

Prof. Lieven Clement

Ghent University, Gent, Belgium

Last update: 13/06/2018

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Bio

Lieven Clement graduated as Master in Bio-Science Engineering at Ghent University in 2000 and obtained a PhD in Environmental Statistics in 2007 at the same University. In his postdoc he reoriented his research to Statistical Genomics and he did several internships with Prof. Ciprian Crainiceanu and Prof. Rafael Irizarry in Johns Hopkins University (Prof. Irizarry is currently based in Harvard University). In 2010 Lieven Clement joined faculty in the Leuven Biostatistics and Statistical Bioinformatics Centre, KU Leuven. He is now Associate Professor of Statistical Genomics at Ghent University, Belgium. He serves as a member of the core team that established a new Master Program in Bioinformatics at Ghent University, as a board member of the Belgian Proteomics Association, as an expert in genomics projects of the Belgian Health Care Knowledge Center (KCE), and as an Associate Editor for the journal *Biometrics* (2011-2017).

Since 2007, Lieven Clement's research focusses on Genomics and Statistical Bioinformatics problems. In particular he developed statistical data analysis methods for microarrays, digital PCR, next-generation sequencing, and mass spectrometry based proteomics. His research efforts resulted in numerous publications on novel methods and tools for, and applied research in, omics data analysis. His lab is built around three strategic research pillars each connected to an omics domain: (meta)genomics, (single cell) transcriptomics and proteomics. He is a strong advocate of open and reproducible science, which he actively propagates in his research and teaching activities. He is also keen on leveraging his expertise in experimental design, omics data analysis and integration to researchers in the life science and to translational research.

Contact

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Education 2007 **PhD in Bioscience Engineering, Ghent University (August 2000 - July 2007)**

PhD Dissertation: Statistical validation and spatio-temporal modelling of river monitoring networks.

Supervisors: Prof. O. Thas & Prof. P. Vanrolleghem

2000 **Master of Science in Bioscience Engineering, Ghent University (October 1995 - July 2000)**
Magna Cum Laude
Master Dissertation: Microbial biosensors for organic micropollutants in gasses.
Supervisor: Prof. W. Verstraete

Occupation 2017– **Associate Professor of Statistical Genomics**
Ghent University

Previous Positions 2012 **Assistant Professor of Statistical Genomics**
Ghent University

2010 **Assistant Professor of Statistical Bioinformatics (20% + 70% postdoc)**
KU Leuven

Guest Professor of Statistical Bioinformatics (10%)

University of Hasselt

2007 **Postdoc**

Ghent University

Supervisor Prof. O. Thas

2003 **Teaching and Research Assistant**

Ghent University

Supervisors Prof. O. Thas & Prof. P. Vanrolleghem

2000 **Research Assistant**

Ghent University

Supervisors Prof. O. Thas & Prof. P. Vanrolleghem

Research

Fellowships 2017 Prof. S. Dudoit, Department of Biostatistics, University of California, Berkeley, USA (2 weeks).
2016 Prof. M. Robinson Lab, Institute of Molecular Life Sciences, University of Zürich, Switzerland (2 weeks).
2011 Prof. C. Crainiceanu & Prof. R. Irizarry, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, USA (4 weeks)
2010 Prof. C. Crainiceanu & Prof. R. Irizarry, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, USA (4 weeks)
2009 Prof. C. Crainiceanu & Prof. R. Irizarry, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, USA (4 weeks)
2008 Prof. C. Crainiceanu & Prof. R. Irizarry, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, USA (10 weeks)

Teaching

University

Courses

Statistical Genomics, 6 ECTS, Master Of Science in Bioinformatics, Ghent University (2014 - Present).

Statistische Genomica, 4 ECTS, Master of Science in Statistical Data Analysis, Ghent University (2013 - Present).

Lecturer of Biostatistics, 4 ECTS, Master of Science in Biochemistry and Biotechnology, Ghent University (2013 - Present).

Lecturer of Statistiek, 4 ECTS, Bachelor of Science in Biology, Ghent University (2012-Present).

Lecturer of Statistiek, 5 ECTS, Bachelor of Science in Biochemistry and Biotechnology, Ghent University (2012 - Present).

Lecturer of Applied Biostatistics, 5 ECTS, Master of Science in Biomedical Sciences, KU Leuven (2011-2012).

Lecturer of Statistical Topics in Food Technology, 4 ECTS, Master of Science in Food Biotechnology, Ghent University (2008 - 2010).

Lecturer of Multivariate Statistics, 3 ECTS, Master of Science in Bioscience Engineering, Ghent University (2007 - 2008).

Other Academic

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| Courses | 2018 | Proteomics Data Analysis (PDA18), Gulbenkian Institute, Oeiras, Portugal. |
| | 2017 | 2 Day Mass spectrometry Data Processing Workshop, BITS, VIB, Ghent. |
| | 2016 | 3 Day Proteomics Informatics Workshop series, Belgium Proteomics Association, Doctoral Schools of Gent University and KU Leuven, hosted by KU Leuven. |
| | 2016 | 3 Day Proteomics Informatics Workshop series, Belgium Proteomics Association, Doctoral Schools of Gent University and KU Leuven, hosted by Ghent University. |

Journal Publications

- A publication list can also be retrieved from [Google Scholar](#) or the [Ghent University Archive](#).
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| 2018 | <p>Van Quickelberghe E, Martens A, Goeminne L, Clement L, van Loo G and Gevaert K (2018). Identification of immune-responsive gene 1 (IRG1) as a target of A20. <i>Journal of Proteome Research</i> 17, 6, 2182-2191.</p> <p>Derycke S, Kéver L, Herten K, Van den Berge K, Van Steenberge M, Van Houdt J, Clement L, Poncin P, Parmentier E and Verheyen E (2018). Neurogenomic Profiling Reveals Distinct Gene Expression Profiles Between Brain Parts That Are Consistent in Ophthalmotilapia Cichlids. <i>Frontiers in Neuroscience</i> 12, 136.</p> <p>Goeminne L, Gevaert K and Clement L (2018). Experimental design and data-analysis in label-free quantitative LC/MS proteomics: A tutorial with MSqRob. <i>Journal of Proteomics</i> 171, 23-36.</p> <p>Van den Berge K, Perraudeau F, Sonesson C, Love M, Risso D, Vert JP, Robinson M, Dudoit S and Clement L (2018). Observation weights to unlock bulk RNA-seq tools for zero inflation and single-cell applications. <i>Genome Biology</i> 19, 1, 24.</p> |
| 2017 | <p>Van den Berge K, Sonesson C, Robinson M and Clement L (2017). stageR: a general stage-wise method for controlling the gene-level false discovery rate in differential expression and differential transcript usage. <i>Genome Biology</i> 18, 1, 151.</p> <p>Sticker A, Martens L and Clement L (2017). Mass spectrometrists should search for all peptides, but assess only the ones they care about. <i>Nature Methods</i> 14, 643-644</p> |

- Jacobs B, Goetghebeur E, Vandesompele J, De Ganck A, Nijs N, Beckers A, Papazova N, Roosens N and Clement L (2017). Model based classification for digital PCR: your Umbrella for rain. *Analytical Chemistry* 89, 8, 4461-4467.
- Broeckx B, Peelman L, Saunders J, Deforce D and Clement L (2017). Using variant databases for variant prioritization and to detect erroneous genotype-phenotype associations. *BMC bioinformatics* 18, 1, 535.
- Pipelers P, Clement L, Vynck V, Hellemans J, Vandesompele J and Thas O (2017). A unified censored normal regression model for qPCR differential gene expression analysis. *PloS one* 12, 8, e0182832.
- Van Nevel S, Buyschaert B, De Roy K, De Gusseme B, Clement L and Boon N (2017). Flow cytometry for immediate follow-up of drinking water networks after maintenance. *Water Research* 111, 66-73.
- 2016 De Tender C, Haegeman A, Vandecasteele B, Clement L, Cremelie P, Dawyndt P, Martine M and Debode J (2016). Dynamics in the strawberry rhizosphere microbiome in response to biochar and botrytis cinerea leaf infection. *Frontiers in Microbiology*, 7, 2062.
- Debyser G, Mesuere B, Clement L, Van de Weygaert J, Van Hecke P, Duytschaever G, Aerts M, Dawyndt P, De Boeck K, Vandamme, P and Devreese, B (2016). Faecal proteomics: a tool to investigate dysbiosis and inflammation in patients with cystic fibrosis. *Journal of Cystic Fibrosis* 15, 2, 242-250.
- Moeys S, Frenkel, J, Lembke, C, Gillard, J, Devos, V, Van den Berge, K, Bouillon, B, Huysman, M, De Decker, S, Scharf, J, Bones, A, Brembu, T, Winge, P, Sabbe, K, Vuylsteke, M, Clement L, De Veylder L, Pohnert, G, Vyverman, W (2016). A Sex-inducing Pheromone Triggers Cell Cycle Arrest and Mate Attraction in the Diatom *Seminavis Robusta*. *Scientific Reports* 6, 19252.
- Props R, Monsieurs P, Mysara M, Clement L, Boon N (2016). Measuring the biodiversity of microbial communities by flow cytometry. *Methods in Ecology and Evolution* 7, 1376-1385.
- Argentini, A, Goeminne L, Verheggen, K, Hulstaert, N, Staes, A, Clement L, Martens L (2016). moFF : a Robust and Automated Approach to Extract Peptide Ion Intensities. *Nature Methods* 13, 12, 962-965.
- Goeminne L, Gevaert K and Clement L (2016). Peptide-level Robust Ridge Regression Improves Estimation, Sensitivity, and Specificity in Data-dependent Quantitative Label-free Shotgun Proteomics. *Molecular & Cellular Proteomics* 15, 2, 657-668.
- 2015 van der Borgh K, Thys K, Wetzels Y, Clement L, Verbist B, Reumers J, van Vlijmen H and Aerssens J (2015). QQ-SNV: Single Nucleotide Variant Detection at Low Frequency by Comparing the Quality Quantiles. *BMC Bioinformatics* 16, 1, 379.
- Verbist B, Klambauer G, Vervoort L, Talloen W, The QSTAR Consortium, Shkedy Z, Thas O, Bender A, Göhlmann H and Hochreiter S (2015). Using transcriptomics to guide lead optimization in drug discovery projects: Lessons learned from the QSTAR project. *Drug Discovery Today*, 20, 5, 505-513. QSTAR Consortium: Angibaud Patrick, Amaratunga Dhammika, Bijmens Luc, De Bondt An, Gijssen Harrie, Göhlmann Hinrich, Osselaer Steven, Peeters Pieter, Talloen Willem, Van Den Wyngaert Ilse, Van Vlijmen Herman, Verbeke Tobias, Verheyen Geert, Vervoort Liesbet, Wegner Jörg, Wroblowski Berthold, Wuyts Dirk, Tresadern Gary. University of Hasselt: Khamiakova Tatsiana, Otava Martin, Perualila Nolen, Shkedy Ziv, Thilakarathne Pushpika. Ghent University: Clement Lieven, Matiello Federico, Thas Olivier, Verbist Bie, Visscher Alain. Johannes Kepler University Linz:

- Bodenhofer Ulrich, Clevert Okko, Heusel Martin, Hochreiter Sepp, Klambauer Günter, Mayr Andreas, Mitterecker Andreas. University of Cambridge: Bender Andreas, Ravindranath Aakash. Durham University: Kasim Adetayo. University of Rochester: McCall Matthew. OpenAnalytics: Bhagwat Aditya, Cougnaud Laure
- Goeminne L, Argentini A, Martens L and Clement L (2015). Summarization vs. peptide-based models in label-free quantitative proteomics: performance, pitfalls and data analysis guidelines. *Journal of Proteome Research* 14, 6, 2457-2465.
- Clauw P, Coppens F, De Beuf K, Dhondt S, Van Daele T, Maleux K, Storme V, Clement L, Gonzalez N, Inze D (2015). Leaf Responses to Mild Drought Stress in Natural Variants of *Arabidopsis thaliana*. *Plant physiology* 168, 3, 1180-1180.
- Verbist B, Clement L, Reumers J, Thys K, Vapirev A, Talloen W, Wetzels Y, Meys J, Aerssens J, Bijmens L and Thas O (2015). ViVaMBC: estimating Viral sequence Variation in complex populations from Illumina deep-sequencing data using Model-Based Clustering. *BMC Bioinformatics* 16, 1, 59.
- Verbist B, Thys K, Reumers J, Wetzels Y, Van der Borght K, Talloen W, Aarsens J, Clement L and Thas O (2015). VirVarSeq: a low-frequency virus variant detection pipeline for Illumina sequencing using adaptive base-calling accuracy filtering. *Bioinformatics* 31, 1, 94-101.
- 2014 De Neve J, Meys J, Ottoy JP, Clement L and Thas O (2014). unifiedWMWqPCR: the unified Wilcoxon–Mann–Whitney test for analyzing RT-qPCR data in R. *Bioinformatics* 30, 17, 2494-5.
- Jacobs B, Goetghebeur E and Clement L (2014). Impact of variance components on reliability of absolute quantification using digital PCR. *BMC Bioinformatics* 15, 283.
- 2013 Yang Y, Foulquié-Moreno M, Clement L, Erdei E, Tanghe A, Schaerlaekens K, Dumortier F and Thevelein J (2013). QTL analysis of high thermotolerance with superior and downgraded parental yeast strains reveals new minor QTLs and converges on novel causative alleles involved in RNA processing. *PLoS genetics* 9, 8, e1003693.
- Forchheh A, Verbeke G, Kasim A, Lin D, Shkedy Z, Talloen W, Göhlmann H and Clement L (2013). beadarrayFilter: An R package to filter beads. *R Journal* 5, 1.
- De Neve J, Thas O, Ottoy JP and Clement L (2013). An extension of the Wilcoxon-Mann-Whitney test for analyzing RT-qPCR data. *Statistical Applications in Genetics and Molecular Biology* 12, 3, 333-46.
- Claesen J, Clement L, Shkedy Z, Foulquié-Moreno M and Burzykowski T (2013). Simultaneous mapping of multiple gene loci with pooled segregants. *PLoS ONE* 8, 2, e55133.
- 2012 De Beuf K, De Schrijver J, Thas O, Van Criekinge W, Irizarry R and Clement L (2012). Improved base-calling and quality scores for 454 sequencing based on a Hurdle Poisson model. *BMC Bioinformatics* 13, 303, 1-11. (Highly accessed).
- De Beuf K, Pipelers P, Andriankaja M, Thas O, Inzé D, Crainiceanu C and Clement L (2012). Analysis of tiling array expression studies with flexible designs in Bioconductor (waveTiling). *BMC Bioinformatics* 13, 234.
- Swinnen S, Schaerlaekens K, Pais T, Claesen J, Hubmann G, Yang Y, Demeke M, Foulquié-Moreno M, Goovaerts A, Souvèreyns K, Clement L, Dumortier F and Thevelein J (2012). Identification of novel causative genes determining the complex trait of high ethanol tolerance in yeast using pooled segregant whole-genome sequence analysis. *Genome Research* 22, 975-984.

- Thas, O, De Neve, J, Clement, L and Ottoy, J (2012). Probabilistic Index Models. *Journal of the Royal Statistical Society B, Statistical Methodology* 74, 4, 623-671. (Discussion paper presented on the Research Section Ordinary Meeting of the Royal Statistical Society, Wednesday, February 15th, 2012)
- Thas O, Clement L, Rayner J, Carvalho B and Van Criekinge W (2012). An Omnibus Consistent Adaptive Percentile Modified Wilcoxon Rank Sum Test with Applications in Gene Expression Studies. *Biometrics* 68, 2, 446-454.
- De Roy K, Clement L, Thas O, Wang Y and Boon N (2012). Flow cytometry for fast microbial community fingerprinting. *Water Research*, 46 (3), 907-919. (De Roy K and Clement L are Joint First Author).
- Forcheh A, Verbeke G, Kasim A, Lin D, Shkedy Z, Talloen W, Göhlmann H and Clement L (2012). Gene Filtering in the Analysis of Illumina Microarray Experiments. *Statistical Applications in Genetics and Molecular Biology*, 11, 2, 3.
- Clement L, De Beuf K, Thas O, Vuylsteke M, Irizarry R and Crainiceanu C (2012). Fast Wavelet Based Functional Models for Transcriptome Analysis with Tiling Arrays. *Statistical Applications in Genetics and Molecular Biology*, 11, 1, 4.
- 2011 Thilakarathne P, Clement L, Lin D, Shkedy Z, Kasim A, Talloen W, Versele M and Verbeke G (2011). The Use of Semi-parametric Mixed Models to Analyze PamChip Peptide Array Data: an Application to an Oncology Experiment. *Bioinformatics*, 27, 20, 2859-2865.
- De Leeneer K, De Schrijver J, Clement L, Baetens M, Lefever S, De Keulenaer S, Van Criekinge W, Deforce D, Van Nieuwerburgh F, Bekaert S, Pattyn F, De Wilde B, Coucke P, Vandesompele J, Claes K and Hellemans J (2011). Practical Tools to Implement Massive Parallel Pyrosequencing of PCR Products in Next Generation Molecular Diagnostics. *PLoS One*, 6, 9, e25531.
- 2009 Wittebolle L, Marzorati M, Clement L, Balloi A, Doffonchio D, Heylen K, De Vos P, Verstraete W and Boon N (2009). Species evenness favors functionality under selective stress. *Nature*, 458, 623-626. (Wittebolle, L and Marzorati, M. are Joint First Author).
- De Clercq E, Clement L and De Wulf R (2009). Monte Carlo simulation of false change in the overlay of misregistered vector maps. *Landscape and Urban Planning*, 91, 1, 36- 45.
- Clement L and Thas O (2009). Nonparametric trend detection in river monitoring network data: a spatio-temporal approach. *Environmetrics*, 20, 3, 283-297.
- Clement L and Thas O (2009). Testing for trends in the violation frequency of an environmental threshold in rivers. *Environmetrics*, 20, 1, 53-67.
- 2007 Clement L, Thas O, Ottoy J and Vanrolleghem P (2007). Data management of river water quality data - a semi-automatic procedure for data validation. *Water Resources Research*, 43, W08429.
- Clement L and Thas O (2007). Estimating and modelling spatio-temporal correlation structures for river monitoring networks. *Journal of Agricultural, Biological, and Environmental Statistics*, 12, 2, 161-176. (Best paper award 2007/2008).
- 2006 Clement L, Thas O, Vanrolleghem P and Ottoy J (2006). Spatio-temporal statistical models for river monitoring networks. *Water Science & Technology*, 53, 1, 9-15.
- 2000 Volcke E, Clement L, Van de Steene M and Vanrolleghem P (2001). An overview of the posters presented at Watermatex 2000. I : Sensor /

Monitoring, control and decision support systems. *Water Science & Technology*, 43, 7, 381-386.

Invited Presentations

- 2018 Clement L. (2018). Experimental design and data-analysis in label-free quantitative MS-based proteomics. 17th Human Proteome World Congress, September 30-October 3 2018, Orlando, USA.
Clement L. (2018). Large-scale inference for RNA-seq experiments. Analytica Conference, April 10-12 2018, Munich, Germany.
- 2017 Clement L. (2017). Statistical analysis of proteomics data on the peptide-level. 4th Computational Biology Workshop 2017, Department of Biochemistry and Molecular Biology, University of Southern Denmark.
Clement L. (2017). Statistical methods for label-free quantitative mass-spectrometry-based proteomics. (IB)2 Seminar, May 5th 2017, Interuniversity Institute Of Bioinformatics in Brussels, Belgium.
- 2016 Clement Lieven (2016). Data driven thresholding of digital PCR fluorescence intensities, your umbrella for heavy rain. 4th qPCR & Digital PCR Congress, October 20th - October 21th 2016, London, UK.
Clement Lieven (2016). Peptide-level robust ridge regression for quantitative label-free Shotgun Proteomics. IMLS Lecture Series in the Molecular Life Sciences, May 17 2017, University of Zurich, Zurich, Switzerland.
- 2014 Clement, L. (2014). Functional Data Analysis of High-Throughput Data. ANed/BMS Summer Meeting: When Biostatistics Meets Omics. Rotterdam, June 13th, 2014.
- 2013 Clement, L. (2013). Wavelet based functional models for omics count profiles, Seminar on Applied Statistics, ETH Zürich, October 24 2013.
Clement L. (2013). Flow cytometry for fast microbial community fingerprinting. 23rd Annual Conference of The International Environmetrics Society. Anchorage, Alaska, USA, June 10-14, 2013.

Advising

- Postdocs 2017 Caroline Detender (external funding until 2020)
- PhD Students 2012 Bart Jacobs, PhD in 2017
title: Confronting bias and precision in digital PCR quantification.
- 2010 Chiara Anyiawung Forcheh PhD in 2013
title: An Statistical models for the Analysis of different types of Microarray Gene Expression Data.
- 2009 Kristof De Beuf PhD in 2013
title: Statistical Methods for High-Throughput Genomic Data.
- 2017 Lisa Joos (expected 2021, external funding)
- 2017 Gwendolien Sergeant (expected 2020)
- 2015 Gust Bilcke (expected 2019, external funding)
- 2014 Koen Van den Berge (expected 2019, external funding)
- 2014 Adriaan Sticker (expected 2018)
- 2013 Ludger Goeminne (expected 2018, external funding)

Awards

- 2017 Award for Best Flash Talk of Young Investigator. Received by PhD student Ludger Goeminne EuBIC European Winter School 2017, January 10-13, 2017, Semmering, Austria.
- 2016 Award for Best Poster. Received by PhD student Koen Van den Berge. XXVIII International Biometric Conference. July 10-15, 2016, Victoria, Canada.
- 2012 Discussion paper: Thas, O., De Neve, J., Clement, L., and Ottoy, J. (2012). Probabilistic Index Models. Journal of the Royal Statistical Society B, Statistical Methodology, accepted. Discussion paper presented on the Research Section Ordinary Meeting of the Royal Statistical Society, London, UK, February 15th, 2012.
- 2011 Award for Best Poster. Received by PhD student Forcheh Chiara, A. Workshop on Computational Statistical Methods for Genomics and Systems Biology. Montreal, Canada, April 18-22 2011.
- 2008 IBS Award for the best paper in the Journal of Agricultural, Biological and Environmental Statistics in 2006/07 (Issued by the International Biometric Society).
- 2007 Award for Best Student Presentation. Ties 2007, August 16-20, Mikulov, Czech Republic.
- 2006 Award for Best Poster. Workshop on Recent Advances in Modelling Spatio-Temporal Data, Southampton, United Kingdom, May 25-26, 2005.

Academic Service

Reviewing

Associate Editor for Biometrics (2011-2017)

Member of the selection committee for the Biometry Best Paper Award for 2012-2013 of the BMS/ANed, Dutch region of the International Biometrics Society.

Referee for Genome Biology, Mathematical Biosciences, Bioinformatics, BMC Bioinformatics, Journal of Proteomics, Biometrics, Environmental and Ecological statistics, Environmetrics, Journal of Hydrology, amongst others

Member of Selection Committees

- 2018 Member of the Selection committee for Research Faculty Position in Biostatistics at the Faculty of Bioscience Engineering, Ghent University, Belgium.
- 2015 Member of the Selection committee for Faculty Position in Statistics at Ghent University Global Campus, Incheon, South Korea.
- 2013 Member of the Selection committee for a Teaching Assistant Position in Statistics at the Faculty of Sciences, Ghent University, Belgium.

Member of PhD Examination Committees

- 2018 Elvis Ndah (2018, Ghent University)
- Matthijs Vynck (2018, Ghent University, Secretary of Examination Committee)
- 2016 Xiaobei Zhou (2016, University of Zürich)
- Yingjie Zhang (2016, Ghent University)

- 2015 Askar Obulkasim (2015, University of Amsterdam)
- Simon Denil (2015, Ghent University)
- 2014 Fatemeh Ghavidel (2014, Hasselt University)
- 2013 Jürgen Claesen (2013, Hasselt University)
- 2012 Antoon Lievens (2012, Ghent University)
- Fanghong Zang (2012, Ghent University)

Program

Committees

Member of the Program committee and of the Core team that established the new Master Program in Bioinformatics, Ghent University. (2013 - Present)

Member of the Program Committee, Master of Science in Statistical Data Analysis, Ghent University. (2012-2017)

Member of the Program Committee, Master of Science in Bioinformatics, KU Leuven. (2011)

Organisation of

Workshops and

Conferences

- 2018 Member of the Local Organising Committee and Scientific Committee of [17th meeting of the EUCARPIA Section Biometrics in Plant Breeding](#), September 3-5 2018, Ghent University.
- 2018 Organiser of the 2 day Hackaton Statistical modelling to improve the quantitative analysis of post-translationally modified peptides at the EubIC Developers meeting, January 9-12, 2018, Gent, Belgium.
- 2015 Co-organiser of the Big Data Science symposium, Gent, May 11, 2015. (Speakers: Paul Vauterin, Multiplicon N.V., Matt Wand, University of Technology, Sydney, Christophe Claramunt, French Naval Academy Research Institute, Tianxi Cao, Harvard University, Susan Holmes, Stanford University, Terry Speed, Walter + Eliza Hall Institute of medical research and UC Berkeley)
- 2012 Organiser and Chair of invited session 12: Statistical Methods for Reducing Batch Effects, Summarization and Gene Filtering in High-Throughput Genomic Data op het 26th International biometric conference, Kobe, 2012 (Jeff Leek, Johns Hopkins University, USA, Matthew N. McCall, University of Rochester, USA, Djork-Arné Clevert, Johannes Kepler University of Linz, Austria, Adetayo Kasim Durham University, UK).