

# Curriculum Vitae

Dr. ir. Frederiek - Maarten Kerckhof

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## General information

### Personalia

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- Last name: Kerckhof
- First names: Frederiek - Maarten Pieter Jozef
- Current adress: Holdaal 72A, 9000 Gent
- Mobile phone: +32477/98.13.12
- 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

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- **2016-current: Postdoctoral research fellow on microbial resource management and synthetic microbial ecology**  
**Funding:** Belgian Science Policy IAP (BELSPO, P7/25)
  - 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 4 PhD students and 2 masters of science students

- **2011-2016: Doctoral thesis on sustainable methanotrophy**

**Promotors:** 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-present: 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

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- 2011-2013 Practical exercises molecular microbial techniques (Msc Bioscience engineering)

- 2013-2015 Practical exercises microbial ecological processes (Bsc Bioscience engineering)
- 2016-2017 Co - teacher theory course molecular microbial techniques (Msc. Bioscience engineering)

## **Internal training**

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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**

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- 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

## **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).
- 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.
- 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.* (2015). Chronic cigarette smoke exposure induces microbial and inflammatory shifts and mucin changes in the murine gut. *Environmental microbiology*.
- 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.
- 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.
- 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.
- De Schrijver, J., Volders, P.-J., Kerckhof, F.-M., Obbels, D., Verleyen, E., Vyverman, W., De Meyer, T. & Van Criekinge, W. (2011). Prokar-seq: An analysis and visualization framework for next-generation sequencing based quantification of prokaryotic communities. In *6th Benelux Bioinformatics Conference (BBC'11)*, pp. 47–47.
- Domingos, J. M. B., Martinez, G. A., Scoma, A., Fraraccio, S., Kerckhof, F.-M., Boon, N., Reis, M. A., Fava, F. & Bertin, L. (2016). Effect of operational parameters in the continuous anaerobic fermentation of cheese whey on titers, yields, productivities and microbial community structure. *ACS Sustainable Chemistry & Engineering*.
- Ho, A., Angel, R., Veraart, A. J., Daebeler, A., Jia, Z., Kim, S. Y., Kerckhof, F.-M., Boon, N. & Bodelier, P. L. (2016). Biotic interactions in microbial communities as modulators of biogeochemical processes: Methanotrophy as a model system. *Frontiers in Microbiology*, 7.
- 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.

- Kerckhof, F.-M. (2016). *The methanotrophic interactome: microbial partnerships for sustainable methane cycling*. Phd thesis, Ghent University.
- Kerckhof, F.-M., Courtens, E. N., Geirnaert, A., Hoefman, S., Ho, A., Vilchez-Vargas, R., Pieper, D. H., Jauregui, R., Vlaeminck, S. E., Van de Wiele, T. *et al.* (2014). Optimized cryopreservation of mixed microbial communities for conserved functionality and diversity. *PloS one*, 9(6):e99517.
- Kerckhof, F.-M., De Rudder, C., Tsilia, V., Props, R., Ho, A., Heylen, K. & Boon, N. (2016a). Functional stabilisation and partner selection during repeated co-cultivation in a methanotrophic interactome. Technical report, PeerJ Preprints.
- Kerckhof, F.-M., Ho, A., De Rudder, C., Heyer, R., Benndorf, D., Heylen, K. & Boon, N. (2016b). Happily ever after? how repeated subcultivation influences a methanotrophic marriage. In *Nederlands Tijdschrift voor Medische Microbiologie*, volume 24. ISSN 0929-0176.
- Kerckhof, F.-M., Ho, A., Granitsiotis, M. S., Heylen, K. & Boon, N. (2015a). Microbial interdependencies in an enriched aerobic mixed methanotrophic community. In *6th Congress of European Microbiologists (FEMS 2015)*, p. 2717. Kenes International Organizers of Congresses.
- Kerckhof, F.-M., Vekeman, B., Geirnaert, A., Courtens, E. N., Vilchez-Vargas, R., Ho, A., Heylen, K. & Boon, N. (2015b). Enhancing microbial cryopreservation: From fastidious microbes to mixed communities. *Cryobiology*, 71(3):549–550.
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- Maza-Márquez, P., Vilchez-Vargas, R., Kerckhof, F.-M., Aranda, E., González-López, J. & Rodelas, B. (2016). Community structure, population dynamics and diversity of fungi in a full-scale membrane bioreactor (mbr) for urban wastewater treatment. *Water Research*, 105:507–519.
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- Scoma, A., Rifai, R. M., Pini, E., Hernandez Sanabria, E., Kerckhof, F.-M. & Boon, N. (2015). Long-chain hydrocarbon degraders from deep-sea. In *VLIZ Young Marine Scientists' Day 2015*, volume 71, pp. 115–115. Vlaams Instituut voor de Zee (VLIZ).

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- Stock, M., Hoefman, S., Kerckhof, F.-M., Boon, N., De Vos, P., De Baets, B., Heylen, K. & Waegeman, W. (2013). Exploration and prediction of interactions between methanotrophs and heterotrophs. *Research in microbiology*, 164(10):1045–1054.
- Tsilia, V., Devos, S., Rajkovic, A., Van de Wiele, T., Heyndrickx, M., Kerckhof, F.-M. & Devreese, B. (2016a). To poison or not?: a proteomic approach to quantify enterotoxins produced from *Bacillus cereus*. In *Symposium on Advances and Applications in Metaproteomics*. Max Planck Institute.
- Tsilia, V., Kerckhof, F.-M., Rajkovic, A., Heyndrickx, M. & Van de Wiele, T. (2016b). *Bacillus cereus* nvh 0500/00 can adhere to mucin but cannot produce enterotoxins during gastrointestinal simulation. *Applied and environmental microbiology*, 82(1):289–296.
- Tsilia, V., Uyttendaele, M., Kerckhof, F.-M., Rajkovic, A., Heyndrickx, M. & Van de Wiele, T. (2015). *Bacillus cereus* adhesion to simulated intestinal mucus is determined by its growth on mucin, rather than intestinal environmental parameters. *Foodborne pathogens and disease*, 12(11):904–913.
- Van den Abbeele, P., Belzer, C., Goossens, M., Kleerebezem, M., De Vos, W., Thas, O., De Weirtdt, R., Kerckhof, F.-M. & Van de Wiele, T. (2012a). Specific butyrate-producing clostridium cluster xiva species colonize the mucosal environment of a novel in vitro gut model. In *8th Joint symposium INRA-IRRI on Gut Microbiology: Gut microbiota: friend or foe?*
- Van den Abbeele, P., Belzer, C., Goossens, M., Kleerebezem, M., De Vos, W., Thas, O., De Weirtdt, R., Kerckhof, F.-M. & Van de Wiele, T. (2012b). Specific clostridium cluster xiva species drive the mucosal butyrate production. In *Gut Day Symposium, 14th, Abstracts*.
- Van den Abbeele, P., Belzer, C., Goossens, M., Kleerebezem, M., De Vos, W. M., Thas, O., De Weirtdt, R., Kerckhof, F.-M. & Van de Wiele, T. (2013). Butyrate-producing clostridium cluster xiva species specifically colonize mucins in an in vitro gut model. *The ISME journal*, 7(5):949–961. URL <http://dx.doi.org/10.1038/ismej.2012.158>.
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