Curriculum Vitae

Personal Information

Name	Karoline Faust
Address	Microbial Systems Biology
	Laboratory of Molecular Bacteriology
	Department of Microbiology and Immunology
	Rega institute, 7th floor, Room 7.A130
	KU Leuven
	Campus Gasthuisberg
	Herestraat 49
	3000 Leuven
	Belgium
E-mail	karoline.faust(at)kuleuven.be
Nationality	German
Date of birth	28 March 1980
KU Leuven	[Home page](#)
ORCiD	[Publications](#)
Publons	[Reviews](#)
ResearchGate	[Profile](#)
Loop	[Profile](#)

Positions

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

Vrancken G, Gregory AC, Huys GRB, Faust K, Raes J
Synthetic ecology of the human gut microbiota
Nature Reviews Microbiology, Accepted (2019)

McBain AJ, O'Neill CA, Amezquita 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, Accepted (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, Accepted (2018)

D'hoe 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'hoe K, Jonckheere K, Homola D, Garcia R, Tigchelaar EF, Eeckhaudt 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, Sarmento 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 JI, 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

16-18th September 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 Feburary 2019	IB2 seminar. Invited oral presentation: "Emergent behaviour in a synthetic gut community". Brussels, Belgium.
4th February 2019	Aarhus University, Department of Bioscience. Invited oral presentation: "Principle, problems and applications of microbial network inference ". Aarhus, Danmark.
23-25th January 2019	Microbiota Data Analysis Workshop. Invited tutorial on: "Microbial network inference and analysis" (lecture and practicals, together with Lisa Röttjers). Zurich, Switzerland.
18th December 2018	Seminar at IBENS. Invited oral presentation: "Emergent behaviour in a synthetic gut community". Paris, France.
19th November 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 October 2018	Seminar at C3BI at the Max Planck Institute for Plant Breeding Research (MPIPZ). Invited oral presentation: "From hairballs to hypotheses - what can we learn from microbial networks?" Cologne, Germany.
4th October 2018	[Seminar at C3BI at the Pasteur Institute.](#) Invited oral presentation: "Signatures of ecological processes in microbial community time series". Paris, France.
15-19th September 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 February-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 February 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 November 2017	Bangor University Seminar. Invited oral presentation: "From sequencing data to community structure: Network analysis of the TARA Oceans data". Bangor, UK.
11-13th September 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 October 2016	Safety of Microbial Reprofiling Workshop. Invited oral presentation: "From microbial networks to community models." Bedford, UK.
4th September 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 March 2016	[Applied Bioinformatics in Life Sciences.](#) Poster: "Inference, analysis and validation of a marine plankton network." Leuven, Belgium.
8-11th March	[Visualizing Biological Data VIZBI 2016.](#) Invited oral presentation: "Ecological network

2016	visualization." Heidelberg, Germany.
25-26th February 2016	[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 December 2015	[Next Generation Sequencing Symposium.](#) Invited oral presentation: "Inference, validation and analysis of marine planktonic interactions with the TARA Oceans data." Helsinki, Finland.
6th November 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 2015	**[Gordon research conference](#)**: Ecological & Evolutionary Genomics. Invited oral presentation: "Network inference meets metagenomics: challenges, tools and applications." Biddeford, USA.
31st-2nd April 2015	[5th International Human Microbiome Congress.](#) Poster: "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 October 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 October 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, Danmark. [[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.

Other scientific activities

I reviewed articles for the following journals:
PNAS, ISME, BMC Systems Biology, Bioinformatics, PLoS Computational Biology, PLoS one, Journal of Bioinformatics and Computational Biology, Computational and Structural Biotechnology Journal and a couple of others.
Please see a summary of my review activities at [publons](#).

Software Development

2014-current	seqtime - R package for the analysis of sequencing data time series and the simulation

of community dynamics
http://hallucigenia-sparsa.github.io/seqtime/

2010-2015	CoNet - Cytoscape plugin for building co-occurrence networks http://systemsbiology.vub.ac.be/conet/
2007-2008	Contribution to NeAT - Path finding and pathway extraction http://embnet.ccg.unam.mx/rsa-tools/index_neat.html

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

English (good)

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

French (good)

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

Dutch (intermediate)

- Mobyus, Level 4 (B1)

Miscellaneous Driving Licence B