Curriculum Vitæ

Dr. Martin Hölzer

Personal Data

Name:	Dr. rer. nat. Martin Hölzer
Gender:	Male
Place and Date of Birth:	Rudolstadt, Germany | 16 March 1988
Nationality:	German
Address:	Jansonstr. 11, 07745 Jena
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Family status:	Single

Scientific Education

01/2018	**Doctorate degree**, Dr. rer. nat. University of Jena Grade: summa cum laude Doctoral thesis: *The Dark Art of Next-Generation Sequencing: fundamental approaches for genomics, transcriptomics, and differential gene expression* Prof. Dr. Manja Marz, RNA Bioinformatics and High-Throughput Analysis Faculty of Mathematics and Computer Sciences
since 06/2017	Leader of a small bioinformatics group at University of Jena
08/2013–06/2017	PhD student at University of Jena
12/2012	**Diploma in Bioinformatics** University of Jena Grade: 1.4 Diploma thesis: *Data management of mass spectra and fragmentation trees with BExIS* Prof. Dr. Sebastian Böcker, Chair of Bioinformatics Faculty of Mathematics and Computer Sciences
10/2007–12/2012	Studies of Bioinformatics at University of Jena
2006–2007	Civilian service, Diakonisches Altenhilfezentrum, Bad Blankenburg
1998–2006	University entrance qualification, Friedrich-Fröbel-Gymnasium, Bad Blankenburg, Grade 2.0

Work Experience

Current | **Post-Doc & group leader**

RNA Bioinformatics/High-Throughput Analysis, Prof. Dr. Manja Marz, University of Jena

Supervision of Next-Generation Sequencing (NGS) projects including the automatization of workflows for assembly, annotation, variant calling, differential gene expression, and visualization of results. Development of novel applications for long-read sequencing data. Head of a fresh, small bioinformatics group at the University of Jena.

since 03/2017 | **EVBC member**

Founding member of the "European Virus Bioinformatics Center" (EVBC), University of Jena

The EVBC is intended to bring together virologists and bioinformaticians across Europe and provide a platform for interdisciplinary collaborative projects. My expertise covers sequencing, design and high-throughput analysis of virus-enriched and -infected biological samples.

08/2013–06/2017 | **PhD student**

RNA Bioinformatics/High-Throughput Analysis, Prof. Dr. Manja Marz, University of Jena

Management of various NGS projects comprising 1) experimental design, 2) selection of appropriate sequencing parameters, and 3) data analysis, visualization and interpretation. Development of pipelines for downstream bioinformatical analyses. Examination of (meta-)genomic/transcriptomic data with a special focus on *de novo* assembly, annotation, and identification of differential expressed protein- and non-coding genes. Contributions to the emerging field of virus bioinformatics.

09/2009–05/2012 | **Student assistant**

Chair of Bioinformatics, Prof. Dr. Sebastian Böcker, University of Jena

Integration of algorithms, data management and visualization for phylogenetic analyses and clustering.

Tasks beyond own research

- **Supervision of practical works**
  Lasse Feldhahn (started 10/2018)
  Jannes Spangenberg (started 10/2018)
  Daria Meyer (started 09/2018)
- **Supervision of bachlor theses**
  Rebekka Köhl (started 07/2018)
- **Supervision of master theses**
  Marie Lataretu (completed summer 2018)
  Ruman Gerst (completed fall 2018)
  Lisa-Marie Barf (started 10/2017)
- **Organization of international conferences and meetings**
  23^{rd} International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME), 2018: Supporting Organizer
  Hackathon on aging-related data, *Stay Young or Die Trying*, 2017: Organizer
  First Meeting of the *European Virus Bioinformatics Centre*, 2017: Supporting Organizer
  Hackathon on virus infected RNA-Seq data, *Fight against Ebola – in silico*, 2014: Organizer
- **Peer-Reviews for international conferences**
  Annual International Conference on Research in Comp. Molecular Biology (RECOMB 2018)
  Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2017)
  German Conference on Bioinformatics (GCB 2014, 2015, 2017)

- **Peer-reviews for journals**
  Virus Research (2018), Molecular Ecology Resources (2018), Bioinformatics (2014)
  Publons: publons.com/author/1521002
- **Third-party funding applications**
  Assistance in writing research grants for third-party funding (DFG, SPP, ERC)

Scholarships

Dec. 2018 – Jan. 2021	Scholarship for an "Add-on Fellowship for Interdisciplinary Life Science" of the Joachim Herz Stiftung (€ **12,500**)

Teaching

at the University of Jena

Teaching instructor

2018	*Practical course*: Viroinformatics *Responsibilitites*: Prepared, supervised, and assisted students in a two-week practical course on the topic of virus detection from meta-transcriptomic NGS data.
2017, 2017/18 2018	*Lecture* & *Practical course*: LaTeX basics for natural scientists *Responsibilitites*: Presented lectures on the document preparation system LaTeX. Supervised and assisted 30 undergraduate students in a one-week full-time course. Graded daily assignments, excercises, and exams.
2017/18	*Practical course*: High-Throughput Bioinformatics *Responsibilitites*: Prepared, supervised, and assisted students in a one-week practical course on the topic of RNA-Seq data analysis.

Teaching assistant

2016/17, 2017/18	*Lecture*: Basic bioinformatic applications *Responsibilities*: Prepared and taught four 1.5-hour lectures on the topic of high-throughput data analysis (*From raw read data to differential expressed genes*). Prepared and supervised practical examples. Graded assignments and course exams.
2014/15, 2015, 2016, 2017	*Lecture*: Virus bioinformatics *Responsibilitites*: Developed and taught hour-long lessons on viral replication, assembly, and sequencing.
2014/15, 2015/16, 2016/17, 2017/18	*Lecture*: High-Throughput Bioinformatics *Responsibilitites*: Developed and taught hour-long lessons on sequencing technologies and protocols, Next-Generation Sequencing design, quality control and data processing, *de novo* and reference-based assembly, read quantification, normalization, and differential gene expression analysis.
2015/16	*Practical course*: High-Throughput Bioinformatics *Responsibilitites*: Prepared, supervised, and assisted students in a one-week practical course on the topic of RNA-Seq data analysis.

Scientific poster presentations

09/2018	German Conference on Bioinformatics, Vienna, Austria *Long reads matter: The advantages of nanopore long-read sequencing.*
05/2017	Bioinformatics Mittelerde Meeting, Leipzig, Germany *PoSeiDon: a web server for the detection of evolutionary recombination events and positive selection.*
03/2017	27th Annual Meeting of the Society for Virology, Marburg, Germany *PoSeiDon: a web server for the detection of evolutionary recombination events and positive selection.*
04/2016	26th Annual Meeting of the Society for Virology, Münster, Germany *A method pipeline for the detection of positively selected sites in silico – exemplarily shown for bat Mx1.*

Scientific oral presentations

07/2018	11th International Conference on Virology and Microbiology, Vancouver, Canada *An Interface between Bioinformatics and Virology* (Keynote Speaker)
06/2018	CRC AquaDiva On Site Retreat, Vitaleum UG Hütten, Germany *Viral diversity, viral de novo assembly, and viral decay in groundwater*
02/2018	33. Winterseminar der Bioinformatik, Bled, Slovenia *PCAGO: An interactive web service to analyze RNA-Seq data with principal component analysis*
08/2017	CRC AquaDiva Recruitment Symposium, Jena, Germany *Next-Generation Sequencing meets viruses*
02/2017	32. Winterseminar der Bioinformatik, Bled, Slovenia *PoSeiDon: A web server for the detection of evolutionary recombination events and positive selection*
10/2016	14. Herbstseminar der Bioinformatik, Doubice, Czech Republic *Fun with PCA: Insights into RNA-Seq based principal component analysis*
02/2016	31. Winterseminar der Bioinformatik, Bled, Slovenia *Evolutionary analyses of positively selected sites in the interferon-induced innate immunity factor Mx1 of bats*
03/2015	25th Annual Meeting of the Society for Virology, Bochum, Germany *Differential transcriptional responses to Ebola and Marburg virus infection in cells from bats and humans*
02/2015	30. Winterseminar der Bioinformatik, Bled, Slovenia *Fight against Ebola – in silico –*
10/2014	12. Herbstseminar der Bioinformatik, Doubice, Czech Republic *Bats and viruses: friend or foe?*
02/2014	29. Winterseminar der Bioinformatik, Bled, Slovenia *Assembly and annotation of Mycobacterium avium subsp. paratuberculosis Typ-III*
10/2013	11. Herbstseminar der Bioinformatik, Doubice, Czech Republic *Assembler comparison and cluster assembly*

Citation Analysis

Total number of publications:	15
No. of peer rev. publications:	11
No. of submissions & preprints:	4
No. of book chapters:	1
h-index:	6
Citations:	65
Average impact factor:	4.2
ORCID	0000-0001-7090-8717
Google Scholar	goo.gl/CY4352

Publications

Peer-reviewed journal publications

Ψ These authors contributed equally

10 D. Steinbach, **M. Hölzer**, M. Marz, M. Gajda, F. C. Von Rundstedt, and M. O. Grimm. Analysis of molecular mechanism of progression of non-muscle-invasive bladder cancer (NMIBC) by genome-wide exome and UTR mutation analysis. *Eur Urol Suppl.* 17(2), e1523, 2018. **IF: 3.5**

9 P. Möbius, G. Nordsiek, **M. Hölzer**, M. Jarek, M. Marz, and H. Köhler. Complete Genome Sequence of JII-1961, a Bovine *Mycobacterium avium* subsp. *paratuberculosis* Field Isolate from Germany. *Genome Announc.* 5(34), 2017. **IF: 1.2**

8 J. Fuchs, **M. Hölzer**, M. Schilling, C. Patzina, A. Schoen, T. Hoenen, G. Zimmer, M. Marz, F. Weber, M. A. Müller, and G. Kochs. Evolution and Antiviral Specificities of Interferon-Induced Mx Proteins of Bats against Ebola, Influenza, and Other RNA Viruses. *J Virol.* 12; 91(15), 2017. **IF: 4.7**

7 P. Möbius, E. Liebler-Tenorio, **M. Hölzer**, and H. Koehler. Evaluation of associations between genotypes of *Mycobacterium avium* subsp. *paratuberculsis* and presence of intestinal lesions characteristic of paratuberculosis. *Veterinary microbiology.* 201, 188-194, 2017. **IF: 2.6**

6 K. Riege$^{\Psi}$, **M. Hölzer**$^{\Psi}$, T. Klassert, E. Barth, J. Bräuer, M. Collatz, F. Hufsky, N. Mostajo, M. Stock, B. Vogel, H. Slevogt, and M. Marz. Massive Effect on LncRNAs in Human Monocytes During Fungal and Bacterial Infections and in Response to Vitamins A and D. *Sci Rep.* 7:40598, 2017. **IF: 4.8**

5 T. E. Klassert, J. Bräuer, **M. Hölzer**, M. Stock, K. Riege, C. Zubiría-Barrera, M. M. Müller, S. Rummler, C. Skerka, M. Marz, and H. Slevogt. Differential Effects of Vitamins A and D on the Transcriptional Landscape of Human Monocytes during Infection. *Sci Rep.* 7:40599, 2017. **IF: 4.8**

4 **M. Hölzer**$^{\Psi}$, V. Krähling$^{\Psi}$, 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. M. Berrospi, R. Ochsenreiter, K. Rieger, 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. *Sci Rep.* 6:34589, 2016. **IF: 4.8**

3 **M. Hölzer**, K. Laroucau, H. H. Creasy, S. Ott, F. Vorimore, P. M. Bavoil, M. Marz, and K. Sachse. Whole-genome sequence of *Chlamydia gallinacea* type strain 08-1274/3. *Genome Announc.* 4(4):e00708–16, 2016. **IF: 1.2**

2 P. Möbius$^{\Psi}$, **M. Hölzer**$^{\Psi}$, M. Felder, G. Nordsiek, M. Groth, H. Köhler, K. Reichwald, M. Platzer, and M. Marz. Comprehensive insights in the *Mycobacterium avium* subsp. *paratuberculosis* genome using new WGS data of sheep strain JIII-386 from Germany. *Genome Biol Evol.* 7(9):2585-2601, 2015. **IF: 3.9**

1 A. H. Sahyoun, **M. Hölzer**, F. Jühling, C. Höner Zu Siederdissen, M. Al-Arab, K. Tout, M. Marz, M. Middendorf, P. F. Stadler, and M. Bernt. Towards a comprehensive picture of alloacceptor tRNA remolding in metazoan mitochondrial genomes. *Nucleic Acids Res.* 43(16):8044–8056, 2015. **IF: 10.2**

Submitted journal publications & preprints

R. Gerst and **M. Hölzer**. PCAGO: An interactive web service to analyze RNA-Seq data with principal component analysis. *bioRxiv.* doi.org/10.1101/433078, 2018.

D. Desirò, **M. Hölzer**, B. Ibrahim and M. Marz. SilentMutations (SIM): a tool for analyzing long-range RNA-RNA interactions in viral genomes and structural RNAs. *bioRxiv.* doi.org/10.1101/424002, 2018.

M. Hölzer and M. Marz. *De novo* transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. *Submitted for publication.* 2018.

Z. Chen, Y. Morita, F. Becker, B. Han, E. Amro, Y. Chen, D. Tang, S. Tao, S. Di Sanzo, **M. Hölzer**, R. Hänold, M. Groth, J. Kirkpatrick, H. Bierhoff, V. Romanov, M. Marz, A. Ori, and K. L. Rudolph. Cohesin-mediated NF-κB signaling limits hematopoietic stem cell self-renewal in aging and inflammation. *Submitted for publication.* 2018.

Book chapter

M. Hölzer and M. Marz. Chapter Nine – Software Dedicated to Virus Sequence Analysis "Bioinformatics Goes Viral". *Adv Virus Res.* (ed. M. Beer), 99:233-257, Academic Press, 2017.

Theses

M. Hölzer. The Dark Art of Next-Generation Sequencing: fundamental approaches for genomics, transcriptomics, and differential gene expression. *PhD thesis*, University of Jena, 2018.

M. Hölzer. Data management of mass spectra and fragmentation trees with BExIS. *Diploma thesis*, in German, University of Jena, 2012.

Soft skills

07/2018	*Fördermöglichkeiten für exzellente Nachwuchswissenschaftler/innen*, Dr. Mareile Knees, Jena
05/2018	*Workshop "Drittmittel einwerben"*, Jana Dümmler, Graduate Academy, Jena
02/2018	*Patente als Chance für meine Forschung*, Dr. Christian Liutik, Patentinformationszentrum FSU, Jena
02/2018	*Pursuing an Academic Career in Germany: Pros and Cons*, Dr. Hanna Kauhaus, Graduate Academy, Jena
02/2018	*Proposal Writing Workshop*, Frank Lauterbach, iRTG AquaDiva, Jena
03/2014	*Mitteldeutscher Fundraisingtag*, Crowdfunding: Chancen und Grenzen, FundraisingForum e.V., Jena
04/2013	*Jugendgruppenleiter Card (JuLeiCa)*, nationwide uniform identity card for voluntary people in youth work, VTPV e.V., Bad Blankenburg
03/2012	*Mitteldeutscher Fundraisingtag*, Fundraising und Freiwillige: wie passt das zusammen? FundraisingForum e.V., Jena
09/2010	*Web 2.0 – für Vereine, Initiativen & Parteien*, Thomas Mergen, Friedrich-Naumann-Stiftung für die Freiheit, Erfurt
since 2002	Various workshops, seminars, and advanced trainings about time and group management, group dynamics, self-motivation, project planning, association and employment law, speech, presentation, administration, and building management.

Leadership Experiences & Non-scientific Activities

Scout association "Bund der Pfadfinderinnen und Pfadfinder" (BdP)

since 2012	*Management board member of "Scoutactive" registered society* Administrative tasks and writing of proposals for staff funding.
since 2008	*Assistant manager of BdP scouting center of Thuringia* Administrative tasks, coordination of staff and volunteers, realization of adventure activities for kids and youths, technical support, web site and hardware supervision.
since 2007	*Assistant leader of BdP "Landesverband Thüringen e.V."* Organization of scout activities in Thuringia and across national borders. Organized events, trainings, and elections.
2005–2015	*Group leader of BdP scout tribe "Falken vom Greifenstein"* Administration of the association. Active participation and mainly responsible for the management and organization of various scout camps, international cooperations, and regular meetings. Managed team conflict and morale, represented the association at national and international events.
since 1998	*Member of BdP*

Water of Life

since 2017 | *Co-Founder and organizer of the Bad Blankenburger "Kessel-Treffen"*
Coordination of Scottish events and whisky tastings, www.kessel-treffen.de.

since 2014 | *Whisky tastings*
Preparation and execution of whisky tastings for beginner and advanced

Music

since 1999 | *Piano*

Languages

German Native language
English Written and spoken fluently

References

Prof. Dr. Manja Marz

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Dr. Konrad K. W. Sachse

1992–2015
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Dr. rer. nat. Martin Hölzer

Jena, October 18, 2018