

# Curriculum Vitae

Frederiek - Maarten Kerckhof

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## Personalia

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## 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

- **2011-present: 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-present: 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: Chosen representative in the student council, work group coordinator.
  - 2009-2011: Chosen year-representative cellular and genetic biotechnology (arranging exam schedule, have a seat in the faculty's student council).

## **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.

- 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 NGS data analysis
- RAxML for phylogenetic tree building
- MG-RAST for metagenomics
- Basic knowledge of Bionumerics, DNASTar lasergenes, PROKKA, CLC workbench, Wolfram Mathematica, Ruby, Java, HTML, php and Visual Basic.

### **Lab skills**

During my master's thesis at LABMET 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 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

- Allais, L., Kerckhof, F.-M., Verschueren, S., Bracke, K., De Smet, R., Laukens, D., Van den Abbeele, P., De Vos, M., Boon, N., Brusselle, G. *et al.* (2014). 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., Verschueren, S., Bracke, K., De Smet, R., Laukens, D., De Vos, M., Boon, N., Brusselle, G., Van de Wiele, T. *et al.* (2013a). 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., Verschueren, S., Bracke, K., De Smet, R., Laukens, D., Devos, M., Boon, N., Brusselle, G., Van de Wiele, T. *et al.* (2013b). P694 chronic cigarette smoke exposure alters the murine gut microbiome. *Journal of Crohn’s and Colitis*, 7(Supplement 1):S289–S289.
- Benner, J., De Smet, D., Ho, A., Kerckhof, F.-M., Vanhaecke, L., Heylen, K. & Boon, N. (2014). Exploring methane-oxidizing communities for the co-metabolic degradation of organic micropollutants. *Applied microbiology and biotechnology*, pp. 1–10.
- 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. 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. (2012b). 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 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.
- 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 Crieginge, 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.
- 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. (2011). *Unconventional electron donors and acceptors for microbial ecosystems*. Master's 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.
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- 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.
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- Van den Abbeele, P., Belzer, C., Goossens, M., Kleerebezem, M., De Vos, W. M., Thas, O., De Weirdt, 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.
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