

Curriculum Vitae

Dr. ir. Frederiek - Maarten Kerckhof

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General information

Personalia

- Last name: Kerckhof
- First names: Frederiek - Maarten Pieter Jozef
- 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)

Education

- **Current: 50% Bio-informatician**
 - Organization of internal workshops for CMET
 - Server management
 - Teaching molecular microbial techniques
 - Bio-informatics support for CMET staff
 - Data stewardship at CMET
- **2016-2018: Postdoctoral research fellow on microbial resource managment 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

- 2016-2018 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 optimiation as well as flowcytometry.

Online Presence

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

Academic publications and conference proceedings

- 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).
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- Allais, L., Kerckhof, F.-M., Verschuere, S., Bracke, K. R., De Smet, R., Laukens, D., Van den Abbeele, P., De Vos, M., Boon, N., Brusselle, G. G. *et al.* (2016). Chronic cigarette smoke exposure induces microbial and inflammatory shifts and mucin changes in the murine gut. *Environmental microbiology*, 18(5):1352–1363.
- 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. (2017). Flow cytometric fingerprinting for microbial strain discrimination and physiological characterization. *Cytometry Part A*.
- 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.

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- 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.
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- 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.
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- De Paepe, K., Kerckhof, F.-M., Verspreet, J., Courtin, C. M. & Van de Wiele, T. (2017). Inter-individual differences determine the outcome of wheat bran colonization by the human gut microbiome. *Environmental Microbiology*.
- De Ryck, T., Boterberg, T., Kerckhof, F., Schrijver, J., Bracke, M. *et al.* (2015). Effects of irradiation on epithelial wound healing and microbial diversity in an in-vitro oral mucosa model. *J Nucl Med Radiat Ther*, 6(218):2.
- De Ryck, T., Grootaert, C., Jaspaert, L., Kerckhof, F.-M., Van Gele, M., De Schrijver, J., Van den Abbeele, P., Swift, S., Bracke, M., Van de Wiele, T. *et al.* (2014). Development of an oral mucosa model to study host-microbiome interactions during wound healing. *Applied microbiology and biotechnology*, 98(15):6831–6846.

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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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- Kerckhof, F.-M. (2016). *The methanotrophic interactome: microbial partnerships for sustainable methane cycling*. Phd thesis, Ghent University.
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- Props, R., Kerckhof, F.-M., Rubbens, P., De Vrieze, J., Sanabria, E. H., Waegeman, W., Monsieus, P., Hammes, F. & Boon, N. (2017). Absolute quantification of microbial taxon abundances. *The ISME journal*, 11(2):584.
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