

Jörg Fallmann

CV

Jahnallee 61
04177 Leipzig

Germany

✉ joerg@fallmann.info
🌐 www.fallmann.info/joerg

0000-0002-4573-9939

🌐 [jfallmann](https://orcid.org/0000-0002-4573-9939)

Summary

Current position: Postdoctoral Researcher Stadler Lab, Department for Mathematics and Informatics; Background in bioinformatics and molecular biology with focus on RNA and cell biology; 32 peer-reviewed publications; International and interdisciplinary collaborations; Organization of scientific and training events as co- and main organizer; Reviewing experience; Teaching experience in computer science, bioinformatics and molecular biology; Mentoring of 4 PhD students together with Peter F. Stadler and 3 Master Students as (Co-)Supervisor.

Research Interests

RNA Biology; Gene Expression Regulation; Bioinformatics; High-throughput Data Analysis; FAIR Data Science; Molecular Biology; Biomarker

Personal Information

Fullname	Jörg Fallmann, PhD.
Date of Birth	26 February 1984.
Place of Birth	Vienna.
Address	Bioinformatics, University of Leipzig, Härtelstr. 16-18, D-04107 Leipzig, Germany.
Nationality	Austria.
Civil Status	Married, 1 child (*2021).
Email	joerg@fallmann.info.
Homepage	https://www.fallmann.info/joerg.
ORCID	https://orcid.org/0000-0002-4573-9939.

Education

since 2016	Postdoctoral researcher with Prof. Peter F. Stadler , <i>Professorship for Bioinformatics, University of Leipzig.</i>
17.11.2016	Ph.D. , <i>University of Vienna.</i>
2012-2016	PhD Thesis , <i>Institute for theoretical Chemistry, University of Vienna, Group Prof. Ivo Hofacker, 1090 Vienna, Bioinformatical analysis of RNA - protein interactions in AU-rich element mediated decay.</i>
16.12.2011	Mag. rer. nat. , <i>University of Vienna, Graduation with distinction.</i>
2010-2011	Master's Thesis , <i>Institute for Theoretical Chemistry, University of Vienna, Group Prof. Ivo Hofacker, 1090 Vienna, Investigation and prediction of interactions between AU-rich binding proteins and AU rich elements and the generation of the 'AREsite' webserver.</i>
2004–2011	Undergraduate studies , <i>Molecular Biology, University of Vienna.</i>
1999–2004	Federal Training and Research Institute for Industrial Chemistry HBLVA Rosensteingasse , <i>1170 Vienna.</i>

Professional Experience

2016-2022	Teaching/Assisting , <i>Algorithms and Data Structures I+II, RNA Regulation, Advanced Methods in Bioinformatics, Institute for Informatics, University of Leipzig, 04107 Leipzig.</i>
2012-2015	University assistant , <i>Institute for Theoretical Chemistry, University of Vienna, 1090 Vienna.</i>
2009-2010	Teaching , <i>Max F Perutz Laboratories, 1030 Vienna, Student assistant in laboratory course: Molecular Biology Techniques.</i>
2008-2008	System Administrator , <i>Institute for Theoretical Chemistry, University of Vienna, 1090 Vienna, Administration of workstations, cluster machines and network.</i>

Parental leave

01-03,08/2022	Paternity leave.
01-04 2023	Part time work 32h (Partnerschaftsmonate).

Reviewing

Since 2011	Manuscripts , <i>Bioinformatics</i> , <i>BMC-Bioinformatics</i> , <i>RNA Biology</i> , <i>NAR genomics and bioinformatics</i> , <i>Molecular Biology and Evolution</i> , <i>Protein and Peptide Letters</i> , <i>others..</i>
2021	Review of proposal , <i>BSF, US-Israel Binational Science Foundation..</i>
2017	Conference proceedings , <i>RECOMB</i> .

Presentations and Posters at Conferences and Seminars

11/2019	Talk , <i>DAAD Seminar: 'RNA bioinformatics'</i> , Sao Paulo, Brazil.
08/2019	Talk , <i>Dagstuhl Seminar 19342: 'Advances and Challenges in Protein-RNA Recognition, Regulation and Prediction'</i> , Wadern, Germany.
11/2018	Talk , <i>DAAD Seminar: 'RNA bioinformatics'</i> , Rio de Janeiro, Brazil.
09/2018	Poster , <i>German Conference on Bioinformatics: 'The RNA Workbench 2.0.19'</i> , Vienna, Austria.
06/2018	Talk , <i>IZBI Workshop „Genome Bioinformatics for Health“: 'de.NBI, Galaxy and my work'</i> , Grimma, Germany.
2016-2020	Poster, annually , <i>de.NBI meeting: 'The RNA bioinformatics center Leipzig'</i> , Bielefeld/Berlin, Germany.
since 2008	Regular talks at seminars almost every year. <ul style="list-style-type: none">○ February: <i>Winterseminar</i>, Bled, Slovenia. Organized by TBI Vienna.○ October: <i>Herbstseminar</i>, Doubice, Czech Republic. Organized by Bioinformatics Leipzig.

List of Courses

01/04/16 - 01/04/23	Teaching winter term , <i>Algorithms and Data structures I</i> assisting Thomas Gatter, Sven Findeiss and Peter F. Stadler.
01/04/16 - 01/04/23	Teaching summer term , <i>Algorithms and Data structures II</i> assisting with Thomas Gatter, Sven Findeiss and Peter F. Stadler.
01/04/21 - 01/07/21	Special Lecture , <i>Advanced Methods in Bioinformatics</i> together with Peter F. Stadler.
01/04/22 - 01/07/22	Special Lecture , <i>Advanced Methods in Bioinformatics</i> together with Thomas Gatter and Peter F. Stadler.

- 01/04/18 - 01/07/18 **Special Lecture**, *RNA Regulation* together with Stephan Bernhart, Stefanie Kehr and Zasha Weinberg.
- 01/02/16 - 31/12/22 **Workshops, on-demand**, *NGS Analysis* together with the de.NBI team of the RNA bioinformatics center Freiburg.
- 09/09/18 - 13/09/18 **Winter school**, *RNA Secondary Structures* together with Kevin Lamkiewicz.
- 25/09/17 - 29/09/17 **Summer school**, *Computational Genomics and RNA Biology* together with Peter F. Stadler and de.NBI RNA bioinformatics center training team.

Theses Supervision

- 2019 - 2022 **Supervision PhD Thesis**, Cristian Velandia: *Workflows for the Large-Scale Assessment of miRNA Evolution* together with Peter F. Stadler.
- 2018 - 2021 **Supervision PhD Thesis**, Rituparno Sen: *Computational Characterization of Long Non-coding RNAs* together with Peter F. Stadler.
- 2017 - 2020 **Supervision PhD Thesis**, Anne Hoffmann: *The marvelous world of tRNAs* together with Peter F. Stadler.
- 2016 - 2019 **Supervision PhD Thesis**, Ali Yazbeck: *Improved Workflows for RNA Homology Search* together with Peter F. Stadler.
- 2020 **Supervision Master student**, Robin Goldmann: *Modular Analysis of Differential Splicing and Transcript Isoform Quantification using RNA-Seq Data*.
- 2020 **Supervision Master student**, Christiane Gärter: *RAP: Ribozeq Analysis Pipeline*.
- 2020 **Co-Supervision Master student**, Christopher Klapproth: *Support vector machine retraining for de novo detection of functional non-coding RNAs*, Main supervisor Sven Findeiss.

Collaborators

Peter F. Stadler (Bioinformatics, Leipzig University), Zasha Weinberg (Bioinformatics, Leipzig University), Christina Weinberg (Institute for Biochemistry, Leipzig University), Mario Mörl (Institute for Biochemistry, Leipzig University), Heike Betat (Institute for Biochemistry, Leipzig University), Anita Marchfelder (Universität Ulm), Thomas Arendt (Universitätsklinikum Leipzig), Peter Kovacs (Universitätsklinikum Leipzig), Jörg Hackermüller (Helmholtz-Zentrum für Umweltforschung), Kristin Reiche (Fraunhofer IZI), Christian Arnold (EMBL Heidelberg), Matthias Blüher (Universitätsklinikum Leipzig), Rolf Backofen (Universität Freiburg), Julian König (IMB Mainz), Manja Marz (Friedrich-Schiller-Universität Jena), Maria Emilia MT Walter (Universidade de Brasília - UnB), Alexandre Paschoal (Federal University of Technology, Paraná/Brazil), Douglas Domingues (University of São Paulo), Steve Hoffmann (FLI Jena), Christoph Grevelding (Institute for Parasitology, Giessen University)

Languages

German: native

English: advanced

Computer skills

Programming: Python, Perl, C++, Bash, JS

OS: Linux, Windows

Misc: R, Latex, Galaxy, Conda, MySQL

Publications

ORCID: <https://orcid.org/0000-0002-4573-9939>

The annotations **XX** report citation numbers according to Google scholar as of writing, **YY%** estimates my contributions.

Peer-Reviewed Publications

- [1] V. J. Olzog, L. I. Freist, R. Goldmann, J. Fallmann, and C. E. Weinberg, “Application of RtcB ligase to monitor self-cleaving ribozyme activity by RNA-seq,” *Biological Chemistry*, Jan. 2022, ISSN: 1437-4315. DOI: 10.1515/hsz-2021-0408 **20%** **2**
- [2] J. Wörtz, V. Smith, J. Fallmann, S. König, T. Thuraisingam, P. Walther, H. Urlaub, P. F. Stadler, T. Allers, F. Hille, and A. Marchfelder, “Cas1 and Fen1 Display Equivalent Functions During Archaeal DNA Repair,” *Frontiers in Microbiology*, vol. 13, 2022, ISSN: 1664-302X **10%** **1**
- [3] R. M. Chakaroun, L. Massier, A. Heintz-Buschart, N. Said, J. Fallmann, A. Crane, T. Schütz, A. Dietrich, M. Blüher, M. Stumvoll, N. Musat, and P. Kovacs, “Circulating bacterial signature is linked to metabolic disease and shifts with metabolic alleviation after bariatric surgery,” *Genome Medicine*, vol. 13, no. 1, p. 105, Jun. 22, 2021, ISSN: 1756-994X. DOI: 10.1186/s13073-021-00919-6 **10%** **8**
- [4] T. Gatter, S. von Löhneysen, J. Fallmann, P. Drozdova, T. Hartmann, and P. F. Stadler, “LazyB: Fast and cheap genome assembly,” *Algorithms for molecular biology: AMB*, vol. 16, no. 1, p. 8, Jun. 1, 2021, ISSN: 1748-7188. DOI: 10.1186/s13015-021-00186-5. pmid: 34074310 **10%** **2**
- [5] A. Hoffmann, L. Erber, H. Betat, P. F. Stadler, M. Mörl, and J. Fallmann, “Changes of the tRNA Modification Pattern during the Development of Dictyostelium discoideum,” *Non-coding RNA*, vol. 7, no. 2, p. 32, May 28, 2021, ISSN: 2311-553X. DOI: 10.3390/ncrna7020032. pmid: 34071416 **25%** **0**
- [6] N. A. N. Jorge, U. Ueberham, M. Knobloch, P. F. Stadler, J. Fallmann, and T. Arendt, “Disturbance of phylogenetic layer-specific adaptation of human brain gene expression in Alzheimer’s disease,” *Scientific Reports*, vol. 11, no. 1, p. 20200, Oct. 12, 2021, ISSN: 2045-2322. DOI: 10.1038/s41598-021-99760-5. pmid: 34642398 **25%** **1**
- [7] C. Klapproth, R. Sen, P. F. Stadler, S. Findeiß, and J. Fallmann, “Common Features in lncRNA Annotation and Classification: A Survey,” *Non-Coding RNA*, vol. 7, no. 4, p. 77, Dec. 2021, ISSN: 2311-553X. DOI: 10.3390/ncrna7040077 **30%** **5**
- [8] E. Parra-Rincón, C. A. Velandia-Huerto, A. Gittenberger, J. Fallmann, T. Gatter, F. D. Brown, P. F. Stadler, and C. I. Bermúdez-Santana, “The Genome of the “Sea Vomit” *Didemnum vexillum*,” *Life*, vol. 11, no. 12, p. 1377, Dec. 2021, ISSN: 2075-1729. DOI: 10.3390/life11121377 **10%** **1**
- [9] H. Saker, R. Machné, J. Fallmann, D. B. Murray, A. M. Shahin, and P. F. Stadler, “Weighted Consensus Segmentations,” *Computation*, vol. 9, no. 2, p. 17, 2 Feb. 2021. DOI: 10.3390/computation9020017 **20%** **0**
- [10] C. A. Velandia-Huerto, J. Fallmann, and P. F. Stadler, “miRNAture—Computational Detection of microRNA Candidates,” en, *Genes*, vol. 12, no. 3, p. 348, Mar. 2021, Number: 3 Publisher: Multidisciplinary Digital Publishing Institute. DOI: 10.3390/genes12030348 **30%** **2**

- [11] L. Erber, A. Hoffmann, J. Fallmann, M. Hagedorn, C. Hammann, P. F. Stadler, H. Betat, S. Prohaska, and M. Mörl, “Unusual Occurrence of Two Bona-Fide CCA-Adding Enzymes in Dictyostelium discoideum,” en, *International Journal of Molecular Sciences*, vol. 21, no. 15, p. 5210, Jan. 2020. DOI: 10.3390/ijms21155210 **15%** **4**
- [12] S. M. Hoser, A. Hoffmann, A. Meindl, M. Gamper, J. Fallmann, S. H. Bernhart, L. Müller, M. Ploner, M. Misslinger, L. Kremser, H. Lindner, S. Geley, H. Schaal, P. F. Stadler, and A. Huettnerhofer, “Intronic tRNAs of mitochondrial origin regulate constitutive and alternative splicing,” *Genome Biology*, vol. 21, no. 1, p. 299, Dec. 2020, ISSN: 1474-760X. DOI: 10.1186/s13059-020-02199-6 **15%** **3**
- [13] L. Massier, R. Chakaroun, S. Tabei, A. Crane, K. D. Didt, J. Fallmann, M. von Bergen, S.-B. Haange, H. Heyne, M. Stumvoll, M. Gericke, A. Dietrich, M. Blüher, N. Musat, and P. Kovacs, “Adipose tissue derived bacteria are associated with inflammation in obesity and type 2 diabetes,” en, *Gut*, gutjnl-2019-320118, Apr. 2020, ISSN: 0017-5749, 1468-3288. DOI: 10.1136/gutjnl-2019-320118 **10%** **86**
- [14] A. Nitsche, C. Arnold, U. Ueberham, K. Reiche, J. Fallmann, J. Hackermüller, F. Horn, P. F. Stadler, and T. Arendt, “Alzheimer-related genes show accelerated evolution,” en, *Molecular Psychiatry*, pp. 1–7, Mar. 2020, ISSN: 1476-5578. DOI: 10.1038/s41380-020-0680-1 **10%** **6**
- [15] I. Nowak, E. Boratyn, S. Student, S. F. Bernhart, J. Fallmann, M. Durbas, P. F. Stadler, and H. Rokita, “MCPIP1 ribonuclease can bind and cleave AURKA mRNA in MYCN-amplified neuroblastoma cells,” *RNA Biology*, vol. 0, no. 0, pp. 1–13, Aug. 2020, ISSN: 1547-6286. DOI: 10.1080/15476286.2020.1804698 **10%** **4**
- [16] R. Sen, J. Fallmann, M. E. M. T. Walter, and P. F. Stadler, “Are spliced ncRNA host genes distinct classes of lncRNAs?” *Theory in Biosciences*, vol. 139, no. 4, pp. 349–359, 2020, ISSN: 1431-7613. DOI: 10.1007/s12064-020-00330-6 **20%** **1**
- [17] N. Bašić, S. J. Berkemer, J. Fallmann, P. W. Fowler, T. Gatter, T. Pisanski, N. Retzlaff, P. F. Stadler, and S. S. Zemljč, “Convexity Deficit of Benzenoids,” en, *Croatica Chemica Acta*, vol. 92, no. 4, pp. 457–466, Nov. 2019, ISSN: 0011-1643. DOI: 10.5562/cca3602 **10%** **3**
- [18] L. Erber, A. Hoffmann, J. Fallmann, H. Betat, P. F. Stadler, and M. Mörl, “LOTTE-seq (Long hairpin oligonucleotide based tRNA high-throughput sequencing): Specific selection of tRNAs with 3'-CCA end for high-throughput sequencing,” *RNA Biology*, vol. 0, Sep. 2019, ISSN: 1547-6286. DOI: 10.1080/15476286.2019.1664250 **20%** **13**
- [19] J. Fallmann, P. Videm, A. Bagnacani, B. Batut, M. A. Doyle, T. Klingstrom, F. Eggenhofer, P. F. Stadler, R. Backofen, and B. Grüning, “The RNA workbench 2.0: next generation RNA data analysis,” *Nucleic Acids Research*, May 2019, ISSN: 0305-1048. DOI: 10.1093/nar/gkz353. eprint: <http://oup.prod.sis.lan/nar/advance-article-pdf/doi/10.1093/nar/gkz353/28578734/gkz353.pdf> **40%** **7**
- [20] A. M. Yazbeck, P. F. Stadler, K. Tout, and J. Fallmann, “Automatic curation of large comparative animal MicroRNA datasets,” *Bioinformatics*, Apr. 2019, ISSN: 1367-4803. DOI: 10.1093/bioinformatics/btz271. eprint: <http://oup.prod.sis.lan/bioinformatics/advance-article-pdf/doi/10.1093/bioinformatics/btz271/28670693/btz271.pdf> **35%** **9**
- [21] B. Grüning, R. Dale, A. Sjödin, B. A. Chapman, J. Rowe, C. H. Tomkins-Tinch, R. Valieris, and J. Köster, “Bioconda: Sustainable and comprehensive software distribution for the life sciences,” En, *Nature Methods*, vol. 15, no. 7, p. 475, Jul. 2018, ISSN: 1548-7105. DOI: 10.1038/s41592-018-0046-7 **10%** **612**

- [22] A. Hoffmann, J. Fallmann, E. Vilardo, M. Mörl, P. F. Stadler, and F. Amman, “Accurate mapping of tRNA reads,” en, *Bioinformatics*, vol. 34, no. 7, pp. 1116–1124, Apr. 2018, ISSN: 1367-4803. DOI: 10.1093/bioinformatics/btx756 20% 32 §
- [23] L. K. Kutsche, D. M. Gysi, J. Fallmann, K. Lenk, R. Petri, A. Swiersy, S. D. Klapper, K. Piracs, S. Khattak, P. F. Stadler, J. Jakobsson, K. Nowick, and V. Busskamp, “Combined Experimental and System-Level Analyses Reveal the Complex Regulatory Network of miR-124 during Human Neurogenesis,” English, *Cell Systems*, vol. 7, no. 4, 438–452.e8, Oct. 2018, ISSN: 2405-4712. DOI: 10.1016/j.cels.2018.08.011 20% 37 §
- [24] F. R. Sutandy, S. Ebersberger, L. Huang, A. Busch, M. Bach, H.-S. Kang, J. Fallmann, D. Maticzka, R. Backofen, P. F. Stadler, K. Zarnack, M. Sattler, S. Legewie, and J. König, “In vitro iCLIP-based modeling uncovers how the splicing factor U2AF2 relies on regulation by cofactors,” en, *Genome Research*, vol. 28, no. 5, pp. 699–713, May 2018, ISSN: 1088-9051, 1549-5469. DOI: 10.1101/gr.229757.117 5% 56 §
- [25] R. Backofen, J. Engelhardt, A. Erxleben, J. Fallmann, B. Grüning, U. Ohler, N. Rajewsky, and P. F. Stadler, “RNA-bioinformatics: Tools, Services and Databases for the Analysis of RNA-based Regulation,” en, *Journal of Biotechnology*, May 2017, ISSN: 01681656. DOI: 10.1016/j.jbiotec.2017.05.019 20% 21 §
- [26] J. Fallmann, S. Will, J. Engelhardt, B. Grüning, R. Backofen, and P. F. Stadler, “Recent advances in RNA folding,” *Journal of Biotechnology*, Bioinformatics Solutions for Big Data Analysis in Life Sciences presented by the German Network for Bioinformatics Infrastructure, vol. 261, pp. 97–104, Nov. 2017, ISSN: 0168-1656. DOI: 10.1016/j.jbiotec.2017.07.007 60% 69 §
- [27] B. A. Grüning, J. Fallmann, D. Yusuf, S. Will, A. Erxleben, F. Eggenhofer, T. Houwaart, B. Batut, P. Videm, A. Bagnacani, M. Wolfien, S. C. Lott, Y. Hoogstrate, W. R. Hess, O. Wolkenhauer, S. Hoffmann, A. Akalin, U. Ohler, P. F. Stadler, and R. Backofen, “The RNA workbench: Best practices for RNA and high-throughput sequencing bioinformatics in Galaxy,” en, *Nucleic Acids Research*, Jun. 2017, ISSN: 0305-1048, 1362-4962. DOI: 10.1093/nar/gkx409 25% 44 §
- [28] J. Fallmann, V. Sedlyarov, A. Tanzer, P. Kovarik, and I. L. Hofacker, “AREsite2: An enhanced database for the comprehensive investigation of AU/GU/U-rich elements,” *Nucleic Acids Research*, no. Database issue 44, 2016 75% 69 §
- [29] M. Hölzer, V. Kräling, F. Amman, E. Barth, S. H. Bernhart, V. A. O. Carmelo, M. Collatz, G. Doose, F. Eggenhofer, J. Ewald, J. Fallmann, L. M. Feldhahn, M. Fricke, J. Gebauer, A. J. Gruber, F. Hufsky, H. Indrischek, S. Kanton, J. Linde, N. Mostajo, R. Ochsenreiter, K. Riege, L. Rivarola-Duarte, A. H. Sahyoun, S. J. SaundeRs, S. E. Seemann, A. Tanzer, B. Vogel, S. Wehner, M. T. Wolfinger, R. Backofen, J. Gorodkin, I. Grosse, I. Hofacker, S. Hoffmann, C. Kaleta, P. F. Stadler, S. Becker, and M. Marz, “Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells,” en, *Scientific Reports*, vol. 6, no. 1, Dec. 2016, ISSN: 2045-2322. DOI: 10.1038/srep34589 10% 53 §
- [30] V. Sedlyarov, J. Fallmann, F. Ebner, J. Huemer, L. Sneezum, M. Ivin, K. Kreiner, A. Tanzer, C. Vogl, I. L. Hofacker, and P. Kovarik, “Tristetraprolin binding site atlas in the macrophage transcriptome reveals a switch for inflammation resolution,” en, *Molecular Systems Biology*, vol. 12, no. 5, pp. 868–868, May 2016, ISSN: 1744-4292. DOI: 10.15252/msb.20156628 35% 61 §
- [31] M. T. Wolfinger, J. Fallmann, F. Eggenhofer, and F. Amman, “ViennaNGS: A toolbox for building efficient next-generation sequencing analysis pipelines,” *F1000Research*, vol. 4, 2015 30% 36 §

- [32] A. R. A. Gruber, J. Fallmann, F. Kratochvill, P. Kovarik, and I. L. Hofacker, "AREsite: A database for the comprehensive investigation of AU-rich elements.," *Nucleic acids research*, vol. 39, no. Database issue, pp. 1–4, Nov. 2011, ISSN: 1362-4962. DOI: 10.1093/nar/gkq990 50% 183

Submitted Manuscripts or Manuscripts in Preparation

- [1] J. Fallmann, R. Goldmann, and P. F. Stadler, "MONSDA: Modular Organizer of Nextflow and Snakemake driven HTS Data Analysis," DOI: 10.31219/osf.io/jeqgr 70% - 8
- [2] J. Fallmann, D. Rabsch, R. Backofen, and P. F. Stadler, "RNAm mediator: RNA secondary structure as mediator of intermolecular interaction," 40% - 8
- [3] S. Fuchs, C. Danßmann, F. Klironomos, A. Winkler, A. Szymansky, J. Naderi, J. Fallmann, S. Bernhart, K. Helmsauer, M.-L. Kirchner, P. Mertins, C. Suenkel, J. Toedling, P. Stadler, P. Hundsdoerfer, H. E. Deubzer, A. Künkele, P. Lang, J. Fuchs, A. Eggert, N. Rajewsky, and F. Hertwig, "Defining the landscape of circular RNAs in neuroblastoma unveils a global suppressive function of MYCN," p. 8, 10% - 8

Theses

- [1] J. Fallmann, "Bioinformatical Analysis of RNA - Protein Interactions in AU-Rich Element Mediated Decay," Ph.D. dissertation, University of Vienna, 2016. [Online]. Available: <http://othes.univie.ac.at/44276/>
- [2] J. Fallmann, "Investigation and Prediction of Interactions between AU-Rich Binding Proteins and AU Rich Elements and the Generation of the AREsite Webserver," M.S. thesis, University of Vienna, 2011. [Online]. Available: <http://othes.univie.ac.at/17132/>

Public Domain Software packages

- [1] Jörg Fallmann, Dominik Rabsch, *RNAm mediator*, 2022. [Online]. Available: <https://github.com/jfallmann/RNAm mediator>
- [2] Jörg Fallmann, Robin Goldmann, *MONSDA: Modular Organizer of Nextflow and Snakemake driven hts Data Analysis*, 2022. [Online]. Available: <https://github.com/jfallmann/MONSDA>
- [3] Ali Yazbeck, Jörg Fallmann, Cristian Velandia, *MIRfix*, 2020. [Online]. Available: <https://github.com/Bierinformatik/MIRfix>
- [4] Björn Grüning, Jörg Fallmann, Pavankumar Videm, *Galaxy RNA Workbench*, 2020. [Online]. Available: <https://github.com/bgruening/galaxy-rna-workbench>
- [5] Cristian Velandia, Jörg Fallmann, *miRNAture*, 2020. [Online]. Available: <https://github.com/Bierinformatik/miRNAture>
- [6] Rainer Machné, Jörg Fallmann, *ConsSeg: Weighted Consensus Segmentation in R*, 2020. [Online]. Available: <https://github.com/Bierinformatik/consseg>
- [7] Bioconda Team, *Bioconda*, 2018. [Online]. Available: <https://github.com/bioconda/bioconda-recipes>

Curriculum Vitae

Bruno Johann Schmidt

Personal Data

Name	Bruno Johann Schmidt
Date of Birth	30.11.1996
Place of Birth	Nordhausen
Address	Kirschbergstraße 68a, 04155 Leipzig, Deutschland
E-Mail	bruno@bioinf.uni-leipzig.de
Phone	+49 152 36867601

Education

since October 2022	PhD Student, Computer Science, Leipzig University, Supervisor: Peter F. Stadler, Topic: Phylogenetic Networks and Clustering Systems
October 2019 - September 2022	Bioinformatics, Master of Science, Leipzig University, Final Grade - 1.1
October 2016 - September 2019	Computer Science, Bachelor of Science, Leipzig University, Final Grade - 1.8
August 2007 - July 2015	A-Levels (Abitur), Staatliches Herder Gymnasium Nordhausen, Final Grade - 1.4

Work Experience

since January 2023

PhD Position
Max Planck Institute for
Mathematics in the Sciences,
Supervisor: Peter F. Stadler

April 2022 - December 2022

Research Assistant
Leipzig University,
Interdisciplinary Center for Bioinformatics IZBI,
Supervisor: Peter F. Stadler

January 2020 - December 2022

Freelance Work,
Courage Netzwerk für Demokratieförderung e.V.,
Consultant

October 2021 - February 2022

Student Assistant
Leipzig University,
Faculty for Bioinformatics
Trainer in the module sequence analysis

September 2021 - December 2021

Student Assistant
Leipzig University,
Interdisciplinary Centre for Bioinformatics (IZBI)
Leipzig
Characterization and identification of short non-coding RNAs

May 2021 - August 2021

Student Assistant
Leipzig University,
Faculty for Bioinformatics
Trainer in the module RNA and protein structures

October 2020 - December 2020

Student Assistant
Leipzig University,
Faculty for Mathematics & Computer Science
Design and revision of lecture slides for the module
algorithms and data structures I

September 2019 - October 2019;

February 2020 - December 2020

Student Assistant
Helmholtz Centre for Environmental Research,
Research Group BioGeoOmics
Database administration, automation, workflow design and implementation

October 2019

Student Assistant
Leipzig University,
Institute for Applied Informatics (InfAI),
Organizational aid at CLARIN
Annual Conference 2019

Additional Interests

Languages

German (native),
English (C1)

Academic Interests

Comparative Genomics, Phylogeny,
Permutations, Sorting Algorithms,
Graph Theory, Cluster Systems, Metrics

Technical Know-How

Python, Java, C, C#, R, bash, HTML, CSS

Date : 29.06.2023

Unterschrift :

A stylized, handwritten signature in black ink, consisting of a large, flowing 'L' shape followed by a horizontal line and a small loop.

CURRICULUM VITAE

NORA BEIER

PERSONAL DETAILS

Name: Nora Beier
Date of birth: 18. September 1987
Place of birth: Dresden

STUDIES

10/2015 - 03/2019 Hochschule Zittau/Görlitz, Zittau
Field of study: Molecular biotechnology
Degree: Bachelor of Science
10/2019 - 05/2022 University Leipzig
Field of study: Biochemie
Degree: Master of Science
10/2019 - 05/2022 Field of study: Bioinformatik
Degree: Master of Science
01/2023 - PhD Position Bioinformatics, University Leipzig

EDUCATION

09/2014 - 10/2015 BSZ of economics „Franz Ludwig Gehe“ Dresden
advanced technical college certificate

PRACTICAL EXPERIENCE

02/2018 - 07/2018 University Hospital Jena
Institute for Experimental Radiology
Intern for Bachelor Practical Module
08/2016 - 09/2016 University Hospital Carl Gustav Carsus Dresden,
Intern facultative
05/2019 - 09/2019 Biotechnology Centre TU Dresden,
Working group Brankatschk
research assistant

FURTHER TRAINING AND CAREER

10/2015 - 08/2014 working as a waiter
08/2007 - 07/2009 BSZ HOGA Schloss Albrechtsberg
Education: waiter
08/2004 - 07/2006 Academy for Information and Communication Design
Education: Technical design assistant



Nora Beier

Prager Straße 31
04315 Leipzig
☎ 0151/ 4044 17 13
✉ nora@bioinf.uni-leipzig.de

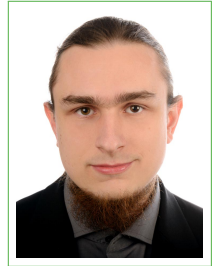
Thomas Gatter

Curriculum Vitae

Einsteinstr. 18
04229 Leipzig
Germany

☎ +49 (0) 1525 4020325
+49 (0) 341 97 16636

✉ thomas@bioinf.uni-leipzig.de



Education

Feb. 2022

Dr. rer. nat., Bioinformatik, Leipzig University, Germany

- final grade: *magna cum laude*
- thesis title: "New Algorithms for Fast and Economic Assembly: Advances in Transcriptome and Genome Assembly"

Sept. 2015

M.Sc. Naturwissenschaftliche Informatik, (*Informatics in the Natural Sciences*), Bielefeld University, Germany

- final grade: 1.0
- thesis title: "Integrating Pareto optimization into the dynamic programming framework Bellman's GAP"

Sept. 2013

B.Sc. Kognitive Informatik, (*Cognitive Informatics*), Bielefeld University, Germany

- final grade: 1.2
- thesis title: "Stream Pipelines for Cloudbased BiBiServ2 Services"

2009

Abitur, (*A-Level equivalent*), Lößnitzgymnasium Radebeul, Germany

- final grade: 1.3

Academic Work Experience

Since Nov. 2015
2023

PhD Student/Postdoctoral Researcher, Leipzig University, Germany

- new methods for RNA transcript isoform prediction and quantification
- new methods for hybrid genome assembly
- research on chemical networks
- AI models in graphs
- (birth of two children Jan. 2018 and Jun. 2021)

2014
2015

Research Assistant for Bellman's GAP, Bielefeld University, Germany

- development of the Bellman's GAP algebraic dynamic programming system
- analysis and extension of the framework to support Pareto Products

2011
2014

Research Assistant for BiBiServ, Bielefeld University, Germany

- development and maintenance of the Bielefeld University Bioinformatics Server
- development of cloud-based services

Teaching

Lecturer WiSe 2021/2022, SoSe 2022, WiSe 2022/2023, SoSe 2023
Lecture: Algorithmen und Datenstrukturen I+II (Algorithm and Data Structures)
Lecture: Graphen und biologische Netze (Graphs and Biological Networks)
Lecture: Fortgeschrittene Methoden der Bioinformatik (Advanced Methods in Bioinformatics)
at Leipzig University

Lead of Tutorials	WiSe 2020/2021, SoSe 2021, WiSe 2021/2022, SoSe 2022, WiSe 2022/2023, SoSe 2023 Lecture: Algorithmen und Datenstrukturen I+II (Algorithm and Data Structures) at Leipzig University
E-Learning Support	WiSe 2020/2021, SoSe 2021 Technical design, planning, setup and management of a recording and streaming service for the Bioinformatics Group at Leipzig University
Tutor	WiSe 2016/2017, WiSe 2019/2020, SoSe 2020 Lecture: Algorithmen und Datenstrukturen I+II (Algorithm and Data Structures) at Leipzig University
Tutor	WiSe 2016/2017, WiSe 2017/2018, WiSe 2019/2020 Lecture: Graphen und biologische Netze (Graphs and biological networks) at Leipzig University

Languages

German	Native	<i>first language</i>
English	Fluent	<i>daily practice, international conferences, experience in academic writing, IELTS Academic exam of 8.0 in 2008</i>
French	Basic Level	<i>4 years of school education</i>

Publications

- [1] Ernesto Parra-Rincón, Cristian A Velandia-Huerto, Jörg Fallmann, Adriaan Gittenberger, Thomas Gatter, Federico D Brown, Peter F Stadler, and Clara I Bermúdez-Santana. The genome of the "sea vomit" didemnum vexillum. *Life*, 2021. Submitted.
- [2] Thomas Gatter, Sarah von Löhneysen, Jörg Fallmann, Polina Drozdova, Tom Hartmann, and Peter F Stadler. Lazyb: fast and cheap genome assembly. *Algorithms for Molecular Biology*, 16(1):1–23, 2021.
- [3] Thomas Gatter and Peter F Stadler. Ryūtō: Improved multi-sample transcript assembly for differential transcript expression analysis and more. *Bioinformatics*, 2021.
- [4] Thomas Gatter, Sarah von Löhneysen, Polina Drozdova, Tom Hartmann, and Peter F. Stadler. Economic genome assembly from low coverage Illumina and Nanopore data. In Carl Kingsford and Nadia Pisanti Pisanti, editors, *20th International Workshop on Algorithms in Bioinformatics (WABI 2020)*, Leibniz International Proceedings in Informatics, page 10, Schloss Dagstuhl, 2020. Dagstuhl Publishing, German.
- [5] Manuela M do Almo, Isabel G Sousa, Waldeyr Mendes Cordeiro da Silva, Thomas Gatter, Peter F Stadler, Steve Hoffmann, Andrea Q Maranhão, and Marcelo Brigido. Anti-cd3 stimulated t cell transcriptome reveals novel ncarnas and correlates with a suppressive profile. In *Brazilian Symposium on Bioinformatics*, pages 180–191. Springer, 2020.
- [6] Thomas Gatter and Peter F Stadler. Ryūtō: network-flow based transcriptome reconstruction. *BMC bioinformatics*, 20(1):1–14, 2019.
- [7] Nino Bašić, Sarah J. Berkemer, Jörg Fallmann, Patrick W. Fowler, Thomas Gatter, Tomaž Pisanski, Nancy Retzlaff, Peter F. Stadler, and Sara Sabrina Zemljič. Convexity deficit of benzenoids. *Croatica Chemica Acta*, 92(4), 2019.

- [8] Sonja J Prohaska, Sarah J Berkemer, Fabian Gärtner, Thomas Gatter, Nancy Retzlaff, Christian Höner zu Siederdisen, Peter F Stadler, et al. Expansion of gene clusters, circular orders, and the shortest hamiltonian path problem. *Journal of mathematical biology*, pages 1–29, 2017.
- [9] Jon Ison, Kristoffer Rapacki, Hervé Ménager, Matúš Kalaš, Emil Rydza, Piotr Chmura, Christian Anthon, Niall Beard, Karel Berka, Dan Bolser, et al. Tools and data services registry: a community effort to document bioinformatics resources. *Nucleic acids research*, 44(D1):D38–D47, 2016.
- [10] Thomas Gatter, Robert Giegerich, and Cédric Saule. Integrating pareto optimization into dynamic programming. *Algorithms*, 9(1):12, 2016.
- [11] Michael Gatter, Thomas Gatter, and Falk Matthäus. Currf (codon usage regarding restriction finder): A free java®-based tool to detect potential restriction sites in both coding and non-coding dna sequences. *Molecular biotechnology*, 52(2):123–128, 2012.

Poster

2014

Krüger J, Gatter T, Henke C, Konermann S, Lückner A, Rumming M and Sczyrba A

BiBiCloud - a Cloud Computing Framework for Big Data Bioinformatics. German Conference on Bioinformatics 2014.

Conferences and Workshops

2016

SPP 1738 Summer School for RNA Bioinformatics, *Organizer and Lecturer*, Leipzig University, Germany

○ introduction to RNA bioinformatics for wet-lab biologists

2014

Cloud Computing Tutorial, *Lecturer*, German Conference on Bioinformatics

2014

ELIXIR Curation Hackathon, *Participant*, CBS-DTU, Denmark

○ development of the ELIXIR Tools & Data Services Registry

○ extension of the EDAM annotation vocabulary

○ annotation of a representative set of tools for the BiBiServ