

# Max Horn

## Curriculum Vitae

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## Education

- Mar. 2018 – Present **PhD in Machine Learning and Computational Biology**, *ETH Zürich (Swiss Federal Institute of Technology Zurich)*.
- Oct. 2015 – Oct. 2017 **M.Sc. Molecular Biosciences: Systems Biology**, *Heidelberg University*, Final Grade: 1.0/A.  
**Thesis title:** “Fully bayesian modelling of covariate effects on the gut microbiome using horseshoe priors for sparsity induction”  
**Additional courses:** Algorithms and Data Structures, Advanced Machine Learning, Introduction to Neuroinformatics, Probabilistic Artificial Intelligence
- Oct. 2012 – Oct. 2015 **B.Sc. Molecular Biotechnology**, *Heidelberg University*, Final Grade: 1.5/A-.  
**Thesis title:** “Clustering and Scoring the Druggability of Transient Protein Pockets”  
**Specialization:** Bioinformatics
- July 2004 – June 2012 **General Qualification for University Entrance**, *Gymnasium Gerabronn*, Final Grade: 1.5/A-.  
**Core courses:** Physics, Biology, Mathematics, German and English

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## Publications

- first author, preprint **Max Horn**, Michael Moor, Christian Bock, Bastian Rieck, and Karsten Borgwardt. “Set Functions for Time Series”. In: *arXiv preprint arXiv:1906.00722* (2019)
- joint first author, preprint Michael Moor, **Max Horn**, Bastian Rieck, and Karsten Borgwardt. “Topological Autoencoders”. In: *arXiv preprint arXiv:1906.00722* (2019)
- accepted, not yet published Stephanie L. Hyland, Martin Faltys, Matthias Hüser, Xinrui Lyu, Thomas Gumbsch, Cristóbal Esteban, Christian Bock, **Max Horn**, Michael Moor, et al. “Machine learning for early prediction of circulatory failure in the intensive care unit”. In: *Nature Medicine* (2019)
- Michael Moor, **Max Horn**, Bastian Rieck, Damian Roqueiro, and Karsten Borgwardt. “Early Recognition of Sepsis with Gaussian Process Temporal Convolutional Networks and Dynamic Time Warping”. In: *Proceedings of the 4th Machine Learning for Healthcare Conference*. Vol. 106. Proceedings of Machine Learning Research. PMLR, 2019
- Bastian Rieck, Matteo Togninalli, Christian Bock, Michael Moor, **Max Horn**, Thomas Gumbsch, and Karsten Borgwardt. “Neural Persistence: A Complexity Measure for Deep Neural Networks Using Algebraic Topology”. In: *International Conference on Learning Representations*. 2019
- Jotham Suez, Niv Zmora, Gili Zilberman-Schapira, Uria Mor, Mally Dori-Bachash, Stavros Bashiardes, Maya Zur, Dana Regev-Lehavi, Rotem Ben-Zeev Brik, Sara Federici, **Max Horn**, et al. “Post-Antibiotic Gut Mucosal Microbiome Reconstitution Is Impaired by Probiotics and Improved by Autologous FMT”. in: *Cell* 174.6 (2018)
- preprint Stefan Ganscha, Vincent Fortuin, **Max Horn**, Eirini Arvaniti, and Manfred Claassen. “Supervised learning on synthetic data for reverse engineering gene regulatory networks from experimental time-series”. In: *bioRxiv* (2018)

Antonia Stank, Daria B Kokh, **Max Horn**, Elena Sizikova, Rebecca Neil, Joanna Panecka, Stefan Richter, and Rebecca C Wade. “TRAPP webserver: predicting protein binding site flexibility and detecting transient binding pockets”. In: *Nucleic acids research* 45.W1 (2017)

Max C. Waldhauer, Silvan N. Schmitz, Constantin Ahlmann-Eltze, Jan G. Gleixner, Carolin C. Schmelas, Anna G. Huhn, Charlotte Bunne, Magdalena Büscher, **Max Horn**, et al. “Backbone circularization of *Bacillus subtilis* family 11 xylanase increases its thermostability and its resistance against aggregation”. In: *Mol. BioSyst.* 11 (12 2015)

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## Academic Experiences

- Feb. 2017 – Oct. 2017 **Fully bayesian modelling of covariate effects on the gut microbiome using horseshoe priors for sparsity induction**, *Visiting student in group of Prof. Eran Elinav, Weizmann Institute of Science, Israel.*
- Sep. 2016 – Feb. 2017 **Detecting network motifs from dynamical time course data using deep learning**, *Visiting student in group of Prof. Manfred Claassen, Institute of Molecular Systems Biology, ETH Zurich.*
- Jan. 2016 – June 2016 **Large scale modeling of *E. coli* chemotaxis using a hybrid ODE-PDE model**, *Complex biological systems group of Prof. Franziska Matthäus, Center for Modeling and Simulation in the Biosciences (BIOMS), Heidelberg University.*
- Feb. 2014 – Nov. 2014 **Utilizing Inteins for the circularization of Proteins**, *Project for the international Genetically Engineered Machine (iGEM) competition of the Heidelberg team 2014.*

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## Open source projects

- `simple_gpu_scheduler` Command line tool to handle a queue of jobs and distribute them among a set of provided GPUs. Can run in background and wait for new commands provided via stdin or named pipes. Written in Python.  
GitHub: [github.com/ExpectationMax/simple\\_gpu\\_scheduler](https://github.com/ExpectationMax/simple_gpu_scheduler)  
PyPI: [pypi.org/project/simple-gpu-scheduler](https://pypi.org/project/simple-gpu-scheduler)
- `bastSim` Library for scalable simulations of interacting bacterial populations using GPUs. Written in C++.  
GitHub: [github.com/ExpectationMax/bastSim](https://github.com/ExpectationMax/bastSim)

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## Sponsorships and Competitions

- Apr. 2017 – June 2017 **Stipend of the PROMOS Programme**, for master’s thesis project in the group of Prof. Eran Elinav, Weizmann Institute of Science, Israel.  
German Academic Exchange Service
- Sep. 2016 – Jan. 2017 **Stipend of the PROMOS Programme**, for research project in the group of Prof. Manfred Claassen, ETH Zürich.  
German Academic Exchange Service
- Feb. 2014 – Nov. 2014 **international Genetically Engineered Machine (iGEM) competition**, as *participant in the Heidelberg 2014 team.*  
Winner of the Grand Prize und Special Prizes of the categories: Best Foundational Advance Project, Best Supporting Software, iGEMer’s prize

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## Work experience

- May 2016 – Feb. 2017 **Student Research Assistent for Web Programming**, *Integrative Bioinformatics and Systems Biology (eislabs), Heidelberg University.*  
Updating and modernizing of web pages from multiple research groups, programming of extensions in Joomla
- Jan. 2015 – Feb. 2017 **Student Research Assistent for Application and Web Programming**, *Molecular and Cellular Modeling Group, Heidelberg Institute for Theoretical Studies (HITS) gGmbH.*  
Updating scientific applications, development of web applications, runtime optimization and extension of scientific software in Python, Java and Fortan
- Nov. 2013 – Apr. 2014 **Student Research Assistent für Data Analysis**, *Institute for Anatomy and Cell Biology, Medical Faculty Heidelberg.*  
Creation and Analysis of fluorescence microscopy images, automation of image analysis using Python scripts
- Apr. 2013 – Mar. 2016 **Network Administrator**, *AXANTIS SOLUTIONS GmbH & Co. KG, Heidelberger Str. 10-12, 69198 Schriesheim.*  
Web development, network and system administration, management of large scale backup system
- Feb. 2011 – Feb. 2014 **Network Administrator, Webdesigner and Programmer**, *Farmbau Fertigsysteme GmbH, Suhlweg 34, 74595 Langenburg.*  
Web application programming, development of a system in C for logging measurements of buildings, network administration
- Sep. 2010 – Feb. 2011 **Assistent for Web Design**, *Advanced Computer Advertisement GmbH, Auchtertstraße 2, 72770 Reutlingen.*  
Design of simple webpages and Administration of small Servers