Thomas Gatter

Curriculum Vitae

Sept. 2013

2009

Since Nov. 2015

2014

2011

2014

2015

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Education Feb. 2022 **Dr. rer. nat.**, *Bioinformatik*, Leipzig University, Germany o final grade: magna cum laude o thesis title: "New Algorithms for Fast and Economic Assembly: Advances in Transcriptome and Genome Assembly" Sept. 2015 Bielefeld University, Germany

M.Sc. Naturwissenschaftliche Informatik, (Informatics in the Natural Sciences),

- o final grade: 1.0
- thesis title: "Integrating Pareto optimization into the dynamic programming framework
- B.Sc. Kognitive Informatik, (Cognitive Informatics), Bielefeld University, Germany
- o final grade: 1.2 o thesis title: "Stream Pipelines for Cloudbased BiBiServ2 Services"
- Abitur, (A-Level equivalent), Lößnitzgymnasium Radebeul, Germany
- o final grade: 1.3

Academic Work Experience

PhD Student/Postdoctoral Researcher, Leipzig University, Germany

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

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

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

Research Assistant for BiBiServ, Bielefeld University, Germany

- o 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 Bioin-

formatics)

at Leipzig University



1/3

Lead of Tutorials WiSe 2020/2021, SoSe 2021, WiSe 2021/2022, SoSe 2022, WiSe 2022/2023, SoSe 2022

2023

Lecture: Algorithmen und Datenstrukturen I+II (Algorithm and Data Structures) at Leipzig University

E-Learning WiSe 2020/2021, SoSe 2021

Support 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 first language

English Fluent daily practice, international conferences, experience in academic writing, IELTS

Academic exam of 8.0 in 2008

French Basic Level

4 years of school education

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 ncrnas 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 Siederdissen, 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.



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

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

o introduction to RNA bioinformatics for wet-lab biologists

Cloud Computing Tutorial, Lecturer, German Conference on Bioinformatics

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

- development of the ELIXIR Tools & Data Services Registry
- extension of the EDAM annotation vocabulary
- o annotation of a representative set of tools for the BiBiServ

2014



2016