

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. Zemljich, “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>