WS 2007/2008 | Teaching assistant, Bielefeld University, <i>Algorithms and Data Structures I</i> , undergraduate lecture |

COORDINATION OF SCIENTIFIC MEETINGS

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|-----------------|------------------------------------------------------------------------------|
| 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

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|-------------------|----------------------------------------------------------------------------------------------|
| 09/2011 – 04/2015 | Mentor in the program “ <i>interKontakt</i> ”, Welcome Centre, Bielefeld University, Germany |
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SCIENTIFIC PORTFOLIO

SCIENTIFIC PUBLICATIONS

Journal Articles

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

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*, application number 13/914,039, 2013

CONFERENCE AND INVITED TALKS

- 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 (RECOMB), 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*