

DR. DANIEL DÖRR

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DATE OF BIRTH	June 1, 1983	
NATIONALITY	German	

SUMMARY

- Dr. rer. nat. in bioinformatics with excellent dissertation
- Long-term researcher in genomics, mathematical modeling and algorithm design
- Interdisciplinary scholar with broad understanding of biological processes, evolutionary in particular
- Junior scientist with excellent communication skills and competence in leading research teams

PROFESSIONAL EXPERIENCE

01/2017 – now	<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

Member	<i>Program Committee for the 18th Workshop on Algorithms in Bioinformatics (WABI), 2018</i>
Member	<i>Program Committee for the 16th RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), 2018</i>

UNIVERSITY EDUCATION

12/2010 – 04/2015	Dr. rer. nat., Faculty of Technology, Bielefeld University, Germany <i>Thesis:</i> <i>Gene Family-free Genome Comparison</i> <i>Graduate schools:</i> <i>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</i>
10/2008 – 11/2010	M. Sc. in Bioinformatics and Genome Research, Bielefeld University, Germany <i>Thesis:</i> <i>Non-additive Substitution Rate Functions in Distance-Based Phylogenetic Reconstructions</i>
10/2005 – 09/2008	B. Sc. in Bioinformatics and Genome Research, Bielefeld University, Germany <i>Thesis:</i> <i>A Feature-based Multiple Alignment Approach for Gas-chromatography-Mass Spectrometry Experiments</i>

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 – 05/2014 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*

SCIENTIFIC PORTFOLIO

SCIENTIFIC PUBLICATIONS

Journal Articles

- 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
- Luhmann, N., Doerr, D., Chauve, C., *Comparative Scaffolding and Gap Filling of Ancient Bacterial Genomes Applied to Two Ancient Yersinia pestis Genomes*, Microbial Genomics, 2017
- Doerr, Balaban, M., D., Feijão, P., Chauve, C., *The Gene Family-free Median of Three*, Algorithms in Molecular Biology, Vol. 12:14, 1, 2017
- 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
- 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
- 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
- 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

Proceedings

- 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
- 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
- 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
- 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
- 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
- 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

Book Chapters

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

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