

Curriculum Vitae

ir. Frederiek - Maarten Kerckhof

February 21, 2018

Personalia

- Last name: Kerckhof
- First names: Frederiek - Maarten Pieter Jozef
- Current adress: Holdaal 72A, 9000 Gent (Belgium)
- 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)

Research interests

I would very much like to conduct a research-oriented task in the environmental biotechnology domain. Due to my doctoral research and training as a bioscience engineer option cellular and genetic biotechnology I consider myself qualified for a function in research and development. My social and organisational skills make me a good collaborator in a research team in which, if necessary, I can take a coordinating task. I have guided or assisted in the guidance of 4 master thesis students and 1 intern, showing that I can delegate my tasks and organize and coordinate them in a research environment. My main interests in environmental biotechnology lie in unravelling microbial interactions that underly the major reactions in nutrient cycling. In my belief the deeper understanding of these complex multicellular behaviour of unicellular organisms will reveal interesting perspectives in engineered ecosystems. Synthetic ecology is a key method in unravelling these interactions. The understanding of the operation of a microbial metabolic network as opposed to the black-box catch-all term 'biomass' that is performing the reactions in e.g. methane oxidation could allow for steering of methane

oxidation rates and valuable by-products formed by methane oxidation partners. My bio-informatics and statistics experience in a great variety of projects in microbial ecological research show that I can be of added value in this research either from a theoretical and applied point of view.

Education

- **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
 - 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)
 - Official teacher "Molecular Microbial Techniques" - 1st Master bioscience engineering, Ghent University (2017-2018)
- **2011-2016: Doctoral thesis on sustainable methanotrophy**
 - Academic papers as first author (see bibliography below, Kerckhof *et al.* (2014))
 - 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**
 - Advanced academic English: conference skills
 - 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 metagenomics 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).
- 2000-2006: Latin - Mathematics, Onze-Lieve-Vrouwecollege Assebroek

Work experience

- Volunteer work
 - 2006-2010: Scout leader.
 - 2007-2009: Materials manager in the Scouts.
 - 2010-2013: Group leader in a team of 3 for Scouts Don Bosco, managing a staff of 30-40 leaders responsible for 200-250 children with weekly activities and yearly camp
 - 2012-2014: District commissary for Scouts District 't Brugse Vrije, pedagogic coordinator of 12 scout groups with 350 leaders and 2000+ children within Bruges
- Extracurricular activities
 - 2004-2006: Editorial and technical staff at OINC-TV (secondary school).
 - 2004-2006: Voted representative in the student council, work group coordinator.
 - 2009-2011: Voted year-representative cellular and genetic biotechnology (arranging exam schedule, have a seat in the faculty's student council).

Teaching experience

- 2011-2013 Practical exercises molecular microbial techniques (Msc Bioscience engineering)
- 2013-2015 Practical exercises microbial ecological processes (Bsc Bioscience engineering)
- 2016-2018 Co - teacher theory course molecular microbial techniques (Msc. Bioscience engineering)

Skills

Informatics

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
- Intermediary in Anvi'o, CONCOCT, IDBA-UD/MegaHIT/metaspades, ... for shotgun metagenomics
- 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.

Lab skills

During my master's thesis at CMET I had the opportunity to be introduced to many methods in microbiological research, which I further developed during my doctoral thesis research.

- Common chemical analytical techniques (VSS/TSS, Kjeldahl-N, COD, CDW, GC-VFA, HPLC, ...).
- Common molecular techniques (PCR, DGGE, qPCR, Illumina MiSeq amplicon data analysis).
- Use of a flowcytometer (BD Accuri, BD FACSVerse) and confocal microscopy.
- Programming and use of Tecan Freedom EVO liquid handling system.
- Biosafety training for a BSL-3 laboratory.

Online Presence

- 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.* (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*.
- 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.
- 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., Jaspert, 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., 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 structures. *ACS Sustainable Chemistry & Engineering*, 5(2):1400–1407.
- Ehsani, E., Hernandez Sanabria, E., Kerckhof, F.-M., Props, R., Vilchez Vargas, R., Vital, M., H Pieper, D. & Boon, N. (2017). Initial evenness determines temporal dynamics in synthetic microbial ecosystem. In *MRM2 conference*.
- 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.
- Garcia Timermans, C., Buysschaert, B., Kerckhof, F.-M., Rubbens, P., Skirtach, A. & Boon, N. (2017). Detecting phenotypes with raman spectroscopy. In *FT-IR Workshop*.
- 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.
- 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*, 7:1285.
- 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., Heyle, K. & Boon, N. (2015b). Enhancing microbial cryopreservation: From fastidious microbes to mixed communities. *Cryobiology*, 71(3):549–550.
- Kuuliala, L., Al Hage, Y., Ioannidis, A.-G., Sader, M., Kerckhof, F.-M., Vanderroost, M., Boon, N., De Baets, B., De Meulenaer, B., Ragaert, P. *et al.* (2018). Microbiological, chemical and sensory spoilage analysis of raw atlantic cod (*gadus morhua*) stored under modified atmospheres. *Food microbiology*, 70:232–244.
- Marzorati, M., Maignien, L., Verhelst, A., Luta, G., Sinnott, R., Kerckhof, F. M., Boon, N., Van de Wiele, T. & Possemiers, S. (2013). Barcoded pyrosequencing analysis of the microbial community in a simulator of the human gastrointestinal tract showed a colon region-specific microbiota modulation for two plant-derived polysaccharide blends. *Antonie Van Leeuwenhoek*, 103(2):409–420.
- 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.
- Mysara, M., Vandamme, P., Props, R., Kerckhof, F.-M., Leys, N., Boon, N., Raes, J. & Monsieus, P. (2017). Reconciliation between operational taxonomic units and species boundaries. *FEMS Microbiology Ecology*, 93(4).
- 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.
- Scoma, A., Coma, M., Kerckhof, F.-M., Boon, N. & Rabaey, K. (2017). Efficient molasses fermentation under high salinity by inocula of marine and terrestrial origin. *Biotechnology for Biofuels*, 10(1):23.
- 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).
- Seuntjens, D., Han, M., Kerckhof, F.-M., Boon, N., Al-Omari, A., Takacs, I., Meerburg, F., De Mulder, C., Wett, B., Bott, C. *et al.* (2017). Pinpointing wastewater and process parameters controlling the aob to nob activity ratio in sewage treatment plants. *Water Research*.
- Stock, M., Hoefman, S., Kerckhof, F., Boon, N., De Vos, P., Heylen, K., De Baets, B. & Waegeman, W. (2012). A kernel-based model to predict interaction between methanotrophic and heterotrophic bacteria. *Communications in agricultural and applied biological sciences*, 78(1):55–60.
- 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-RRI 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>.
- van der Ha, D., Nachtergaele, L., Kerckhof, F.-M., Rameiyanti, D., Bossier, P., Verstraete, W. & Boon, N. (2012). Conversion of biogas to bioproducts by algae and methane oxidizing bacteria. *Environmental science & technology*, 46(24):13425–13431.
- Van Meervenne, E., Van Coillie, E., Kerckhof, F.-M., Devlieghere, F., Herman, L., De Gelder, L., Top, E. & Boon, N. (2012a). An environmental multiresistance plasmid can be transferred to foodborne pathogens. In *Microbial Ecology, 14th International symposium, Abstracts*.
- Van Meervenne, E., Van Coillie, E., Kerckhof, F.-M., Devlieghere, F., Herman, L., De Gelder, L., Top, E. & Boon, N. (2012b). An environmental multiresistance plasmid can be transferred to foodborne pathogens. In *FoodMicro 2012, Abstracts*.
- Van Meervenne, E., Van Coillie, E., Kerckhof, F.-M., Devlieghere, F., Herman, L., De Gelder, L. S., Top, E. M. & Boon, N. (2012c). Strain-specific transfer of antibiotic resistance from an environmental plasmid to foodborne pathogens. *BioMed Research International*, 2012.
- Vekeman, B., Kerckhof, F.-M., Cremers, G., de Vos, P., Vandamme, P., Boon, N., Op den Camp, H. J. & Heylen, K. (2016). New methyloceanibacter diversity from north sea sediments includes methanotroph containing solely the soluble methane monooxygenase. *Environmental microbiology*, 18(12):4523–4536.

Zekker, I., Vlaeminck, S., Bagchi, S., Courtens, E., De Clippeleir, H., Kerckhof, F.-M. & Boon, N. (2012). Selecting nitrifying inocula on different ammonium concentrations. *Communications in agricultural and applied biological sciences*, 77(1):275–279.