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Personal Information

Name	Karoline Faust
Address	Microbial Systems Biology Laboratory of Molecular Bacteriology

Department of Microbiology, Immunology and
Transplantation
Rega institute, 7th floor, Room 7.A130
KU Leuven
Campus Gasthuisberg
Herestraat 49
3000 Leuven
Belgium

E-mail [karoline.faust\(at\)kuleuven.be](mailto:karoline.faust@kuleuven.be)

KU Leuven [Home page](#)

ORCID [Publications](#)

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Science [Reviews/Citations](#)

ResearchGate [Profile](#)

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Positions

10/2021 to
present Associate Professor in Microbiological Bioinformatics at
KU Leuven

10/2016 to 9/
2021 Assistant Professor in Microbiological Bioinformatics at
KU Leuven

10/2013 to 9/
2016 FWO grant prolongation for post-doctoral position with
Prof. Raes

Topic: "Exploration of microbial community dynamics
by metagenomic time series analysis, community
model development and validation"

10/2010 to 9/
2013 FWO grant for post-doctoral position with Prof. Raes
Topic: "Development of computational approaches for

the prediction and analysis of species interaction networks from metagenomics data"
2/2010 to 9/2010 Post-doctoral position in the Research Group of Bioinformatics and (Eco)-Systems Biology headed by Prof. Raes

Education

February 12th, 2010 Public PhD defense at ULB ([pdf](#))

September 8th, 2006 DEA in Bioinformatics at ULB ([pdf](#))

12/2005 to 1/2010 PhD in the laboratory "Bioinformatique des Génomes et des Réseaux" (BiGRe) at ULB (Brussels)
Topic: "Inferring metabolic pathways from clusters of co-expressed genes in yeast."
Supervisor: Prof. Jacques van Helden

September 15th, 2005 Diplom in Biology at Humboldt University, Berlin ([pdf](#)) (equivalent to Master, qualifies recipient for PhD)

12/2004 to 9/2005 Diplomarbeit with the Sers group (Charite university hospital) and the Institute for Theoretical Biology (Humboldt University)
Title: "Effects of Oncogenic Ras on Gene Expression: Clustering of Microarray Data and Screening for Potential Serum Response Factor Targets"
Supervisors: PD Dr. Christine Sers, Prof. Hanspeter Herzel

2003 to 2004 Additional subject (Zusatzfach): Applied computer science at Humboldt University (Berlin)

2002 to 2003 Study of Biology at University of York (UK) (Undergraduate courses)

1999 to 2002 Study of Biology at Humboldt University (Berlin)
Major subject: Biochemistry
Minor subjects: Microbiology, Theoretical biology

Publications

Liu B*, Garza DR*, Gonze D, Krzynowek A, Simoens K, Bernaerts K, Geirnaert A and [Faust K](#)
*Starvation responses impact interaction dynamics of human gut bacteria *Bacteroides thetaiotaomicron* and *Roseburia intestinalis**
[The ISME Journal 17, 1940-1952 \(2023\)](#)

Bonal M, Goetghebuer L, Joseph C, Gonze D, [Faust K](#) and George IF
Deciphering Interactions Within a 4-Strain Riverine Bacterial Community
[Current Microbiology 80, 238 \(2023\)](#)

Garza DR, Gonze D, Zafeiropoulos H, Liu B and [Faust K](#)
Metabolic models of human gut microbiota: Advances and challenges
[Cell Systems 14\(2\), 109-121 \(2023\)](#)

van de Velde C, Joseph C, Simoens K, Raes J, Bernaerts K and [Faust K](#)
Technical versus biological variability in a synthetic human gut community
[Gut Microbes 15, 2155019 \(2023\)](#)

Van Nguyen T, Viver T, Mortier J, Liu B, Smets I, Bernaerts K, [Faust K](#), Lavigne R, Poughon L, Dussap CG and Springael D
Isolation and characterization of a thermophilic chain elongating bacterium that produces the high commodity chemical n-caproate from polymeric carbohydrates [Bioresource Technology, 367 128170 \(2022\)](#)

Krawczyk AI, Röttjers S, Coimbra-Dores MJ, Heylen D, Fonville M, Takken W, [Faust K](#) and Sprong H

Tick microbial associations at the crossroad of horizontal and vertical transmission pathways [Parasites & Vectors 15:380 \(2022\)](#)

Krawczyk AI, Röttjers S, Fonville M, Takumi K, Takken W, [Faust K](#) and Sprong H

Quantitative microbial population study reveals geographical differences in bacterial symbionts of Ixodes ricinus [Microbiome 10, 120 \(2022\)](#)

Khalighi M, Sommeria-Klein G, Gonze D, [Faust K](#) and Lahti L

Quantifying the impact of ecological memory on the dynamics of interacting communities [PLoS Computational Biology 18\(6\), e1009396 \(2022\)](#)

van de Velde CC, Joseph C, Biclôt A, Huys GRB, Pinheiro VB, Bernaerts K, Raes R and [Faust K](#)

Fast quantification of gut bacterial species in cocultures using flow cytometry and supervised classification [ISME Communications 2, 40 \(2022\)](#)

Beller L, Deboutte W, Vieira-Silva S, Falony G, Tito RY, Rymenans L, Yonda CK, Vanmechelen B, Van Espen L, Jansen D, Shi C, Zeller M, Maes P, [Faust K](#), Van Ranst M, Raes J, Matthijnssens J

The virota and its transkingdom interactions in the healthy infant gut [PNAS, 119\(13\), e2114619119 \(2022\)](#)

Beller L, Deboutte W, Falony G, Vieira-Silva S, Tito RY, Valles-Colomer M, Rymenans L, Jansen D, Van Espen L, Papadaki MI, Shi C, Yinda CK, Zeller M, [Faust K](#), Van Ranst M, Raes J, Matthijnssens J

Successional Stages in Infant Gut Microbiota Maturation [mBio 12\(6\), e01857-21 \(2021\)](#)

Röttjers S and [Faust K](#)

Fast and flexible analysis of linked microbiome data with mako [Nature](#)

[Methods 19, 51-54 \(2021\)](#)

Röttjers S, Vandeputte D, Raes J and [Faust K](#)
Null-model-based network comparison reveals core associations [ISME Communications 1, 36 \(2021\)](#)

[Faust K](#)
Open challenges for microbial network construction and analysis [The ISME Journal 15, 3111-3118 \(2021\)](#)

Martinez Arbas S, Narayanasamy S, Herold M, Lebrun LA, Hoopmann MR, Li S, Lam TJ, Kunath B, Hicks DH, Liu CM, Price LB, Laczny CC, Gillece JD, Schupp JM, Keim PS, Moritz RL, [Faust K](#), Tang H, Ye Y, Skupin A, May P, Muller EL & Wilmes P
Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. [Nature Microbiology 6, 123-135 \(2021\)](#)

Ma B, Wang Y, Ye S, Liu S, Stirling E, Gilbert JA, [Faust K](#), Knight R, Jansson JK, Cardona C, Röttjers L and Xu J
Earth microbial co-occurrence network reveals interconnection pattern across microbiomes [Microbiome 8:82 \(2020\)](#)

Röttjers L and [Faust K](#)
manta - a clustering algorithm for weighted ecological networks [mSystems 5, e00903-19 \(2020\)](#)

Vrancken G, Gregory AC, Huys GRB, [Faust K](#), Raes J
Synthetic ecology of the human gut microbiota [Nature Reviews Microbiology 17, 754-763 \(2019\)](#)

McBain AJ, O'Neill CA, Amezcua A, Price LJ, [Faust K](#), Tett A, Segata N, Swann JR, Smith AM, Murphy B, Hoptroff M, James G, Reddy Y,

Dasgupta A, Ross T, Chapple IL, Wade WG, Fernandez-Piquer J
*Consumer Safety Considerations of Skin and Oral Microbiome
Perturbation* [Clinical Microbiology Reviews](#) 32, e00051-19 (2019)

Faust K

*Towards a Better Understanding of Microbial Community Dynamics
through High-Throughput Cultivation and Data Integration* [mSystems](#) 4,
e00101-19 (2019)

Goetghebuer L, Bonal M, Faust K, Servais P, George IF

*The Dynamic of a River Model Bacterial Community in Two Different
Media Reveals a Divergent Succession and an Enhanced Growth of Most
Strains Compared to Monocultures*
[Microbial Ecology](#) 78(2), 313-323 (2019)

Röttjers L and Faust K

Can we predict keystones? [Nature Reviews Microbiology](#) 17, 193 (2018)
Correspondence, not peer-reviewed

Faust K

Microbial Consortium Design Benefits from Metabolic Modeling [TIBTECH](#)
37(2), 123-125 (2018)
Spotlight, not peer-reviewed

Joossens M, Faust K, Gryp T, Nguyen ATL, Wang J, Eloot S, Schepers E,
Dhondt A, Pletinck A, Vieira-Silva S, Falony G, Vaneechoutte M,
Vanholder R, Van Biesen W, Huys GRB, Raes J, Glorieux G
Gut microbiota dynamics and uraemic toxins: one size does not fit all
[Gut](#) 68(12), 2257-2260 (2018)

D'hoë K*, Vet S*, Faust K*+, Moens F, Falony G, Gonze D, Lloréns-
Rico V, Gelens L, Danckaert J, De Vuyst L*, Raes J*+
Integrated culturing, modeling and transcriptomics uncovers complex

interactions and emergent behavior in a three-species synthetic gut community [eLife 7, e37090 \(2018\)](#)

Röttjers L and [Faust K](#)

From hairballs to hypotheses - biological insights from microbial networks [FEMS Microbiology Reviews 42, 761-780 \(2018\)](#)

Ma B, Zhao K, Lv X, Su W, Dai Z, Gilbert JA, Brookes PC, [Faust K](#), Xu J
Genetic correlation network prediction of forest soil microbial functional organization [The ISME Journal 12, 2492-2505 \(2018\)](#)

Gonze D, Coyte KZ, Lahti L, [Faust K](#)

Microbial communities as dynamical systems [Current Opinion in Microbiology 44, 41-49 \(2018\)](#)

[Faust K](#)+, Bauchinger F, Laroche B, de Buyl S, Lahti L, Washburne AD, Gonze D, Widder S+

Signatures of ecological processes in microbial community time series [Microbiome 6, 120 \(2018\)](#)

Vet S, de Buyl S, [Faust K](#), Danckaert J, Gonze D, Lendert G

Bistability in a system of two species interacting through mutualism as well as competition: chemostat vs. Lotka-Volterra equations [PLoS ONE, 13\(6\), e0197462 \(2018\)](#)

Muller EL, [Faust K](#), Widder S, Herold M, Martinez Arbas S, Wilmes P

Using metabolic networks to resolve ecological properties of microbiomes [Current Opinion in Systems Biology 8, 73-80 \(2018\)](#)

Parente E, Zotta T, [Faust K](#), De Filippis F, Ercolini D

Structure of association networks in food bacterial communities [Food Microbiology 73, 49-60 \(2018\)](#)

Gonze D, Lahti L, Raes J, [Faust K](#)
Multi-stability and the origin of microbial community types [The ISME Journal](#) 11, 2159-2166 (2017)

Wang H, Wei Z, Mei L, Gu J, Yin S, [Faust K](#), Raes J, Deng Y, Wang Y, Shen Q, Yin S
Combined use of network inference tools identifies ecologically meaningful bacterial associations in a paddy soil [Soil Biology and Biochemistry](#) 105, 227-235 (2017)

Pérez-Valera E, Goberna M, [Faust K](#), Raes J, García C, Verdú M
Fire modifies the phylogenetic structure of soil bacterial co-occurrence networks [Environmental Microbiology](#) 19, 317-327 (2016)

[Faust K](#) and Raes J, *CoNet app: inference of biological association networks using Cytoscape*. [F1000](#) 5:1519, [Cytoscape apps Channel](#) 5, 1519 (2016)

[Faust K](#) and Raes J, *Host-microbe interaction: Rules of the game for microbiota*. [Nature News & Views](#) (2016), not peer-reviewed

Günther S, [Faust K](#), Schumann J, Harms H, Raes J, Müller S
Species-sorting and mass-transfer paradigms control managed natural metacommunities. [Environmental Microbiology](#) 18, 4862-4877 (2016)

Bálint M, Bahram M, Eren AM, [Faust K](#), Fuhrman J, Lindahl B, O'Hara R, Opik M, Sogin M, Unterseher M, Tedersoo L
Millions of reads, thousands of taxa: microbial community structure and associations analyzed via marker genes. [FEMS Microbiology Reviews](#) fuw017 (2016)

Falony G*, Joossens* M, Vieira-Silva* S, Wang* J, Darzi Y, [Faust K](#), Kurilshikov A, Bonder, MJ, Valles-Colomer M, Vandeputte D, Tito RY,

Chaffron S, Rymenans L, Verspecht C, Sutter LD, Lima-Mendez G, D'hoë K, Jonckheere K, Homola D, Garcia R, Tigchelaar EF, Eeckhaut L, Fu J, Henckaerts L, Zhernakova A, Wijmenga C, Raes J
Population-level analysis of gut microbiome variation. Science 352 (6285), 560-564 (2016)

Mattiello F, Verbist B, Faust K, Raes J, Shannon WD, Bijnens L, Thas O
A Web Application for Sample Size and Power Calculation in Case-Control Microbiome Studies. Bioinformatics 32, 2038-2040 (2016)

Weiss S, Van Treuren W, Lozupone C, Faust K, Friedman J, Deng Y, Xia LC, Xu ZZ, Ursell L, Alm EJ, Birmingham A, Cram JA, Fuhrman JA, Raes J, Sun F, Zhou J, Knight R
Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. The ISME Journal 10, 1669-1681 (2016)

Edwards RA, McNair K, Faust K, Raes J, Dutilh B
Computational approaches to predict bacteriophage-host relationships. FEMS Microbiology Reviews fuv048 (2015)

Faust K, Lima Mendez G, Lerat J-S, Sathirapongsasuti JF, Knight R, Huttenhower C, Lenaerts T and Raes J
Cross-biome comparison of microbial association networks. Frontiers in Microbiology 6, 01200 (2015)

Lima Mendez G*, Faust K*, Henry N*, Decelle J, Colin S, Carcillo F, Chaffron S, Ignacio-Espinosa J, Roux S, Vincent F, Bittner L, El Darzi Y, Wang J, Audic S, Berline L, Bontempi G, Cabello A, Coppola L, Cornejo-Castillo F, d'Ovidio F, De Meester L, Ferrera I, Garet-Delmas M, Guidi L, Lara E, Pesant S, Royo-Llonch M, Salazar G, Sánchez P, Sebastian M, Souffreau C, Dimier C, Picheral M, Searson S, Kandels-Lewis S, Tara Oceans coordinators, Gorsky G, Not F, Ogata H, Speich S, Stemmann L, Weissenbach J, Wincker P, Acinas S, Sunagawa S,

Bork P, Sullivan M, Karsenti E, Bowler C, de Vargas C, Raes J
Determinants of community structure in the global plankton interactome. [Science 348 \(6237\), \(2015\)](#)

Faust K*, Lahti L*, Gonze D, de Vos W, Raes J
Metagenomics meets time series analysis: unraveling microbial community dynamics. [Current Opinion in Microbiology 25, 56-66 \(2015\)](#)

Navarrete AA, Tsai SM, Mendes LW, Faust K, Hollander M, Cassman NA, Raes J, Veen JA, Kuramae EE
Soil microbiome responses to the short-term effects of Amazonian deforestation. [Molecular Ecology 24 \(10\), 2433-2448 \(2015\)](#)

Hingamp P, Grimsley N, Acinas SG, Clerissi C, Subirana L, Poulain J, Ferrera I, Sarmiento H, Villar E, Lima-Mendez G, Faust K, Sunagawa S, Claverie J-M, Moreau H, Desdevises Y, Bork P, Raes J, de Vargas C, Karsenti E, Kandels-Lewis S, Jaillon O, Not F, Pesant S, Wincker P and Ogata H
Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. [ISME 7, 1678-1695 \(2013\)](#)

Faust K, Raes J. *Microbial interactions: from networks to models.* [Nature Review Microbiology 10, 538-550 \(2012\)](#)

Faust K*, Sathirapongsasuti, JF*, Izard J, Segata N, Gevers G, Raes J*, Huttenhower C*. *Microbial Co-occurrence Relationships in the Human Microbiome.* [PLoS Computational Biology 8 \(7\), e1002606 \(2012\)](#)

The Human Microbiome Project Consortium. *Structure, function and diversity of the healthy human microbiome.* [Nature 486, 207-214 \(2012\)](#)

The Human Microbiome Project Consortium. *A framework for human*

microbiome research. [Nature 486, 215-221 \(2012\)](#)

Lozupone C, [Faust K](#), Raes J, Faith JJ, Frank DN, Zaneveld J, Gordon JL, Knight R. *Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts.* [Genome Research 22, 1974-1984 \(2012\)](#)

[Faust K](#), van Helden J. *Predicting Metabolic Pathways by Sub-network Extraction.* [Book chapter 7 in "Bacterial Molecular Networks"](#), edited by van Helden, J., Toussaint A. and Thieffry, D., volume 804 in series "Methods in Molecular Biology" (2011)

[Faust K](#), Croes D, van Helden J. *Prediction of metabolic pathways from genome-scale metabolic networks.* [BioSystems, 105 \(2\), 109-121 \(2011\)](#)

[Faust K](#), Dupont P, Callut J, van Helden J. *Pathway discovery in metabolic networks by subgraph extraction.* [Bioinformatics, 26 \(9\), 1211-1218 \(2010\)](#)

[Faust K](#), Croes D, van Helden J. *In response to "Can sugars be produced from fatty acids? A test case for pathway analysis tools".* [Bioinformatics, 25 \(23\), 3202-3205 \(2009\)](#)

[Faust K](#), Croes D, van Helden J. *Metabolic path finding using RPAIR annotation.* [Journal of Molecular Biology 388 \(2\), 390-414 \(2009\)](#)

Brohée S, [Faust K](#), Lima-Mendez G, Vanderstocken G, van Helden J. *Network Analysis Tools: from biological networks to clusters and pathways.* [Nature protocols 3 \(10\), 1616-1629 \(2008\)](#)

Brohée S, [Faust K](#), Lima-Mendez G, Sand O, Janky R, Vanderstocken G, van Helden J. *NeAT: A toolbox for the analysis of biological networks, clusters, classes and pathways.* [Nucleic Acids Research 36, W444-W451](#)

(2008)

Lazarus D, Faust K, Popova-Goll I. *New species of prunoid radiolarians from the Antarctic Neogene*. [Journal of Micropalaeontology](#), 24 (2), 97-121 (2005)

Conferences, Seminars and Workshops

- 20th Oct 2023 [CNB Seminar Cycle](#). Invited oral presentation: "Lessons from synthetic human gut bacterial communities". Madrid, Spain
- 11th-13th Sep 2023 [Summer School on Microbial Community Design and Control](#). **Main organizer**. Lecture: "Metabolic modelling of microbial communities". Leuven, Belgium
- 25th July 2023 [European Conference on Computational Biology \(ECCB\)](#). **Keynote speaker**: "From hairballs to hypotheses: network analysis applied to microbiome data". Lyon, France
- 29th June 2023 [CMESS Lecture Series](#). Invited oral presentation: "Top down and bottom up exploration of the human gut microbiome". Vienna, Austria
- 17th May 2023 FDA Microbiome Working Group. Invited oral presentation: "Lessons from synthetic human gut bacterial communities". Online.
- 28th April 2023 [Channing Microbiome Seminar Harvard Medical School](#). Invited oral presentation: "Lessons from synthetic human gut bacterial communities". Online.
- 28th March 2023 [Lecture Series in Ecology and Evolution Bern](#) Invited oral presentation: "Lessons from synthetic human gut communities". Online.
- 21-22nd March 2023 [Pharmabiotics conference](#) Invited oral presentation: "Lessons from synthetic human gut communities". Lyon, France.

- 2-3rd February 2023 [Statistical Methods for Post Genomic Data \(SMPGD\) workshop](#) Invited oral presentation: "From hairballs to hypotheses: microbial network analysis". Ghent, Belgium.
- 5th December 2022 [Symposium: ecology and evolution of the microbiome](#) Invited oral presentation: "Lessons from synthetic human gut communities". Kortrijk, Belgium.
- 10-14th October 2022 [INI Workshop: Microbial communities: current approaches and open challenges](#) Invited oral presentation: "Application of microbial community models to human gut bacteria – challenges and insights". Cambridge, UK.
- 26-27th September 2022 [Workshop on human microbiome & e-DNA research for public health & the environment](#) Invited oral presentation: "In-vitro exploration and modelling of human gut microbial interactions". Utrecht, The Netherlands.
- 13-15th September 2022 [Applied Hologenomics Conference](#) Oral presentation: "Exploring the origin of alternative microbial community types". Bilbao, Spain.
- 14-19th August 2022 [18th International Symposium on Microbial Ecology \(ISME\)](#). Poster presentation: "Microbial Network Analysis". Lausanne, Switzerland.
- 28st June 2022 [Cell Economy Forum](#). Invited oral presentation: "Lessons from synthetic human gut communities". Online.
- 21st June 2022 [Modelling in Ecology and Evolution \(MEEM\)](#). Invited oral presentation: "Exploring the origin of human gut community types". Online.
- 10th May 2022 [ISCB academy webinar](#). Invited oral presentation: "From hairballs to hypotheses: microbial network analysis".
- 5th May 2022 [Innsbruck Microbiology Seminar Series](#). Invited oral presentation: "Top-down and bottom-up exploration of

- the human gut microbiome" Innsbruck, Austria (took place online).
- 23-29th April 2022 [EMBO course: "Integrated multi-omic analyses of microbial communities"](#) Invited lecture: "Inference and analysis of microbial networks from sequencing data" Luxembourg city, Luxembourg.
- 22-24th Feb 2022 [First International Iranian Conference on Bioinformatics](#). **Keynote speaker:** "From hairballs to hypotheses: Microbial network analysis" Kish, Iran (joined online).
- 2-4th Nov 2021 [School of Microbial Time Series Analysis](#). **Main organizer.** Lecture on: "Insights from microbial time series data" Leuven, Belgium (took place online).
- 20-23rd April 2021 [Microbiome Data Analysis Workshop](#). Invited lecture: "Introduction to microbial network inference and analysis." Hasselt, Belgium (took place online).
- 8th April 2021 [GELIFES seminar](#). Invited oral presentation: "Emergent behavior in a three-species human gut community." Groningen, The Netherlands (took place online).
- 29-31st Mar 2021 [MiCom 2021](#). **Keynote speaker:** "Top-down and bottom-up exploration of gut microbial community dynamics." Jena, Germany (took place online).
- 11-15th Jan 2021 [Ecology and co-evolution: from models to data and back](#). Invited oral presentation: "Emergent behavior in a three-species human gut community." Paris, France (took place online).
- 30th Sep 2020 Virtual Mini Symposium Microbial metabolism on a computer: from single-cells to complex communities. Invited oral presentation: "How to count bacteria in communities?"
- 15th Sep 2020 Colloquium on Networks, Lateral Gene Transfer, Symbiosis and Evolution. Invited oral presentation: "The eight challenges of microbial network inference." Paris,

- France (took place online).
- 29th May 2020 Symposium: Frontiers in Evolutionary Biology (Arenberg Doctoral School). Lecture: "[The tangled microbial bank: structure and dynamics of microbial communities.](#)"
Leuven, Belgium (took place online).
- 11-12th Feb 2020 [Netherlands Annual Ecology Meeting](#). Oral presentation: "Microbial network analysis – where do we stand?" Lunteren, The Netherlands.
- 11-13th Dec 2019 [4th Thünen Symposium on Soil Metagenomics](#). **Keynote lecture:** "Opportunities and limitations of microbial network analyses." Braunschweig, Germany.
- 23-25th Oct 2019 [Wellcome Genome Campus: Exploring Human Host-Microbiome Interactions in Health and Disease](#). Invited oral presentation: "Emergent behaviour in a synthetic gut community." Hinxton, UK.
- 16-18th Sept 2019 [Summer school on Microbial Community Modeling](#). **Main organizer.** Lecture: "Introduction to qualitative metabolic modelling." Leuven, Belgium.
- 14-19 July 2019 [Gordon Research Conference in Applied and Environmental Microbiology: Shaping the Earth's Microverse](#) Invited oral presentation: "Emergent Behavior in a Synthetic Gut Community". Mount Holyoke College, USA.
- 20-24 June 2019 [ASM Microbe 2019](#). Invited oral presentation: "Signatures of ecological processes in microbial community time series". San Francisco, USA.
- 26-30 May 2019 [15th Symposium on Bacterial Genetics and Ecology](#). Invited oral presentation: "Mechanisms behind alternative community types (and how to distinguish them)". Lisbon, Portugal.
- 20-22 May 2019 [Microbiome & Probiotics series: Europe](#). Invited oral presentation: "Insights from synthetic gut communities". Rotterdam, The Netherlands.

- 8th Feb 2019 [IB2 seminar](#). Invited oral presentation: "Emergent behaviour in a synthetic gut community". Brussels, Belgium.
- 4th Feb 2019 Aarhus University, Department of Bioscience. Invited oral presentation: "Principle, problems and applications of microbial network inference ". Aarhus, Denmark.
- 23-25th Jan 2019 [Microbiota Data Analysis Workshop](#). Invited tutorial on: "Microbial network inference and analysis" (lecture and practicals, together with Lisa Röttjers). Zurich, Switzerland.
- 18th Dec 2018 [Seminar at IBENS](#). Invited oral presentation: "Emergent behaviour in a synthetic gut community". Paris, France.
- 19th Nov 2018 Microbial Population Dynamics and Time Series Methods, Experiments and Data workshop. Invited oral presentation: "Signatures of ecological processes in microbial community time series." Ghent, Belgium.
- 10th Oct 2018 Seminar at C3BI at the Max Planck Institute for Plant Breeding Research (MIPZ). Invited oral presentation: "From hairballs to hypotheses - what can we learn from microbial networks?" Cologne, Germany.
- 4th Oct 2018 [Seminar at C3BI at the Pasteur Institute](#). Invited oral presentation: "Signatures of ecological processes in microbial community time series". Paris, France.
- 15-19th Sep 2018 [ERS International Congress](#). Invited oral presentation: "What can we learn from microbial networks?" Paris, France.
- 12-17th August 2018 [17th International Symposium on Microbial Ecology \(ISME\)](#). Poster (418A): "Emergent behaviour in a synthetic gut community". Leipzig, Germany.
- 12th March 2018 [Think tank: Host-microbiome research](#). Invited oral presentation: "Signatures of ecological processes in microbial community time series". Amsterdam, The Netherlands.

- 28th Feb-6th March 2018 [Advanced Lecture Course on Systems Biology](#). Invited to contribute to the "Understanding Microbes" symposium, topic: "Microbial network inference and analysis". Innsbruck, Austria.
- 13-14th Feb 2018 [The Netherlands Ecology Meeting](#). Co-organizer of session: " MICROBIAL ECOLOGY; Community composition and dynamics". Presentation: "Exploring the dynamics of a synthetic gut community". Lunteren, The Netherlands.
- 24th Nov 2017 Bangor University Seminar. Invited oral presentation: "From sequencing data to community structure: Network analysis of the TARA Oceans data". Bangor, UK.
- 11-13th Sep 2017 [Summer school on ecological network inference and analysis](#). **Main organizer**. Microbial network inference tutorial. Leuven, Belgium.
- 6-11th August 2017 [Ecological Society Annual Meeting](#). Invited oral presentation: "Multi-stability in host-associated microbial communities" Portland, US.
- 2nd June 2017 [Journée Réseaux du GDR Génomique Environnementale](#). **Keynote speaker**: "On the origin of microbial community types." Nantes, France.
- 16th May 2017 [Young Investigators Research Day](#). **Keynote speaker**: "Microbial Systems Biology." Kiel, Germany.
- 3rd May 2017 Pasteur Institute Seminars. Invited oral presentation: "Modelling the dynamics of a synthetic gut community." Paris, France.
- 13-17th March 2017 CIFAR-Gordon & Betty Moore Foundation Workshop: "Message in a bottle" - Chemical Symbiotic Interactions in the Oceans. Invited oral presentation: "From sequencing data to community structure: Network analysis of the TARA Oceans data." Eilat, Israel.
- 24-25th Oct Safety of Microbial Reprofilng Workshop. Invited oral

- 2016 presentation: "From microbial networks to community models." Bedford, UK.
- 4th Sep 2016 [European Conference on Computational Biology \(ECCB\), Pre-Meeting on Recent Computational Advances in Metagenomics \(RCAM\)](#). **Keynote speaker:** "Network inference meets metagenomics: challenges, tools and evaluations." Den Haag, The Netherlands.
- 17-18th [Applied Bioinformatics in Life Sciences](#). Poster:
- March 2016 "Inference, analysis and validation of a marine plankton network." Leuven, Belgium.
- 8-11th March [Visualizing Biological Data VIZBI 2016](#). Invited oral presentation: "Ecological network visualization." Heidelberg, Germany.
- 25-26th Feb [Simons Foundation: First Workshop on Challenges in Microbiome Data Analysis](#). Invited oral presentation: "On the removal of environmentally driven microbial associations." New York, USA.
- 10-11th Dec [Next Generation Sequencing Symposium](#). Invited oral presentation: "Inference, validation and analysis of marine planktonic interactions with the TARA Oceans data." Helsinki, Finland.
- 6th Nov 2015 [Symposium: Ecology and evolution in microbial communities](#). Invited oral presentation: "Network science meets metagenomics: what can we learn from microbial association networks?" Lausanne, Switzerland.
- 12-17th July [Gordon research conference: Ecological & Evolutionary Genomics](#). Invited oral presentation: "Network inference meets metagenomics: challenges, tools and applications." Biddeford, USA.
- 31st-2nd [5th International Human Microbiome Congress](#). Poster:
- April 2015 "Time-varying network construction with CoNet". Luxembourg City, Luxembourg.

- 29th Jan 2015 [8th Finnish Gut Day](#). Invited oral presentation: "Metagenomics Meets Network Inference - What Can We Learn From Microbial Networks?". Helsinki, Finland.
- 10-12th Nov 2014 [Meta-Omics and Bioinformatics in Microbial Ecology workshop](#). Invited oral presentation: "Microbial Interactions: From Network to Models". Piracicaba, Brazil.
- 8-11th Sep 2014 [3S Biology Summer School](#). Invited tutorial on: "Inference and analysis of microbial association networks" (2h). Trento, Italy. [\[URL\]](#)
- 24-30th August 2014 [15th International Symposium on Microbial Ecology](#). Invited oral presentation: "Comparative analysis of co-occurrence networks across biomes". Seoul, South Korea.
- 2nd April 2014 [Metagenomics Approaches and Data Analysis course](#). Invited session on microbial association network construction (3h). Nijmegen, The Netherlands. [\[URL\]](#)
- 19th March 2014 [Seminar at the CUBE, University of Vienna](#). Invited oral presentation: "Inference of microbial association networks from metagenomic data - challenges, tools and results". Vienna, Austria.
- 9-10th Dec 2013 [Benelux Bioinformatics Conference 2013](#). Poster: "Comparative Analysis of Biome-Specific Microbial Association Networks". Brussels, Belgium. [\[F1000\]](#)
- 22nd Nov 2013 [IB2 seminar](#). Oral presentation: "Inference of microbial association networks from metagenomic data - challenges, tools and results". Brussels, Belgium.
- 4th Oct 2013 [CMC Symposium 2013](#). **Keynote speaker**: "Microbial interactions: from networks to models". Copenhagen, Denmark.
- 26-29 June 2013 [SocBiN 2013](#). Invited oral presentation: "Detection of microbial relationships from metagenomics data using network inference". Torun, Poland.

- 6-7 March 2013 Gordon & Betty Moore workshop on incorporating -omics data into models. Invited oral presentation: "Detecting microbial relationships using network inference techniques". Miami, USA.
- 5-6 Feb 2013 [Netherlands Annual Ecology Meeting](#). Poster: "CoNet - a co-occurrence Network inference tool". Lunteren, The Netherlands. [\[pdf\]](#)
- 3-4 Dec 2012 [Networks in Biodiversity Research Workshop](#). Invited oral presentation: "Detecting bacterial associations in the human microbiome". Berlin, Germany. [\[pdf\]](#)
- 7-12 Oct 2012 [Bertinoro Computational Biology 2012](#). Invited oral presentation: "Detecting bacterial associations in the human microbiome". Bertinoro, Italy. [\[pdf\]](#)
- 19-24 August 2012 [14th International Symposium on Microbial Ecology \(ISME\)](#). Poster: "CoNet - a Co-occurrence Network inference tool". Copenhagen, Denmark. [\[pdf\]](#)
- 18-20 April 2012 [VIB seminar](#). Oral presentation: "Microbial co-occurrence relationships in the human microbiome". Blankenberge, Belgium. [\[pdf\]](#)
- 28-30 March 2012 [MICROME training workshop](#). Invited teacher for session: "Predicting operons, regulons and metabolic pathways from bacterial genomes". Marseille, France.
- 19-21 March 2012 [International Human Microbiome Congress](#). Recipient of travel grant. Poster: "Prediction of microbial relationships from metagenomic data sets." Paris, France. [\[pdf\]](#)
- 12-13 Dec 2011 [Benelux Bioinformatics Conference \(BBC\)](#). Poster: "Prediction of bacterial relationships in the human microbiome." Luxembourg city, Luxembourg. [\[pdf\]](#)
- 9-13 March 2011 [International Human Microbiome Congress](#). Poster: "From Parts Lists to Ecosystem Networks: Development of a 2nd Generation Toolkit for Meta-Omics Analysis." Vancouver, Canada. [\[pdf\]](#)

- 15 Oct 2010 [Workshop: ICSB 2010 IOMPA](#). Oral presentation: "Predicting metabolic pathways from functionally linked genes." Edinburgh, UK. [\[pdf\]](#)
- 26-29 Sept 2010 [European Conference of Computational Biology \(ECCB\) 2010](#). Chair of Technology Track session TT4-6. Poster: "Predicting metabolic pathways from bacterial operons and regulons." Gent, Belgium. [\[pdf\]](#)
- 26-30 Oct 2009 [Workshop: "Metabolic Pathways Analysis 2009"](#). Leiden, The Netherlands.
- 7-11 Sept 2009 [Workshop: "Summer School on Metabolomics and Metabolic Networks"](#). Leuven, Belgium.
- 15-16 Dec 2008 [Benelux Bioinformatics Conference](#). Poster: "Discovery of metabolic pathways using graph algorithms." Maastricht, The Netherlands. [\[pdf\]](#)
- 13 Sept 2008 [Machine Learning in Systems Biology \(MLSB\) Conference](#). Oral presentation: "Metabolic Pathway inference using Random Walks and Shortest-Paths Algorithms." Brussels, Belgium. [\[pdf\]](#)
- 14-21 June 2008 [Summer School: "Biological Networks: Evolution, Interaction and Computation"](#). Lipari, Italy.
- 12-13 Nov 2007 [Benelux Bioinformatics Conference \(BBC\)](#). Oral presentation: "Inference of pathways from metabolic networks by subgraph extraction." Leuven, Belgium. [\[pdf\]](#)
- 10-12 Sept 2007 [Integrative Bioinformatics Workshop](#). Poster: "Improved metabolic path finding using RPAIR annotation." Gent, Belgium. [\[pdf\]](#)
- 7-11 May 2007 [Workshop: "Complexity of Biological networks"](#). Evry, France.

Supervision

I am currently supervising 2 postdocs, 1 research associate, 6

PhD students (3 of these as co-supervisor) and 3 Master students. Previously, I supervised 1 postdoc (Daniel Garza), 2 PhD students (Sam Röttjers & Clémence Joseph), 13 visiting students and 5 Master students.

Grants

- KUL Starter Grant (STG/16/006), 2016-2018, Main PI
 - FWO ERC Runner-up Grant (G0I0918N), 2018-2022, Main PI
 - ERC Starter Grant (EcoBox 801747), 2019-2023, Main PI
 - FWO Research Project (G046721N), 2021-2024, Main PI
 - KUL IDN Grant (IDN/20/010), 2021-2025, Co-PI
 - RIA Grant (3D-omics 101000309-2), 2021-2025, Co-PI
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Teaching

Together with my PhD students Sam Röttjers and Anna Krzynowek, I created the MOOC: "[How to analyse a microbiome](#)". I am also contributing to "[Omics Techniques and Data Analysis](#)" (B-KUL-I0V62a), "[Hot Topics in Microbiology](#)" (B-KUL-E05N6A) and "[Advanced Microbiology](#)" (B-KUL-E05N5A) at KU Leuven and to "[Modeling dynamical systems in biology](#)" (BINF-F404) at ULB. In addition, I also created an [online tutorial on microbial network inference](#).

Roles and Memberships

I am senior editor at [The ISME Journal](#), editor at [mSystems](#) and secretary of the board of the [Belgian Society for Microbiology](#). In addition, I served as a jury member in 13 Master thesis defences, 10 PhD defences and 1 habilitation.

Reviewer Activities

I reviewed articles for PNAS, ISME, Nature Communications, Microbiome, Bioinformatics, PLoS Computational Biology and mSystems among many others. Please see a summary of my reviewer activities at [publons](#). In addition, I am regularly reviewing grant applications, including for NWO, ISF, ERC, Helmholtz and other institutions.

Supervision of Software Development

Yu Gao & Daniel Rios Garza miaSim - R package for the simulation of community dynamics
<http://bioconductor.org/packages/release/bioc/html/miaSim.html>
Co-developed with Emma Gheysen, Yagmur Simsek and Leo Lahti

Clémence Joseph CellScanner - flow cytometry data analysis tool
<http://msysbiology.com/cellscanner.html>

Sam Röttjers mako - microbiome data and network querying tool
https://ramellose.github.io/mako_docs/

Sam Röttjers anuran - network comparison tool
<https://github.com/ramellose/anuran>

Sam Röttjers manta - microbial network clustering tool
<https://github.com/ramellose/manta>

Software Development

2018-2022 seqgroup - R package for the analysis of microbial

- sequencing data with group structure
<http://hallucigenia-sparsa.github.io/seqgroup/>
- 2014-2020 seqtime - R package for the analysis of longitudinal microbial sequencing data and the simulation of community dynamics
<http://hallucigenia-sparsa.github.io/seqtime/>
- 2010-2015 CoNet - Cytoscape plugin for building co-occurrence networks
<http://msysbiology.com/conet/>
- 2007-2008 Contribution to NeAT - Path finding and pathway extraction
http://rsat.sb-roscoff.fr/NeAT_home.php
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Skills

- Computer Science
- Java:
- course: Programmation Java: advanced topics (Technofutur, 2007)
 - course: Web applications: servlet & JSP (Technofutur, 2008)
 - course: Enterprise Java Beans 3.0 (Technofutur, 2008)
 - IDE: Eclipse
- Other general purpose languages:
- Perl (intermediate)
 - C++ (basic)
- Statistical languages:
- R (good)

- Matlab (basic)

Good knowledge of HTML/CSS and PHP

Basic knowledge in bash, Latex and SQL

Experience with Windows, UNIX and Mac OS

Languages German (native speaker)

English (proficient)

- Cambridge Certificate in Advanced English (2003, Grade A)
- TOEFL (2001, 233 out of 300 points)

French (good)

- Kamer voor Handel en Nijverheid van Brussel (2008, Frans Module 3.2)

Dutch (intermediate)

- Interuniversitaire Taaltest Nederlands voor Anderstaligen (2021, B2)

Miscellaneous Driving Licence B

Karoline Faust

October 2023

