

Here you can find all application files (excluding certificates) in a single file.

Curriculum Vitæ ..... 1 - 8

Teaching Statement incl. Evaluations .....9 - 19

List of Publications ..... 20 - 27

Research Statement ..... 28 - 31

# Marc Hellmuth

## Curriculum Vitae

Västgötaresan 15  
75754 Uppsala, Sweden  
☎ (0049) 176 225 01 495  
✉ [mhellmuth@mailbox.org](mailto:mhellmuth@mailbox.org)  
📄 [marc-hellmuth.github.io](https://github.com/marc-hellmuth)

## Personal Information

---

Date and Place of Birth June 25, 1980. Nordhausen, Germany  
Nationality German  
Family status married  
Children Jonna (March 4th, 2013), Mattis Max (May 6th, 2015), Lotta Merle (Jan. 22nd, 2019)  
Desk address Stockholm University  
Faculty of Science  
Department of Mathematics  
SE - 106 91 Stockholm, Sweden

## Education

---

11/2022 **Promotion to Docent in “Computer Science”** (*Venia Legendi*)  
Stockholm University (Dpt. of Mathematics), Sweden

11/2017 **Positive Interim Evaluation: Junior Professorship**  
**“Computer Science”** (non-tenured)  
University of Greifswald (Dpt. of Mathematics and Computer Science), Germany

12/2016 **Habilitation in Bioinformatics** (*Venia Legendi*)  
Saarland University (Faculty of Mathematics and Computer Science), Germany

04/2010 **PhD in Computer Science** (*Dr. rer. nat.*)  
University of Leipzig, Faculty of Mathematics and Computer Science, Germany  
(*summa cum laude - very good with distinction*)

01/2007 **Diploma in Econometrics**  
University of Leipzig (Faculty of Mathematics and Computer Science), Germany

2001 – 2007 **Student of Econometrics** (University of Leipzig, Germany)

2000 – 2001 **Student of Computer Science** (University of Leipzig, Germany)

1991 – 1999 **High school** (Humboldt Gymnasium, Nordhausen, Germany)

## Research Experience

---

- 12/2020 – now **Associate Professor for Computer Science**  
Faculty of Science, Department of Mathematics, Stockholm University, SE
- 03/2020 – 12/2020 **Lecturer** (permanent)  
Group *Applied Computing in Life Sciences and Algorithms and Complexity*  
School of Computing, University of Leeds, UK
- 12/2016 – now **Adj. Prof. (Priv.-Doz.) for Bioinformatics**  
Dept. Math. and Comp. Sci., Saarland University, Saarbrücken, DEU
- 04/2015 – 03/2020 **Junior Professorship for Computer Science**  
re-denomination 2018 to **Biomathematics and Computer Science**  
Dept. Math. and Comp. Sci., University of Greifswald, Greifswald, DEU

### Postdoctoral Positions

- 12/2011 – 03/2015 Center for Bioinformatics, Saarland University, Saarbrücken, DEU  
Head of Group: *Prof. Dr. Hans-Peter Lehnhof*
- 04/2011 – 11/2011 Max-Planck-Institute for Computer Science, Saarbrücken, DEU  
Head of Group: *Prof. Dr. Kurt Mehlhorn*
- 07/2010 – 03/2011 Interdisciplinary Center for Bioinformatics, University Leipzig, DEU  
Head of Group: *Prof. Dr. Peter F. Stadler*
- 04/2010 – 07/2010 Max-Planck-Institute for Mathematics in the Sciences, Leipzig, DEU  
Head of Group: *Prof. Dr. Jürgen Jost*

### PhD student

- 02/2007 – 04/2010 Interdisciplinary Center for Bioinformatics, University Leipzig, DEU  
Head of Group: *Prof. Dr. Peter F. Stadler*  
*and*  
Max-Planck-Institute for Mathematics in the Sciences, Leipzig, DEU  
Head of Group: *Prof. Dr. Jürgen Jost*

### Visiting Researcher

- 03/2024, 10/2009 at Vienna Univ. of Economics and Business, Dept. Math. & Statistics, AUT  
09/2007 – 10/2007 Head of Group: *Prof. Dr. Josef Leydold*
- 04/2018, 01/2009 at University of Southern Denmark, IMADA, SDU Odense, DNK  
Head of Group: *Prof. Dr. Daniel Merkle*
- 02/2012, 02/2018 at University of East Anglia, School of Computing Sciences, Norwich, GBR  
Head of Group: *Prof. Dr. Vincent Moulton, Dr. Katharina Huber*
- 08/2017 at Université de Montréal, Dept. of Comp. Sci. and Operations Res., CAN  
Head of Group: *Prof. Dr. Nadia El-Mabrouk*
- 08/2014 – 09/2014 at University of Ljubljana, Dept. of Mathematics and Physics, SVN  
Head of Group: *Prof. Dr. Sandi Klavžar*
- 2007 – 2013 *Research Assistant and Visiting Researcher*  
Frequent visits (*up to 8 months at a time*) at MU Leoben, Dept. Appl. Math., AUT  
Head of Group: *Prof. emer. Dr. Wilfried Imrich*

(cont.)

### Third Party Funds

- |               |  |
|---------------|--|
| 2024          | Swedish Research Council (in review)<br><a href="#">Decomposing Complexity: Unveiling Hidden Structures in Discrete Objects to Tackle Hard Problems</a><br><i>Head:</i> Marc Hellmuth<br><i>Amount:</i> 5 194 000 SEK (~457 000 EUR)   |
| Aug 1-5, 2022 | Institute Mittag-Leffler (Royal Swedish Academy of Sciences)<br><a href="#">Emerging Mathematical Frontiers in Molecular Evolution</a><br><i>Head:</i> Marc Hellmuth, Kathi Huber, Peter F. Stadler, Guillaume Scholz<br><i>Amount:</i> Coverage of all costs for a one week conference in Stockholm, SE incl. accomodation for 30 participants  |
| 2019-2021     | State Program Mecklenburg-Vorpommern: Digital Teaching<br><a href="#">Virtual and Augmented Reality (VR / AR) for knowledge transfer, formation of hypothesis and research learning in pharmacy</a><br><i>Head:</i> Marc Hellmuth and Andreas Link<br><i>Amount:</i> 50 000 EUR (Hardware)   |
| 2016 – 2019   | Competitive PhD-Grant (Excellence Research at the Univ. Greifswald, GER)<br><a href="#">Theoretical Computer Science meets Chemistry and Biology</a><br><i>Head:</i> Marc Hellmuth<br><i>Amount:</i> 107 000 EUR   |
| 2011 – 2014   | European Science Foundation: <a href="#">Geometric representations and symmetries of graphs, maps and other discrete structures and applications in science</a> (ESF-EUROCORES (GreGAS))<br><i>Head:</i> Tomaz Pisanski<br><i>Own Position:</i> Co-investigator of IP Project “Graphs in Molecular Biology” (229 680 EUR) and AP Project “Near Graph Products” (318 408 EUR)<br><i>Amount:</i> 1 590 288 EUR |
| 2009 – 2010   | Max-Planck-Research-School PhD stipend <a href="#">MPI for Mathematics in the Sciences</a><br><i>Head:</i> Marc Hellmuth<br><i>Amount:</i> Stipend (~ 15 000 EUR)  |

## Lectures and Presentations

---

### SCIENTIFIC CONFERENCES (SELECTION).....

- 09/2024 “Symbolic Ultrametrics and Beyond”  
[Discrete Mathematics and Biology: the legacy of Andreas Dress, MPI Leipzig, DEU](#)
- 06/2023 “On a generalization of median graphs: k-median graphs”  
[10th Slovenian International Conference on Graph Theory, Bled, SVN](#)
- 08/2022 “Clustering Systems of Level-1 Networks”  
[Institute Mittag-Leffler, SWE](#)
- 12/2020 “Horizontal gene transfer and Fitch’s xenology relation”  
[Online Seminar: Algorithms and Complexity in Phylogenetics](#)
- 06/2019 “Best Match Graphs”  
[9th Slovenian International Conference on Graph Theory, Bled, SVN](#)
- 04/2019 **INVITED SPEAKER:** “Orthologs and Best Matches”  
[Workshop “Phylogenetics”, University Bielefeld, GER](#)
- 10/2017 **INVITED SPEAKER:** “The Matroid Structure of Representative Triple Sets”  
[15th Bioinformatics Autumn-Seminar, Doubice, CZE](#)
- 05/2016 **INVITED SPEAKER:** “Evolutionary Event Types and Phylogenetics”  
[Chemolution: From Chemistry to Evolution \(Symposium dedicated to Prof. emer. Peter Schuster on the occasion of his 75th birthday\), Vienna, AUT](#)
- 08/2015 “Phylogenomics with Paralogs”  
[19th Evolutionary Biology Meeting at Marseille \(EBMM\), FRA](#)
- 06/2015 “A first step towards determining biological traits from phenotypespaces: The strong product of di-graphs”  
[8th Slovenian International Conference on Graph Theory, Kranjska Gora, SVN](#)
- 02/2013 “Approximative Graph Products”  
[28th TBI-Winterseminar, Bled, Slovenia](#)
- 09/2012 **INVITED SPEAKER:** “Graphs, Relations and Some Answers to Some Biological Questions” [Symposium - 10th Anniversary of the Chair of Bioinformatics, Leipzig, DEU](#)
- 09/2011 “Symbolic ultrametrics, orthology and co-graphs”  
[25th Ljubljana-Leoben-Seminar on Graph Theory, Leoben, AUT](#)
- 06/2011 “Cartesian S-prime Graphs and a Local PFD Algorithm”  
[7th Slovenian International Conference on Graph Theory, Bled, SVN](#)
- 02/2010 “A general approach for the recognition of approximate graph products”  
[25th TBI-Winterseminar on Computational Biology, Bled, SVN](#)
- 09/2009 “Converting DNA to Music: ComposAlign” (together with M. Marz, T. Ingalls)  
[German Conference on Bioinformatics, Jena, DEU](#)
- 08/2009 “On the Design of RNA Sequences for Realizing Extended Shapes”  
[International Joint Conference on Bioinformatics, Computational Biology and Intelligent Computing, Shanghai, CHN](#)

06/2009 “On Local Covering Approaches for Approximate Products”,  
Conf. on Algebraic Graph Theory 2009, Dubrovnik, HRV

OTHER THAN SCIENTIFIC CONFERENCES AS **INVITED SPEAKER** (SELECTION).....

- 03/2024 “Explicit Modular Decomposition”  
Research Seminar - WU Vienna, Dept. Math. & Statistics, AUT
- 02/2023 “Explicit Modular Decomposition”  
Mathematics-Physics Celebration Evening, Stockholm University, SWE
- 06/2019 “Dot, dot, comma, dash and the House of Santa Claus:  
From simple mathematical objects to insights in the sciences”  
Public Talk “University in the City Hall”, Greifswald, DEU
- 09/2018 “Inference of Phylogenetic Trees from Homology-Relations”  
Research Seminar “Discrete Spectral Theory”, University Potsdam, DEU
- 09/2018 “Homology Relations”  
1st Greifswald Summer School on Mathematics of Evolution, Greifswald, DEU
- 04/2018 “The Fitch-Relation”  
University of Southern Denmark, IMADA, DNK
- 02/2018 “From Homology-Relations to Gene and Species Trees.”  
University of East Anglia, School of Computing Sciences, Norwich, GBR
- 08/2017 “From Evolutionary Event-Relations to Gene and Species trees”  
Université de Montréal, Dept. of Comp. Sci. and Operations Res., CAN
- 01/2015 “Phylogenomics with Paralogs”  
Jena Centre for Bioinformatics, University Jena, DEU
- 06/2014 “(Approximate) Graph Products”  
Technical University of Munich, Dept. Mathematics, DEU
- 03/2012 “Orthology Relations, Symbolic Ultrametrics, and Co-Graphs”  
University of East Anglia, School of Computing Sciences, Norwich, GBR
- 11/2011 “Abstracting the length of a dogs tail” (together with S.J. Prohaska)  
Jena Centre for Bioinformatics, University Jena, DEU
- 08/2011 “A general approach for the recognition of approximate graph products”  
Cambridge University, Unilever Centre for Molecular Informatics, GBR
- 12/2010 “Die Abstraktion der Schwanzlänge des Hundes” (together with S.J. Prohaska)  
Symposium - Realistic Abstraction, ArtSociety Leipzig, DEU
- 10/2010 “(Approximate) Graph Products”  
Bielefeld University, Center for Biotechnology, DEU
- 05/2010 “Phenotypes, Biological Traits and Graph Products”  
Yale University, Dept. Ecol. & Evol. Bio., New Haven, USA
- 10/2009 “(Approximate) Graph Products”  
Vienna Univ. of Economics and Business, Dept. Math. & Statistics, AUT
- 08/2009 “(Approximate) Graph Products”  
CAS-MPG PICB, Shanghai, CHN

## Other Research Activities

---

Acad. self-administration at Stockholm University	Head-Coordinator for Bachelor Projects in Computer Science Director of the Mathematical Computer Science Symposium
Member	German Mathematical Society (Deutsche Mathematiker-Vereinigung - DMV), Specialist Group “Discrete Mathematics” Expert Panel of National Science Centre (Computer Science), Poland, 2022
Organizer	Conference at Institute Mittag-Leffler (Royal Swedish Academy of Sciences) <a href="#">Emerging Mathematical Frontiers in Molecular Evolution</a> (Aug 1-5, 2022) Several Colloquiums at the Institute for Mathematics and Computer Science, University of Greifswald
Program Committee	19th Workshop on Algorithms in Bioinformatics (WABI) Niagra Falls, NY, USA (Sept. 2019) 9th Slovenian International Conference on Graph Theory Invited Organizer of Special Session: <i>Biomathematics and Bioinformatics</i> Bled, SVN (June 2019)
Examining Boards	Member of many BSc, MSc and PhD examining boards in Germany, England, Denmark and Sweden. Among other things, I was responsible for compliance with regulations and writing referee reports and final grading.
External Examiner (viva voce)	for PhD-Thesis “ <i>New algorithms and mathematical tools for unlocking complex signals left behind by evolution</i> ” by Guillaume E. Scholz at University of East Anglia, School of Computing Sciences, Norwich, GBR (Feb. 2018)
Referee for Grants	Natural Sciences and Engineering Research Council of Canada (NSERC), CAN Leverhulme Trust Fellowship, UK National Science Center, POL
Referee for Journals	Algorithms for Molecular Biology, Ars Mathematica Contemporanea, Art of Discrete and Applied Mathematics, Asian-European Journal of Mathematics, Australasian Journal of Combinatorics, Bulletin of Mathematical Biology, Combinatorica, Discrete Applied Mathematics, Discrete Mathematics, Electronic Journal of Combinatorics, European Journal of Combinatorics, Journal of Graph Theory, Journal of Mathematical Biology, Mathematics in Computer Science, Nucleic Acids Research, Springer Nature Computer Science, Systematic Biology, Theoretical Computer Science, Theory in Biosciences
Referee for Books	Classes of Directed Graphs, J. Bang-Jensen and G. Gutin (Springer, 2018) Handbook of Product Graphs - 2nd Edition, R. Hammack W. Imrich and S. Klavžar (Taylor & Francis, 2011)
Referee for Proceedings	ACM/BCB 2017; ESA 2020; GCB 2012; ISMB/ECCB 2013, 2022, 2024; RECOMB 2016; WABI 2011/2016/2017/2019; ISAAC 2019

## Job Offers and Rankings

---

- 07/2023 Professor (W3) in “Discrete Structures” at Technical University Freiberg, Germany  
[ranked 2nd](#)
- 08/2022 Professor (W3) in “Mathematical Data Science” at University of Augsburg, Germany - [ranked 3rd](#)
- 09/2020 Associated Professor in “Computer Science” at Stockholm University, Sweden  
[ranked 1st \(accepted\)](#)
- 09/2019 Lecturer in “Computer Science” (research track, permanent) at the University of Leeds, England - [ranked 1st \(accepted\)](#)
- 10/2014 Junior Professorship for “Computer Science” at the University Greifswald, Germany - [ranked 1st \(accepted\)](#)
- 03/2012 Lecturer in “Computational Biology” at the University of East Anglia, Norwich, UK - [ranked 1st \(declined\)](#)
- 03/2012 Tenured junior professorship for “Discrete Biomathematics” at the University Greifswald, Germany - [ranked 2nd](#)

## Awards

---

- 11/2022 Promotion to Dozent in Computer Science (*Venia Legendi*)
- 11/2017 Nomination: Excellent Teaching Award (Honorable Mention)
- 11/2017 Positive interim evaluation of my Junior Professorship “Computer Science” (renewed contract till 2021 and new denomination)
- 11/2017 Personal invitation to attend at the *Dagstuhl Seminar "Algorithmic Cheminformatics"* (17452), Schloss Dagstuhl in Germany
- 12/2016 Habilitation in Bioinformatics (*Venia Legendi*)
- 11/2014 Personal invitation to attend at the *Dagstuhl Seminar "Algorithmic Cheminformatics"* (14452), Schloss Dagstuhl in Germany
- 10/2012 Best Poster Award at 10th RECOMB-CG 2012, Niteroi, Brazil
- 2012 Nominated for the Richard-Rado-Preis 2012
- 06/2011 Best Poster Award at JOBIM 2011, Paris, France
- 04/2010 PhD with highest honor (*summa cum laude*)



## Other Jobs and Internships

---

- 02/2012–03/2012 Coordinator and Project Manager for Mirador e.V. in Guatemala  
Project: *Building a First Aid Station in Chocruz, GT*
- Since 2010 Cofounder and Board Member (2010-2018) of Mirador e.V. - a non-profit association that supports weakly infrastructural developed regions worldwide  
[www.mirador-ev.org](http://www.mirador-ev.org)
- 2004–2007 Employee as Tutor at 'Gesellschaft für Nachhilfeunterricht mbh & CoKG', Germany
- 2004–2006 Guitar Teacher at Wabe e.V., Jugendzentrum "Kanal 28", Leipzig, Germany  
CD - record of "Marc Hellmuth - Stimmen der Stadt", PCS-Records, Leipzig
- 2003–2004 Student Assistant with Prof. Dr. Friedbert Prüfer, Faculty of Mathematics and Computer Science, University Leipzig, Germany
- 1999–2000 Civilian Service at Südharzkrankenhaus, Nordhausen, Germany

## Other Skills

---

- Languages German (Mothertongue)  
English (Very good, working language)  
Swedish (Basics)
- Computer Skills C, C++, JAVA, PYTHON, HTML,  $\text{\LaTeX}$ , Linux
- Instruments Guitar

# Marc Hellmuth

## *Teaching Concept*

I strongly believe that besides imparting knowledge, teaching has further essential goals. A good teacher motivates the students to always think critical and ask profound questions. This requires creating a comfortable and motivating atmosphere where students feel respected. Both the students and the teacher will obviously profit from the arising discussions. Thus, my primary pedagogical goal is to help students learn how to ask, to dare to ask, how to search for answers, and how to apply their knowledge.

I have taught a wide variety of courses for undergraduate and graduate students. The lectures consist of one or two lessons of 90 minutes per week, some are accompanied by an exercise course in which the knowledge the students have acquired during the lectures can be applied in practical exercises.

To prepare my lectures, I usually determine which prerequisites the students already should have, based on their preceding must-attend lecture. Moreover, I investigate which topics would broaden the skills of the students and, in addition, which ones fit into the current research activities of the faculty.

I always put all the class information including script, additional lecture notes, exercises or useful research articles online, see e.g.

<https://marc-hellmuth.github.io/DiscreteOptimization.html>

<https://marc-hellmuth.github.io/DatastructuresAlgorithms.html>

This online material is weekly updated. Usually, I prepare 30-50 slides for a 90 minutes lecture. Difficult topics or proofs that need to be established step by step are presented on a blackboard.

I do not see a rigid dividing line between research and teaching, especially in my role as a teacher for graduate and PhD students. I always include recent research results and open questions in my lectures and encourage the students to discover the excitement that can be found in research. However, depending on the course, I use different course materials. While I prefer well-known text books as a basis for the more fundamental courses, I provide my own compilations (based on textbooks or recent research papers) in the graduate courses. In addition, a script for most of my lectures is provided. For an example follow the link for a current script of the course “Algorithms and Datastructures”: <https://marc-hellmuth.github.io/ADS.pdf>

To deepen the student’s knowledge, I prepare (1 or 2-weekly) exercises. I often mix exercises that are easy with exercises that seem to be easy, but are not. This teaches the students to have an open mind and to apply diverse methods and techniques they learned. The exercise results also indicate, which parts of the lectures were easy to solve and which were difficult. This in turn, helps me to understand, if some topics must be investigated in more detail in the lecture or tutorial. I made the experience, that my students usually ask me in the lecture to recap or present some topics more detailed, whenever necessary.

Besides the official office hours and the lecturing time I make myself available to students at other times as well. Although I am responsible for grading the students, I try to create a personal and relaxed atmosphere, yet still never losing track of the high expectations I have. Especially before exams I encourage all students to come to my office hours. I personally offer them the possibility for a conversation not only concerning the content of the exam, but also how to deal with their possible anxieties. Experience has shown, that students appreciate this offer and especially weaker students benefit from using this opportunity.

For thesis topics, I usually select the subject together with the student, based on interesting current research topics as well as the student’s interest. For me it is important to always stay in touch with my BSc/MSc/PhD students and I usually meet them several times per month. I don’t have fixed office opening hours, as students can usually come to my office with their questions or research results at any time. In that way, I can easily judge in which state the student’s work is and the students can usually faster continue with their current work.

The supervision of my students is also reflected in my publication list and should justify the success of my teaching methods from a research and supervision point of view. My co-authors Anna Lindeberg, Lydia Ostermeier (nee Gringmann), Sarah Berkemer, Nikolai Nøjgaard, Nicolas Wieseke, Tilen Marc, Manuel Noll, Kevin Gitzhofer, Adrian Fritz, John Anders, David Schaller and Carsten Seemann were supervised by me during their PhD, MSc or BSc thesis and were all able to publish their research results in international journals.

## Outreach activities

---

Besides dozens of scientific talks I gave, Prof. Sonja Prohaska (Univ. Leipzig, GER) and me started a project to transfer our knowledge also to a non-scientific community in 2010. The aim of this project is besides imparting knowledge, to show people how exciting science can be. We gave several talks with the title “*Die Abstraktion der Schwanzlänge des Hundes (The Abstraction of the Length of a Dog Tail)*” for non-scientific and scientific audience. We regularly repeated this talk, which comprises topics originated in bioinformatics and discrete mathematics and shows how these different disciplines are intertwined.

In 2019, I represented the talk “*Dot, dot, comma, dash and the House of Santa Claus: From simple mathematical objects to insights in the sciences*” as part of the lecture series “University in the City Hall” in Greifswald, Germany. The series is organized jointly by city and university. That the lectures take place in the town hall and not in the university is part of the concept and is intended to reach a broad audience, in particular, the population of Greifswald and surrounding area. In this talk, I presented classical results established by Leonhard Euler and its connection to current research topics in life sciences.

In addition, we have briefly summarized parts of our current research, that is concerned with the evolutionary history of the species, in an easy and understandable way for a non-scientific audience. Extracts of this summary are released by the German and Austrian press (German only), see e.g.

<http://derstandard.at/2000011192605/Mit-paralogen-Genen-zu-praezisieren-Stammbaeumen-des-Lebens>

Beyond my scientific interest, I am one of the project coordinators of Mirador e.V., a non-profit organisation that supports infrastructural weakly developed regions worldwide, see <http://www.mirador-ev.org/>. We built facilities in Guatemala, Haiti, Nepal and South Africa. Public presentations that I gave in Germany, serve as a basis to transfer knowledge, and to sensitize people for cross-cultural topics.

## Course List

---

All lectures and seminars at the Stockholm Univ., Univ. Leeds and Univ. Greifswald as well as the lecture “Discrete Computational Biology” (Univ. Saarbrücken) are completely on my own authority. The lectures and seminars comprises both: undergraduate and graduate level. The number of participants ranged from 8 to 70. Other lectures and seminars are shared with Prof. Dr. Peter F. Stadler or Prof. Dr. Hans-Peter Lenhof.

*I wish to emphasize that most of my lectures are adjusted to fit the requirements and content of the respective institute where I have worked. As a computer scientist, mathematician, and bioinformatician, I am also able and willing to teach further undergraduate and graduate courses.*

### Stockholm University (Sweden)

Lectures: <a href="#">Algorithms and Complexity</a> (WS 20/21, 21/22, 22/23, 23/24)	//4 HPW, 7.5 ECTS
<a href="#">Algorithms and Datastructures</a> (SS 24)	//4 HPW, 7.5 ECTS
<a href="#">Computational Biology</a> (WS 21/22, 20/21, 21/22, 22/23, 23/24)	//4 HPW, 7.5 ECTS

### University of Leeds (UK) / Southwest Jiaotong University in Chengdu (China)

Lectures: <a href="#">Computer Processors</a> (SS 20)	//3 HPW, 10 ECTS
---	------------------

### University Greifswald

Lectures: <a href="#">Combinatorics</a> (SS 19)	//4 HPW, 6 ECTS
<a href="#">Efficient Algorithms and Data Structures</a> (WS 18/19, 19/20)	//4 HPW, 9 ECTS
<a href="#">Graph Theory</a> (WS 17/18, 19/20)	//4 HPW, 6 ECTS
<a href="#">Discrete Optimization</a> (WS 15/16, 16/17, SS 18)	//4 HPW, 6 ECTS
<a href="#">Bioinformatics</a> (SS 15, 16, 17)	//2 HPW, 6 ECTS
<a href="#">Software Engineering</a> (SS 18)	//4 HPW, 6 ECTS
Seminars: <a href="#">FUN with Algorithms</a> (WS 18/19)	//2 HPW, 3 ECTS
<a href="#">Mathematical Phylogeny</a> (SS 17)	//2 HPW, 3 ECTS
<a href="#">Products of Graphs and Hypergraphs</a> (SS 16, 19)	//2 HPW, 3 ECTS

### University Saarbrücken

Lectures: <a href="#">Discrete Comput. Biology</a> (WS 11/12, 12/13, 13/14, 14/15)	//3 HPW, 5 ECTS
<a href="#">Bioinformatics Lecture Series</a> (WS 11/12, 12/13, 13/14, 14/15)	//3 HPW, 3 ECTS
Seminars: <a href="#">Efficient Algorithms for RNA molecules</a> (SS 11, 12, WS 11/12)	//1 HPW, 5 ECTS
<a href="#">Bioinf. Approaches for Cancer Research</a> (SS 11, 12, WS 11/12)	//1 HPW, 5 ECTS
<a href="#">Selected Topics in Molecular Docking</a> (SS 11, 12)	//1 HPW, 7 ECTS
<a href="#">Modelling and Analyzing Biological Networks</a> (SS 12)	//1 HPW, 7 ECTS

### University Leipzig

Lectures: <a href="#">Phenotypespace and Approximate Graph Products</a> (WS 10/11)	//3 HPW, 5 ECTS
<a href="#">Mathematics in Bioinformatics</a> (WS 07/08, 08/09)	//2 HPW
<a href="#">Graph Theory</a> (SS 07, 08)	//2 HPW
Seminars: <a href="#">Algorithms and Data Structures</a> (WS 08/09, 10/11)	//1 HPW

## Supervision of Students

---

### CURRENTLY SUPERVISED STUDENTS (POSTDOC: 1 / PHD: 2 / BSc: 5).....

PostDoc	Sandhya Thekkumpadan Puthiyaveedu (since 2022)
PhD Comp.Sci.	Carsten R. Seemann (expected graduation 2024)
PhD Comp.Sci.	Anna Lindeberg (expected graduation 2027)
Bsc Comp.Sci.	Anton Alfonsso (expected graduation 2024)
Bsc Comp.Sci.	Timothy Lindquist Marongiu (expected graduation 2024)
Bsc Comp.Sci.	Tom Alexander Hessler (expected graduation 2024)
Bsc Comp.Sci.	Joakim Axner (expected graduation 2024)
Bsc Comp.Sci.	Michael Laurila (expected graduation 2024)

### COMPLETE LIST OF FINISHED POJECTS (PHD: 3 / MSc: 16 / BSc: 23).....

#### PhD students

The theses of all of my PhD students were graded “**summe cum laude**” ([with highest honors](#)). In addition, David Schaller won the price for the best German dissertation in bioinformatics (FaBI, 2022).

PhD Comp.Sci.	David Schaller (Oct. 2021): <a href="#">Gene Family Histories: Theory and Algorithms</a>
PhD Math.	Nikolai Nøjgaard (April 2020): <a href="#">Graph Theoretical Problems in Life Sciences</a>
PhD Comp.Sci.	Nicolas Wieseke (Sep. 2017): <a href="#">From Homologous Genes to Phylogenetic Species Trees</a>

#### MSc / Diploma students

MSc Math.	Anna Lindeberg: (Aug 2023): <a href="#">The Structure of Primitive Edge-Colored Graphs: A Galled Tree Perspective</a>
MSc BioMath.	Svenja Fischer: (Jan 2023): <a href="#">About a generalization of median graphs</a>
MSc BioMath.	Linda Knuever: (March 2021): <a href="#">On balance of phylogenetic networks</a> <i>[work has been extended and published as a joint paper]</i>
MSc BioMath.	Carmen Bruckmann: (Aug. 2019): <a href="#">Median graph-Like Relations</a> <i>[work has been extended and published as a joint paper]</i>
MSc Math.	Carsten Seemann: (Aug. 2018): <a href="#">Generalized Fitch Relations</a> <i>[work has been extended and published as a joint paper]</i>
MSc BioMath.	Anne Schütz: (Aug. 2018): <a href="#">Spanning Tree Based Edge-Vitality of Graphs</a>
MSc Math.	Sebastian Brinkop: (May 2018): <a href="#">Local Factorization Algorithms for the Strong Product of Directed Graphs</a>
MSc Math.	Paul Klemm (Feb. 2018): <a href="#">How Much Information is Provided by Induced P4's for the Characterization of Orthology Data?</a>
MSc Bioinf.	John Anders (June 2017): <a href="#">Fitch's Xenology Relation</a> <i>[work has been extended and published as a joint paper]</i>
MSc Math.	Sebastian Lüersen (Aug. 2016): <a href="#">Approximate Cartesian Products of Digraphs</a>
MSc Biomath.	Maria Hartmann (June 2016): <a href="#">Design of Methods to Align NMR-Spectra</a>
MSc Bioinf.	Kevin Gitzhofer (Aug. 2015): <a href="#">Heuristic approaches for the reconstruction of minimally resolved phylogenetic trees</a>

MSc Bioinf.	Adrian Fritz (June 2015): <a href="#">A Heuristic for Cograph-Editing</a> <i>[work has been extended and published as a joint paper]</i>
MSc Math.	Tilen Marc (Aug. 2014): <a href="#">Infinite median graphs</a>
MSc Comp.Sci.	Manuel Noll (Dez. 2013): <a href="#">On Several Strong Hypergraph Products - Existence and Computation of Unique Prime Factor Decomposition</a> <i>[work has been extended and published as a joint paper]</i>
Diplom Math.	Lydia Gringmann (Feb. 2010): <a href="#">Hypergraph Products</a> <i>[work has been extended and published as a joint paper]</i>
<b>BSc students</b>	
BSc Comp.Sci	Emanuel Berggren (Aug. 2023): <a href="#">Graph coloring using modular decomposition</a>
BSc Comp.Sci	Oliver Tryding (May 2022): <a href="#">Clustering systems and Level-1 Networks</a>
BSc Comp.Sci	Daniel Westerlund (May 2022): <a href="#">Designing and Implementing a Median Graph-Generating Algorithm through Convex Expansion</a>
BSc Comp.Sci	Fredrik Eklind (May 2022): <a href="#">Generating Level-k Phylogenetic Networks</a>
BSc Comp.Sci	Mohammed Habib (Aug. 2021): <a href="#">Later-Divergence-Time Graphs</a>
BSc Comp.Sci	Nicolai Moerdrup (May 2021): <a href="#">Complete Edge-Colored Permutation Graphs</a>
BSc Comp.Sci	Anna Lindeberg (May 2021): <a href="#">Maximum matchings in Graph Products</a>
BSc BioMath.	Nicola Döring (Feb. 2020): <a href="#">Best Match Heuristics</a>
BSc Math.	Mira Michel (Aug. 2019) <a href="#">Combining Orthology- and Fitch-Relations</a> <i>[work has been extended and published as a joint paper]</i>
BSc Biomath.	Linda Knüver (March 2018): <a href="#">Fitch Graphs</a>
BSc Biomath.	Lars Berling (March 2018): <a href="#">A Comparison of Triple Based Heuristics for Supertree Reconstruction</a>
BSc Math.	Fynn Marlin Leitow (Feb. 2018): <a href="#">Heuristics and Exact Algorithms for the Di-Cograph Editing Problem</a>
BSc Math.	Casten Seemann (March 2017): <a href="#">Splits und triples in rooted trees, the construction of the closure, and representative triple sets</a> <i>[work has been extended and published as a joint paper]</i>
BSc Math.	Felix Becker (Feb. 2017): <a href="#">Efficient Primfactor-Decomposition of Cartesian Product Graphs</a>
BSc Biomath.	Anica Hoppe (Nov. 2016): <a href="#">On the relationship between phylogenetic trees on four leaves and estimated orthology relations</a>
BSc Biomath.	Sonja Türpitz (Nov. 2016): <a href="#">On the reconstruction of slightly disturbed symbolic ultrametrics</a>
BSc Biomath.	Jan Oldenburg (Aug. 2016): <a href="#">Protein Design with Machine Learning Methods</a>
BSc Bionf.	Jannik Luxenburg (Aug. 2015): <a href="#">Efficient Generation and Structural Analysis of RNA-Phenotype Spaces</a>
BSc Bioinf.	Christian Brossette (June 2014): <a href="#">Efficient Algorithms for the Densest-k Subgraph problem</a>
BSc Bioinf.	Kevin Gitzhofer (June 2013): <a href="#">New Results in Finding Species Trees</a>
BSc Bioinf.	Miriam Bah (Oct. 2012): <a href="#">Measuring the relevance of topology in networks for finding deregulated subgraphs</a>
BSc Bionf.	Sarah Berkemer (Aug. 2012): <a href="#">Cograph Editing: An Approach to Adjust the Orthology Relation for the Reconstruction of Phylogenetic Trees</a> <i>[work has been extended and published as a joint paper]</i>
BSc Bionf.	Anna Feldmann (April 2012): <a href="#">Retrieving optimally discriminative Subnetwork Markers to predict response to Chemotherapy using a Color-coding Technique</a>



## Nomination: Excellent Teaching Award (2018)

2

### Würdigung Ihres Engagements für die Lehre bei der Studierendenumfrage für die Universitätspreise für Hervorragende Lehre im Sommersemester 2018 (anonymisiert)

Institut bzw. Fachrichtung	Familienname der vorgeschlagenen Lehrperson/en	Vornamen (falls bekannt)	Akademischer Grad der vorgeschlagenen Lehrperson/en	Bitte begründen Sie Ihren Vorschlag: Was zeichnet die Lehre der von Ihnen für den Lehrpreis vorgeschlagenen Person/en besonders aus?
----------------------------	--	--------------------------	---	--

Mathematik und Informatik

Hellmuth

Marc

Prof. Dr.

Professor Hellmuth hält ausgezeichnete Tafelvorlesungen, da er sein Skript nicht nur für die Studierenden, sondern auch für sich stets herleitet. Auf diese Weise versteht er selbst die vorgestellten Themen jedes Mal neu und befindet sich mit den Studierenden auf Augenhöhe. Er regt durch Fragen und kleine „Fingerübungen“ an, in der Vorlesung mitzudenken. Deshalb lohnt es sich, die Vorlesung zu besuchen und nicht nur das zur Verfügung gestellte Skript eigenständig durchzuarbeiten. So hat er mein Interesse auch in Fachbereichen wecken können, die ich ursprünglich für weniger interessant hielt. Daher habe ich mittlerweile sämtliche von ihm angebotenen Module gehört. Nun zählen seine Fachbereiche zu meinen Stärken. Prof. Hellmuth geht stets auf die Bedürfnisse der Studierenden ein, sei es bei Prüfungsterminen oder Vorlesungszeiten. Er unterstützt die Studierenden außergewöhnlich stark und motiviert sie, insbesondere bei Abschlussarbeiten über sich selbst hinauszuwachsen. Dabei sind die betreuten Abschlussarbeiten forschungsorientiert, sodass man seine Forschungsarbeit nicht nur kennen lernt, sondern auch daran mitwirken kann. Darüber hinaus unterstützt Prof. Hellmuth die Studierenden individuell, indem er den Kontakt zu anderen Arbeitsgruppen außerhalb Greifswalds herstellt und ihnen somit weitere Schritte auf dem Lebensweg erleichtert. Daher nominiere ich Professor Hellmuth für den Lehrpreis (Preis für hervorragende Lehre an der Universität Greifswald) im Bereich „Integrative Vorlesung“.

#### Translation of student statement (excerpt)

He gives excellent lectures-

He is at eye level with the students

The students get part of the lecture, based on open questions and "finger exercise"

He was able to arouse my interest in subjects that I originally thought were less interesting.

He always addresses the needs of the students.

He supports the students exceptionally strong, and encourages us to surpass oneself

The thesis topics are research-oriented, so that one can contribute to recent research

He supports the students individually

Mathematik und Informatik

Hellmuth

Marc

Prof. Dr.

Professor Hellmuth erklärt verständlich und spricht begeistert von jedem vorgestellten Thema, sodass die Vorlesung auch bei schwierigen Themen stets lohnenswert ist. Dabei wird auch der Bezug zur aktuellen Forschung hergestellt. Die dabei entstehenden Fragen werden umfassend beantwortet und bei Bedarf auch im persönlichen Gespräch geklärt. Zusätzlich zur detaillierten Vorlesung wird ein hilfreiches Skript zur Verfügung gestellt. Bei der Festlegung der Vorlesungstermine wird jeder Teilnehmer berücksichtigt und auch Prüfungstermine können individuell festgelegt werden. Die vorgestellten Themen sind anspruchsvoll und das erworbene Wissen lässt sich nicht nur auf Problemstellungen in anderen Modulen im Studium übertragen, sondern haben auch über das Studium hinaus Anwendungspotential. Dadurch erweitert sich die Anzahl an möglichen Strategien zur Lösung von mathematischen Problemen. Aus all diesen Gründen nominiere ich Professor Hellmuth für den Lehrpreis im Bereich integrative Vorlesung.

#### Translation of student statement (excerpt)

He explains clearly and speaks enthusiastically about each presented topic, so that the lecture is always worthwhile, even on difficult topics.

Questions are comprehensively answered and, if necessary, also clarified in a personal meeting.

Examination dates can be set individually.

The topics are challenging, but the acquired knowledge can be transferred to different problems in other lectures.

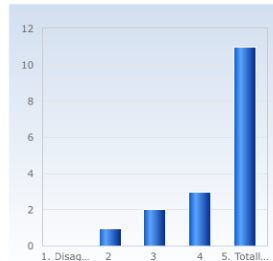
## Evaluation of Lecture *Algorithm and Complexity* (Fallsemester HT23)

### Course Evaluation DA4005 Algoritmer och komplexitet HT23

Respondents: 46  
Answer Count: 17  
Answer Frequency: 36,96 %

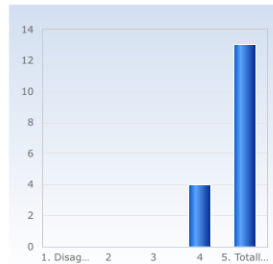
#### 1. Overall, I am satisfied with the course.

Overall, I am satisfied with the course.	Number of responses
1. Disagree	0 (0,0%)
2	1 (5,9%)
3	2 (11,8%)
4	3 (17,6%)
5. Totally agree	11 (64,7%)
Total	17 (100,0%)



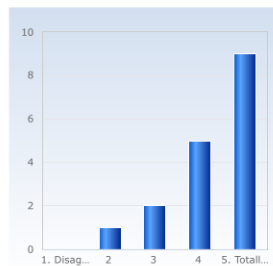
#### 2. The content of the course was relevant to me for achieving the intended learning outcomes.

The content of the course was relevant to me for achieving the intended learning outcomes.	Number of responses
1. Disagree	0 (0,0%)
2	0 (0,0%)
3	0 (0,0%)
4	4 (23,5%)
5. Totally agree	13 (76,5%)
Total	17 (100,0%)



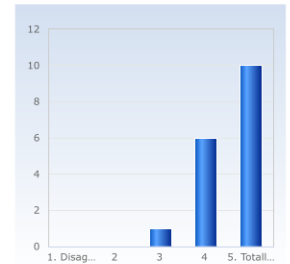
#### 3. The teaching gave me good conditions to achieve the intended learning outcomes.

The teaching gave me good conditions to achieve the intended learning outcomes.	Number of responses
1. Disagree	0 (0,0%)
2	1 (5,9%)
3	2 (11,8%)
4	5 (29,4%)
5. Totally agree	9 (52,9%)
Total	17 (100,0%)



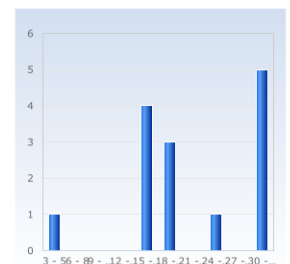
#### 4. The examination/assessment tested how well I achieved the intended learning outcomes.

The examination/assessment tested how well I achieved the intended learning outcomes.	Number of responses
1. Disagree	0 (0,0%)
2	0 (0,0%)
3	1 (5,9%)
4	6 (35,3%)
5. Totally agree	10 (58,8%)
Total	17 (100,0%)



#### 5. On average, I have spent approximately the following number of hours per week on the course, total time, including self-study.

On average, I have spent approximately the following number of hours per week on the course, total time, including self-study.	Number of responses
3 - 5	1 (7,1%)
6 - 8	0 (0,0%)
9 - 11	0 (0,0%)
12 - 14	0 (0,0%)
15 - 17	4 (28,6%)
18 - 20	3 (21,4%)
21 - 23	0 (0,0%)
24 - 26	1 (7,1%)
27 - 29	0 (0,0%)
30 - 32	5 (35,7%)
Total	14 (100,0%)





## Profillinie

Teilbereich: LE\_Mathematik und Informatik (MNF)  
 Name der/des Lehrenden: Prof. Dr. Marc Hellmuth  
 Titel der Lehrveranstaltung: Datenstrukturen und effiziente Algorithmen  
 (Name der Umfrage)

Vergleichslinie: Durchschnitt MNF-Vorlesungen

Verwendete Werte in der Profillinie: Mittelwert

## Bewertung von Lehrperson und Veranstaltung

Frage	trifft überhaupt nicht zu	trifft nicht zu	trifft vollst. zu	n	mw	md	sd
Die/der Lehrende spricht verständlich und anregend.				n=8	mw=96,0	md=100,0	s=7,4
Die/der Lehrende engagiert sich bei der Lehrtätigkeit.				n=8	mw=96,0	md=100,0	s=7,7
Die/der Lehrende ist kooperativ und aufgeschlossen.				n=8	mw=98,0	md=100,0	s=4,6
Eigene Beiträge, Fragen und aktive Mitarbeit werden gefördert.				n=8	mw=95,0	md=100,0	s=10,7
Die Studierenden erhalten zu ihren Fragen und Beiträgen hilfreiches Feedback.				n=8	mw=98,0	md=100,0	s=4,6
Der inhaltliche Aufbau der Veranstaltung ist nachvollziehbar.				n=8	mw=95,0	md=100,0	s=7,6
Zum Mitdenken und Durchdenken des Themas wird angeregt.				n=8	mw=98,0	md=100,0	s=4,6
Die Bedeutung bzw. der Nutzen der behandelten Themen wird vermittelt.				n=8	mw=95,0	md=100,0	s=7,6
Die Arbeitsmaterialien (z. B. Handouts, Skripte, Literaturhinweise) waren hilfreich.				n=8	mw=89,0	md=95,0	s=15,5

### Bewertung von Anforderungen und Lerngewinn

Meine Vorkenntnisse waren ausreichend, um der Veranstaltung zu folgen.	trifft überhaupt nicht zu	trifft vollständig zu	n=8 n=3442	mw=89,0 mw=82,0	md=90,0 md=90,0	s=13,6 s=21,5
Ich habe den Stoff verstanden.	trifft überhaupt nicht zu	trifft vollständig zu	n=8 n=3404	mw=90,0 mw=81,0	md=90,0 md=90,0	s=10,7 s=18,5
Ich lerne viel in der Veranstaltung.	trifft überhaupt nicht zu	trifft vollständig zu	n=8 n=3420	mw=98,0 mw=79,0	md=100,0 md=80,0	s=4,6 s=20,7
Die Veranstaltung fördert mein Interesse am Fach.	trifft überhaupt nicht zu	trifft vollständig zu	n=8 n=3440	mw=98,0 mw=78,0	md=100,0 md=80,0	s=4,6 s=24,1
Der Besuch der Veranstaltung lohnt sich.	trifft überhaupt nicht zu	trifft vollständig zu	n=8 n=3378	mw=100,0 mw=82,0	md=100,0 md=90,0	s=0,0 s=21,3
Ich empfinde den für diese Veranstaltung zu erbringenden Arbeitsaufwand als angemessen.	trifft überhaupt nicht zu	trifft vollständig zu	n=8 n=3379	mw=94,0 mw=83,0	md=95,0 md=90,0	s=7,4 s=19,7

## Lehrveranstaltung: Gesamteinschätzung

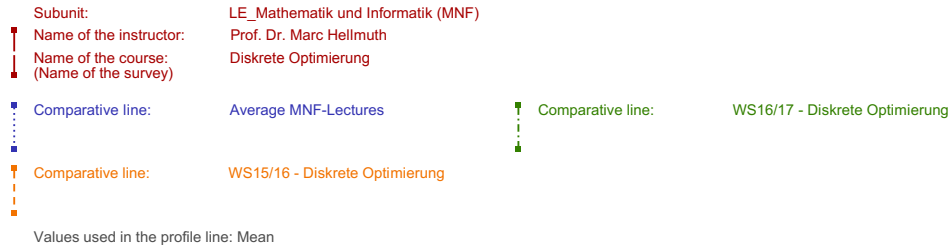
Welche Note würden Sie der Lehrveranstaltung insgesamt geben (sehr gut/gut/befriedigend/ausreichend/mangelhaft)?

n=8    mw=1,1    md=1,0    s=0,4  
n=3058    mw=1,8    md=2,0    s=0,8

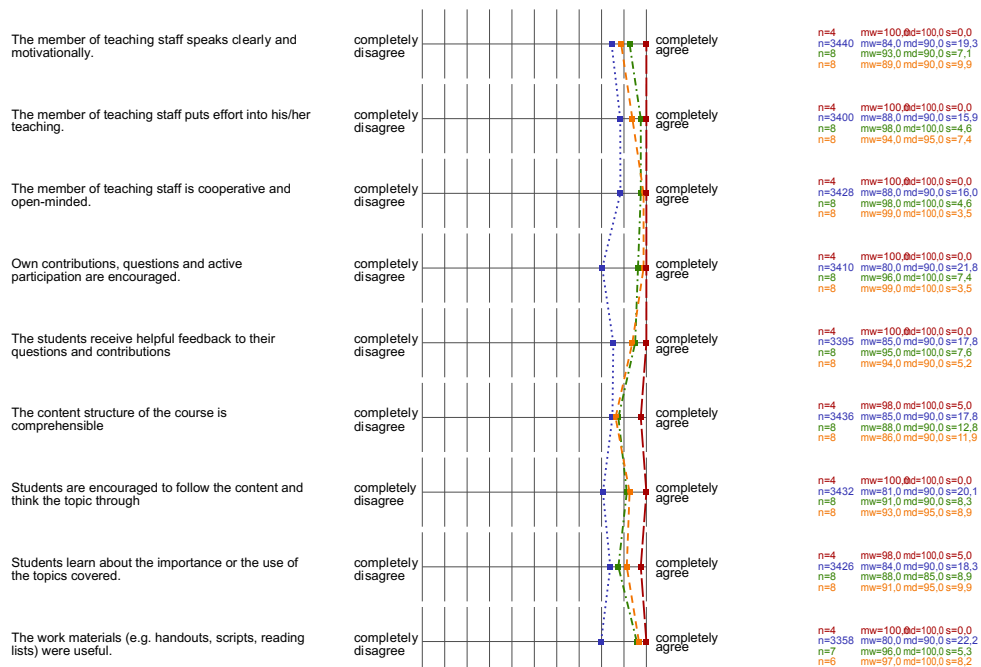
# Evaluation of Lecture *Discrete Optimization* (WS17/18; WS16/17; WS15/16)

Prof. Dr. Marc Hellmuth, Diskrete Optimierung

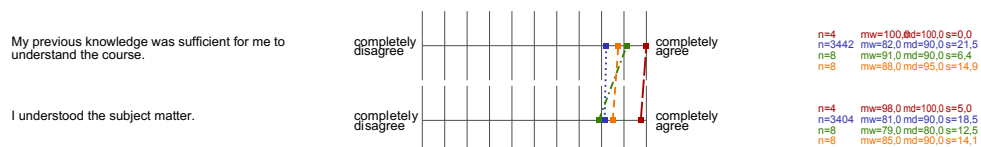
## Profile



### Evaluation of the Member of Teaching Staff and the Course



### Evaluation of Requirements and Gain of Knowledge



03.09.2018

EvaSys Auswertung

Seite 5

## Profile

Subunit:	LE_Mathematik und Informatik (MNF)
Name of the instructor:	Prof. Dr. Marc Hellmuth
Name of the course: (Name of the survey)	Graphentheorie (5501151)
Comparative line:	Durchschnitt MNF-Vorlesung Englisch

Values used in the profile line: Mean

### Evaluation of the Member of Teaching Staff and the Course

[illegible]

### Evaluation of Requirements and Gain of Knowledge

Statement	trifft überhaupt nicht zu	trifft überhaupt vollständig zu	Statistics
My previous knowledge was sufficient for me to understand the course.	trifft überhaupt nicht zu	trifft vollständig zu	n=14 av=98,0 md=100,0 dev=4,3 n=3480 av=82,0 md=90,0 dev=21,4
I understood the subject matter.	trifft überhaupt nicht zu	trifft vollständig zu	n=13 av=93,0 md=90,0 dev=8,5 n=3442 av=81,0 md=90,0 dev=18,4
I learn a lot at the course.	trifft überhaupt nicht zu	trifft vollständig zu	n=14 av=91,0 md=90,0 dev=9,5 n=3458 av=79,0 md=80,0 dev=20,7
The course fosters my interest in the subject.	trifft überhaupt nicht zu	trifft vollständig zu	n=14 av=88,0 md=95,0 dev=16,7 n=3478 av=78,0 md=80,0 dev=24,0
It is worth attending the course.	trifft überhaupt nicht zu	trifft vollständig zu	n=14 av=93,0 md=100,0 dev=11,4 n=3416 av=82,0 md=90,0 dev=21,3
I think the workload for this course is appropriate	trifft überhaupt nicht zu	trifft vollständig zu	n=14 av=85,0 md=90,0 dev=19,9 n=3417 av=83,0 md=90,0 dev=19,7

### Overall Evaluation of the Course

Which overall mark would you give for the course  
(excellent/good/satisfactory/sufficient/inadequate)?

sehr gut  mangelhaft

n=14 av=1,6 md=1,0 dev=0,8

## Profile

Subunit: LE\_Mathematik und Informatik (MNF)

Name of the instructor: Prof. Dr. Marc Hellmuth

Name of the course: Bioinformatik (Vorlesung)  
(Name of the survey)

Comparative line: MNF-Vorlesung Englisch 2014/15-2016/17

Values used in the profile line: Mean

### Evaluation of the Member of Teaching Staff and the Course

Item	trifft überhaupt nicht zu	trifft nicht zu	trifft zu	trifft vollständig zu	n	av	md	av=90,0	md=90,0	dev
The member of teaching staff speaks clearly and motivationally.					n=15	av=96,0	md=100,0	dev=6,3		
					n=3476	av=85,0	md=90,0	dev=19,3		
The member of teaching staff puts effort into his/her teaching.					n=15	av=93,0	md=90,0	dev=6,2		
					n=3438	av=88,0	md=90,0	dev=15,8		
The member of teaching staff is cooperative and open-minded.					n=15	av=94,0	md=90,0	dev=6,3		
					n=3464	av=88,0	md=90,0	dev=16,0		
Own contributions, questions and active participation are encouraged.					n=15	av=94,0	md=90,0	dev=6,3		
					n=3447	av=80,0	md=90,0	dev=21,8		
The students receive helpful feedback to their questions and contributions					n=15	av=93,0	md=90,0	dev=6,2		
					n=3432	av=85,0	md=90,0	dev=17,8		
The content structure of the course is comprehensible					n=15	av=87,0	md=90,0	dev=13,5		
					n=3471	av=85,0	md=90,0	dev=17,7		
Students are encouraged to follow the content and think the topic through					n=15	av=85,0	md=90,0	dev=5,2		
					n=3470	av=81,0	md=90,0	dev=20,1		
Students learn about the importance or the use of the topics covered.					n=15	av=93,0	md=90,0	dev=6,2		
					n=3464	av=84,0	md=90,0	dev=18,2		
The work materials (e.g. handouts, scripts, reading lists) were useful.					n=15	av=85,0	md=90,0	dev=12,5		
					n=3394	av=80,0	md=90,0	dev=22,2		

### Evaluation of Requirements and Gain of Knowledge

Statement	trifft überhaupt nicht zu	trifft vollständig zu	n	av	md	dev
My previous knowledge was sufficient for me to understand the course.	trifft überhaupt nicht zu	trifft vollständig zu	n=16 n=3480	av=81,0 av=82,0	md=95,0 md=90,0	dev=10,2 dev=2
I understood the subject matter.	trifft überhaupt nicht zu	trifft vollständig zu	n=16 n=3442	av=91,0 av=81,0	md=90,0 md=90,0	dev=7,7 dev=18,4
I learn a lot at the course.	trifft überhaupt nicht zu	trifft vollständig zu	n=16 n=3458	av=86,0 av=79,0	md=90,0 md=80,0	dev=11,5 dev=20,7
The course fosters my interest in the subject.	trifft überhaupt nicht zu	trifft vollständig zu	n=16 n=3478	av=88,0 av=78,0	md=90,0 md=80,0	dev=13,3 dev=24,0
It is worth attending the course.	trifft überhaupt nicht zu	trifft vollständig zu	n=15 n=3416	av=89,0 av=82,0	md=90,0 md=90,0	dev=12,5 dev=21,3
I think the workload for this course is appropriate	trifft überhaupt nicht zu	trifft vollständig zu	n=15 n=3417	av=88,0 av=83,0	md=90,0 md=90,0	dev=10,8 dev=19,7

### Overall Evaluation of the Course

Which overall mark would you give for the course  
(excellent/good/satisfactory/sufficient/inadequate)?

sehr gut | | | | mangelhaft

n=16 av=1,6 md=1,0 dev=0,9

# Marc Hellmuth

## Publications

All publications where I am the corresponding author are marked with “★”.

### International Journals (peer-reviewed)

---

- ★ [1] M. Hellmuth and G.E. Scholz. *Resolving prime modules: The structure of pseudo-cographs and galled-tree explainable graphs*. **Discrete Applied Mathematics**, 343:25–43, 2024
- ★ [2] David Schaller, Tom Hartmann, Manuel Lafond, Peter F. Stadler, Nicolas Wieseke, and Marc Hellmuth. *Relative timing information and orthology in evolutionary scenarios*. **Algorithms for Molecular Biology**, 18(1):16, 2023
- [3] David Schaller, Marc Hellmuth, and Peter F. Stadler. *Orientation of fitch graphs and reconciliation-free inference of horizontal gene transfer in gene trees*. **SIAM Journal on Discrete Mathematics**, 37(3):2172–2207, 2023
- ★ [4] M. Hellmuth, D. Schaller, and P.F. Stadler. *Clustering systems of phylogenetic networks*. **Theory in Biosciences**, 2023. doi:10.1007/s12064-023-00398-w
- [5] M. Hellmuth, K. T. Huber, V. Moulton, G. E. Scholz, and P. F. Stadler. *Injective split systems*. **Graphs and Combinatorics**, 39(4):65, 2023
- [6] A. Korchmaros, D. Schaller, M. Hellmuth, and P.F. Stadler. *Quasi-best match graphs*. **Discrete Applied Mathematics**, 331:104–125, 2023
- ★ [7] C.R. Seemann, V. Moulton, P.F. Stadler, and M. Hellmuth. *Planar median graphs and cubesquare-graphs*. **Discrete Applied Mathematics**, 331:38–58, 2023
- ★ [8] M. Hellmuth and G.E. Scholz. *From modular decomposition trees to level-1 networks: Pseudo-cographs, polar-cats and prime polar-cats*. **Discrete Applied Mathematics**, 321:179–219, 2022
- ★ [9] A. Lindeberg and M. Hellmuth. *Construction of  $k$ -matchings in graph products*. **Art Discrete Appl. Math.**, 6(2):#P2.02, 2023
- [10] D. Schaller, M. Hellmuth, and P.F. Stadler. *AsymmeTree: A flexible python package for the simulation of complex gene family histories*. **Software**, 1(3):276–298, 2022
- ★ [11] M. Hellmuth, D. Schaller, and P.F. Stadler. *Compatibility of partitions with trees, hierarchies, and split systems*. **Discrete Applied Mathematics**, 314:265–283, 2022
- ★ [12] T. Hartmann, M. Bannach, M Middendorf, Stadler P.F., N. Wieseke, and M. Hellmuth. *Complete edge-colored permutation graphs*. **Advances in Applied Mathematics**, 139:102377, 2022

- [13] D.I. Valdivia, M. Geiß, M. Hernández Rosales, P.F. Stadler, and M. Hellmuth. *Hierarchical and modularly-minimal vertex colorings*. **Art Discrete Appl. Math.**, 6(2):#P2.01, 2023
- [14] D. Schaller, M. Geiß, M. Hellmuth, and P.F. Stadler. *Best match graphs with binary trees*. **IEEE/ACM Transactions on Computational Biology and Bioinformatics**, (01):1–1, 2022. DOI: 10.1109/TCBB.2022.3143870
- ★ [15] C. Bruckmann, P.F. Stadler, and M. Hellmuth. *From modular decomposition trees to rooted median graphs*. **Discrete Applied Mathematics**, 310:1–9, 2022
- [16] C. Flamm, M. Hellmuth, D. Merkle, N. Nøjgaard, and P.F. Stadler. *Generic context-aware group contributions*. **IEEE/ACM Transactions on Computational Biology and Bioinformatics**, 19(1):429–442, 2022
- [17] D. Schaller, M. Hellmuth, and P.F. Stadler. *A simpler linear-time algorithm for the common refinement of rooted phylogenetic trees on a common leaf set*. **Algorithms Mol. Biol.**, 16(23), 2021. DOI: 10.1186/s13015-021-00202-8
- [18] D. Schaller, M. Geiß, M. Hellmuth, and P.F. Stadler. *Least resolved trees for two-colored best match graphs*. **Journal of Graph Algorithms and Applications**, 25(1):397–416, 2021
- [19] D. Schaller, M. Geiß, M. Hellmuth, and P.F. Stadler. *Heuristic algorithms for best match graph editing*. **Algorithms Mol. Biol.**, 16(19), 2021. DOI: 0.1186/s13015-021-00196-3
- ★ [20] D. Schaller, M. Lafond, P.F. Stadler, W. Wieseke, and M. Hellmuth. *Indirect identification of horizontal gene transfer*. **J. Math. Biology**, 83(1):1–73, 2021
- [21] M. Hellmuth, C.R. Seemann, and P.F. Stadler. *Generalized Fitch graphs III: Symmetrized Fitch maps and sets of symmetric binary relations that are explained by unrooted edge-labeled trees*. **Discrete Mathematics & Theoretical Computer Science**, 23:1, 2021
- [22] David Schaller, Manuela Geiß, Marc Hellmuth, and Peter F. Stadler. *Arc-completion of 2-colored best match graphs to binary-explainable best match graphs*. **Algorithms**, 14(4), 2021
- [23] M. Hellmuth, W. Fontana, D. Merkle, and N. Nøjgaard. *Cayley graphs of semi-groups applied to atom tracking in chemistry*. **Journal of Computational Biology**, 28(7):701–715, 2021
- [24] D. Schaller, M. Geiß, E. Chávez, M. González Laffitte, A. López Sánchez, B.M.R. Stadler, D.I. Valdivia, M. Hellmuth, M. Hernández Rosales, and P.F. Stadler. *Corrigendum to “best match graphs”*. **J. Math. Biology**, 82(47):1–9, 2021
- ★ [25] D. Schaller, P.F. Stadler, and M. Hellmuth. *Complexity of modification problems for best match graphs*. **Theoretical Comp. Sci.**, 865:63–84, 2021
- ★ [26] D. Schaller, M. Geiß, P.F. Stadler, and M. Hellmuth. *Complete characterization of incorrect orthology assignments in best match graphs*. **J. Math. Biology**, 82(20):1–64, 2021

- ★ [27] M. Lafond and M. Hellmuth. *Reconstruction of time-consistent species trees*. **Algorithms Mol. Biol.**, 15(16):1–27, 2020
- ★ [28] M. Hellmuth, C.R. Seemann, and P.F. Stadler. *Generalized Fitch graphs II: Sets of binary relations that are explained by edge-labeled trees*. **Discrete Appl. Math.**, 283:495 – 511, 2020
- [29] P.F. Stadler, M. Geiß, D. Schaller, A. López Sánchez, M. González Laffitte, D.I. Valdivia, M. Hellmuth, and M. Hernández Rosales. *From pairs of most similar sequences to phylogenetic best matches*. **Algorithms Mol. Biol.**, 15(5):1–20, 2020
- ★ [30] M. Hellmuth, M. Geiß, and P.F. Stadler. *Complexity of modification problems for reciprocal best match graphs*. **Theoretical Comp. Sci.**, 809:384 – 393, 2020
- ★ [31] M. Hellmuth, A. Fritz, N. Wieseke, and P.F. Stadler. *Cograph editing: Merging modules is equivalent to editing P4’s*. **Art Discrete Appl. Math.**, 3:P2.01, 2020
- [32] M. Geiß, M. González Laffitte, A. López Sánchez, D.I. Valdivia, M. Hellmuth, M. Hernández Rosales, and P.F. Stadler. *Best match graphs and reconciliation of gene trees with species trees*. **J. Math. Biology**, 80:1459–1495, 2020
- ★ [33] M. Geiß, P.F. Stadler, and M. Hellmuth. *Reciprocal best match graphs*. **J. Math. Biology**, 80:865–953, 2020
- ★ [34] M. Hellmuth. *Generalized Fitch graphs: Edge-labeled graphs that are explained by edge-labeled trees*. **Discr. Appl. Math.**, 267:1 – 11, 2019
- ★ [35] M. Hellmuth, K.T. Huber, and V. Moulton. *Reconciling event-labeled gene trees with MUL-trees and species networks*. **J. Math. Biology**, 79:1885–1925, 2019
- ★ [36] M. Hellmuth and C.R. Seemann. *Alternative characterizations of Fitch’s xenology relation*. **J. Math. Biology**, 79(3):969–986, 2019
- [37] M. Geiß, E. Chávez, M. González Laffitte, A. López Sánchez, B.M.R. Stadler, D.I. Valdivia, M. Hellmuth, M. Hernández Rosales, and P.F. Stadler. *Best match graphs*. **J. Math. Biology**, 78(7):2015–2057, 2019
- ★ [38] M. Geiß, J. Anders, P.F. Stadler, N. Wieseke, and M. Hellmuth. *Reconstructing gene trees from Fitch’s xenology relation*. **J. Math. Biology**, 77(5):1459–1491, 2018
- [39] T. Siems, M. Hellmuth, and V. Liebscher. *Simultaneous credible regions for multiple changepoint locations*. **J. Comp. Graph. Statistics**, 0(0):1–9, 2018. DOI 10.1080/10618600.2018.1513366
- [40] M. Geiß, M. Hellmuth, Y. Long, and P.F. Stadler. *A short note on undirected Fitch graphs*. **Art Discrete Appl. Math.**, 1(1):#P1.08, 2018
- ★ [41] Carsten R. Seemann and Marc Hellmuth. *The matroid structure of representative triple sets and triple closure computation*. **European J. Combin.**, 70:384 – 407, 2018
- ★ [42] N. Nøjgaard, M. Geiß, D. Merkle, P.F. Stadler, N. Wieseke, and M. Hellmuth. *Time-consistent reconciliation maps and forbidden time travel*. **Algorithms Mol. Biol.**, 13(1):2, 2018

- [43] M. Hellmuth, M. Hernandez-Rosales, Y. Long, and P.F. Stadler. *Inferring phylogenetic trees from the knowledge of rare evolutionary events*. **J. Math. Biology**, 76(7):1623–1653, 2018
- ★ [44] M. Hellmuth and N. Wieseke. *On tree representations of relations and graphs: Symbolic ultrametrics and cograph edge decompositions*. **J. Comb. Opt.**, 36(2):591–616, 2018
- ★ [45] M. Hellmuth. *Biologically feasible gene trees, reconciliation maps and informative triples*. **Algorithms Mol. Biol.**, 12(1):23, 2017
- ★ [46] M. Hellmuth, P.F. Stadler, and N. Wieseke. *The mathematics of xenology: Di-cographs, symbolic ultrametrics, 2-structures and tree-representable systems of binary relations*. **J. Math. Biology**, 75(1):199–237, 2017
- [47] R. Batra, N. Alcaraz, K. Gitzhofer, J. Pauling, H. Ditzel, M. Hellmuth, M List, and J. Baumbach. *On the performance of de novo pathway enrichment*. **Nature PJ Systems Biology and Applications**, 3(1):6, 2017
- ★ [48] M. Hellmuth and F. Lehner. *Fast factorization of Cartesian products of (directed) hypergraphs*. **J. Theor. Comp. Sci.**, 615:1–11, 2016
- ★ [49] R.H. Hammack, M. Hellmuth, L. Ostermeier, and P.F. Stadler. *Associativity and non-associativity of some hypergraph products*. **Math. Comp. Sci**, 10(3):403–408, 2016
- ★ [50] M. Hellmuth, W. Imrich, and T. Kupka. *Fast recognition of partial star products and quasi Cartesian products*. **Ars Math. Cont.**, 9(2):233 – 252, 2015
- ★ [51] M. Hellmuth, N. Wiesecke, M. Lechner, H.P. Lenhof, M. Middendorf, and P.F. Stadler. *Phylogenomics with paralogs*. **Proc. Natl. Acad. Sci. USA (PNAS)**, 112(7):2058–2063, 2015
- ★ [52] S. Berkemer, R. Chaves, A. Fritz, M. Hellmuth, M. Hernandez-Rosales, and P.F. Stadler. *Spiders can be recognized by counting their legs*. **Math. Comput. Sci**, 9(4):437–441, 2015
- [53] M. Hellmuth, L Ostermeier, and P.F. Stadler. *The relaxed square property*. **Australas. J. Combin.**, 62(3):240–270, 2015
- ★ [54] M. Hellmuth and T. Marc. *On the Cartesian skeleton and the factorization of the strong product of digraphs*. **J. Theor. Comp. Sci.**, 565(0):16–29, 2015
- ★ [55] M. Hellmuth, L. Ostermeier, and M. Noll. *Strong products of hypergraphs: Unique prime factorization theorems and algorithms*. **Discr. Appl. Math.**, 171:60–71, 2014
- [56] M. Hernandez-Rosales, M. Hellmuth, N. Wieseke, and P. F. Stadler. *Simulation of gene family histories*. **BMC Bioinformatics**, 15(Suppl 3):A8, 2014
- [57] M. Hellmuth, L. Ostermeier, and P. F. Stadler. *Unique square property, equitable partitions, and product-like graphs*. **Discr. Math.**, 320(0):92 – 103, 2014
- [58] M. Hellmuth, J. Leydold, and P.F. Stadler. *Convex cycle bases*. **Ars Math. Cont.**, 7(1):123 – 140, 2014



- ★ [59] M. Hellmuth, W. Imrich, and T. Kupka. *Partial star products: A local covering approach for the recognition of approximate Cartesian product graphs*. **Math. Comput. Sci**, 7(3):255–273, 2013
- [60] M. Hellmuth, M. Hernandez-Rosales, K. T. Huber, V. Moulton, P. F. Stadler, and N. Wieseke. *Orthology relations, symbolic ultrametrics, and cographs*. **J. Math. Biology**, 66(1-2):399–420, 2013
- ★ [61] M. Hellmuth. *On the complexity of recognizing S-composite and S-prime graphs*. **Discr. Appl. Math.**, 161(7-8):1006 – 1013, 2013
- [62] M. Hernandez-Rosales, M. Hellmuth, N. Wieseke, K. T. Huber, V. Moulton, and P. F. Stadler. *From event-labeled gene trees to species trees*. **BMC Bioinformatics**, 13(Suppl 19):S6, 2012
- ★ [63] L. Ostermeier, M. Hellmuth, and P. F. Stadler. *The Cartesian product of hypergraphs*. **J. Graph Theory**, 70(2):180–196, 2012
- ★ [64] M. Hellmuth, L. Ostermeier, and P.F. Stadler. *Diagonalized Cartesian products of S-prime graphs are S-prime*. **Discr. Math.**, 312(1):74 – 80, 2012. Algebraic Graph Theory - A Volume Dedicated to Gert Sabidussi on the Occasion of His 80th Birthday
- [65] M. Hellmuth, L. Ostermeier, and P.F. Stadler. *A survey on hypergraph products*. **Math. Comput. Sci**, 6:1–32, 2012
- [66] M. Hellmuth, P.J. Ostermeier, and P.F. Stadler. *Minimum cycle bases of lexicographic products*. **Ars Math. Cont.**, 5:223–234, 2012
- ★ [67] M. Hellmuth. *A local prime factor decomposition algorithm*. **Discr. Math.**, 311(12):944–965, 2011
- [68] S. Jänicke, C. Heine, M. Hellmuth, P.F. Stadler, and G. Scheuermann. *Visualization of graph products*. **IEEE Transactions on Visualization and Computer Graphics**, 16(6):1082–1089, 2010
- [69] T. Biyikoglu, M. Hellmuth, and J. Leydold. *Largest eigenvalues of the discrete p-Laplacian of trees with degree sequences*. **Electron. J. Linear Algebra**, 18:202–210, 2009
- ★ [70] M. Hellmuth, D. Merkle, and M. Middendorf. *Extended shapes for the combinatorial design of RNA sequences*. **Int. J. of Computational Biology and Drug Design**, 2(4):371–384, 2009
- ★ [71] M. Hellmuth, W. Imrich, W. Klöckl, and P. F. Stadler. *Local algorithms for the prime factorization of strong product graphs*. **Math. Comput. Sci**, 2(4):653–682, 2009
- [72] P.J. Ostermeier, M. Hellmuth, K. Klemm, J. Leydold, and P.F. Stadler. *A note on quasi-robust cycle bases*. **Ars Math. Cont.**, 2:231–240, 2009
- [73] M. Hellmuth, W. Imrich, W. Klöckl, and P. F. Stadler. *Approximate graph products*. **European J. Combin.**, 30(5):1119 – 1133, 2009

- [74] J.A. Ramírez-Rafael, A. Korchmaros, K. Aviña-Padilla, A. López Sánchez, A.A. España-Tinajero, M. Hellmuth, P.F. Stadler, and M. Hernández-Rosales. *Revolutionh-tl: Reconstruction of evolutionary histories tool*. In **Comparative Genomics (RECOMB-CG)**, pages 89–109, Cham, 2024. Springer Nature Switzerland
- [75] A.V. Shanavas, M. Changat, M. Hellmuth, and P.F. Stadler. *Unique least common ancestors and clusters in directed acyclic graphs*. In **Algorithms and Discrete Applied Mathematics: 10th International Conference, CALDAM 2024**, page 148–161. Springer-Verlag, 2024
- [76] M. Hellmuth and G.E. Scholz. *Linear time algorithms for NP-hard problems restricted to GaTeX graphs*. In **Computing and Combinatorics: 29th International Conference, COCOON 2023, Part I**, page 115–126. Springer-Verlag, 2023
- ★ [77] M. Hellmuth, P.F. Stadler, and S. Thekkumpadan Puthiyaveedu. *Fitch graph completion*. In **Computing and Combinatorics: 29th International Conference, COCOON 2023, Part II**, page 225–237. Springer-Verlag, 2023
- [78] M. Hellmuth, M. Michel, N. Nøjgaard, D. Schaller, and P.F. Stadler. *Combining orthology and xenology data in a common phylogenetic tree*. **Advances in Bioinformatics and Computational Biology (BSB2021)**, 13063:53–64, 2021
- [79] D. Schaller, M. Geiß, M. Hellmuth, and P.F. Stadler. *Best match graphs with binary trees*. **Algorithms for Computational Biology (ALCoB)**, 12715:82–93, 2021
- [80] M. Hellmuth, D. Merkle, and N. Nøjgaard. *Atom tracking using Cayley graphs*. In **Bioinformatics Research and Applications (ISBRA)**, pages 406–415, Cham, 2020. Springer International Publishing
- [81] J.L. Andersen, M. Hellmuth, D. Merkle, N. Nøjgaard, and M. Peressotti. *A graph-based tool to embed the pi-calculus into a computational DPO framework*. **46th International Conference on Current Trends in Theory and Practice of Computer Science (SOFSEM)**, 2020
- ★ [82] N. Nøjgaard, N. El-Mabrouk, D. Merkle, N. Wieseke, and M. Hellmuth. *Partial homology relations - satisfiability in terms of di-cographs*. In **24th International Computing and Combinatorics Conference (COCOON), 2018**, pages 403–415, Cham, 2018. Springer International Publishing
- [83] M. Hellmuth, A.S. Knudsen, M. Kotrbčik, D. Merkle, and N. Nøjgaard. *Linear time canonicalization and enumeration of non-isomorphic 1-face embeddings*. **SIAM: 2018 Proceedings of the Twentieth Workshop on Algorithm Engineering and Experiments (ALENEX)**, pages 154–168, 2018
- ★ [84] N. Nøjgaard, M. Geiß, D. Merkle, P.F. Stadler, N. Wieseke, and M. Hellmuth. *Forbidden time travel: Characterization of time-consistent reconciliation maps between trees*. **Leibniz International Proceedings in Informatics (LIPIcs)**, 88(17):1–12, 2017. 17th International Workshop on Algorithms in Bioinformatics (WABI 2017)
- ★ [85] M. Hellmuth and N. Wieseke. *On symbolic ultrametrics, cotree representations, and cograph edge decompositions and partitions*. In **Computing and Combinatorics: 21st International Conference (COCOON), 2015**, pages 609–623, Cham, 2015. Springer International Publishing

- ★ [86] T. Ingalls, G. Martius, M. Marz, S.J. Prohaska, and M. Hellmuth. *Converting DNA to music: ComposAlign*. In **German Conference on Bioinformatics '09**, pages 93–103, 2009
- ★ [87] M. Hellmuth, D. Merkle, and M. Middendorf. *On the design of RNA sequences for realizing extended shapes*. In **Bioinformatics, Systems Biology and Intelligent Computing, 2009. IJCBS'09. International Joint Conference on**, pages 167–173. IEEE, 2009

## Monographs (Theses)

---

- ★ [88] M. Hellmuth. *On the decomposition and reconstruction of discrete structures: Characterization, approximation and computation*. **Habilitation thesis**, University Saarbrücken, Department of Mathematics and Computer Science, 2016
- ★ [89] M. Hellmuth. *Local prime factor decomposition of approximate strong product graphs*. **PhD thesis**, University Leipzig, Department of Mathematics and Computer Science, 2010
- ★ [90] M. Hellmuth. *Konstruktion von Worten mit Matchingeigenschaften und Anwendung auf das RNA design*. **Diploma thesis**, University Leipzig, Department of Mathematics and Computer Science, 2006

## Book Chapter

---

- [91] M. Hellmuth and P.F. Stadler. *The Theory of Gene Family Histories*, pages 1–32. Springer US, New York, NY, 2024
- ★ [92] M. Hellmuth and N. Wieseke. *From sequence data incl. orthologs, paralogs, and xenologs to gene and species trees*. In **Evolutionary Biology**, pages 373–392, Cham, 2016. Springer International Publishing. DOI: 10.1007/978-3-319-41324-2\_21

## Public Domain Software Packages

---

- Ref. [74] Ramírez-Rafael et al.  
REvolutionH-tl: a Python-based tool designed for evolutionary analysis tasks.  
<https://pypi.org/project/revolutionhtl/>
- Ref. [10] Schaller et al.  
AsymmeTree: a Python-based library for the simulation and analysis of phylogenetic scenarios. <https://github.com/david-schaller/AsymmeTree>
- Ref. [81] J.L. Andersen, M. Hellmuth, D. Merkle, N. Nøjgaard and M. Peressotti  
EpiM: a Python-based library for computing execution spaces of  $\pi$ -calculus processes. <http://cheminf.imada.sdu.dk/epim>
- Ref. [16] C. Flamm, M. Hellmuth, D. Merkle, N. Nøjgaard and P.F. Stadler  
Context AwaRe Group cOntribution (CARGO). <https://imada.sdu.dk/Employees/daniel/cargo/>
- Ref. [42] N. Nøjgaard, M. Geiß, D. Merkle, P.F. Stadler, N. Wieseke and M. Hellmuth  
TimeCons-Reconciliation. <https://github.com/Nojgaard/tc-recon>

- Ref. [51] M. Hellmuth, N. Wiesecke, M. Lechner, H.P. Lenhof, M. Middendorf and P.F. Stadler  
ParaPhylo. [pacosy.informatik.uni-leipzig.de/paraphylo](http://pacosy.informatik.uni-leipzig.de/paraphylo)
- Ref. [67] M. Hellmuth  
LocalPFD. <https://math-inf.uni-greifswald.de/institut/ueber-uns/mitarbeitende/hellmuth/software/>
- Ref. [83] M. Hellmuth, A.S. Knudsen, M. Kotrbčik, D. Merkle and N. Nøjgaard  
GapEST. <https://github.com/nojgaard/DoubleTrace>
- Ref. [86] T. Ingalls, G. Martius, M. Marz, S.J. Prohaska and M. Hellmuth  
ComposAlign. <http://composalign.bioinf.uni-leipzig.de/>

# Marc Hellmuth

## Research Statement

*Bridging the gap between computer science and mathematics forms the core of my research with a specific emphasis on the characterization of discrete data, the design of efficient algorithms, as well as computational complexity theory.*

I studied mathematics and economy in Leipzig (Germany) and since April 2010, I hold a PhD in computer science that was graded with highest honor (*summa cum laude*). Following PostDoc positions in Leipzig and Saarbrücken, I was Juniorprofessor for Computer Science at the University of Greifswald, Germany (2015-2020). In 2020, I worked as a lecturer (permanent, research track) within the group *Algorithms and Complexity* at the University of Leeds, UK. Since Dec 2020, I am associate professor for computer science at the Stockholm University in Sweden. In addition, I have received the *Venia Legendi* (habilitation) in bioinformatics from the Saarland University in 2016 and in computer science from Stockholm University in 2022. Currently, my research group consists of one postdoctoral researcher and two PhD students.

My research lies at the interface of theoretical computer science and discrete mathematics with a focus on computational complexity and the design of efficient algorithms for tackling combinatorial optimization problems. Besides establishing novel research fields in theoretical computer science and discrete mathematics, our developed theoretical findings have played a crucial role in creating practical and innovative applications and software solutions. This holistic perspective underscores the relevance and impact of bridging the gap between theoretical computer science, abstract mathematical concepts, and pragmatic problem-solving in diverse research fields.

In a nutshell, my main research fields are located in the following areas (for each of them representative references are selected):

- Complexity Theory (e.g. (Co)NP-completeness and Fixed-Parameter Tractability (FPT)) [11, 25, 30, 44, 61]
- Design of efficient algorithms with a focus on
  - linear-time algorithms (where possible) [3, 17, 59, 76, 83]
  - heuristics [6, 19]
  - exact algorithms, e.g. Integer Linear Programs [26, 39, 44, 51]
  - approximation and parameterized algorithms [11, 30, 38]
- Algorithmic and mathematical analysis of large data sets [2, 16, 26, 39, 51, 82, 92]
- Finding efficient representation of data for the design of robust and fast algorithms [1, 2, 6, 8, 15]
- Discrete Mathematics (incl. Discrete Optimization, Combinatorics, (Hyper)Graph Theory) [7, 9, 12, 48, 67]
- Algorithmic Network Analysis [16, 19, 29, 47]
- Computational Geometry [83] and Matroid Theory [41]
- Algorithms in Life Sciences (Reciprocal Best Matches, Horizontal Gene Transfer, Self-assembling Nano structure, Atom Tracking in Chemical Reaction Networks, Combinatorial RNA structures) [10, 23, 27, 70, 83]

In what follows, I present some of my research activities in some more detail.

*Bibliography references can be found in Attachment “List of Publications”*

**Tackling Hard Problems with Explicit Modular Decomposition.** Modular decomposition is a widely used technique for representing nested "substructures" (modules) of discrete data, pairwise relationships, or graphs in form of a rooted tree. In a graph  $G = (V, E)$ , for example, a subset  $M \subseteq V$  is considered a module if all its vertices share the same set of neighbors among the vertices not in  $M$ . The modular decomposition of a graph  $G$  consists of non-overlapping modules, forming a hierarchy and thus, a rooted tree known as the modular decomposition tree  $\text{MDT}(G)$ . In the absence of so-called "prime" vertices in  $\text{MDT}(G)$ , the graph  $G$  is referred to as a *cograph*, and  $\text{MDT}(G)$  fully *explains*  $G$ , i.e., the existence of edges and non-edges is determined by  $\text{MDT}(G)$ . As a result, modular decomposition trees without "prime" vertices become invaluable guides for algorithms to efficiently solve many computationally hard problems on cographs. These problems include graph isomorphism, as well as classical NP-hard problems such as minimum independent set, maximum clique, or minimum vertex coloring.

In general, "prime" modules can obstruct and challenge the algorithmic utility of modular decomposition trees. To circumvent this issue, we aim to use [modular decomposition networks](#) instead of trees, leading to the concept of [explicit modular decomposition](#). In other words, we aim at finding rooted DAGs (networks) to explain the underlying graphs  $G$  [1, 8, 15]. As a proof of concept, we demonstrated that all (edge-colored) graphs have a natural network representation by replacing "prime" vertices in modular decomposition trees with so-called half-grids [15]. We further characterized graphs that can be explained by 0/1-labeled rooted networks (called galled-trees) that are obtained from  $\text{MDT}(G)$  by replacing "prime" vertices with simple rooted 0/1-labeled cycles [8]. This eventually led to the discovery of the new graph classes of pseudo-cographs and, more general, GATEx graphs. We showed in [1] that GATEx graphs form a superclass of cographs but are at the same time permutation graphs that are linear-time perfectly orderable and that have bounded twin-width. Moreover, GATEx are characterized by a set of 24 forbidden subgraphs. Importantly, we have shown in [76] how to employ the structure of these networks explaining a GATEx graph  $G$  in order to solve many NP-hard problems (maximum clique, minimum vertex-coloring, maximum independent set, perfect ordering) in [linear-time](#). Many complexity results established for graphs with bounded twin-width (e.g. fixed-parameter tractability or approximation results) become applicable for GATEx graphs as well.

We are currently investigating the interplay between the structure of modular decomposition networks explaining a given graph  $G$ , the structure of  $G$ , and the ability of the network to guide algorithms in efficiently solving hard problems on such graphs. These networks essentially provide a sliding window through which we can observe the points at which structural properties of  $G$  allow underlying NP-hard problems to be solved in polynomial time or become NP-hard in the underlying graph class of  $G$ . All these ideas can be generalized to other discrete objects, e.g., hypergraphs, 2-structures, matroids or Boolean functions. Thus, explicit modular decomposition opens a fundamental new way to study and discover new classes of discrete objects and we have, together with the networks that explain the underlying objects, an extremely powerful tool in hand to explore the computational complexity of many problems. This in turn, will lead to the development of new methods to tackle challenging computational problems.

**(Approximate) Product Structures of Set Systems.** A further part of my work that established an entire new research field in algorithmic graph theory, is concerned with determining the prime factors of products of set systems (e.g. graphs or hypergraphs). Products of set systems are a common way of constructing larger objects from smaller building blocks. For graphs, hypergraphs, and related set systems there is not only a one but a few types of products. These often (but not always) satisfy a unique prime factor decomposition (PFD) property. It is of key interest then to understand the structure of a large object by decomposing it into its prime factors.

We established characterizations of graphs and hypergraphs and their unique PFD w.r.t. different types of products [49, 55, 57, 63, 65]. In addition, we designed efficient algorithms to determine the prime factors of a given set system [48, 54, 55, 67, 71]. In particular, I developed the currently fastest algorithm to determine the prime factors of graphs w.r.t. the strong product which runs linear-time for graphs with fixed maximum degree [67]. Contrary to existing approaches, this method utilizes the information of small local factorizable patches, which are then combined to determine the original prime factors of the graph. In addition, we designed the currently fastest algorithm for the PFD of Cartesian products of hypergraphs [48].

Graph products arise in a variety of different contexts, from mathematics and computer science to theoretical

biology or computational engineering. In all applications of practical interest, however, the considered set systems are derived from real data or simulations. Hence, they are notoriously incomplete and/or plagued by measurement errors. In order to deal with such inaccuracies we introduced the concept of approximate products and product-like structures. The central question is: *Is a graph an approximate product and how close is the approximate product to an exact product?* We showed the (Co)NP-completeness of certain types of such products [61, 64] and designed several heuristics for approximate products [50, 57, 59].

In the classical reference [Handbook of Product Graphs](#), 2nd Edition (CRC Press, 2011) by Hammack, Imrich and Klavžar several sections are provided that present many results of my work.

**1-Face Embeddings and Linear-Time Isomorphism Test.** Orientable 1-Face Embeddings, which are specific planar representations of graphs on a generalized torus, are equivalent to antiparallel strong traces (types of walks in graphs that utilize each edge exactly twice) within the examined graphs. These embeddings play a vital role in designing self-assembling protein or DNA strands. Such traces can be computed by means of the underlying automorphism groups, which, however, is significantly inefficient. In contrast, we introduced a novel canonical form invariant for antiparallel strong traces, offering a linear-time isomorphism test for these traces and, consequently, for orientable 1-face embeddings of graphs as well. Remarkably, this algorithm remains independent of the graph's automorphism group size. This breakthrough eventually paved the way for the first large-scale enumeration of non-isomorphic embeddings and the exploration of their characteristics. Parts of this work were presented at the SIAM conference on Algorithm Engineering and Experiments (ALENEX) [83] one of the leading conference in algorithms and data structures.

**Matroids meet Phylogenetics.** A matroid is a structure that abstracts and generalizes the notion of linear independence in vector spaces. We used this type of generalization to solve the following problem: An important set-operation is the closure  $\text{cl}(R)$  of a set  $R$  of triples (rooted binary trees on three leaves) since it provides essential information about tree-like relations that are shown by any supertree that displays all triples in  $R$ . In [41], we investigated the structure of so-called representative triple sets (RTS), that is, those subsets  $R'$  of  $R$  for which  $\text{cl}(R') = \text{cl}(R)$ . For decades, it was conjectured that the computation of a minimum-sized RTS is NP-hard. In contrast, we have shown that RTS form the basis of a matroid and thus must all have the same size. As a consequence, RTS can be computed in polynomial time using a simple greedy algorithm. This algorithm, in particular, enhances the 1995 algorithm for computing triple closures, achieving a remarkable improvement by a factor of  $|R||L|$ , where  $L$  is the set of vertices on which the triples in  $R$  are defined. This mathematical result has far-reaching consequences in bioinformatics, as RTS serve as the foundation for many heuristics whose runtime can now be significantly improved by considering smaller inputs.

**Trees and Networks in Biology.** Several of the problems I've explored have real-world applications. This encompasses characterizing the mathematical structure of complex networks or relations between genomic sequence data and delving into the computational complexity of the underlying optimization problems (see, for instance, [25, 26, 30, 44, 45]). Typically, our initial task in tackling biological problems is to formalize and examine their mathematical structure. When solving specific optimization problems, we analyze their computational complexity and design efficient algorithms, including exact algorithms, heuristics, or ILP and FPT algorithms.

By way of example, the study of evolution involves exploring genetic mechanisms that drive species' transformations over generations, with significant implications for understanding biodiversity and drug resistance in bacteria, developing next year's flu vaccine, and even crime detection. The challenge arises from the inability to directly observe the past due to extinct ancestor species, limiting predictions to the genetic material of current species. The study often starts with identifying homologous regions within or across species. Homologous genes can be further classified into orthologs, paralogs, and xenologs. Many methods infer such pairwise homology relationships based on sequence data.

In [38, 40, 43, 44, 46, 60], we established characterizations of "valid" evolutionary homology relations and showed their close relationship with heritable classes of graphs. We introduced novel algorithms for determining "closest" homology relations and, based on this, algorithms for recovering the evolutionary history of genes or species in terms of trees or networks. In particular, we showed that finding the closest homology



relations that fit the data is NP-complete, but fixed-parameter tractable (FPT) and Integer Linear Program (ILP) algorithms have been established [38, 42, 45, 46, 51, 60, 62, 84, 92].

For species history reconstruction, usually restricted sets of allowed genes (typically less than 10% of the genetic material, 1:1 orthologs) are used. Our mathematical characterizations opened a new way to refine and adjust estimated event relations, allowing the use of the entire genetic material and considerably increasing information about evolutionary history. Parts of this work were published in the [Proceedings of the National Academy of Sciences \(PNAS\)](#) [51].

Parts of this work were published in the [Proceedings of the National Academy of Sciences \(PNAS\)](#) [51].

**Further Topics in Structural and Algorithmic Graph Theory.** The study of cycle bases in graphs is crucial for understanding their underlying structure and has significant applications in various fields, including chemistry and network analysis. The cycle space of a graph consists of all subgraphs where every vertex has an even degree. This space can be algebraically described as a vector space over the two-element finite field. The goal is to construct a cycle basis, a set of fundamental cycles from which all other cycles in the cycle space can be generated. While finding a cycle basis is straightforward, identifying cycle bases with special properties, such as minimum, robust, quasi-robust, or convex bases, is more challenging. These specialized bases are important for practical applications, especially in chemical reaction networks. We developed algorithms to recognize and characterize these special classes of cycle bases, highlighting their central role in mathematical and practical contexts [58, 66, 72],

We also explored the Laplace matrix of a graph  $G$ , which serves as a representation of a discrete Laplace operator. The eigenvalues of this matrix, known as the Laplacian spectrum, are closely related to the structure of  $G$ . For instance, the 2nd smallest Laplacian eigenvalue  $\lambda_2$  indicates whether  $G$  is disconnected ( $\lambda_2 = 0$ ) or not ( $\lambda_2 > 0$ ). We characterized trees with the greatest maximum  $p$ -Laplacian eigenvalue for a given degree sequence, showing that such extremal trees are uniquely determined by a breadth-first search with non-increasing vertex degrees [69]. Further generalizations to graphs with cycles, but almost tree-like structures, are in progress.

In our study of heritable graph classes, we focused on graphs with hereditary properties, which are characterized by forbidden induced subgraphs. A prominent example is complement reducible graphs (cographs), which do not contain induced paths on four vertices. Many heritable graph classes have been introduced under various names. We demonstrated the close connection between cographs and symbolic ultrametrics and generalized this to edge-colored cographs. We discussed several optimization problems, proved their NP-hardness, and provided Integer Linear Programs (ILPs) to solve them [44, 46, 60, 85]. Furthermore, we established the equivalence between symbolic ultrametrics (introduced by Andreas Dress) and unip 2-Structures (introduced by Ehrenfeucht and Rozenberg), characterizing unip 2-Structures as directed cographs, and developed a quadratic-time recognition algorithm. These results bridge gaps between different mathematical fields and play a crucial role in phylogenomics, as the classes of event-relations form a heritable family [46].