

Curriculum Vitae

Personal Data

Title	Prof. Dr.
First name	Marc-Thorsten
Name	Hütt
Current position	Full Professor of Computational Systems Biology
Current institution(s)/site(s), country	Constructor University (formerly Jacobs University), Bremen, Germany
Identifiers/ORCID	0000-0003-2221-423X

Qualifications and Career

Stages	Periods and Details
Physics	1988 – 1991, Göttingen, Germany 1991 – 1992, Paris, France 1992 – 1994 Göttingen, Germany
Ph.D.	1997, <i>supervisor</i> : Prof. Dr. Martin Schumacher, Nuclear Physics, Georg-August-Universität Göttingen, Germany
Stages of academic/professional career	
Full Professor	since 2013, Computational Systems Biology, Jacobs University Bremen (since January 2023: <i>Constructor University Bremen</i>), Germany
Professorship (W3)	2013, Medical Systems Biology, Kiel University, <i>offer rejected</i>
Associate Professor	2006 – 2013, Computational Systems Biology, Jacobs University Bremen, Germany
Professorship (W2)	2005, Bioinformatics, TU Darmstadt, <i>offer rejected</i>
Assistant Professor (Juniorprofessor)	2002 – 2006, Theoretical Biology and Bioinformatics, TU Darmstadt, Germany
Postdoctoral Researcher	1998 – 2001, DFG Center of Graduate Studies 340 "Communication in biological systems" at TU Darmstadt, Germany

Short-term research stays (1-3 months)

Warsaw/Poland (1992), Novosibirsk/Russia (1996; 1997; 1998), Biosphere II Research Center Oracle/USA (2002; 2003), Florida Atlantic University, Boca Raton/USA (2005), Institut des Hautes Etudes Scientifiques (IHES) Paris/France (2008; 2010; 2011), Niels Bohr Institute Copenhagen/Denmark (2010, 2015), Arizona State University, Tempe/USA (each year between 2010 and 2018; 2023), Université Pierre et Marie Curie Paris/France (each year between 2017 and 2024).

Engagement in the Research System

Member of the Editorial Boards of PLOS Complex Systems (Section Editor since 2024), Advances in Complex Systems (since 2007), BMC Evolutionary Biology (since 2010) and EPJ Nonlinear Biomedical Physics (Section Editor-in-Chief 2013–2017) and Genomics, Proteomics & Bioinformatics (2014–2020).

Member of organizing committees of more than 30 conferences, workshops and summer schools. *Examples:* Dynamics Days Europe, international conference, Bremen/Germany 2024; Networks: A Language for Understanding Complex Systems, workshop, Hamburg/Germany, 2023; How Mathematics and Physics explain biological patterns, summer school, Nice/France, 2016; Heraeus Physics School *The Physics Behind Systems Biology*, Bremen/Germany, 2015.

Invited talks, colloquia and conference contributions at more than 140 events and institutions. *Examples:* talk at AI-NET spring workshop (online), 2025; invited colloquium talk at *Laboratoire de Physique Théorique de la Matière Condensée* (Paris/France), 2024; invited talk at COMBINE 2024 (Stuttgart/Germany); invited talk at 2nd International Workshop on Machine Learning and Quantum Computing Applications in Medicine and Physics (Warsaw/Poland), 2024; invited talk at SBMC 2018 (Systems Biology of Mammalian Cells), (Bremen/Germany); invited colloquium talk at School of Mathematical Sciences, Arizona State University, (Phoenix/USA), 2016.

Funding

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Supervision of Researchers in Early Career Phases

Postdoctoral Researchers (last five years)

Ali Salehzadeh-Yazdi (since 2022; industry project), **Johannes Falk** (since 2019; industry project), **Piotr Nyczka** (2015 – 2021; BMBF e:med program, grant 01ZX1306D), **Santhust Kumar** (2018 – 2022; industry project).

PhD students (last five years)

Sanghita Bose (since 2021; DFG HU 937/27) *Emergence of synchronization in manufacturing systems and its effect on logistic performance*, **Viktor Dinkel** (since 2021; Helmholtz Graduate School MarDATA), *Bioinformatics and network analyses of ancient DNA shotgun data from marine sediment cores*, **Eda Cakir** (since 2021; institutional funds) *Connectivity patterns of disease-related genes*, **Jyoti Jyoti** (since 2020; industry project) *A Boolean network approach to analyzing microbiome data*, **Dzmitry Rumiantsev** (since 2020; VW 9A174) *Understanding attractors in stylized gene regulatory networks*, **Selim Haj Ali** (2020 – 2025; EU ITN, grant 859937) *Simulation and analysis of collective patterns in dynamics on graphs*, **Venetia Voutsas** (2020 – 2025; EU ITN, grant 859937) *Minimal models of dynamics on graphs to study generic relationships between structural and functional connectivity*, **Alexey Lyutov** (2017 – 2023; industry project; joint PhD student with Prof. Yilmaz Uygur) *Application of machine learning and optimization to problems in supply*

network management, Daniel Merten (2017 – 2023; industry project; joint PhD student with Prof. Yilmaz Uygun) Improved steel production planning through data analysis and optimization, Mauricio Moreno-Zambrano (2016 – 2021; industry project)) Mathematical modeling of cocoa bean fermentation.

Scientific Results

Journal Publications (ten most relevant)

(1) Jyoti, J., and Hütt, M. T. (2025). Evaluating changes in attractor sets under small network perturbations to infer reliable microbial interaction networks from abundance patterns. *Bioinformatics*, **41**, btaf095. *Here we consider microbial abundance patterns as – binary – attractors of the underlying microbial interaction network. This view allows us to formulate a new network inference method.*

(2) Popova, M., Hilgetag, C. C., and Hütt, M.-Th. (2024). Perturbation therapies for neurodegenerative disorders: How attractors of excitable networks can help. *Physical Review* **E110**, 054406. *This work combines several concepts from statistical physics to better understand excitation patterns in signed directed graphs and their structural regulators.*

(3) Zimmermann, H. H., Stoof-Leichsenring, K. R., Dinkel, V., Harms, L., Schulte, L., Hütt, M.-Th, Nürnberg, D., Tiedemann, R. and Herzsuh, U. (2023). Marine ecosystem shifts with deglacial sea-ice loss inferred from ancient DNA shotgun sequencing. *Nature Communications*, **14**, 1650. *In this collaborative work within the Helmholtz Graduate School MarDATA we analyze sedimentary ancient DNA covering 20,000 years. Applying network methods to sedimentary DNA we identify marine ecosystem dynamics across a broad taxonomic spectrum and establish ancient DNA as an important new tool in identifying long-term ecosystem responses to climate transitions.*

(4) Jablonski, K. P., Carron, L., Mozziconacci, J., Forné, T., Hütt, M.-Th, and Lesne, A. (2022). Contribution of 3D genome topological domains to genetic risk of cancers: a genome-wide computational study. *Human Genomics*, **16**, 2. *Studying the distribution of SNPs across chromosomal domains, we find that, compared to non-cancer diseases, cancers have a larger proportion of SNPs clustered in the boundary regions of chromosomal domains, suggesting a markedly different functional interpretation of GWAS data than SNP-gene mappings.*

(5) Moretti, P. and Hütt, M.-Th. (2020) Link-usage asymmetry and collective patterns emerging from rich-club organization of complex networks. *PNAS* **117**, 18332-18340. *This publication provides the theoretical foundation of self-organized waves on graphs in excitable dynamics.*

(6) Klosik, D., Grimbs, A., Bornholdt, S. and Hütt, M.-Th. (2017) The interdependent network of gene regulation and metabolism is robust where it needs to be. *Nature Communications* **8**, 534. *This work presents the main result of the project DFG HU 937/9. Using approaches from network science we show that the joint system of gene regulation and metabolism in a bacterial cell is genetically sensitive and metabolically robust.*

(7) Hütt, M.-Th., Kaiser, M. and Hilgetag, C.C. (2014) Network-guided pattern formation of neural dynamics. *Phil. Trans. Roy. Soc. B* **369**, 20130522. *This work represents a summary of findings of the project DFG HU 937/7. We show how the*

notion of self-organized spatiotemporal patterns can be transferred to networks.

(8) Sonnenschein, N., Golib Dzib, J.F., Lesne, A., Boulkroun, S., Zennaro, M.-C., Benecke, A. and Hütt, M.-Th. (2012) *A network perspective on metabolic inconsistency*. **BMC Systems Biology** **6**, 41.

This publication is based on the methodology developed in DFG HU 937/8. We analyze transcriptomics data from disease cohorts based on metabolic network clustering.

(9) Müller-Linow M., Hilgetag C., and Hütt M.-Th. (2008) *Organization of excitable dynamics in hierarchical biological networks*. **PLoS Computational Biology** **4**, e1000190.

This publication provides first evidence of self-organized waves around hubs in excitable dynamics on graphs.

(10) Rascher U., Hütt M.-T., Siebke K., Osmond C. B., Beck F. and Lüttge U. (2001) *Spatiotemporal variation of metabolism in a plant circadian rhythm: the biological clock as an assembly of coupled individual oscillators*. **PNAS** **98**, 11801-11805.

This publication is the first evidence that photosynthesis on a plant leaf is spatiotemporally organized like spatially coupled oscillators.

Books and Patents

Textbooks

Hütt, M.-Th. and Dehnert, M. (2016) Methoden der Bioinformatik. Eine Einführung für Biologie und Medizin. 2nd (extended) Edition. Springer-Verlag: Berlin, Heidelberg.

Hütt, M.-Th. (2001) Datenanalyse in der Biologie. Springer-Verlag: Berlin, Heidelberg

Edited Volumes

Uygun, Y., Özgür, A. and Hütt, M.-Th. (Editors) (2024) Steel 4.0. Digitalization in Steel Industry. Springer Nature.

Vec M., Freund A.M. and Hütt, M.-Th. (Editors) (2006) Selbstorganisation. Ein Denksystem für Natur und Gesellschaft. Böhlau-Verlag.

Beck F., Hütt, M.-Th. and Lüttge U. (Editors) (2003) Nonlinear dynamics and the spatiotemporal principles of biology. Nova Acta Leopoldina, 332, Halle/Sahle.

Patents

Windt, K. and Hütt, M.-T. (2024). Method and computer programme for discovering possible errors in a production process, US Patent 12,182,750

Academic Distinctions

Fellow of the Hamburg Institute of Advanced Study (HIAS), Hamburg, Germany (2023)

The Hütt group has won the **PEGS DREAM Data Challenge 2024** organized by the National Institute of Environmental Health Sciences (NIEHS) in the United States.

Member of the European Academy of Sciences and Arts (since 2019).

Member of Die Junge Akademie (an institution of Berlin-Brandenburgische Akademie der Wissenschaften and Deutsche Akademie der Naturforscher Leopoldina) (2000 – 2005)