

Curriculum Vitae

Dr. ir. Frederiek - Maarten Kerckhof

April 21, 2021

General information

Personalia

- Last name: Kerckhof
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- Current adress: Holdaal 72A, 9000 Gent
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- E-mail: frederiekmaarten.kerckhof@ugent.be
- Date and place of birth: November 14, 1988 (Bruges)
- Affiliation: Ghent University, Faculty of bioscience engineering, Center for Microbial ecology and technology (CMET).
- Address: Coupure Links 653, 9000 Gent, Belgium
- Family: Varvara Tsilia (spouse) and Phileas Kerckhof Tsilias (son, ★15/09/16)

Experience

- **2020-current: VLAIO IM Spin-off mandate**
 - VLAIO IM Spin-off mandate HBC.2019.2601: "Innovative management strategies for yeast-driven fermentations"
 - Back-end development and support for cloud architecture
 - see www.kytos.be
- **2018-2020: 50% Bio-informatician and 50% IOF-Postdoc**
 - IOF-Postdoc
 - * IOF StepStone project "KYTOS": on-time microbial management for sustainable bioprocesses

- * As part of the team with a focus on applications in Fermentation industry
 - * see www.kytos.be
- Bio-informatician
 - * Organization of internal workshops for CMET
 - * Teaching molecular microbial techniques
 - * Bio-informatics support for CMET staff
 - * Data stewardship at CMET
- **2016-2018: Postdoctoral research fellow on microbial resource management and synthetic microbial ecology**
Funding: Belgian Science Policy IAP (BELSPO, P7/25), GOA Crohn (BOF17/GOA/032)
 - Coordinating day-to-day management of inter-university attraction poles programme P7/25 "micro-manager: microbial resource management in engineered and natural ecosystems"
 - Organization of internal workshops for the IUAP network and CMET
 - Guidance of 5 PhD students and 2 masters of science students
 - ARB/sILVA course "from primer to paper (P2P) (2016)"
 - TT skills course (Ugent TTO): research valorization, IP, bridge funding etc.
 - EBAME3: Workshop on Computational Microbial Ecogenomics (2017)
- **2011-2016: Doctoral thesis on sustainable methanotrophy**
Promoters: prof. dr. ir. Nico Boon & Dr. Kim Heylen
Funding: Ghent University GOA (BOF09/GOA/005) and Belgian Science Policy IAP (BELSPO, P7/25)
 - Academic papers as first author (see bibliography below, Kerckhof *et al.* (2014) and 2 submitted)
 - Many co-authorships as bio-informatics or statistical consultant (see bibliography below)
 - Guided master thesis and internship students
 - Teaching assistant in practical exercises molecular microbial techniques and microbial ecological processes.
 - Organizing internal courses on statistics, bio-informatics and version control
- **2011-2016: Ghent university doctoral schools**
 - IVPV specialist course: Advanced statistical methods - nonparametric methods
 - IVPV specialist course: Advanced statistical methods - multivariate methods
 - FLAMES specialist course: Advanced R - Programming in R and beyond
 - Specialist course: UGent High Performance computing (Linux shell scripting, Python, HPC usage)
 - Specialist course: Introduction to MG-RAST

- **2006-2011: Msc. Bioscience engineering in cellular and genetic biotechnology, major computational biology at Ghent University.**
 - Bachelorpaper: 'Competition and diversity: apparent opposites?'. About (mathematic modelling of) ecological competition on both macro- and micro-ecological levels and possible applications (preemptive colonisation, pre- and pro-biotics).
 - Combined project statistics for genome analysis and bio-informatics: analysis of 454-pyrosequencing amplicon data
 - Masters thesis: 'The impact of the physical state of electron donors and acceptors on microbial physiology and morphology'. Fundamental research concerning microbial electron metabolism in bio-electrochemical systems (microbial fuel cells). - Supervisors: dr. Jan B. Arends, prof. dr. ir. Willy Verstraete & prof. dr. ir. Nico Boon
- 2000-2006: Latin - Mathematics, Onze-Lieve-Vrouwecollege Assebroek

Teaching experience

Practical exercises

- 2011-2013 Practical exercises molecular microbial techniques (Msc Bioscience engineering)
- 2013-2015 Practical exercises microbial ecological processes (Bsc Bioscience engineering)

Theory classes

- 2016-2019 Co - teacher theory course molecular microbial techniques (Msc. Bioscience engineering)

Internal training

Training organized for all collaborators within CMET to enhance the quality of research of the group.

- Amplicon NGS analysis: basic training for all collaborators on use of linux command line, mothur and R.
- Statistics and experimental design: introduction to R, proper experimental design and one-way multiple comparisons.
- Version control: use of Git/GitHub for collaborative code editing.

Services

Internal services

- 2011-present: server management of CMETs core computational infrastructure: setup of 3 linux servers, user and software management
- 2014-2015: organization of internal research cluster meetings on NGS sequencing and microbial ecology and interactions.
- 2015: Benchmarking of amplicon sequencing pipelines using mock communities - design of amplicon sequencing SOP.
- 2016: setup and management of shiny application server, setup of Pathwaytools server

Skills

Dry lab

As a major in computational biology I sure know my way around computers, below are listed some of the specific software applications that I am familiar with.

- Advanced knowledge of R, bioconductor and many R packages for statistical analysis.
- The Mathworks Matlab and simulink for modelling and advanced mathematics.
- Perl/Bioperl & Python/Biopython for scripting
- ImageJ and comstat for bio-imaging.
- Advanced in mothur and knowledge of Qiime for amplicon NGS data analysis
- RAxML for phylogenetic tree building
- MG-RAST for metagenomics
- Basic knowledge of Bionumerics, DNASTar lasergenes, PROKKA, PathwayTools (EcoCyc/MetaCyc), CLC workbench, Wolfram Mathematica, Ruby, Java, HTML, php and Visual Basic.

Wet lab

I have familiarized myself with many molecular biology tools within the lab, so I am aware of possible biases when generating e.g. NGS data. Furthermore I have experience with (q)PCR primer design and optimisation as well as flowcytometry.

Entrepreneurial skills

In gearing up towards the perspective spin-off company Kytos I took a few courses to make sure I would have the entrepreneurial skill-set to start a company.

- Participated in business competitions: Cleantech challenge 2012 and Batle of Talents 2010
- UGent TechTransfer TT-skills course: essentials of IP & funding
- UGent TechTransfer/Capture "disciplined entrepreneurship" course: semi-intensive program on getting from the idea to a start-up using the book "Disciplined entrepreneurship" by Bill Aulet
- Thriving business community BaLinCa+: 2 day financial awareness and business experience course
- VOKA/UGent "from PhD to SME"
- (ongoing) Vlerick Business school "Learn to speak business"

Online Presence

- LinkedIn
- ResearchGate
- ResearcherID
- ORCID
- Contributor to stack Exchange fora (StackOverflow, CrossValidated, Ask Ubuntu, TeX)

Academic publications and conference proceedings

- Acosta, N., Sakarika, M., Kerckhof, F.-M., Law, C. K. Y., De Vrieze, J. & Rabaey, K. (2020). Microbial protein production from methane via electrochemical biogas upgrading. *Chemical Engineering Journal*, 391:123625.
- Allais, L., Kerckhof, F.-M., Verscheure, S., Bracke, K., De Smet, R., Laukens, D., De Vos, M., Boon, N., Brusselle, G., Van de Wiele, T. & Cuvelier, C. (2013a). Chronic cigarette smoke exposure alters the murine gut microbiome. In *Mucosal Immunology, 16th International congress, Abstracts*. Society for Mucosal Immunology.
- Allais, L., Kerckhof, F.-M., Verscheure, S., Bracke, K., De Smet, R., Laukens, D., Van den Abbeele, P., De Vos, M., Boon, N., Brusselle, G. *et al.* (2014a). The effect of chronic cigarette smoke exposure on gut microbial diversity in healthy mice. In *9th Joint symposium Rowett-INRA 2014: Gut microbiology: from sequence to function*.
- Allais, L., Kerckhof, F.-M., Verscheure, S., Bracke, K., De Smet, R., Laukens, D., Van den Abbeele, P., De Vos, M., Boon, N., Brusselle, G. *et al.* (2014b). The effect of chronic cigarette smoke exposure on the gut microbiome in healthy mice. In *BSM Annual meeting 2014: Cell signaling in host-microbe interactions*. Belgian Society for Food Microbiology (BSFM).
- Allais, L., Kerckhof, F.-M., Verschuere, S., Bracke, K., De Smet, R., Laukens, D., De Vos, M., Boon, N., Brusselle, G., Van de Wiele, T. & Cuvelier, C. (2013b). Chronic cigarette smoke exposure alters the murine gut microbiome. In *ACTA GASTRO-ENTEROLOGICA BELGICA*, volume 76. ISSN 0001-5644.
- Allais, L., Kerckhof, F.-M., Verschuere, S., Bracke, K., De Smet, R., Laukens, D., De Vos, M., Boon, N., Brusselle, G., Van de Wiele, T. *et al.* (2013c). Chronic cigarette smoke exposure alters the murine gut microbiome. In *8th Congress of ECCO*, pp. 167–167. European Crohn’s and Colitis Organisation (ECCO).
- Allais, L., Kerckhof, F.-M., Verschuere, S., Bracke, K., De Smet, R., Laukens, D., Devos, M., Boon, N., Brusselle, G., Van de Wiele, T. *et al.* (2013d). P694 chronic cigarette smoke exposure alters the murine gut microbiome. *Journal of Crohn’s and Colitis*, 7(Supplement 1):S289–S289.
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- Alloul, A., Muys, M., Hertoghs, N., Kerckhof, F.-M. & Vlaeminck, S. E. (2021). Cocultivating aerobic heterotrophs and purple bacteria for microbial protein in sequential photo-and chemotrophic reactors. *Bioresource Technology*, 319:124192.
- Benner, J., De Smet, D., Ho, A., Kerckhof, F.-M., Vanhaecke, L., Heylen, K. & Boon, N. (2015). Exploring methane-oxidizing communities for the co-metabolic degradation of organic micropollutants. *Applied microbiology and biotechnology*, 99(8):3609–3618.

- Buysschaert, B., Kerckhof, F.-M., Vandamme, P., De Baets, B. & Boon, N. (2018). Flow cytometric fingerprinting for microbial strain discrimination and physiological characterization. *Cytometry Part A*, 93(2):201–212.
- Callewaert, C., De Maeseneire, E., Kerckhof, F.-M., Verliefde, A., Van de Wiele, T. & Boon, N. (2014a). Microbial odor profile of polyester and cotton clothes after a fitness session. *Applied and environmental microbiology*, 80(21):6611–6619.
- Callewaert, C., Kerckhof, F.-M., Granitsiotis, M., Van Gele, M., Van de Wiele, T. & Boon, N. (2012a). The human axillary environment harbors 2 microbiome ecotypes. In *42nd Annual meeting of the European Society for Dermatological Research (ESDR)*, volume 132, pp. S115–S115.
- Callewaert, C., Kerckhof, F.-M., Granitsiotis, M., Van Gele, M., Van de Wiele, T. & Boon, N. (2012b). The human axillary environment harbors 2 microbiome ecotypes. In *Journal of investigative dermatology*, volume 132, pp. abstract 656:S115–abstract 656:S115. ISSN 0022-202X.
- Callewaert, C., Kerckhof, F.-M., Granitsiotis, M. S., Van Gele, M., Van de Wiele, T. & Boon, N. (2013). Characterization of staphylococcus and corynebacterium clusters in the human axillary region. *PloS one*, 8(8):e70538.
- Callewaert, C., Kerckhof, F.-M., Van de Wiele, T. & Boon, N. (2012c). The bacterial fingerprint of the armpit and its variation in time. In *17th PhD Symposium on Applied Biological Sciences*, volume 77.
- Callewaert, C., Kerckhof, F.-M., Van Gele, M., Van de Wiele, T. & Boon, N. (2012d). The human axillary environment harbors two microbiome ecotypes. In *Belgian Society for Cell and Developmental Biology (BSCDB) Fall meeting 2012: Epidermal cell biology*.
- Callewaert, C., Kerckhof, F.-M., Van Keer, T., Plaquet, T., Meunier, M., Bostoen, J., Verhofstadt, L., Van de Wiele, T. & Boon, N. (2014b). Characterisation of the human malodorous axillary microbiome and a novel treatment to obtain a better body odour. In *44th Annual meeting of the European Society for Dermatological Research (ESDR)*, volume 134, pp. S78–S78.
- Callewaert, C., Van Nevel, S., Kerckhof, F.-M., Granitsiotis, M. S. & Boon, N. (2015). Bacterial exchange in household washing machines. *Frontiers in microbiology*, 6:1381.
- Chalermwatanachai, T., Vilchez-Vargas, R., Holtappels, G., Lacoere, T., Jáuregui, R., Kerckhof, F.-M., Pieper, D. H., Wiele, T., Vaneechoutte, M., Zele, T. *et al.* (2018). Chronic rhinosinusitis with nasal polyps is characterized by dysbacteriosis of the nasal microbiota. *Scientific reports*, 8(1):7926.
- Cichocki, N., Hübschmann, T., Schattenberg, F., Kerckhof, F.-M., Overmann, J. & Müller, S. (2020). Bacterial mock communities as standards for reproducible cytometric microbiome analysis. *Nature Protocols*, 15(9):2788–2812.
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- Ehsani, E., Hernandez-Sanabria, E., Kerckhof, F.-M., Props, R., Vilchez-Vargas, R., Vital, M., Pieper, D. H. & Boon, N. (2018). Initial evenness determines diversity and cell density dynamics in synthetic microbial ecosystems. *Scientific reports*, 8(1):340.
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- García-Timermans, C., Rubbens, P., Heyse, J., Kerckhof, F.-M., Props, R., Skirtach, A. G., Waegeman, W. & Boon, N. (2019). Characterizing phenotypic heterogeneity in isogenic bacterial populations using flow cytometry and raman spectroscopy. *bioRxiv*, p. 545681.
- García-Timermans, C., Rubbens, P., Heyse, J., Kerckhof, F.-M., Props, R., Skirtach, A. G., Waegeman, W. & Boon, N. (2020). Discriminating bacterial phenotypes at the population and single-cell level: a comparison of flow cytometry and raman spectroscopy fingerprinting. *Cytometry Part A*, 97(7):713–726.
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- García Timermans, C., Rubbens, P., Kerckhof, F.-M., Props, R., Waegeman, W. & Boon, N. (2018). Single-cell bacterial characterization using flow cytometry and raman spectroscopy. In *2018 Symposium of the Belgian Society for Microbiology: Microbes in the spotlight*.
- Garcia Timermans, C., Rubbens, P., Props, R., Kerckhof, F.-M., Waegeman, W. & Boon, N. (2019). Fingerprinting microbial communities through flow cytometry and raman spectroscopy. In *15th Symposium on Bacterial Genetics and Ecology (BAGECO 15): Ecosystem drivers in a changing planet*, pp. 155–155.
- Gryp, T., De Paepe, K., Kerckhof, F.-M., Van Biesen, W., Vanholder, R., Joossens, M., Vaneechoutte, M. & Glorieux, G. (2019). Fo079 concentrations of p-cresyl-and indoxyl sulfate and their precursors in different stages of chronic kidney disease: From feces to urine. *Nephrology Dialysis Transplantation*, 34(Supplement_1):gfz096–FO079.
- Gryp, T., De Paepe, K., Vanholder, R., Kerckhof, F.-M., Van Biesen, W., Van de Wiele, T., Verbeke, F., Speeckaert, M., Joossens, M., Couttenye, M. M. *et al.* (2020). Gut microbiota generation of protein-bound uremic toxins and related metabolites is not altered at different stages of chronic kidney disease. *Kidney international*, 97(6):1230–1242.
- Hawinkel, S., Kerckhof, F.-M., Bijmens, L. & Thas, O. (2019). A unified framework for unconstrained and constrained ordination of microbiome read count data. *PloS one*, 14(2):e0205474.
- Hernandez-Sanabria, E., Slomka, V., Herrero, E. R., Kerckhof, F.-M., Zaidel, L., Teughels, W. & Boon, N. (2017). In vitro increased respiratory activity of selected oral bacteria may explain competitive and collaborative interactions in the oral microbiome. *Frontiers in Cellular and Infection Microbiology*, 7:235.
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- Ho, A., Kerckhof, F.-M., Luke, C., Reim, A., Krause, S., Boon, N. & Bodelier, P. L. (2013). Conceptualizing functional traits and ecological characteristics of methane-oxidizing bacteria as life strategies. *Environmental microbiology reports*, 5(3):335–345.
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