Part I: Personalia

First Name:	Kristel
Last Name:	Van Steen
Place of birth, Date:	Dendermonde, 3 June 1969
Address:	Krijgsbaan 147, D – 9140 Temse, Belgium
Residence:	see address
Contact information:	
Phone:	+32 (0)4 366 2692 (work)
	+32 (0)485 766597 (private)
E-Mail:	kristel.vansteen@ulg.ac.be

Part II: Study background

II.1. Study background section A: Obtained master degrees

a) **Diploma 1**:

Master in Exact Sciences; Mathematics
Ghent University; 28 June 1991
Grade: summa cum laude

Thesis:

"Inleiding tot de gebouwentheorie."
Promotor: Prof Dr H Van Maldeghem

Detailed information:

- This training is useful in giving me a firm foundation to acquire knowledge as a basis for future study and research activities,
- and developing a logical and structural thinking mentality.

b) **Diploma 2**:

Master in Biostatistics
Hasselt University; 5 oktober 1999
Grade: magna cum laude

Thesis:

"Analysis of longitudinal, ordinal, categorical, quality of life data with dropout."
Promotor: MSc D Curran; Co-promotors: MSc L Collette and Prof Dr G Molenberghs.

Detailed information:

- The extensive training in biostatistics gives me the opportunity to translate a purely mathematical background into a practical social engagement.
- Project-driven group assignments during the training are useful in developing skills to enhance team working.
- The apprenticeship is enriching and is a first real exposure to the business community.
- The nature of the student population – the majority were VLIR students from developing countries (this is: in Belgium with a Flemish Inter-university Board grant) – is extremely stimulating to adopt a positive international attitude and mentality.

II.2. Study background section B: Doctorate or special doctorate

a) **Diploma 1**:

PhD in Exact Sciences: Mathematics
Ghent University; 21 May 1996
Grade: summa cum laude

Thesis:

"Non-spherical buildings of rank 3."
Promotor: Prof Dr H Van Maldeghem

Publications:

- Van Maldeghem H, **Van Steen K** (1999) Characterizations by Automorphism Groups of Some Rank 3 Buildings IV. Hyperbolic p-adic Moufang Buildings of Rank 3, Geometriae Dedicata 75: 115-122.
- **Van Steen K** (1999) Characterizations by Automorphism Groups of Some Rank 3 Buildings III. Moufang-Like Conditions, Geometriae Dedicata 74: 225-240.
- Van Maldeghem H, **Van Steen K** (1999) Characterizations by Automorphism Groups of Some Rank 3 Buildings II. A Half Strongly-Transitive Locally Finite Triangle Building is a Bruhat-Tits Building, Geometriae Dedicata 74: 113-133.
- Van Maldeghem H, **Van Steen K** (1998) Characterizations by Automorphism Groups of Some Rank 3 Buildings I. Some Properties of Half Strongly-Transitive Triangle Buildings, Geometriae Dedicata 73: 119-142.
- Van Maldeghem H, **Van Steen K** (1997) Moufang Affine Buildings have Moufang Spherical Building at Infinity, Glasgow Math. J. 39: 237-241.

Detailed information:

- During my research years in fundamental mathematics I considered it a challenge to convey abstract concepts in a teachable and exciting way to a varied audience. During symposia and workshops it becomes clear that communicative skills are essential in building out a career, independently of the discipline or type of work floor. Under the leadership of my promotor in those days, Prof Dr H Van Maldeghem, the first building stones are laid to canalize and further develop skills in communication.
- The preparations for my first doctoral degree have accentuated my sense of analysis and synthesis, and are essential to nourish an independent and critical attitude.
- From a scientific viewpoint the study of fundamental mathematics at this level is a good basis for study and research work in other specialties. **Mathematicians can thrive in diverse sectors due to their analytic problem solving and logical thinking.**

b) **Diploma 2:**

PhD in medical sciences – biomedical science
Hasselt University / Maastricht University; 20 December 2005
Grade: not applicable

Thesis:

"Genomic screening methodology for common diseases and complex traits -
Multiplicity and missingness: a statistical hurdle?"
Promotor: Prof Dr G Molenberghs; Co-promotor: Prof Dr NM Laird

Publications:

- **Van Steen K**, Laird NM, Markel P, Molenberghs G (2006) Approaches to
  handle incomplete data in family-based association testing. Ann Hum Genet
  71: 141-151.
- **Van Steen K**, Mcqueen MB, Herbert A, Raby B, Lyon H, Demeo DL, Murphy
  A, Su J, Datta S, Rosenow C, Christman M, Silverman Ek, Laird NM, Weiss
  St, Lange C (2005) Genomic screening and replication using the same data set
  in family-based association testing, Nature Genetics 37 (7) 683 – 691.
- **Van Steen K**, Lange C (2005) PBAT: a comprehensive software package for
  genome-wide association analysis of complex family-based studies (Invited
  submission) Journal of Human Genomics 2 (1): 1-3.
- **Van Steen K**, Tahri N, Molenberghs G (2004) Introducing the multivariate
  Dale model in population based genetic association studies, Biometrical
  Journal 46 (2):187-202.

Detailed information:

- An important part of this thesis is the result of my work at the Harvard School
  of Public Health as a post-doctoral fellow. At this school I am made aware of
  different English writing styles (European versus non-European) and am given
  useful comments on increasing the success rate of publications in American and
  non-American journals. I learn that adopting the correct conventions, etiquette
  and writing style can severely increase the rate of accepted project proposals.
- A publication is not a private affair. Every manuscript is read by some internal
  specialists, heavily discussed upon with the authors, provided with comments to
  increase the value of the publication and only then released for submission in a
  scientific journal. Corporate thinking brought into practice …
- According tot he American website Careercast (2014), **mathematicians,
  tenured university professors and statisticians embody the top 3 best jobs,
  with a world of unlocked opportunities, continued growth and growing
  demands in science, industry and society.**

A copy of diplomas and obtained certificates can be obtained upon request.

II.3. Study background section C: Additional Study Certificates (a selection)

Diploma or certificate	Grade	University / Institute	Year
Workshop in Mixture Estimation and Applications	Certificate	International Centre for Mathematical Sciences (ICMS), Edinburgh (UK)	2011
IFRES 6+ Dispensation officielle (tenue compte de ma formation de communication WECOM)		ULg (Belgium)	
IFRES 5 (séance de base) Un guide pour l'enseignant, un guide pour l'étudiant: l'engagement pédagogique		ULg (Belgium)	2010
IFRES 4 Organisation et évaluation des stages		ULg (Belgium)	2010
IFRES 3 Le titurat pour l'apprentissage par problems et en petits groupes		ULg (Belgium)	2010
IFRES 2 Introduction générale au PBLet au rôlede tuteur		ULg (Belgium)	2010
IFRES 1 Construction et gestion qualité de teste		ULg (Belgium)	2009
Statistical analysis of Networks	Certificate	UCL (Belgium)	2009
Cours : Français		Nationale Handels Academie Antwerp (Belgium)	2008
Continuing medical education: post genome respiratory epidemiology II: an interdisciplinary challenge	Certificate	Cernay-la-Ville (France)	2008
Workshop: Statistical analysis of genetic data in families	Certificate	FaBeR – KUL, (Belgium)	2008
FAMHAP – haplotype frequency estimation and association analysis	Certificate	Rheinische Friedrich-Wilhelms-Universität, Bonn (Germany)	2008
Good practice in DNA micro-array analysis	Certificate	Klinikum Großhadern, Munich (Germany)	2007
Erasmus Summer Program; Modules Genetic epidemiology of complex diseases, Introduction to genomics en Searching genes of complex disorders	Certificate	Erasmus Medical Centre Rotterdam (the Netherlands)	2006
SAS JMP genetics course	Certificate	Department of Cardiovascular Diseases – KUL (Belgium)	2006
S.A.G.E. course: statistical analysis for genetic epidemiology	Certificate	Department of Cardiovascular Diseases –	2006

		Catholic University Leuven (Belgium)	
37th International training workshop on the use of GelCompar II and Bionumerics	Certificate	Applied Maths headquarters in Sint-Martens-Latem (Belgium)	2006
Doctoral Training: Medical Sciences	**Certificate**	**Antwerp University (Belgium)**	**2005**
Biotechnology Project Management	**Certificate**	**Harvard Extension School – Massachusetts Biotechnology Council (USA)**	**2005**
Short course: Mathematical approaches to the analysis of complex phenotypes	Certificate	The Jackson Laboratory Bar Harbor – n (USA)	2003
Short course: Bayesian hierarchical modelling using WinBUGS, IBConf	Certificate	Universität Freiburg (Germany)	2002
Interculturele Communicatietraining		**Universiteit Hasselt**	**2001**
Advances in population-based studies of complex genetic disorders	Certificate	Erasmus Medical Centre Rotterdam (the Netherlands)	2001
Course: module 2: Bio-informatics	Certificate	ICES University Ghent (Belgium)	2001
Course: module 1: Bio-informatics	Certificate	ICES University Ghent (Belgium)	2001
WECOM: training in scientific communication: written communication	**Certificate**	**Limburg University Centre Hasselt (Belgium)**	**2001**
WECOM: training in scientific communication: oral communication	**Certificate**	**Limburg University Centre (Belgium)**	**2001**
Advances in population-based studies of complex genetic disorders	Certificate	Erasmus Medical Centre Rotterdam (the Netherlands)	2001
Course: Handling Non-response	Certificate	ESRC university Southampton (United Kingdom)	2000
Workshop: Statistical Inference	Certificate	University Hasselt (Belgium)	2000
Workshop: Sensitivity analysis for incomplete data	Certificate	Biostatistical center de K.U.Leuven, LUC et university Gent (Belgium)	2000
Workshop: Statistical analysis of discrete structures	Certificate	Institut für Statistik Munich (Germany)	2000
Multivariate Statistics in Practice	Certificate	Groningen University (the Netherlands)	1997
Computerintensive Methods in Statistics; Density Estimation, Smoothing in S+	18/20	Hasselt University Belgium)	1997

Detailed information:

- During the period 1997-1999 the emphasis lies on gaining in-depth scientific biostatistics knowledge. Persistent training is necessary to surpass a simple executive function as a biostatistician. It enables me to closely follow the trends and evolutions in my discipline and to carry out creative and innovative scientific work.
- This resulted, from 2000 onwards, in a period of self–study. I am feeling scientifically well-prepared to successfully start methodological research in biostatistics. Intense focus within this discipline has the risk of becoming alienated with other disciplines. That is why I choose for a doctoral training beyond the frontiers of pure statistics. For the aforementioned reason I also take training in scientific communication.
- The invitation to work at the Harvard School of Public Health (2003-2005) as a post-doctoral fellow allows me to make most of my chances to expand my work area. The vivid team spirit, the scientific discussions and enriched personal scientific research, led to a **publication in Nature Genetics, despite the methodological nature of its content**. At Harvard I also get the opportunity to expand my knowledge in non-statistics disciplines: biotechnology project management.
- From 2006 onwards, the emphasis temporarily is on exploring and mapping new trends and evolutions in Europe regarding statistical genetics. This focus, rather than carrying out pure methodological research at the fullest, is due to my 50% commitment as a project manager for the Ghent University to the European Network of Excellence GA^{2}LEN (www.ga2len.com) up until the end of 2007.
- The year 2008 is the start of a bioinformatics tenure track position at the University of Liège. As the only statistician at the department of Electrical Engineering and Computer Science (Montefiore Institute) I formulate the **mission to introduce statistical genetics in the research unit of "Systems and Modelling" and to start up a multi-disciplinary group** that can make significant contributions to disentangle the genetics of human complex diseases, hereby developing a **think tank for systems genetics and systems medicine**. Efforts focus on becoming tenured in 2011 (which I achieved).
- Because of the desired permanent position, courses followed during 2008-2010 are restricted to courses related to academic teaching (cfr. IFRES training and certificates). These courses supplemented past intensive WECOM (**wetenschappelijke communicatie**) training I had already taken in 2001.

Part III: Knowledge and competences in a professional context

III.1. My curriculum

Overview:

Identification employer	Start	End	Position	Full time/ part-time %
University of Liége – GIGA-R	1/1/2016	15/2/2018	**Director of GIGA-R Medical Genomics thematic research unit**	
University of Liége	1/10/2015	30/9/2019	**WELBIO researcher**	50% (research)
University of Liége – GIGA-R	1/1/2014	31/12/2015	**Director of Systems Biology and Chemical Biology (SB&CB) thematic research unit**	
University of Liège – Dept of Electrical Engineering and Computer Science	1/1/2008 1/1/2011 **1/1/2017**	31/12/2010 31/12/2016 **-**	Assistant professor Associate professor **Professor**	**100**
Catholic University of Leuven – Department of Biomolecular Medicine	1/5/2008 **1/10/2016**	20/4/2018 **30/9/2021**	(honorary) guest-professor **Professor (hoogleraar)**	**10**
Ghent University – Department of Biomolecular Medicine	1/10/2020	30/9/2025	(honorary) guest-professor	5
Ghent University – Dept of Medical Genetics	1/10/2008	30/9/2020	(honorary) guest-professor	5
Ghent University – Dept ORL	1/2/2008	30/9/2011	(honorary) post-doctoral researcher	10
Univeritair Ziekenhuis UZ Ghent; De Pintelaan 185, 5B2, 9000 Ghent	1/1/2006	31/12/2007	Post-doctoral scientific researcher (status: expert) – Project Manager GA2LEN Ghent University	50
Ghent University – Dept of applied mathematics and computer science	1/1/2006	31/12/2007	Guest Professor	50
StepGen cvba	**26/1/2006**	**31/1/2010**	**Co-founder and scientific director**	
Ghent University – FP6 project GA2LEN	15/6/2005	31/12/2005	Post-doctoral scientific collaborator – Project Manager GA2LEN Ghent University	100
Hasselt University - Censtat	1/9/2003	31/12/2007	(honorary) scientific collaborator	
Harvard School of Public Health – Department of Biostatistics, Boston MA 02115, USA	5/5/2003	31/5/2005	Post-doctoral fellow researcher on statistical genetics	100
Hasselt University (LUC – Censtat)	1/9/1999	31/5/2003	Post-doctoral researcher	100
Hasselt University (LUC – Censtat)	16/5/1999	31/8/1999	Scientific researcher	100
E.O.R.T.C (Quality of Life Unit) – Avenue Mounier 83, 1200 Brussel	16/11/1998	15/5/1999	Fellow statistician	100
Ghent University	1/9/1994	31/1/1998	Assistant Geometry	100

	1/2/1992	31/8/1994		50

III.2. Situating the most important evolutions in my knowledge acquisition related to professional activities mentioned in III.1.

a) Know-how 1: Logical thinking

Research topics in mathematics included:

Affine and Euclidean building theory
Finite geometry
Trees
(Algebraic) Topology

Conclusions in these domains are the result of pure reasoning, starting from a set of basic assumptions. My academic activities as a researcher in fundamental mathematics (from 1/9/1994 to 31/1/1998) mark a period of further development in logical and structural thinking.

Overview 3rd cycle educational training – Orientation Mathematics:

- Training ULBrussel, 10 1996 (3 lectures):
- Training RGhent University, 1994-95 (7 lectures).
- **D**(iscrete) **A**(lgebra and) **G**(eometry) –days (1993-1995).
- 3rd cyclus NFWO, KUL-Ghent University: Linear algebraic groups (1992-1993).
- 3rd Cyclus: Buildings UL/Brussel (1992-1993).
- Sommerschule Gebäude. Bielefeld University (Germany) 8-15 September 1991.

Reference Mathematics:

Prof Dr H Van Maldeghem
Vakgroep Zuivere Wiskunde en Computeralgebra
Ghent University
Galglaan 2
B-9000 Ghent
E-Mail: hvm@cage.ugent.be

b) Know-how 2: Biostatistics

Research topics in biostatistics include:

During and after my Master training in Biostatistics, I developed interst in the topics:

Coarsening
Complex data structures
Genetic epidemiology
Local influence

Missing data mechanisms and handling
Multicollinearity
Multiple testing
Multivariate modeling
Quality of life data
Statistical genetics

Overview 3rd cycle educational training - Orientation Life Sciences:

- ICES Course bio-informatics.
  Module 1: Ghent University 20 September, 3 October and 11 October 2001.
  Module 2: Ghent University 26 September, 18 October and 25 October 2001.
- Inference for mixed populations KULeuven 12-13 July 2001.
- Course: Advances in population-based studies of complex genetic disorders, Erasmus Medical Centre Rotterdam (The Netherlands) 26-30 March 2001.
- Course on "Handling Non-response", Southampton (UK) 17-19 May 2000.
- Course Medical Biology, Hasselt University, February 2000.
- Course Survey Methodology, Hasselt University, January-February 2000.
- SAS course on data step programming and macro writing (P. Meyvisch) EORTC 29 March - 1 April 1999.
- Course: Multivariate Statistics in Practice, Groningen University (The Netherlands) 24-27 November 1997.
- Course: computerintensieve methods in statistics (S+ environment) Hasselt University, 1997.

Reference Biostatistics:

Prof. Dr. Andreas Ziegler
Institut fuer Medizinische Biometrie und Statistik
Universitaet zu Luebeck
Ratzeburger Allee 160
23538 Luebeck
Germany
E-Mail: ziegler@imbs.mu-luebeck.de

c) **Know-how 3: Statistical genetics**

Research topics in statistical genetics include:

Components analysis and dimensionality reduction techniques
Data fusion
Data integration
Family-Based Association Testing
Gene-environment interactions
Gene-gene interactions and interaction graphs
Genetic heterogeneity
Genome-wide association analysis
Integrative analysis
Integromics
Kinship and genomic background
Multifactor Dimensionality Reduction strategies

Multi-locus or combined group approaches
Noisy or erroneous data handling
Omics meta-analysis
Phenocopies
Population stratification
Predictive disease models
Pre-screening algorithms and approaches
Simultaneous signficicance assessment
Winner's curse

Overview 3rd cycle educational training - Orientation Life Sciences:

- Webex training "Approaches to microbiome analysis", 16 May 2012.
- Workshop: Statistical analysis of genetic data in families, Leuven, Belgium, 11-15 August 2008.
- FAMHAP, Bonn, Germany, 6-7 June 2008.
- Good practice in DNA microarray analysis, Munich, Germany, 26-29 November 2007.
- 37th International training workshop on the use of GelCompar II and Bionumerics, Sint-Martens-Latem, Belgium, 25-26 September 2006.
- S.A.G.E. course: statistical analysis for genetic epidemiology; Department of Cardiovascular Diseases KUL, Belgium, 17-20 July 2006.
- SAS JMP genetics course; Department of cardiovascular diseases KUL, Belgium, 21-22 July 2006.
- Erasmus Summer Program at Erasmus Medical Centre Rotterdam (The Netherlands) 7-25 augustus 2006:
  - Genetic epidemiology of complex diseases (Cornelia Van Duijn – Erasmus MC Rotterdam, The Netherlands / Bertram Müller – Max Planck Institute Munich, Germany).
  - Introduction to genomics and bioinformatics (Cornelia Van Duijn – Erasmus MC Rotterdam, The Netherlands).
  - Searching genes of complex disorders (Ben Oostra – Erasmus MC, André Uitterlinden – Erasmus MC.
- Course Bar Harbor, 9-15 October 2003 "Short course on mathematical approaches to the analysis of complex phenotypes" , with topics including:
  - Complex trait analysis (Gary Churchill, The Jackson Laboratory) / Introduction to QTL mapping in model organisms (Karl Broman, Johns Hopkins University).
  - A missing data perspective on QTL mapping (Saunek Sen, University of California, San Fransisco).
  - Introduction to human genetic linkage (Josee Dupuis, Genome Therapeutics Corporation).
  - Issues in contemporary human genetic analysis: haplotype maps, bioinformatics tools, and novel statistical tools (Nicholas Schork, Univerisity of California, San Diego).
  - Experimental design for cDNA microarrays (Gary Churchill, The Jackson Laboratory).
  - Gene expression with signature sequencing (Natalie Blades, The Jackson Laboratory).
  - ANOVA methods for microarray analysis (Gary Churchill, The Jackson Laboratory) / Analysis of microarray time course data (Christina Kendziorski, University of Wisconsin).
  - Bioinformatics resources for complex traits (Carol Bult, The Jackson Laboratory).

<u>Reference Statistical Genetics and Precision Medicine</u>*:*

Prof Dr N Laird (emeritus)
Department of Biostatistics
655 Huntington Avenue
Building II 4th Floor, Room 447
Boston, MA 02115
USA
E-Mail: laird@hsph.harvard.edu

Prof Dr EK Silverman
Brigham and Women's Hospital
Department of Medicine
Channing Division of Network Medicine
75 Francis Street
Boston, MA 02115USA
E-Mail: ed.silverman@channing.harvard.edu

<u>Fundamental research at Montefiore (2008-):</u>

Details: III.3. Activities related to professional knowledge acquisition (other than education)

<u>Fundamental research at Harvard (2003-2005):</u>

Harvard School of Public Health, department of Biostatistics, Boston MA, USA :

start :   05/05/2003
end: 31/05/2005
purpose :   post-doctoral fellow researcher on statistical genetics

My tasks involved fundamental research. I was a member of several work groups to expand my know-how:

- Computing Work Group
- Environmental Statistics
- Gene-environment Interactions
- Psychiatric Biostatistics
- Longitudinal Data Working Group
- HIV Working Group

The Channing Seminar Series (organizer: Channing Laboratories at Harvard Medical School) were invaluable to translate practical problems into research ideas. These topics have largely determined my current activities as an advisor or researcher.

Research domains (2008-):

- During 2006-2007, I mainly focused on continued research on Asthma and Allergies with Harvard (School of Public Health and Channing Laboratories) and partners of the European FP6 network GA2LEN. My position in the project management gives me the opportunity to explore the scientific "genomics" landscape in Europe.
- Within 4 years after occupying the bioinformatics tenure track position at ULg, I assembled a group of three post-doctoral students at ULg, two PhD students at ULg, a PhD student co-supervised at Ghent University, a PhD student co-supervised at the Catholic University of Louvain, a PhD student co-supervised with CNIO (Madrid, Spain) / ULg.
- From 2011 onwards, and in parallel to the initial research line on epistasis, a second line of research emerges, now in the field of "integromics" (i.e., omics data integration). Since 2014, a third line of research is launched on patient subtyping and molecular reclassification, towards personalized/stratified medicine:
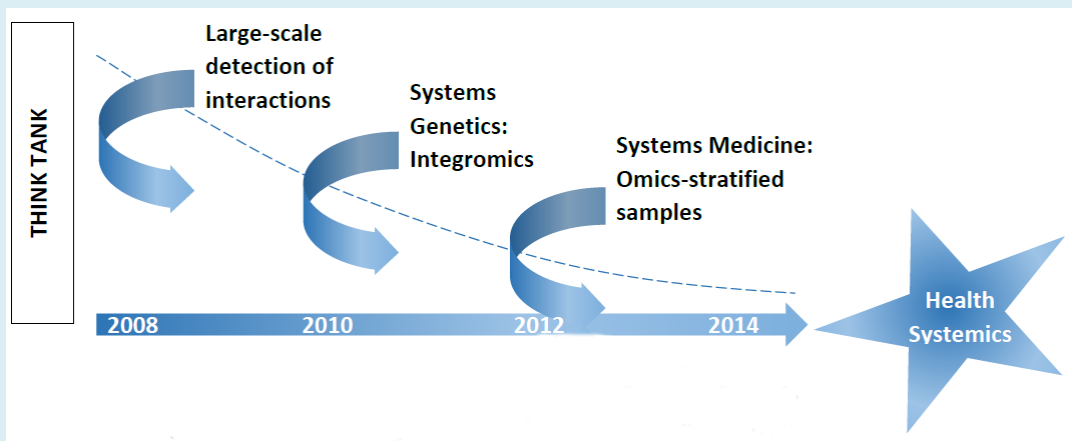
- In 2013 I decided to formally refer to my group as "BIO3", in order to better reflect that our research and offered training activities are situated **at the intersection of Biostatistics, Biomedicine and Bioinformatics**, and to **increase visibility and transparency (http://bio3.giga.ulg.ac.be/)**.

- Currently, BIO3 is part of GIGA-R (http://www.giga.uliege.be), from which BIO3 steers training, research and consult. I have been appointed director of GIGA-R Systems Biology and Chemical Biology (1/1/2014-31/12/2015) and of GIGA-R Medical Genomics (1/1/2016 – 31/12/2020), giving me the opportunity to reach out to external institutes, including the Maastricht Centre for Systems Biology (MaCSBio), towards developing a joint programme in **Systems Health or Health Systemics**.
- Throughout, **great care is taken in maintaining my scientific network** (see **III.4. c)**), **providing scientific advice to institutions in Belgium and abroad** (section **III.4. b)**), **and contributing to teaching at basic and advanced levels at ULg and in institutions in Belgium and abroad** (see **III.2. d)**).

d) Know-how 4: Education and development

<u>Teaching experience:</u>

- Teaching courses in different faculties and even at different universities is an important way to showcase acquired expertise, and is ideal to spot promising future interdisciplinary researchers.
- In particular, in my own area of systems genomics/systems medicine, I promote collaborative teaching that involves pushing the boundaries of one's own background disciplines. One example is the ULg course "GBIO0002: Genetics and Bioinformatics", for which I am the responsible. Whereas analytic aspects are covered by me, genetic aspects of the course are covered by Prof. Franck Dequiedt, who acts as co-teacher. The entire course is meant to be a synergetic interplay between both aspects.
- During the academic year 2015-2016, I developed several new courses which are strongly inspired by the principles of "Learning from Data". Within each course, students can choose between 2 thematic options.

At the University of Liège (ULg):

Ac. Year	Course code	Description (*)	Cycle
2015-	GBIO0030-1	Computational approaches to statitical genetics, 25h Th, 15h Pr, 35h Proj.	2
2015-	GBIO0031-1	Learning from genomic data, 150h Proj.	2
2014-	GBIO0002-1(**)	Genetics and bioinformatics, 30h Th, 30h Pr	1 + 2
2011-2012	MATH0062-1(***)	Eléments du calcul des probabilités, 15h Th, 15h Pr	1
2009-2012	MATH0008-2	Introduction to probability and statistics, 15h Th, 15h Pr	1
2008-	GBIO0009-1	Topics in bioinformatics, 25h Th, 15h Pr, 35h Proj.	2
2008-	GBIO0015-1	A tour in genetic epidemiology, 15h Th, 15h Pr, 60h Proj.	2
2008-2016	EPID0754-1	Introduction à l'épidémiologie génétique, 20h Th, 20h	2
2008-2009	ELEN0441-1	A tour in genetic epidemiology, 15h Th, 15h Pr	2
2007-2010	GBIO0001-1	Introduction au génie biomédical, 30h Th, 30h Pr	1+2

(*) Th: theory, Pr: practicals, Proj: project
(http://progcours.ulg.ac.be/cocoon/en/enseignant/U205435.html)
(**) Course responsible; co-tutor: F Dequiedt (genetics components of course)
(***) Shared course responsibility: L Wehenkel and K Van Steen

Other experience in teaching (advanced):

- Advanced summer school courses: **1) "Reductionism and complexity in the omics era", and 2) "Living in a world of interactions", as part of the Summer School "Genomic Medicine – briding research and the clinic" [Portoroz, Slovenia, May 2016]**
- COST Action BM1204 TRAINING SCHOOL "Statistical Interactions/Interactome" jointly organized with the Belgian Society of Statistics and CSCDA2016 [Antwerp, 2016]
- Course in Genetic Epidemiology (3ECT) in the "Masters Epidemiology" (UA) [20 hours during spring, since 2013]
- Block-course 1.4: Cancer, metabolic syndrome and chronic disease in "Master in Systems Biology" (Maastricht University). Course coordinator: I Arts / Project 1.2: Modelling life in "Master in Systems Biology" (Maastricht University). Course coordinator: R Westra [for both, co-teaching starts in 2016; curriculum adapts to needs and expectations];
- Lecture in the advanced course "Molecular Epidemiology of Chronic Diseases" entitled "Interactions and Human Variation", Maastricht, the Netherlands, 19 June, 2014
- Short course on "Scientific Communication" (oral and written communication, critical reading) at the 1st Marie Curie ITN Machine Learning for Personalized Medicine Summerschool in Tübingen, 23-27 September 2013.
- Lecture in the advanced course "Molecular Epidemiology of Chronic Diseases" entitled "Interactions and Human Variation",Genome-wide association interaction (GWAI) studies: mission impossible?", Maastricht, 18 April, 2013
- 7th SNU BIBS STOM workshop (Statistical Analysis of Omics Data): "Genome-Wide Association Interaction (GWAI) Studies", Seoul - South Korea, 23 February 2013
- Lecture in advanced course "Molecular Epidemiology of Chronic Diseases" Entitled "Travelling a world of interactions", Maastricht, April 23-27, 2012
- Lecture in short course "Epidem&OMICS: The "omics" era of cancer epidemiology" entitled "", Spanish National Cancer Research Centre (CNIO), Madrid, November 28-29, 2011
- Short course: Genome-wide association studies (with co-teacher Andreas Ziegler – University of Luebeck/Germany) – Brazil (Dec 2010).
- Short course: Gene-gene and gene-environment interactions – An overview of methods and available software, UMCG, Groningen – the Netherlands (8 May 2009)
- Short course: Family-based designs in genetic association studies, UVic – Spain, 30 June, 2008
- Short course: FBAT/PBAT course in Europe; Institute of Biology, Lille – France, March 30-31, 2005
- Short course: Using FBAT and PBAT to Analyze Family-Based Association Studies in Genetics; Harvard School of Public Health (HSPH) Boston – VS, January 24-26, 2005
- Short course: The Analysis of Family Based Association Studies in Genetics; Department of Medical Epidemiology and Biostatistics (MEB) Karolinksa Institutet, Stockholm – Sweden, March 24-26, 2004

Other experience in teaching (non-advanced):

- **Honorary invited teacher for "Genetic Epidemiology" in the Masters in Epidemiology track at the University of Antwerp (2012-2016)**.
- Teacher and responsible for courses in statistics (3rd Bachelor Dentistry; Medische Statistiek en Methodologie van Onderzoek, Ghent University, Ghent, Belgium (2006-2008).
- University teacher and responsible for Statistical Genetics, Master of Statistical Data Analysis, Ghent University, Ghent, Belgium (2005-2006; 2007-2008).
- University teacher and/or responsible for modules in statistics (2de Bachelor in Mathematics; "Kansrekenen en wiskundige statistiek", Ghent University, Ghent, Belgium 2005-2008).
- University teaching assignments for different modules in statistiek (Calculus for Statistics, Multivariate Techniques, Statistical Reading) Master of Applied Statistics Program Hasselt University, Diepenbeek, Belgium (1999-2002).
- Assistant for the practical training sessions in "analyse, lineare algebra en analytische meetkunde", Bachelor of Science Program, Ghent Univeristy, Ghent, Belgium (1993-1997).
- Assistant of introductory summer courses for students in civil engineering, fysics, mathematics and informatics: "meetkunde en algebra", Ghent University, Ghent, Belgium (1992-1996).

Involvement in PhD theses:

Supervision of 9 doctoral students since 2008 (±1 PhD thesis defense every 2 years)

- Ahmed Debit (Université de Liège); Tentative title: Integrated statistical epistasis networks – promotor; co-promotor: V Bours (GIGA-cancer) – ongoing (since October 2015).
- Benjamin Dizier (GSK); Tentative title: Machine Learning for Stratified Cancer Medicine (since September 2014) – stopped due to move from GSK to UCB, where he became director of the Experimental Medicine and Diagnostics Group.
- Ramouna Fouladi (Université de Liège) – ITN Marie Curie fellow; Tentative title: An -omics integrated flexible framework for interaction analysis - promotor (defense foreseen in 2018)
- Kridsadakorn Chaichoompu (Université de Liège); Title: Capturing fine-scale population structure – towards molecular reclassification of patients – promotor. Thesis defended 6 October 2017.
- Kyrylo Bessonov (Université de Liège); Title: From statistical to biological networks via omics integration – promotor. Thesis defended on 4 July 2016.
- François Van Lishout (Université de Liège); Title : An efficient and flexible software tool for genome-wide association interaction studies– promotor ; co-promotor : L Wehenkel. Thesis defended on 14 June 2016.
- Silvia Pineda (CNIO, Madrid, Spain / Université de Liège); Title: Statistical approaches for the integration of 'omics' and epidemiological data. An application to bladder cancer – promotor in co-promotorship with CNIO, Madrid, Spain. Thesis defended on 27 October 2015.
- Jestinah Mahachie (Université de Liège); Title: Genomic association screening methodology for highly dimensional and complex data structures - detecting n-order interactions – promotor. Thesis defended on 20 December December 2012.

- Jeroen Huyghe (Universiteit Antwerpen); Title: Identification of genes contributing to human complex diseases and traits in the genetically isolated Saami and the general European population - co-promotor. Thesis defended on 6 April 2011.

Expert consultant for 12 doctoral students since 2004

- Erwin Dreezen (Laboratory for Pharmaceutical Biology KULeuven); tentive title: Integrating disease progression modeling and population based pharmacokinetics to refine the optimal therapeutic window and stratify dosing of biopharmaceuticals used to treat inflammatory bowel disease patients (start date: 2014).
- Iris Detrez (Laboratory for Pharmaceutical Biology KULeuven); tentative title: Development, validation and clinical application of assas in order to perform blood concentration measurements of biological (start date: 2013)
- Gaëlle Pillault (Laboratory for Pharmaceutical Biology KULeuven); tentative title: Pharmacokinetic/Pharmacodynamic modelling of anti-TNF therapeutics (start date: 2013).
- Sylviane De Viron (VIV-ISP); tentative title: Public health genomics and smokingOngoing (start date: 2012).
- Lize Bollen (Laboratory for Pharmaceutical Biology KULeuven); tentative title: venous thromboembolism. Doctoral thesis defended in 2015
- Christine Breynaert (KULeuven); Topic: Tolaribility of altered infliximab infusion times in Crohn's Disease. Doctoral thesis defended in 2014.
- Marie Joossens (KULeuven); Topic: Gut microbiota in relation to Crohn's disease. Doctoral thesis defended in 2010.
- Ingrid Arijs (KULeuven); Topic: micro-array analyses of Crohn patients prior to and after therapy. Doctoral thesis defended in 2010.
- Lizzy De Lobel (UGent); Topic: Alternative methods to detect gene-gene interactions (start date: 2008).
- Peter Konings (KULeuven); Topic: Statistical and machine learning methods for genetype-phenotype correlation and association studies of copy number variations. (start date: 2008).
- Marieke Pierik (KULeuven); Topic: Susceptibility to inflammatory bowel diseases and pharmacogenetic predictors of treatment outcome in the Flemish population. Doctoral thesis defended in 2006.
- Olga Bijnens (Hasselt Universiteit); Topic: Het gebruik van cycloongas en staalgrit bij de "in situ" immobilisatie van metaalgecontamineerde bodems: een statistische benadering. Doctoral thesis defended in 2006.

Member of the PhD thesis jury of 16 students (since 2008)

- Yuanlong (INSERM, Paris, France); Topic: Development of network-based analysis methods with application to the genetic component of asthma". Thesis defended in November, 2017.
- Iryna Nikolayeva (Institut Pasteur, Paris, France); Topic: Network and machine learning approaches to dengue omics data. Thesis defended in October, 2017.
- Harland Chad Simeon (ULg); Topic: Mutation and recombination in the cattle germ-line : genome analysis and impact fertility. Thesis defended in September, 2017.
- Sarah Daakour (ULg); Topic: Perturbations of interactome networks in acute lymphoblastic leukemia: identification of EXT-1 tumor suppressor as a Notch pathway regulator. Thesis defended in March, 2016.

- Bryan Guillaume (UM, Maastricht, Netherlands/ Ulg); Title: Improving Group Inference for fMRI Clinical Trials with Task or Task-Free Designs. President of the jury. Thesis defended in September, 2015.
- Wanbo Li (ULg); Topic: Studying the genetics of Mendelian and complex traits with high-throughput genotyping and sequencing in cattle. Thesis defended in April 2015.
- Laura Grange (Institut Pasteur, Paris, France); Topic: Epistasis in genetic susceptibility to infectious diseases: methods comparison and developments, application to severe dengue susceptibility in Asia. Thesis defended in July 2014.
- Anne Collard (ULg) ; Topic : Traitement statistique d'images définies sur des espaces non linéaires et application à l'imagerie célébrale de tenseurs de diffusion. Thesis defended in September 2013.
- Vincent Botta (ULg); Topic:Apprentissage automatique appliqué à la génomique. Thesis defended in November 2013.
- Marenne Gaëlle (CNIO, Madrid, Spain); Topic: Statistical methods to combine SNP and CNV information in genome-wide association studies: an application to bladder cancer. Thesis defended in September 2012.
- SeptemberNovember François Schnitzler (ULg); Topic: Mixtures of Tree-Structured Probabilistic Graphical Models for Density Estimation in High Dimensional Spaces. Thesis defended in September 2012.
- Van Anh Huynh-Thu (ULg); Topic: Machine learning-based feature ranking: Statistical interpretation and gene network inference. Thesis defended in January 2012.
- **Carolien Bettens (Antwerp University); Topic: The genetic architecture of Alzheimer disease: in search of risk factors. Thesis defended in October 2010.**
- Hugues Aschard (INSERM, France; étudiant de Florence Demenais); Topic: Analyses multi-marqueurs et multi-phénotypes dans les études génétiques des maladies multifactorielles – exemple de l'asthme dans l'étude EGEA. Thesis defended in December 2009.
- Michel Journée (ULg); Topic: Geometric algorithms for component analysis with a view to gene expression data analysis (4 June 2009).
- Erik Quaeghebeur (UGent, Belgium; étudiant de Gert de Cooman); Topic: Learning from samples using coherent lower previsions — Leren uit monsters met coherente onderprevisies. Thesis defended in January 2009.

Member of the thesis (progress) committee of 8 doctoral students (since 2008)

- Arnaud Lavergne (ULg); Topic: Analyse du transcriptome des cellules pancréatiques et des gènes régulés par Pax6 chez les vertébrés. PhD student of Bernard Peers (start 2014).
- Alice Desbuleux (ULg); Topic: Towards a better understanding of genotype-phenotype relationships using networks biology. PhD thesis committee of student in Marc Vidal's lab (Boston). PhD student of Jean-Claude Twizere (start 2014).
- Iryna Nikolayeva; Topic: Integrative network analysis of dengue genome-wide association studies. PhD Thesis Advisory Committee member at Institut Pasteur, Paris, France (start: 2014).
- Wenric Stéphane (ULg - Sciences biomédicales et pharmaceutiques) ; Topic : Integrated multi-omics analysis of human cancer (start: 2013).
- Gaëlle Marenne (CNIO, Madrid, Spain); Topic: Statistical methods to combine SNP and CNV information in genome-wide association studies: an application to bladder cancer. Thesis defended in September 2012.

- Wanbo Li (ULg); Topic: Studying the genetics of Mendelian and complex traits with high-throughput genotyping and sequencing in cattle. Thesis defended in April 2015.
- Olivier Stern (ULg : Faculté des Sciences Appliquées - Electricité, électronique et informatique Sc. Ing.); Topic: Intégration de données génomiques et protéomiques et de banques de connaissances biologiques pour la découverte de biomarqueurs et la biologie systémique.
- Vincent Botta (ULg -Informatique Sciences); Topic:Apprentissage automatique appliqué à la génomique. Thesis defended in November November 2013.

Member of the ULg committee "diplômes d'études approfondies" (since 2008)

- Zhiyang Zhang (GIGA, Liège University); Title: Marker imputation with low-density marker panels in Holstein cattle (2009-2010)
- Vincent Botta (Ulg); Title: Prédiction du risque génétique par apprentissage automatique supervisé dans le cadre des maladies complexes (2007-2008)

Involvement in master theses:

Promotor or co-promotor at the University of Liège (since 2008)

- Arnaud Blanjean; Tentative title: Random Jungle for statistical genetics.
- Thomas Leysen; Tentative title: Efficient genome-wide two-locus epistasis testing in disease association studies (on Erasmus Exchange from ULg to University of Vic. Promotor at host institution: Malu Calle) (2010-2011)
- Jose Rial; Tentative title: Association testing in the presence of gene-gene interactions : MB-MDR compared to BOOST (on Erasmus Exchange from computer science at the University of A Coruña, in Spain, to ULg) (2010-2011)

Promotor or co-promotor at the University of Antwerp (Belgium)

- Leen Thielemans; Topic: Integrating existing multiple myeloma data sets to identify treatment-independent survival markers and new biological insights. Master thesis at UA, Antwerpen, Belgium. In collaboration and under a confidentiality agreement with Janssen Research & Development Oncology Biomarkers. Co-PhD advisor: Tine Casneuf from Janssen Research & Development, Belgium (2014-2015)

Promotor or co-promotor at Hasselt University (Belgium) - Master of Science in Biostatistics

- Marc Joiret; Topic: The Impact of Correlated Genetic Markers on Large-scale DNA-based Gene-Gene Interaction Studies – Internship of student at BIO3. UH responsible: Ziv Skhedy (2017-2018).
- Samuel Kawa; Topic: The effects of linkage disequilibrium in gene-gene interaction studies– Internship of student at BIO3. UH responsible: Herbert Thijs (2014-2015).
- Dominik Grathwohl; Topic: A Model-Based 40 to 1 Algorithm in Microarray Analysis. Thesis defended in 2002.
- Chris Muller; Topic: The EigenApples Approach. Thesis defended in 2002.
- Mbah Alfred Kubong; Topic: Growth of Dutch PKU Patients. Thesis defended in 2002.

Promotor or co-promotor at Hasselt University - Master of Science in Applied Statistics

- He Liang; Topic: Dealing with Discreteness: Confidence Intervals for Difference in Proportions. Thesis defended in 2002.
- Petra Goyens; Topic: Evolution and Effect of Trans Fatty Acids during Pregnancy. Thesis defended in 2002.
- Valerie Poulart; Topic: Checking for proportional hazards assumption in survival studies. Thesis defended in 2002.
- Maarten Borremans; Topic: The comparison of DNA sequences using a Mahalanobis-type distance measure: a sensitivity analysis? Thesis defended in 2001.
- Nahson Sigalla; Topic: Sampling Schemes for Large Units (co-supervisor). Thesis defended in 2001.
- Anthony Gichangi; Topic: Missing data in the health interview survey 1997. Thesis defended in 2000.

Jury member at the University of Liège - not promotor (since 2008)

- Geoffrey Salvoni ; Topic : Multivariate statistics for the joint analysis of quantitative maps (2017-2018)
- Quentin Garnier; Topic : Apprentissage sure des paires – application en bioinformatique (2014-2015)
- Liliane La ; Topic : Analysis of local field potentials recorded in rats during drug self-administration (2014-2015)
- Lionel Perpète; Topic: Inférence de régulations génétiques différenciéespar apprentissage automatique (2013-2014)
- Loïc Joine; Topic: Integration and validation of a wireless ECG on a cardiovascular ultrasound system (2012-2013)
- Thomas Wehenkel; Topic: Inférence contextuelle de réseau de régulation génétique par apprentissage automatique (2012-2013)
- Antonio Sutera ; Topic : Characterization of variable importance measures derived from decision trees (2012-2013)
- Marc Stroykov ; Topic : Prise en compte de la topologie pour l'inférence supervisée de graphes (2012-2013)
- Jean-Yves Nicolas; Topic: Identification de signatures multiples par ensemble d'arbres de décision (2010-2011)
- Arnaud Joly; Topic: Amélioration des forêts aléatoires dans le cadre de problèmes à très haute dimension. Thesis defended in 2010-2011
- Sébastien Roland; Topic: Prioritisation de gènes par ensembles d'arbres de decision (2009-2010)
- Aline Serteyn; Topic: Wearable ECG-monitor for real-time epileptic seizure detection (2009-2010)
- Stéphane Wenric; Topic: Complétion du réseau OMIM par apprentissage automatique (2009-2010)
- François Ghilain; Topic: Algorithmes de réduction de données transcriptomiques temporelles (2008-2009)

Stimulating ERASMUS (Lifelong Learning programme) collaborations and student exchanges:

ERASMUS

- Participating in « Programa de Doctorado de Epidemiologia y Salud Pública de la Comunitad de Madrid coordinado por la Universitad de Alcalá » in collaboration with Nuria Malats, CNIO Madrid, Spain. (signed in January 2014)
- Initiative taker of « Conventions bilaterals » between UPC and Ulg for 2008-2013 (signed in 2009).
- Initiative taker "Conventions bilaterals » between University of Vic and Ulg for 2008-2013 (signed in 2009).

DREAM

I was involved in the "DREAM" project which aims to give to Flemish schools and students the opportunity to experience life at ULg (2007-2013). Under the supervision of their teacher, students at the age of 16-19 years can have an encounter with a "DREAM witness". The exchange of information lasts for about 2 hours and can take place at the school of the students or at the work floor of the DREAM witness. More information at www.dreamday.be.

Fostering international student exchanges*

Who	Position	From	To	Status**
Milka Grk	PhD-student	Institute of Human Genetics, Begrade	BIO3 ULg (service de K Van Steen), Belgium	Under negotiation – Topic to be determined
	PhD-student	University of Hong Kong (Maggie Wang)	BIO3 ULg (service de K Van Steen), Belgium	Under negotiation – Topic: robust epistasis detection
	Phd-student	SNU, South Korea (Taesung Park)	BIO3 Ulg (service de K Van Steen), Belgium	Under negotiation– Topic: Creating a GPU version of MB-MDR
	Post-doc student in statistics	Univerity of Göttingen (H Bickeböller)	BIO3 Ulg (service de K Van Steen), Belgium	Under negotiation- Topic: Kernels for integrating large-scale omics data
Marc Joiret	Master student	University of Hasselt (Z Skhedy)	BIO3 Ulg (service de K Van Steen), Belgium	OK (2017) - Finished
Mélanie Fernández Pradier	Phd-student	UC3 Madrid (Fernando Perez-Cruz)	BIO3 ULg (service de K Van Steen), Belgium	OK (May – June 2016) Stochastic modeling and graphical models for the analysis and prediction of phenotype interactions / Indian buffets – Marie Curie ITN MLPM secondment

Cristóbal Esteban	Phd-student	Siemens Germany (Volker Tresp)	BIO3 ULg (service de K Van Steen), Belgium	OK (September – December 2015) Marie Curie ITN MLPM secondment on Learning Decision Support for Personalized Medicine
Menno Witteveen	PhD student	ETH Zürich, Karten Borgwardt lab	BIO3 ULg (service de K Van Steen), Belgium	OK (2014) – short stay in November 2014 OK (April -June 2015) Marie Curie ITN MLPM secondment:
K Bessonov	Phd Student	BIO3 ULg (service de K Van Steen), Belgium	Institut Pasteur, Paris, France (Anavaj Sakuntabhai)	OK (in 2014 + 2015) – Topic: Cis-trans epistasis accountance in integrated networks
R Fouladi	PhD student	BIO3 ULg (service de K Van Steen), Belgium	Mines ParisTech (J-Ph Vert) Pharmatics (Felix Agakov)	OK (2014) Kernels for sequence analysis (Marie Curie ITN MLPM secondment) (OK (May-June 2016) – secondment Marie Curie ITN MLPM
Samwel Kawa	Master student	University of Hasselt (H Thijs)	BIO3 Ulg (service de K Van Steen), Belgium	OK (2014) – Finished
Silvia Pineda	PhD student (cotutelleà	CNIO, Madrid, Spain	BIO3 Ulg (service de K Van Steen), Belgium	OK (2014) – Finished
Iryna Nikolayeva	PhD student	Institut Pasteur, France (A Sakubanthai)	BIO3 Ulg (service de K Van Steen), Belgium	OK (2014) - Finished
F Gadaleta	Post-doc	BIO3 Ulg (service de K Van Steen), Belgium	Univerity of Göttingen (H Bickeböller) INTEGROMICS, company in Spain	OK (2014) Topic: Speeding up kernel methods for GWAs OK (2014)- Finished
Carl Johann Simon-Gabriel	PhD student – Marie Curie	Max Planck, Tübingen, Germany (Karsten Borgwardt)	BIO3 ULg (service de K Van Steen), Belgium	OK (2014) - Finished
K Chaichoompu	PhD student	BIO3 Ulg (service de K	Institut Pasteur, France (A Sakubanthai)	OK (2014) – Finished

		Van Steen), Belgium	IPATIMUP, Portugal (Luisa Pereira)	Under negotiation Topic: Epigenetics to explain population stratification
Laura Grange	PhD student	Institut Pasteur, Paris, France (A Sakubanthai)	BIO3 Ulg (service de K Van Steen), Belgium	OK (2014) - Finished
E Gusareva	Post-doc	BIO3 ULg (service de K Van Steen), Belgium	INSERM genetic epidmiology unit, France (F Demenais)	OK (2014) - Finished
F Van Lishout	PhD Student	BIO3 ULg (service de K Van Steen), Belgium	Darthmouth Geisel School of Medicine, USA (J Moore)	OK (2013) - Finished

* **Several former members of BIO3 are still official honorary collaborator to the group** (agreement via legal office). **This allows them to further continue their activities, including contributing to initiated projects or pursue further training in systems genetics or systems medicine.** Examples of such members: Fentaw Abegaz, Elena Gusareva, Jestinah Machachie John, Kris Chaichoompu, Kirill Bessonov. For the BIO3 team composition, see Section **III.3. a)**).

**OK = formal arrangement made or exchange already took place

Realization of supervised self-study and development of didactical tools:

> During my professional activities I have been giving both basic and specialized courses. Self-study became increasingly important. This explains my search for alternative educational tools that stimulate self-study, and simultaneously allow for fast detection of problems and implementation of remedial measures.

- I have had a shared responsibility in work package WP 1.1. of the Global Allergy and Asthma European Network GA2LEN with the Charité (Germany), in particular for the part on *e-learning and e-testing*. In order to create an extensive compendium of useful material, I worked out new goals for the 4th work year of GA2LEN on e-learning and e-testing and created the basis for an Instructional Design template to be used for pre- and post-testing knowledge during future GA2LEN Allergy Schools. A reflection of aforementioned activities is highlighted in the publication "Education via E-testing" in GA2LEN News – Spreading excellence in allergy and asthma, nr 10, devoted to "Creating excellence through education & training" (http://www.GA2LEN.net//files_new/filesPublic/Publication_GA2LEN%20News10.pdf).

- *Students' dean*: Together with Prof B Müller-Myhsok (Max Planck Institute, Munich), I have been acting as students' dean in the Marie Curie Initial Training Networks (ITN) MLPM-ITN-2012 call (Call: FP7-PEOPLE-2012-ITN). Tasks included: i) giving the students a voice in the ITN supervisory board (besides the student representative), in particular on the quality of training by research and by summer schools in the ITN, ii) monitor that all partners commit to equal opportunity (e.g., in gender questions) and adequate working conditions for the

ESRs and iii) act as mediator in cases when controversies between advisor, PhD committee and ESR arise.

- Based on my experience in GA^{2}LEN and "***Learning from Data***" (a programme in Problem-Based Learning I was asked to work out at the Hasselt University for the Masters Programmes in Applied Statistics/Biostatistics and Prof. Herman Callaert, in close collaboration with an expert group in Maastricht), I worked out an exciting high-quality training programme within the new consortium "TranSYS" I created in 2016-2017 ("TranSYS": a new ETN proposal coordinated by me, within MSCA-ITN-2018).

Reference Education:

      Prof Dr J A Thas
      Vakgroep Fundamentele en Computergerichte Wiskunde
      Ghent University
      Galglaan 2 B-9000 Ghent
      E-Mail: jat@cage.ugent.be

Reference E-learning for GA^{2}LEN:

      Prof Dr T Zuberbier
      Charité - Universitätsmedizin Berlin
      Klinik für Dermatologie, Venerologie und Allergologie
      Charitéplatz 1
      D - 10117 Berlin
      E-Mail: torsten.zuberbier@charite.de

Participation in committees and working groups with respect to education:

- **Training Advisor to the 2018 ITN MLFPM**: responsible for all issues related to the training in the network. She monitors the quality and transparency of the recruitment process, as well as the organisation and the quality of joint training events (in particular summer schools and closing conference). I also see to the participation of all ESRs in the training events, the completion and updates of all individual career development plans, and the implementation of the secondments. If difficulties occur with the organisation or conduction of a planned secondment, my tasks consists of providing support and proposing solutions.
- **Consultant for new Graduate Program of GIGA**, as member of GIGA Board of Directors (2017-2018) [realized via several private brainstorming discussions with Marianne Bevova].
- **Member of the initial Study Programme Committee for the Masters in Systems Biology (organized at the Univerity of Maastricht and accredited since 2015-2016).** The Committee monitors the quality of education of the master in Systems Biology and advises the Dean of the Faculty on the Education and Examination Rules, the Course Catalogue and all other relevant educational matters, on request or on personal initiative. Also it reviews the course evaluations and provides feed-back to the course and project coordinators. The

Study Programme Committee comprises of the Scientific Programme Director (FHML), three staff members (UM- FHS/ FPN, ULg) and four student members.

- **Initiator to present a novel type of hands-on courses in the faculty of Applied Sciences (ULg) [informatics, bioinformatics, biomedicine] in the spirit of "Capita Selecta in Problem Solving"**. "Problems" include "network construction", "network inference", "epistasis detection using SNPs", "interaction detection using integrated data". Result in 2015: I set up a new series of courses offered by the Faculty of Applied Sciences, coordinated by K Van Steen (e.g., GBIO0030, GBIO0031).
- Co-brainstormer during the development phase of a novel Master in Global Health in Flanders (contact: Niel Hens, Hasselt University)
- Initiator of a task force to introduce novel courses in the faculty of Medicine (ULg), Public Health, which can serve as stand-alone courses or can be inserted as part of existing courses. The courses are organized around 4 components: "problem identification", "data collection and quality control", "selection of the appropriate analytic tool", "analysis and interpretation". The courses cover a range of analytic tools, varying from "multiple regression" to "survival analysis". Contact person: Olivier Bruyère.
- Participation in "Education Conference" organized by KUL LOKO: module "Leren in hoorcolleges, kan dat? Gesprek tussen partners: professoren & studenten" [motivation: brainstorm about ideas to enhance the educational value of teaching in front of large groups of students]
- External consulent for Bioinformatics and Systems Biology (coordinated by R Westra – Unversity Maastricht, the Netherlands) to compose the programme content (2012-)
- Task force group to reorganize Probability / Statistics / Stochastics in the Bachelors of the Engineering curriculum (2011-2012)
- Work group to create a new "Masters in Epidemiology" at Antwerp University (responsible for programme item "Genetic epidemiology"). Start of group activities: 2010; Accepted start of Masters Programme: academic year 2012-2013
- Initiator of Educational Work Group between the University of Maastricht (R Westra) and the University of Liège concerning giving guest-lectures within the corresponding existing bioinformatics programs and beyond. Practical start: academic year 2010-2011
- Secretary of Educational Board – Biomedical Civil Engineering (Ulg; 2008-)
- Member of AIM, Association des Ingénieurs de Montefiore (2008 -)
- Learning from data project: coordination of practical implementation, Hasselt university in close collaboration with University of Maastricht, the Netherlands (2002)

e) **Know-how 5: Communication and knowledge dissemination**

Dissemination of research and science:

- Via involvement in GA^{2}LEN, in particular WP 1.1
- Via research activities
- Via involvement in BioScope-IT, a FlandersBio's Bioinformatics Service Project to reduce the gap between Flemish biotech companies to implement bioinformatics applications.

Press reports of scientific research, targeting a non-scientific audience:

- "In Utero Smoke Exposure and Impaired Response to Inhaled Corticosteroids in Children with Asthma." (Ulg REFLEXIONS, February 2011)
- "'StepGen' nieuwe spin-off " (Maandblad Gent Universiteit, June 2008).
- "UGent lanceert nieuwe medische spin-off' (Trends, 17 April 2008).
- " 'StepGen' nieuwe spinoff van de UGent" (UGent Press Release / Technologie Transer, 9 April 2008).
- "Statistical method provides unprecedented look at genetic underpinnings of complex diseases" – appeared in Harvard School of Public Health Press Releases, after an interview by Christina Roache of the HSPH press department with Dr C Lange and myself.
- "Een massa gegevens" - appeared in Knack, Mens & Cultuur 3, nr 28-29, 13 - 26 July 2005. This publication was composed by D Draulans on the basis of a text proposed by myself.

Overview 3rd cycle educational training – Orientation Communication:

- Advocacy workshop on developing the basic skills of doing advocacy and lobbying work (Miriam Stein, lobbyist with Cooperative Metropolitan Ministries) Newton (USA) 16 May 2005.
- Biotechnology project management, spring term course organised by the Harvard Extension School and the Massachusetts Biotechnology Council, 2005
- Inter-university doctoral training: Wecom – orald and written scientific communication, Hasselt University, 2001.
- Interculturele Communicatietraining, Hasselt University, 6-7 September 2001.

Reference Biotechnology Project Management:

Lydia Harris, MGA,
Co-Chair of the Project Management Committee,
Massachusetts Biotechnology Education Foundation,
Massachusetts Biotechnology Council.
E-Mail: lydia_harris@massbio.org

f) Know-how 6: Creating a culture of innovation

I was a **co-founder and the scientific director of** an SME (2006-2010) that offers service in statistics, in particular in biostatistics, statistical genetics and genetic epidemiology. Since December 2007, this SME has been acknowledged as an official **spin-off of the Ghent University**. In 2008, StepGen also became an official "collaborating centre" to the European EU funded network of Excellence GA^{2}LEN.

Building upon the expertise acquired in StepGen, lobbying activities were set up at ULg and with Dr Michael Rossbach from the Singapore Human Genome Center. These resulted in a draft business plan that can serve as a template to create a new spin-off with two poles, one in Europe and one in Asia. The focus is on omics integration for personalized medicine. The framework envisages a **high-throughput pipeline service from raw samples to end product**, in close collaboration with other service providers and pharmaceutical companies. Once global economic stability has returned, we envisage to revise these plans and to implement them.

In 2014, I started investigating the possibility to **patent the methodology behind the C++ software MB-MDR** (contact person: Anne-Stéphanie Adibime, Ulg). This software tool was developed in my group and implements most analytic strategies on epistasis detection that my group worked out and validated. The follow-up of these activities are incorporated as integral part of recently obtained WELBIO grants (DEST*in*CT and 2-DEST*in*CT).

Also in 2014, I agreed to officially closely follow the **iPhi-Pod project** (convention nr 1217600), as part of the First Spin-off program. The project aims to **develop the necessary devices and infrastructure to give ownership to patients of their medical history**. Being able to access this information, at any time, at any place, in several languages, may be the difference between life and death in emergency situations. The project allowed adding on innovative methodologies to analyse or visualize the data and hence closely connecting to ongoing research activities in my BIO3 team.

As part of an international collaboration, my team contributed to the statistical analysis for the identification of airway disease subtypes via expired air profiles. In 2017, this led to a **European patent** application (patent ref. EP 3 143 930 A1), in collaboration with the University Hospital of Liège, Pneumology-Allergology, Prof. Renaud Louis and Florence Schleich: "Method for the diagnosis of airway disease inflammatory subtype". In 2018, we also submitted a **US patent application** (ref. P75696US0).

g) Know-how 7: Corporate thinking

At an international level I have established a network of researchers, with varying backgrounds, to tackle problems related to gene-environment or gene-gene interactions large-scale screening and systems medicine, as well as to assess the impact of biological and genetic (integrated) networks to disease development. It is my strong belief, and the belief of those in the virtual network, that these types of problems can only be dealt with when gears are shifted and when different viewpoints are synergetically merged.

In 2010, my virtual network led to an FP7 consortium COMED (consortium on omics for better medicine) in Europe, bringing together top-notch researchers in medicine, genetic epidemiology, statistical genetics, genomics and bioinformatics. It also led to several Transatlantic working groups. One such group has been the Gene-Environment working group to catalogue gene-environment detection methods, to identify niches for future research, and to form subprojects tackling subproblems. Activities within this working group resulted in an invited article submission under my guidance: "Challenges and opportunities in Genome-Wide Environmental Interaction (GWEI) studies". Another such group is the STRATOMIX working group, dealing with challenges and opportunities related to omics-stratified precision medicine.

h) Know-how 8: Project management

During my stay in the US I took the Biotechnology Project Management course at the Harvard Extension School. Whether it is a large or a small project, good management is a determining factor for its success. The course focused on identifying and understanding responsibilities, activities and competences that are required for excellent project management in a biotech environment. Topics included: drug development, regulatory bodies, project life cycle, group structures and leadership, problem solving

techniques, communication skills, project monitoring, project closure. During the course of my career I have had ample opportunity to bring theory into practice (for instance, GA^{2}LEN, FP7-ICT-2009-6, FP7-HEALTH-2009-2.1.1-3, COMED, …).

Overview 3rd cycle educational training - Orientation: Management:

- FP7 competitive writing, KUL 2009
- ERC grant applications, KUL 2009
- EU preparatory course (http://www.e-t-i.be/eu_concours.asp) 2008
- Biotechnology project management, spring term course jointly organized by the Harvard Extension School and the Massachusetts Biotechnology Council, 2005

Reference:

Prof Dr P Van Cauwenberge (emeritus)
Former Rector Ghent University
Sint-Pietersnieuwstraat 25
B-9000 Ghent
E-Mail: Paul.VanCauwenberge@UGent.be

III.3. Activities related to professional knowledge acquisition (other than education)

a) Scientific animation in a research group

<u>Life and organization of research @ BIO3:</u>

BIO3's spirit

BIO3's spirit is templated on the Broad Institute's new way of doing science, empowering this generation of researchers to:

- **Act nimbly:** Encouraging creativity often means moving quickly, and taking risks on new approaches and structures that often defy conventional wisdom [www.creativityatwork.com].
- **Work boldly:** Meeting the biomedical challenges of this generation requires the capacity to mount projects at any scale — from a single individual to teams of hundreds of scientists.
- **Share openly:** Seizing scientific opportunities requires creating methods, tools and massive data sets — and making them available to the entire scientific community to rapidly accelerate biomedical advancement.
- **Reach globally:** Biomedicine should address the medical challenges of the entire world, not just advanced economies, and include scientists in developing countries as equal partners whose knowledge and experience are critical to driving progress

Short-term goals of BIO3 are:

- **Sharing** – open policy of sharing within the team
- **Multitasking** – do not bet on one horse
- **Networking** - collaborate with those from whom you can learn
- **Keeping standards high** – SOPs, replication
- **Enhancing team dynamics** – conversations, talent review and training

Composition of BIO3*:

hD Student	Post-doc	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	Nationality	Background	
																			Year
Vanessa De Wit		X	X														Belgian	Engineering cell and gene biotechnology	Research Fellow at Laboratory for Pharmaceutical Biotechnology; Scientific Institute of Public Health
	Tom Cattaert	X	X	X	X	X											Belgian	Physics, Biostatistics	Data Scientist at P95 (consultancy business in consulting business in epidemiology and pharmacovigilance)
Jestinah Mahachie		X	X	X	X	X	X										Zimbabwean	Biostatistics	EORTC fellow; Johnson & Johnson; Veramed (GSK, J&J); Senior Biostatistician at GCE Solutions (UK CRO and IT business solutions provider)
	Elena Gusareva				X	X	X	X	X	X							Russian	Biology, Genetics, Cytology	Microbial ecology research fellow at SCELCE (Singapore Center for Environmental Life Sciences Engineering)
François Van Lishout				X	X	X	X	X	X	X							Belgian	Software engineer	Post-doctoral researcher in artificial intelligence at ULg; project manager
	Bärbel Maus				X	X	X										German	Statistics	Senior statistician at Medtronic (NL - world's largest medical device company)
Kirill Bessonov						X	X	X	X	X							Canadian	Biochemistry, Biotechnology, Bioinformatics	Bioinformatician and NGS software developer / researcher at Public Health Agency of Canada
Silvia Pineda							X	X	X	X							Spanish	Statistics	Postdoc at the University of California, San Francisco (UCSF)
	Francesco Gadelata						X										Italian	Computer engineering, Artificial intelligence	Post-doc Human Genetic KULeuven; Advanced Analytics Team of Johnson&Johnson; Abe AI (AI-Powered Banking Solutions); Co-founder of fitchain.io the decentralised machine learning factory; Director at Amethix Technologies amethix.com (pharma/finances business solutions using e.g AI)
Ramouna Fouladi							X	X	X	X	X	X					Iranian	Electrical engineering (telecom., biomedical), bioinf.	Product Analyst at Restore – a Centrica business solutions company
Kris Chaichoompu							X	X	X	X	X						Thai	Computer engineering	Post-doctoral staff scientist Max Planck Munich

Name		Nationality	Expertise	Position
Benjamin Dizier		Belgian	Molecular biology, Experimental medicine and diagnostics	Director of Immunology Translational Medicine at UCB (UK/Belgium)
	Ahmed Tawfik	Egyptian	Computer and systems engineering, computer science	Post-doc at Institut Pasteur (Parisian world famous dengue/malaria lab of Anavaj Sakuntabhai)
Ahmed Debit		Algerian	Engineer Informatics, Bioinformatics and modelling	
	Fentaw Abegaz	Ethiopian	Statistics, Statistical genomics	Post-doc researcher at Probability and Statistics Univ of Groningen
Myriam Nemry (scientist programmer)		Belgian	Computer science, Programming	
	Archana Bhardwaj	Indian	Bioinformatics, Comput. biology, Plant biology	
Israt Jahan		Bangladesh	Biostatistics	Lecturer at University in Bangladesh
	Sandra Negro	Belgium	Biologist, Agricultural Genomics	
Diane Duroux		France	Statistics and Bioinformatics	
Aldo Camargo		Peru	Computer Science, Programming	
Junior Ocira		Uganda	Data science, Biostatistics	
	Ahmed Tawfik	Egypt	Computer and systems engineering, Bioinformatics	

Bottom counts: 3 3 3 5 6 9 8 9 10 7 9 6 5 2 1

*Since 2017, efforts are made to create a another pillar of BIO3 outside ULg, namely at the Center of Human Genetics at KU Leuven. These efforts mainly focus on **attracting top PhD students, via the instrument MARIE SKŁODOWSKA-CURIE INNOVATIVE TRAINING NETWORKS – ETN, and in particular the proposal "TranSYS" I submitted as coordinator in January 2018.**

Each member of my team is involved in 3-5 projects at a time. These projects have components that are unique to the interests ad expertise of the team member, but also have components that require collaboration with at least one other team member. The large number of projects in which my team is involved, imposes special needs in project management. In practice, in the past I have invested in tools such as Wrike to manage all aspects related to projects: internal and external milestones and deliverable due date, (dependencies) relationships between projects, human resources available at any time during the lifetime of the project, when new funding must be acquired to ensure the maintenance of research themes, etc.

BIO3's strengths are the international and interdisciplinary composition of the team (see foregoing table) and having established an environment of openness. Forming "bioinformatics subgroups", ideally consisting of at least 3 team members who have something to offer with respect to a) biology, b) informatics and c) statistics, allows approaching problems from different angles and enhances the initiation of truly novel methods. Obviously, being able to form such subgroups is conditional on the constitution of the team. However, it has already shown to be very beneficial in my group BIO3: it not only speeds up the project work (e.g., field-specific language problem can more rapidly be resolved), but it also helps young researchers to learn how to keep their own identity and how to profile themselves in an interdisciplinary context, while still being surrounded by a comfortable and protective environment.

Creating a critical mass:

So far, all of my mentors from the past have told me that establishing a minimal critical mass of (at least) 1 permanent position in the team is critical for the optimal functioning of it and in order to be competitive with top institutions. It also ensures continuity in terms of "operations" and "consulting". Since 2008 I have been trying to build up such a critical mass, without success, because of the worsening economic situation at my institution and a shrinking number of available research positions in the region between 2008 and 2016. However, I have put the following measures in place to temporarily deal with this problem:

- After 1 year in BIO3, each post-doc in my group is assigned one or two **managerial tasks**. This task may relate to "Consultancy", "Operational" (for instance enhancing communication and information exchanges within the team), "Big Data", "Computational Needs", and "Special Events" management, depending on the the person's background and his/her talents. Detailed task descriptions are available via the team's shared repository and WordPress site.
- I have experienced that a team works much more efficiently when there is a clear structure in the operational functioning of it, so that everyone can take up his/her responsibility and is aware of good common conduct and general expectations within BIO3. I have put in place a "semi-automated" system for operational functioning, via for instance WordPress and a growing number of SOPs that are securely stored under a "virtual super-user" to which any team member can link.
- **Life at BIO3 is dynamic, and hence all aspects are discussable in the team at any moment**.

A genuine weakness in the BIO3 team is that the team does not have a dedicated technical assistant to take care of issues related to the IT infrastructure or software management. Efficient problem-solving (e.g., accessing clusters within ULg and outside ULg, adapting programming code to be applicable to particular computer environment) largely depends on the availability of IT knowledge at the post-doctoral level. Unavailability of this knowledge in the past has caused huge delays in producing deliverables in time. The situation has improved to some extent by physically moving to the GIGA premises, which has fostered discussions between my team and other teams who experience similar problems and which has opened up new avenues towards creating sustainable solutions in the future.

Research dynamics:

Internally, in my group, the strategy to achieve research-related objectives is "**find motive, seek opportunity, develop means**". The strategy is implemented in an open atmosphere of "sharing expertise and knowledge" and "promoting" research at the national and international level via an extensive number of collaborative efforts. Research discussions are held in vivo or via Skype and alternative web-based platforms such as GoToMeeting.

Group dynamics and feed-in of novel ideas is accelerated via regular research meetings within BIO3 or at the GIGA:

- **Brainstorming meetings**
  - These are kept limited to twice a month, max 90 minutes each.
  - At the start of each meeting a "secretary" is identified. This person takes notes / minutes (electronically). By doing so you one learns how to report about topics that are out of one's comfort zone…
  - Each team member uses Wordpress posts /presentations to explain in 10 minutes the progress of the past two weeks (incl points out new posts). This facilitates using Wordpress as a communication channel and knowledge repository. During half an hour, one team member explains a particular problem in more detail. This problem is discussed in the group. The presenter is identified at the previous team meeting.
  - Everyone should complete his/her agenda points, following a fixed template (https://drive.google.com), sent around by a team member, who will twice a year (in June and in December) move all team meeting agenda's and minutes to the team's "shared folders". The template foresees items related to administration, research and education. Although research meetings will only handle the research related aspects, the provided items will be used by the PI to take further actions regarding educational or administrative issues. Each research team meeting will end with a 10 minutes skimming over these items, after which action points are identified (and reported by the secretary) and the meeting is closed.

- **Medical Genomics – section BIO3 meetings**
  - Research highlights: a 45 min presentation about a team member's research or research by an invited speaker (approx. 6 a year; between March-May and Oct-December)
  - Journal clubs: a 45 min presentation of papers relevant to a particular (sub)topic of a team member's research (approx. 6 a year; between March-May and Oct-December
  - These events are reported on the Medical Genomics google calendar created by BIO3. All PI's within the GIGA Medical Genomics unit or designated persons are able to access this google calendar and to add events of joint interest.

Creating an environment that stimulates growth:

Growing as a researcher, in my view, goes beyond expanding one's knowledge about a particular topic. Ultimately, BIO3 aims to shape researchers that meet modern requirements about skills, competences and abilities, as imposed by potential future employers:

- managerial and leadership skills
- the ability to communicate with the public
- the ability to connect with foreign colleagues in networks
- administration of projects
- dealing with and understanding political circumstances
- negotiating with business partners
- cultural understanding

In order to assess whether BIO3's aims have been met, I have put a series of **evaluation tools** in place: guiding questions to (self-) evaluate the progress of a team member. **Once a year or upon request of the team member, the results of a(n) (self)-evaluation can be discussed**. For examples, see **Appendix 1**.

Life and organization of research @ GIGA-R Medical Genomics:

Stimulated by the positive reviews on my team's management (see **Appendix 1.a**)), I took the lead over the GIGA-R Systems Biology and Chemical Biology research group in January 2014. The university's instituational reorganization in 2015-2016 led to a decomposition of this unit and in fact its diseappearance. Since January 2016, BIO3's new home is the GIGA-R Medical Genomics Thematic Reseatrch Unit.

As a director, the following action points are listed high on the priority list:

- to increase the synergy between PI's in the Medical Genomics unit
- to investigate the possibilities for a longer-term strategic plan in the context of understanding biology of disease, developing and offering large-scale omics analyses techniques, and valorizing research towards improved global, public and personalized health,
- to explore the options of creating a virtual Systems Biology group at ULg, embracing multiple disparate groups with explicit links to systems genomics or systems biology. Given the evolutions in our neighbouring countries (including the Netherlands and Luxembourg) there is a clear need for such a highly visible platform, not exclusively focusing on human health.

b) Participation at international conferences and symposia

> - I highly appreciate interdisciplinary collaboration. Since 2002, more than 100 abstracts have been submitted and accepted, for which no publication information is available. Since 2000, I have more than 150 accepted abstracts (as first, last, or contributing author) that have resulted in publications other than articles (see also the following Section **III.3. c)**).
> - In recent years, I have mainly been involved in international conferences that cover aspects of the analysis of rare or complex diseases, in the context of modern genetic epidemiology, systems genetics and personalized medicine.

Conference Name*	Town	Country	Date	Participation
BIT's 9thWorld Gene Convention-2018	Singapore	Singapore	13-15/11/2018	Invited oral presentation
Benelux **Personalized Medicine Forum** (PMF)	Utrecht	The Netherlands	12-13/6/2018	Invited oral presentation
INSERM Workshop 248: Use of next generation sequencing data in the study of human diseases: **statistical methods and applications**	Bordeaux	France	27-29/9/2017	Invited oral presentation
ECML PKDD 2017	Skopje	Macedonia	20-24/9/2017	Invited oral presentation at DLPM 2017 workshop on (**Deep Learning for Precision Medicine**)
DDTWC 2017	Boston	USA	6-15/7/2017	Track Chair + invited oral presentation
ESHG 2017 Annual Conference	Copenhagen	Denmark	27/5-1/6/2017	SPC + **chair educational session E13 (Network Medicine) + Workshop organizer and moderation (Big Data)**
ICG 2017	Xi'an	China	23-30/4/2017	Invited oral presentation
COST CA15120 meeting	Porto	Portugal	19-21/2/2017	Representing WP leader (as co-leader): activity report, past –

				present – future of the WP
ITN MLPM Closing Event	Munich	Germany	19-21/10/2016	Node presentation; Board meeting: the future of MLPM; preparation of follow-up Marie Curie proposal
Max-Planck Section Symposium on Complex Trait Genetics	Berlin	Belgium	6-7/10/2016	Oral presentation - invited
ITN MLPM Annual Conference	Barcelona	Spain	21-24/5/2016	Workshop moderator and chair
ESHG 2016 Annual Conference	Barcelona	Spain	19-20/5/2016	SPC + **chair educational session E08 (Clinical interpretation of genetic variants) + Workshop organizer and moderation (Big Data)**
Summer School Genomic Medicine	Portoroz	Slovenia	3-7/5/2016	Presenter (2), Chair (2)
In-FLAME Annual Meeting	Maastricht	the Netherlands	1-3/4/2016	Presenter at the Systems Biology Workshop
First joint meeting Belgian Society of Human Genetics and Nederlandse Vereniging voor Humane Genetica "Genetics & Scoiety"	Leuven	Belgium	4-5/2/2016	Society member, European Society of Human Genetics SPC member
Combined EFISDS & EPC Meeting "Burning issues in pancreatology"	Cluj	Romania	6-7/11/2015	Oral presentation (invited) and session chair
COST BM1204 Annual Conference	Cluj	Romania	5/11/2015	WG2 presentator on omics integration in PDAC
ASHG 2015	Baltimore	USA	6-10/10/2015	Session chair
IGES 2015	Baltimore	USA	4-6/10/2015	Board of Directors Meetings
3rd MLPM Summer School	Manchester	UK	21-25/9/2015	Node leader, Board Member

COST Action BM1204 Omics Integration In Pdac Workshop: "Cancer genomics and personalised medicine workshop: focus on pancreas cancer"	Barcelona	Spain	1/7/2015	Organizer (local organizer: Nuria Lopéz-Bigas)
ESHG 2015	Glasgow	Scotland	6-9/6/2015	Program Board Member; session chair
Korean Statistical Society Meeting	Seoul	South Korea	29-30/5/2015	Invited discussant
3rd International Symposium on Statistical Genetics (ISSG)	Seoul	South Korea	27-28/5/2015	Keynote lecture (invited)
Bioinformatics and biostatistics applications in cancer genomics research (BBACGR2015)	Doha	Qatar	26-28/4/2015	Keynote lecture (invited)
ERCIM 2014	Pisa	Italy	5-8/12/2014	Oral presentation (invited)
CSCDA2014 / COST Action BM1204 WG2 workshop	Liege	Belgium	24-26/11/2014	Organizer - Chair
2nd MLPM Summer School	Paris	France	11-19/9/2014	Presenter (invited); Node leader, Board Member
IBS2014	Florence	Italy	6-11/7/2014	Oral presentation (invited)
HGM 2014	Geneva	Switzerland	26-30/04/2014	Research meetings
ERCIM2013	London	UK	14-16/12/2013	Oral presentation (invited)
1st Pancreatic Cancer Forum	Madrid	Spain	29-30/11/2013	EU COST Action BM1204; WG2 Coordinator
Annual Meeting of the American Society of Human Genetics (ASHG)	Boston	USA	22-26/10/2013	-
1st MLMP Summer School	Tübingen	Germany	23-27/9/2013	Presenter (invited); Node leader, Board Member
Annual Meeting of the International Genetics and Epidemiology Society (IGES)	Chicago	USA	15-17/9/2013	Annual Meeting IGES Board of Directors
IWSM 2013	Palermo	Italy	8-12/7/2013	-

Annual Meeting of the European Society of Human Genet. (ESHG)	Paris	France	8-11/6/2013	**-**
European Mathematical and Genetics Meeting (EMGM)	Leiden	The Netherlands	25-27/4/2013	Chair
BioIT World Conference	Boston	USA	9-11/4/2013	**-**
5th International Conference of the ERCIM WG on COMPUTING & STATISTICS (ERCIM 2012)	Oviedo	Spain	1-3/12/2012	Oral presentation
Capita Selecta in Complex Disease Analysis (CSCDA)	Liège	Belgium	30-31/5 – 1/6/2012	Organizer
HGM 2012	Sydney	Australia	10-15/03/2012	Poster and research meetings with Singapore Human Genome Center team
12th BeSHG meeting	Liège	Belgium	2/3/2012	-
Epidem&OMICS: The "omics" era of cancer epidemiology	Madrid	Spain	28-29/11/2011	Oral presentation - invited short course
5th Annual PQG Conference – Quantitative issues in genomic medicine	Boston	USA	17-18/11/2011	(encapsulated in research stay at Harvard School of Public Health)
Annual Meeting of the European Society of Human Genetics (ESHG)	Amsterdam	The Netherlands	28-31/05/2011	Research meetings Medical Center Groningen team
15th Human Genome Meeting - 4th Pan Arab Human Genetics Conference	Dubai	United Arab Emirates	14-17/03/2011	Poster
International Biometric Society (IBS)	Florianópolis-SC	Brasil	5-10/12/2010	Short course provider
Annual Meeting of the American Society of Human Genetics (ASHG)	Washington DC	USA	2-6/11/2010	Research meetings Vanderbilt team / Poster
Annual Meeting Belgian Statistics Society (BSS)	Spa	Belgium	14-15/10/2010	Scientific committee
Annual Meeting of the International Genetics and Epidemiology Society (IGES)	Boston, Massachusetts	USA	10-12/10/2010	Poster

Capita Selecta in Complex Disease Analysis (CSCDA)	Leuven	Belgium	25-27/08/2010	Organizer
Annual Meeting of the Benelux Bioinformatics Conference (BBC)	Liège	Belgium	14-15/12/2009	Local organizing committee
Annual Meeting Belgian Statistics Society (BSS)	Lommel	Belgium	15-16/10/2009	-
Annual Meeting of the European Society of Human Genetics (ESHG)	Vienna	Austria	23-26/05/2009	Oral
Annual Belgian-Dutch Conference on Machine Learning (BENELEARN)	Tilburg	The Netherlands	18-19/05/2009	Chair
PHOEBE-P3G-BBMRI Annual meeting	Brussels	Belgium	25-27/03/2009	Invited oral
Conference of the Eastern Mediterranean Region of the International Biometric Society	Istanbul	Turkey	10-14/05/2009	-
Hannover Biometric Colloquium	Hannover	Germany	17-18/03/2009	Invited oral
Benelux Bioinformatics Conference (BBC)	Maastricht	The Netherlands	16/12/2008	Poster
Meeting of the UK/European Molecular Epidemiology Group (MEG)	Barcelona	Spain	12/12/2008	Poster
Annual Meeting of the American Society of Human Genetics (ASHG)	Philadelphia, Pennsylvania	USA	11-15/11/2008	Poster
Annual Belgian-Dutch Conference on Machine Learning (BENELEARN)	Spa	Belgium	19-20/05/2008	Program committee
Scientific symposium on new methodologies for multi-factorial disease genetics	Malmö	Sweden	3-4/04/2008	Invited oral
AllerGen's 3rd annual research conference	Alberta	Canada	10-12/02/2008	Invited discussant

Annual Meeting Belgian Statistics Society (BSS)	Antwerp	Belgium	19-20/10/2007	-
GA²LEN Annual Conference	London	UK	20/04/2007	GA²LEN Management Office
World Immune Regulation Meeting - WIRM	Davos	Switzerland	11-15/04/2007	GA²LEN Management Office
GA²LEN Annual Conference	Berlin	Germany	31/03/2006	GA²LEN Management Office
Annual Hawaii International Conference on statistics, mathematics and related fields	Honolulu	Hawaii	16-18/01/2006	Oral
Annual Meeting of the American Society of Human Genetics (ASHG)	Salt Lake City, Utah	USA	25-29/10/2005	-
Annual Meeting of the International Genetics and Epidemiology Society (IGES)	Park City, Utah	USA	23-24/10/2005	Invited oral + 2 GAW (genetic analysis workshop) papers
Eastern Mediterra-nean Region-International Biometric Society Conference (EMR-IBS)	Corfu	Greece	10-12/05/2005	Oral
Annual Meeting of the International Genetics and Epidemiology Society (IGES)	Noordwijkerhout	The Netherlands	11-12/09/2004	Poster
Annual Meeting of the International Genetics and Epidemiology Society (IGES)	New Orleans, Los Angeles	USA	15-16/11/2002	Poster
Annual Meeting of the American Society of Human Genetics (ASHG)	Baltimore, Maryland	USA	15-19/10/2002	Poster
European Mathematical and Genetics Meeting (EMGM)	Sheffield	UK	6-7/04/2002	Poster
Annual Meeting of the American Society of Human Genetics (ASHG)	San Diego, California	USA	12-16/10/2001	Poster
Annual Meeting of the International Genetics	Garmisch	Germany	2-4/09/2001	Poster

and Epidemiology Society (IGES)				
1st Dutch-Belgian Biometric Conference (BBC)	Centerparcs Erperheide, Peer	Belgium	28-29/05/2001	Poster
Annual conference of the International Society of Clinical Biostatistics (ISCB)	Trento	Italy	4-8/09/2000	Oral
Annual conference of the International Society of Clinical Biostatistics (ISCB)	Heidelberg	Germany	13-17/09/1999	Oral

*confirmed participation in the future – in italic

c) Detailed information about scientific announcements – a selection

<u>Contributions to announcements at international conferences and symposia which resulted in publications other than articles:</u>

1. Abegaz F, Chaichoompu K, **Van Steen K** (2017). Epistasis detection for human complex diseases in structured populations. Genet Epi 41(7): 678-678.
2. Chaichoompu K , Yazew FA ,Tongsima S, Shaw PJ, Sakuntabhai A, Cavadas B, Pereira L, **Van Steen K** (2017). Using IPCAPS to Identify Fine-Scale Population Structure. Genet Epi 41(7): 656-656.
3. Chaichoompu K, Cleynen I, Fouladi R, Ellinghaus D, Ubenthal MH, **Van Steen K**, IIBDGC: Detecting patient subgroups using reduced set of disease-related markers with iterative pruning Principal Component Analysis (ipPCA). Genetic Epidemiology 2015, 39:536-537.
4. Dizier B, **Van Steen K**: An extension of Conditional Inference Forest methodology for predictive biomarkers and personalized medicine applications. Genetic Epidemiology 2015, 39:544-544.
5. Fouladi R, Schurmann C, Bessonov K, Vert JP, Loos RJF, **Van Steen K**: A novel gene-based analysis method based on MB-MDR. Genetic Epidemiology 2015, 39:548-548.
6. De Greef E, et al. (2014). The Belgian Registry of Pediatric Crohn's Disease (BELCRO): growth status after 3 year follow up. Gastroenterology. Abstract submitted for DDW 2014
7. De Greef E, et al. (2014). Disease severity after 3 years of treating newly diagnosed pediatric Crohn's disease patients (the BELCRO cohort). Gastroenterology. Abstract submitted for DDW 2014
8. Machiels K et al. (2014). Predominant gut microbiota predict pouchitis following colectomy and IPAA in ulcerative colitis. Gastroenterology. Abstract submitted for DDW 2014.
9. Machiels K et al. (2014). Predominant gut microbiota predict pouchitis following colectomy and IPAA in ulcerative colitis. Acta Gastroenterol. Bel. Abstract submitted for Belgian Week 2014.
10. Breynaert C, et al. (2014)/ MRI T2 relaxometry to image fibrosis in patients with Crohn's disease. Gastroenterology. Abstract submitted for DDW 2014.

11. Benitez Cantero JM et al. (2014). Genetic predictors of non reversible tissue damage in inflammatory bowel disease. Journal of Crohn's and Colitis. Abstract submitted for ECCO 2014.

12. Benitez Cantero JM et al. (2014). Genetic predictors of non reversible tissue damage in inflammatory bowel disease. Acta Gastroenterol. Bel - Abstract submitted for Belgian Week 2014

13. Billiet T, Cleynen I, Ballet V (et al.) (2013). Familial aggregation in the response to anti-TNF in inflammatory bowel disease patients. Gastroenterology: vol. 144 (5). Digestive Disease Week. Orlando: FL, 18-21, 2013, S647-S647.

14. Cleynen I, Konings P, Theatre E, Amiminejad L, Laukens D, Davani NA, Cuppens H, Machiels K, Coopmans T, Robberecht C, Wollants W-J, Claes K, Organe S, Rutgeerts P, Franchimont D, De Vos M, Louis E, **Van Steen K**, Georges M, Moreau Y, Vermeesch J, Vermeire S (2013) Genome-wide copy number variation scan identifies Complement Component C4 as novel susceptibility gene for Crohn's Disease. Gut, Abstract submitted for UEGW 2013.

15. de Bruyn M et al. (2013). Serum neutrophil gelatinase B-associated lipocalin - matrix metalloproteinase-9 (NGAL-MMP-9) complex as a surrogate marker for mucosal healing in ulcerative colitis. Journal of Crohn's and Colitis. Abstract submitted for ECCO2013

16. de Bruyn, M., Arijs, I., Wollants, W., Machiels, K., **Van Steen, K**., Ferrante, M., Rutgeerts, P., Vermeire, S., Opdenakker, G. (2013). Neutrophil Gelatinase B-Associated Lipocalin-Matrix Metalloproteinase-9 (NGAL-MMP-9) Complex As a Surrogate Serum Marker for Mucosal Healing in Ulcerative Colitis. Gastroenterology: vol. 144 (5). Digestive Disease Week. Orlando: FL, 18-21, 2013, S417-S418.

17. De Greef E et al. (2013) Diagnosing and treating pediatric Crohn's disease patients: is there a difference between adult and pediatric gastroenterologist's practices? Resuls of the BELCRO cohort. Journal of Crohn's and Colitis. Abstract submiited for ECCO2013.

18. Li Z et al. (2013) Simultaneously Restoration of Foxp3 (+) Regulatory T cells Subsets, Type 1-Like Regulatory T cells and B cells Correlates With Clinical Response to Infliximab Therapy for IBD. Journal of Crohn's and Colitis. Abstract submitted for ECCO2013

19. Li Z et al. (2013) Simultaneously Restoration of Foxp3 (+) Regulatory T cells Subsets, Type 1-like regulatory T cells and B cells correlates with clinical response to infliximab therapy for IBD. Acta Gastroenterol. Bel - Abstract submitted for Belgian Week 2013

20. Malats N, La Vecchia C, Esposito I, **Van Steen K**, Hahn S, Brand A – on behalf of the EU Pancreas members (2014) De La Célula A La Sociedad: Eupancreas, Plataforma Europea Multidisciplinar Sobre Cáncer De Páncreas – abstract submitted to the Spanish Epidemiology Society.

21. Vande Casteele N (2013). Randomised controlled trial of drug level versus clinically based dosing of infliximab maintenance therapy in IBD: Final results of the Taxit study. Gut. UEGW 2013

22. Veereman G, Mahachie John JM, De Greef E, Smets E, Van Biervliet S, **Van Steen K**, and BELCRO working group (2013). Therapeutic strategy and patient outcome during the first 2 years of pediatric Crohn's disease. Gastroenterology. Abstract submitted for DDW 2013.

23. Veereman G, Mahachie John JM, De Greef E, Smets E, Van Biervliet S, **Van Steen K**, and BELCRO working group (2013). Therapeutic strategy and patient

outcome during the first 2 years of pediatric Crohn's disease. Abstract submitted for ESPGHAN 2013.

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Selection of accepted abstracts – no publication information available:

The year 2016 is marked by first output within BIO3's third research line on Stratified Medicine. We intensively advertise our work, hereby covering the European, American and Asian continent while presenting our work on the detection of fine-scale structure in populations and patients. Feedback to increase translatability of findings in molecular reclassification exercises is incorporated in several (draft) manuscripts involving Kridsadakorn Chaichoompu from BIO3.

130. Abegaz F, Chaichoompu K, **Van Steen K** (2017). Epistasis detection for human complex diseases in structured populations – DDTWC2017

131. Chaichoompu K, Abegaz FA, Tongsima S, Shaw PJ, Sakuntabhai A, Cavadas B, Pereira L, **Van Steen K** (2017). Using IPCAPS to identify fine-scale population structure – IGES2017

132. Chaichoompu K, Abegaz FA, Tongsima S, Shaw PJ, Sakuntabhai A, Pereira L, **Van Steen K** (2017). Determining fine population structure using iterative pruning – ICG2017

133. Chaichoompu K, Abegaz FA, Tongsima S, Shaw PJ, Sakuntabhai A, **Van Steen K** (2017). Using unsupervised clustering method and SNP-based information to identify fine-level population structure – DDTWC2017

134. Deliu N, Efficace F, Collins G, Anota A, Bonnetain F, **Van Steen K**, Cella D, Cottone F (2017) Modelling strategies to improve estimates of prognostic factors analyses with patient reported outcomes: a simulation study – ISOQOL 2017

135. Noël G, Chaichoompu K, Leclercq G, Fabre E, Gengler N, **Van Steen K** & Francis F (2017). Human based genetic tools to refine genetic population structure of honey bees (Apis mellifera ssp L.) (Hymenoptera: Apoidea: Apidae) colonies at regional scale - European Phd Network "Insect Science" | Giornate Culturali Di Entomolo 2017

136. Chaichoompu K, Abegaz F, Tongsima S, ShawPJ, Sakuntabhai A, **Van Steen K** (2016). Using SNP-based information and unsupervised clustering method to dentify fine-level population structure – GIGA Day 2016

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141. Chaichoompu et al. **Van Steen** K, IIBDGC Consortium (2015) Detecting patient subgroups using reduced set of disease-related markers with iterative pruning Principal Component Analysis (ipPCA) – ASHG2015

142. Fouladi et al., **Van Steen** (2015) A novel gene-based analysis method based on MB-MDR – ASHG2015

143. Fouladi et al., **Van Steen** (2015) A novel gene-based analysis method based on MB-MDR – IGES2015

144. Gusereva et al, **Van Steen**, IIBDGC Consortium (2015) Epistasis associated to inflammatory bowel disease (IBD) in humans – IGES2015

145. Gusareva et al., **Van Steen** (2015). Biological validation of statistical epistasis signals. Presented at COST Action (BM1204): An integrated European platform for pancreas cancer research: from basic science to clinical and public health interventions for a rare disease.

146. Gusareva et al., **Van Steen** (2015). Gene-based replication strategy and meta-analysis in the context of epistasis: application for Alzheimer's disease, accepted to Functional Genomics & Predictive Medicine Conference

147. Holly et al., **Van Steen** K, Moore JH, Ritchie MD (2015) Data-Driven Genetic Encoding: A robust approach for detecting diverse action in main effect models and genetic interactions – ASHG

148. **Van Steen** K (2015). Balancing between dimensionality reduction and modelling complexity – accepted to the workshop "Recent developments in statistical methods with applications to genetics and genomics", Oberwolfach, Germany - invited

149. Bessonov K et al. (2014) Regulatory gene network inference from expression data via conditional inference trees, accepted to CSCDA2014

150. Chaichoompu K et al. (2014) Iterative pruning principal component analysis to retrieve population structure – accepted to CSCDA2014

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152. Chaichoompu K, Fouladi R, Wangkumhang P, Wilantho A, Chareanchim W, Tongsima S, Sakuntabhai A, **Van Steen K** (2014) LD-based haplotype encoding scheme with iterative pruning principal component analysis – abstract accepted for poster presentation at HGM 2014

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154. Fouladi R et al. (2014) A novel gene-based analysis method based on MB-MDR– accepted to CSCDA2014

155. Fouladi R, Bessonov K, Van Lishout F, Moore J, **Van Steen K** (2014) Genomic MB-MDR for rare variant analysis - abstract accepted for oral presentation at EMGM 2014

156. Fouladi R, Bessonov K, Van Lishout F, Moore J, **Van Steen K** (2014) A novel integrated framework for large scale association analysis - abstract accepted for poster presentation at HGM 2014

157. Gadaleta F et al., **Van Steen** (2014) Are we far from correctly inferring gene interaction networks? – CSCDA2014
158. Gusareva et al., **Van Steen** (2014) Genome-wide association interaction analysis for Alzheimer's disease, submitted to GIGA-DAY 2014.
159. Pineda-Sanjuán S et al. (2014) Integration analysis of OMICS data using penalized regression methods: An application to bladder cancer – accepted to CSCDA2014
160. Pineda-Sanjuán S, Malats K, **Van Steen K** (2014). Integration analysis of genomics, epigenomics and transcriptomics in bladder cancer – accepted to EAU 2015.
161. Pineda-Sanjuán S**, Van Steen K**, Real F, Kogevinas M, Malats N (2014). Análisis de intgración de datos "omics" mediante regresión penalizada: aplicación en cáncer de vejiga - accepted to SEE 2014
162. Bessonov K, Croteau-Chonka D, Qi W, Carey VJ, Raby BA, **Van Steen K** (2013) Identification of asthma-related trans-acting epistatic eQTL using Model-Based Multifactor Dimensionality Reduction. Poster session presented at Annual Society of Human Genetics Annual Meeting 2013, Boston, USA
163. Bessonov, K., & **Van Steen, K**. (2013, September 17). Replication of large-scale epistasis studies: an example on ankylosing spondylitis. Poster session presented at International Genetic Epidemiology Society (IGES) 2013, Chicago, USA.
164. Gadaleta F,Bessonov K,Chaichoompu K,Pineda S,**Van Steen K** (2013) Network-based omics integration framework:overcoming the obstacle of high dimensional data - abstract accepted for oral presentation at ERCIM 2013
165. Gusareva E, Bellenguez C, Cuyvers E,Colon S, Carrasquillo MM, Graff-Radford NR,Petersen RC, Dickson DW,Younkin SG,Van Broeckhoven C,Harold D, Williams J,Amouvel P, Sleegers K,Ertekin-Taner N,Lambert J-C,**Van Steen K** (2013) Genome-wide association interaction analysis (GWAI) for complex diseases:an example on Alzheimer's disease.- abstract accepted for oral presentation Israel 2013
166. Gusareva E, Bellenguez C, Cuyvers E,Colon S, Carrasquillo MM, Graff-Radford NR,Petersen RC, Dickson DW,Younkin SG,Van Broeckhoven C,Harold D, Williams J,Amouvel P, Sleegers K,Ertekin-Taner N,Lambert J-C,**Van Steen K** (2013) Genome-wide association interaction analysis (GWAI) for complex diseases: an example on Alzheimer's disease – abstract accepted for oral presentation Seoul 2013
167. Gusareva E, Bellenguez C, Cuyvers E,Colon S, Carrasquillo MM, Graff-Radford NR,Petersen RC, Dickson DW,Younkin SG,Van Broeckhoven C,Harold D, Williams J,Amouvel P, Sleegers K,Ertekin-Taner N,Lambert J-C,**Van Steen K** (2013) Genomewide epistasis screening for Alzheimer's disease – abstract accepted for poster presentation at ACMG Phoenix 2013
168. Mahachie John JM, Van Lishout F, Gusareva E, **Van Steen K** (2013) A Robustness Study of Parametric and Non-parametric Tests in Model-Based Multifactor Dimensionality Reduction for Epistasis Detection – abstract accepted for oral presentation at BeSHG 2013
169. Pineda-Sanjuán S, Milne Roger, **Van Steen K**, Malats N (2013). Statistical approaches for the integration of "omics" and epidemiological data: an application to bladder cáncer – submitted to Biometria 2013
170. Van Lishout, F., Bessonov, K., Duan, Q., Gusareva, E., Mahachie John, J., Tantishira, K., & **Van Steen, K**. (2013, October 25). Genome-wide environmental interaction analysis using multidimensional data reduction principles to identify asthma pharmacogenetic loci in relation to corticosteroid therapy. Poster session presented at Annual Society of Human Genetics Annual Meeting 2013, Boston, USA

171. **Van Steen K** and E Gusareva (2013) To interact or not to interact – abstract accepted for oral presentation at Annual Meeting of Statistical Modeling Society 2013

172. **Van Steen K**, Fouladi R, Bessonov K, Van Lishout F, Moore J (2013 Genomic MB-MDR for rare variant analysis – abstract accepted for oral presenation (invitation to sesión "Advances of rare variant analysis in large scale genetic association studies") at ERCIM 2013

173. De Greef E, Hoffman I,D'haens G, Van Biervliet S, Smets F, Scaillon M, Dewit O, Peeters H, Paquot I, Alliet P, Arts W, Hauser B, Vermeire S, Van Gossum A, Rahier JF, Etienne I, Louis E, Coche JC, Mahachie John J, **Van Steen K**, Veereman G and Bird and Bespghan (2012). Safety And Cost Of Infliximab For The Treatment Of Belgian Pediatric Patients With Crohn's Disease – ESPGHAN, 2012

174. De Greef E, Mahachie John J, Hoffman I, Smets F, Van Biervliet S, Scaillon M, Hauser B, Paquot I, Alliet P, Arts W, Dewit O, Peeters H, Baert F, D'haens G, Rahier JF, Etienne I, Bauraind O, Van Gossum A, Vermeire S, Fontained F, Muls V, Louis E, Van de Mierop F, Coche JC, **Van Steen K**, Veereman G and Bird and Bespghan (2012). Factors determining therapeutic strategy at diagnosis and evolution of disease severity in a cohort of Belgian pediatric Crohn's Disease patients (Belcro). – ESPGHAN, 2012

175. Dresselaers T, Breynaert C, Cremer J, **Van Steen K**, Perrier C, Vermeire S, Rutgeerts P, Ceuppens J, Van Assche G, Himmelreich U (2012). Longitudinal T_2 relaxometry to monitor repeated cycles of DSS inducing a chronically relapsing inflammation - International Society of Magnetic Resonance in Medicine, 5-11th 2012 Melbourne (AU).

176. Gusareva E, **Van Steen K** (2012). Integrating Biological Information in Genome-Wide Association Interaction (GWAI) Studies – abstract accepted for oral presentation at CSCDA2012, Liege, Belgium

177. Gusareva E, Mahachie John J, Isaacs A, **Van Steen K** (2012). Application of mixed polygenic model to control for cryptic/genuine - abstract accepted for poster presentation at HGM 2012, Sydney, Australia

178. Li, Z., Vermeire, S., Bullens, D., Ferrante, M., **Van Steen, K.**, Noman, M., Rutgeerts, P., Ceuppens, J. L., & Van Assche, G.(2012, October). Restoration Of B Cells Correlates With Clinical Response To Anti-Tnf Therapy. Poster session presented at united european gastroenterology.

179. Li, Z., Vermeire, S., Bullens, D., Ferrante, M., **Van Steen, K.**, Noman, M., Rutgeerts, P., Ceuppens, J. L., & Van Assche, G. (2012, October). Active Foxp3 (+) Regulatory T Cells Rather Than Other Foxp3 (+) T Cells Subsets CorrelateWith Clinical Response To Infliximab Therapy For IBD. Poster session presented at united european gastroenterology.

180. Mahachie John J, Gusareva E, Van Lishout F, **Van Steen K** (2012). A robustness study of parametric and non-parametric tests in modelbased multifactor dimensionality reduction for epistasis detection - abstract accepted for poster presentation at HGM 2012, Sydney, Australia

181. Mahachie John J, Gusareva E, Van Lishout F, **Van Steen K** (2012). A robustness study of parametric and non-parametric tests in modelbased multifactor dimensionality reduction for epistasis detection - abstract submitted for ESHG 2012, Nürnberg, Germany

182. Mahachie John J, Gusareva E, Van Lishout F, **Van Steen K** (2012). Omics integration and the importance of quantifying and verifying underlying model assumptions – abstract accepted for oral presentation at CSCDA2012, Liege, Belgium

183. Maus B, Génin E, Mahachie John J, **Van Steen K** (2012). Inference and comparison of different genetic stratification techniques – abstract accepted for oral presentation at CSCDA2012, Liege, Belgium

184. Ummarino D, **Van Steen K**, Ruggiero Pellegrino N, Staiano A, Hauser B, Vandenplas Y (2012). Baseline esophageal impedance in children differs with age– ESPGHAN, 2012

185. Van Lishout, F., Vens, C., Urrea, V., Calle, M. L., Wehenkel, L., & **Van Steen, K**. (2012, December 03). Survival analysis: finding relevant epistatic SNP pairs using Model- Based Multifactor Dimensionality Reduction. Paper presented at 5th International Conference of the ERCIM WG on COMPUTING & STATISTICS, Oviedo, Spain.

186. **Van Steen K**, Gusareva E, Cattaert T (2012). Making sense of epistasic findings from different methodologies- abstract accepted for poster presentation at HGM 2012, Sydney, Australia

187. Breynaert C, Ferrante F, Fidder H, **Van Steen K**, Noman M, Ballet V, Vermeire S, Rutgeerts P, Van Assche G (2011). Tolerability of shortened infliximab infusion times in patients with inflammatory bowel diseases: a single center cohort study – NVGE, Veldhoven, the Netherlands 2011

188. Cattaert T, **Van Steen K** (2011) The impact of genotyping error on power and type-I error of quantitative trait genetic association studies – EMGM 2011, London, United Kingdom

189. Cattaert T, Van Lishout F, Rial J, **Van Steen K** (2011). Comparison of MB-MDR to BOOST andRAPID for detecting epistasis in unrelated - 6th EMR-IBS, Crete, Greece

190. Cattaert T., Rial Garcia J. A., Gusareva E., **Van Steen K** (2011). Comparison Of Different Methods For Detecting Gene-Gene Interactions In Case-Control Data, IGES 2011 Heidelberg, Germany, 19 September 2011

191. De Greef E, Hoffman I, Smets F, Van Biervliet S, Scaillon M, Hauser B, Paqout I, Alliet Ph, Arts W, Dewit O, Peeters H, Baert F, D'Haens G, Rahier J-F, Etienne I, Bauraind O, Van Gossum A, Vermeire S, Fontaine F, Muls V, Louis E, Van de Mierop F, Coche JC, Mahachie John JM, **Van Steen K**, Veereman G (2011). Profil d'une population d'enfants et d'adolescents attaints de maladie de Crohn – GFGHNP de Liège

192. De Greef I, Hoffman I, Smets F, Van Biervliet S, Scaillon M, Hauser B, Paquot I, Alliet P, Arts W, Dewit O, Peeters H, Baert F, D'Haens G, Rahier JF, Etienne I, Bauraind O, Van Gossum A, Vermeire S, Fontaine F, Muls V, Louis E, Van de Mierop F, Coche JC, Mahachie John JM, **Van Steen K**, Veereman G (2011). Profile of Belgian Pediatric Crohn Disease (CD) Patients: Presentation and Diagnostic Features – BVK Brussels 2011

193. De Greef I, Hoffman I, Smets F, Van Biervliet S, Scaillon M, Hauser B, Paquot I, Alliet P, Arts W, Dewit O, Peeters H, Baert F, D'Haens G, Rahier JF, Etienne I, Bauraind O, Van Gossum A, Vermeire S, Fontaine F, Muls V, Louis E, Van de Mierop F, Coche JC, Mahachie John JM, **Van Steen K**, Veereman G (2011). Profile of Belgian Pediatric Crohn Disease (CD) Patients: Presentation and Diagnostic Features – ESPGHAN, Sorento 2011

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Bauraind O, Van Gossum A, Vermeire S, Fontaine F, Muls V, Louis E, Van de Mierop F, Coche JC, Mahachie John JM, **Van Steen K**, Veereman G (2011). Profile of Belgian Pediatric Crohn Disease (CD) Patients: Associations between variables at diagnosis – ESPGHAN, Sorento 2011

196. Grady B J, Cattaert T, **Van Steen K** and Ritchie MD (2011). An Ensemble Pipeline to Enable Detection of Epistasis in Genomic Data , IGES 2011 Heidelberg, Germany, 20 September2011

197. Grady B J, Cattaert T, **Van Steen K** and Ritchie MD (2011). An Ensemble Pipeline to Enable Detection of Epistasis in Genomic Data (2011), ASHG 2011

198. Gusareva E, Huyghe J, **Van Steen K** (2011). Genome-wide epistasis screening for asthma associated traits – submitted for ISM2011 / Joint Statistical Meetings, Miami Beach, Florida USA

199. Haerynck F, **Van Steen K**, Cattaert T, Loeys B, Van Daele S, Schelstraete P & De Baets F (2011). Association of FCN1 and FCN2 gene polymorphisms with earlier onset of chronic pseudomonas aeruginosa (Pa) colonisation in cystic fibrosis (CF) patients, ERS 2011, Amsterdam, Pays-Bas, 25 September 2011

200. Mahachie John JM, Cattaert T, Van Lishout F, **Van Steen K** (2011). A detailed view on model-based multifactor dimensionality reduction with quantitative traits for detecting gene-gene interactions: different ways of adjusting for lower-order effects - Human Genetics Meeting, Dubai, United Arab Emirates

201. Mahachie John JM, Cattaert T, Van Lishout F, **Van Steen K** (2011). A detailed view on model-based multifactor dimensionality reduction with quantitative traits for detecting gene-gene interactions: different ways of adjusting for lower-order effects – ESHG 2011, Amsterdam, the Netherlands

202. Mahachie John JM, Gusareva E, Van Lishout F, **Van Steen K** (2011). A robustness study to investigate the performance of parametric and non-parametric tests used in Model-Based Multifactor Dimensionality Reduction Epistasis Detection. Accepted for poster presentation at the International Genetics Epidemiology Society(IGES), Heidelberg, Germany, September 18-20, 2011.

203. Van Lishout, F., Cattaert, T., Mahachie John, J., Gusareva, E., Urrea, V., Cleynen, I., Theatre, E., Charloteaux, B., Kvasz, A., Calle, M. L., Wehenkel, L., & **Van Steen, K**. (2011, December 13). An Efficient Algorithm to Perform Multiple Testing in Epistasis Screening. Paper presented at Benelux Bioinformatics Conference 2011, Luxembourg, Luxembourg

204. Van Lishout F, Cattaert T, Mahachie John JM, Wehenkel L, **Van Steen K** (2011). A Memory Efficient Algorithm to Perform Multiple-Testing in Epistasis Screening- 6th EMR-IBS, Crete, Greece

205. Vieira M, **Van Steen K**, Salvatore S, Vandenplas Y (2011) Effects of domperidone on Qtc interval in infants. – ESPGHAN 2011

206. **Van Steen K** (2011). Got heritability lost in a world of interactions? - Human Genetics Meeting, Dubai, United Arab Emirates

207. Cattaert T, De Lobel L, **Van Steen K** (2010). Using mixed models with a mixture of normal distributions for the random residual effect leads to a fast and powerful genomewide association test –25th International Biometric Conference IBC2010, Florianopolis, Brasil.

208. Cattaert T, Mahachie John JM, Van Lishout F, **Van Steen K** (2010). Alternative risk cell definitions based on ranking improve performance of model-based multifactor dimensionality reduction for epistasis detection –IGES 2010

209. Cattaert T, Mahachie John JM, Van Lishout F, **Van Steen K** (2010). Alternative risk cell definitions based on ranking improve performance of Model-Based Multifactor Dimensionality Reduction for epistasis detection – First edition of Capita Selecta in Complex Disease Analysis CSCDA2010

210. Cattaert T, Calle ML, Dudek SM, Mahachie John JM, Van Lishout F, Urrea V, Ritchie MD, **Van Steen K** (2010). A detailed view on several Model-Based Multifactor Dimensionality Reduction methods for detecting gene-gene interactions in case-control data in the absence and presence of noise – ECCB 2010, Ghent , Belgium

211. Cleynen I, Mahachie John JM, Henckaerts L, Van Moerkercke W, Rutgeerts P, **Van Steen K**, Vermeire S (2010). Molecular reclassification of Crohn's disease by cluster analysis of genetic variants –First edition of Capita Selecta in Complex Disease Analysis CSCDA2010

212. De Lobel L, Thijs L, Kouznetsova T, Staessen J, **Van Steen K** (2010). A Family-based Association Test to Detect Gene-Gene Interactions in the Presence of Linkage –First edition of Capita Selecta in Complex Disease Analysis CSCDA2010

213. De Lobel L, Thijs L, Kouznetsova T, Staessen JA, **Van Steen K** (2010). A Family-Based Association Test to Detect Gene-Gene Interactions in the Presence of Linkage –25th International Biometric Conference IBC2010, Florianopolis, Brasil.

214. Haerynck F, Loeys B, **Van Steen** K, van Daele S, Schelstraete P, Rossau R, De Baets F (2010). Association of MASP3 and FCN2 gene polymorphisms with the age of onset of chronic Pseudomonas aeruginosa (Pa) - ECFS (European Cystic fibrosis society) congress- Valencia

215. Haerynck F, Loeys B, **Van Steen** K, van Daele S, Schelstraete P, Rossau R, De Baets F (2010) Association of MASP3 and FCN2 gene polymorphisms with the age of onset of chronic Pseudomonas aeruginosa (Pa) - ESID (European Society for Immune deficiencies) congress - Istanbul

216. Huyghe JR, Van Camp G, **Van Steen K** (2010). Elucidating the Molecular Etiology of Asthma using Genome-Wide Association Study Pathway Analysis. – First edition of Capita Selecta in Complex Disease Analysis –First edition of Capita Selecta in Complex Disease Analysis CSCDA2010

217. Mahachie John JM, Cattaert T, Van Lishout F, **Van Steen K** (2010). Model-Based Multifactor Dimensionality Reduction to detect epistasis for quantitative traits in the presence of error-free and noisy data – IGES 2010

218. Mahachie John JM, Cattaert T, Van Lishout F, **Van Steen K** (2010). A detailed view on model-based multifactor dimensionality reduction with quantitative traits for detecting gene-gene interactions: different ways of adjusting for lower-order effects –25th International Biometric Conference IBC2010, Florianopolis, Brasil.

219. Mahachie John JM, Cattaert T, Van Lishout F, **Van Steen K** (2010). A detailed view on model-based multifactor dimensionality reduction with quantitative traits for detecting gene-gene interactions: different ways of adjusting for lower-order effects. –First edition of Capita Selecta in Complex Disease Analysis CSCDA2010

220. Mahachie John JM, Van Lishout F, **Van Steen K** (2010). Model-Based Multifactor Dimensionality Reduction to detect epistasis for quantitative traits in the presence of error-free and noisy data. Accepted for poster presentation at the European Conference on Computational Biology (ECCB), Gent, Belgium, September 27-29, 2010.

221. Savenije OEM, Mahachie John JM, Kerkhof M, Postma DS, **Van Steen K** & Koppelman GH (2010). Genetic epistasis in the IL1RL1 pathway and wheezing phenotypes: multinomial MB-MDR analyses–First edition of Capita Selecta in Complex Disease Analysis CSCDA2010 (responsible author).

222. **Van Steen K**, Cattaert T, Calle ML, Dudek SM, Mahachie John JM, Van Lishout F, Urrea V, Ritchie MD (2010). A detailed view on Model-Based Multifactor Dimensionality Reduction for detecting gene-gene interactions in case-control data in the absence and presence of noise. Accepted for poster presentation at the

International Genetics Epidemiology Society(IGES), Boston, USA, October 10-12, 2010.

223. **Van Steen K**, Cattaert T, Calle ML, Dudek SM, Mahachie John JM, Van Lishout F, Urrea V, Ritchie MD (2010). Model-Based Multifactor Dimensionality Reduction for detecting gene-gene interactions in case-control data in the absence and presence of noise. Submitted to the American Society of Human Genetics (ASHG), Washington, USA,November, 2010

224. Arijs I, Quintens R, Van Lommel L, **Van Steen K**, De Hertogh G, Van Assche G, Vermeire S, Geboes K, Schuit F, Rutgeerts P. (2009). TECK and MADCAM-1 mucosal expression in active IBD: the effect of infliximab therapy - submitted for the National Cross-Disciplinary symposium on Immune Mediated Inflammatory Diseases 2009.

225. Arijs I, Quintens R, Van Lommel L, **Van Steen K**, De Hertogh G, Van Assche G, Vermeire S, Geboes K, Schuit F, Rutgeerts P (2009). TECK and MADCAM-1 mucosal expression in active IBD: the effect of infliximab therapy. Accepted for oral presentation at the National Cross-Disciplinary symposium on Immune Mediated Inflammatory Diseases, Dolce La Hulpe, March 13 - 14, 2009.

226. Cattaert T, Mahachie John JM, De Wit V, **Van Steen K** (2009). Selecting multiple epistatic models using MB-MDR –BVS 2009

227. Cattaert T, Mahachie John JM, **Van Steen K** (2009). Selecting multiple epistatic models using MB-MDR – submitted for BBC 2009

228. Cattaert T, Mahachie John JM, **Van Steen K** (2009). Selecting multiple epistatic models using MB-MDR – submitted for DYSCO 2009

229. Cattaert T, Urrea V, Calle ML, De Wit V, Mahachie John JM, **Van Steen K** (2009). Unified framework for epistasis detection in (un)-relateds – 5th conference of the Eastern Mediterranean Region of the Internation Biometric Society IBS 2009

230. Cattaert T, Mahachie John JM, **Van Steen K** (2009). Selecting multiple epistatic models using MB-MDR. Abstract Book of the Annual meeting of the American Society of Human Genetics 2009,1848

231. Cattaert T, Mahachie John JM, De Wit V, **Van Steen K** (2009). Selecting multiple epistasis models using MB-MDR. Accepted for oral presentation at the Benelux Bioinformatics Conference, Liége, Belgium, December 14 -15, 2009.

232. De Wit V, Vermeirssen V, Huyghe J, Van de Peer Y, **Van Steen K** (2009). Epistasis detection using MB-MDR, guided by prior biological knowledge –IGES 2009

233. Cattaert T, Urrea V, Calle M, De Wit V, Malats N, **Van Steen K** (2008). FAM-MDR: A method for genetic association studies with epistasis using families – DYSCO 2008

234. Perez-Alvarez N, Konings P, **Van Steen K**, Nadia T (2008). Analysis of an outcome beyond a detection limit: Application to HIV RNA data – IBC 2008

235. Van Der Gucht B, Konings P, Rooms J, Van Wanzeele F, Pelgrom J, Verhofstede C, **Van Steen K**, Blot S, Vandekerckhove L, Vogelaers D (2008). High success rates in virologic suppression in initial HAART regimens: a tool for benchmarking quality of HIV care? – AIDS 2008

236. De Lobel L, **Van Steen K**, De Meyer H, (2007). Alternative methods to detect gene-gene interactions – 15th Annual meeting of the Belgian Statistical Society (BVS) Antwerp, 19-20 October 2007.

237. Kogevinas M, Castro-Giner F, de Cid R, Jarvis D, **Van Steen K**, Anto J-M, Wjst M and the ECRHS study group (2007). Replication of positionally cloned asthma genes in an international population-based cohort study (ECRHS-II). – ERS 2007, Stockholm, Sweden, 17-19 September 2007.

238. Willemarck N, Van Poucke M, **Van Steen K**, Maes S, Van Zeveren A, Peelman LJ (2007). PRNP polymorphisms associated with PRNP mRNA expression in blood in Belgian sheep population. – Prion 2007 congress Edinburgh, 26 - 28th September 2007.
239. Wark PA, Souverein OW, **Van Steen K**, Van 'T Veer P (2002). Onderzoeken van etiologische heterogeniteit van kanker met behulp van multinomiale logistische regressie. In: WEON (Werkgroep Epidemiologisch Onderzoek Nederland) 2002, Nijmegen, s.l.

Selection of oral presentations at international conferences in life sciences (as presenter):

1. BIT's 9th international gene convention: "Translational Systemics for Precision Medicine", 13-15 November 2018, Singapore, Singaproe
2. INSERM Workshop 248 on the **use of NGS data in the study of human diseases**: "**Systems Genomics for Precision Medicine**", 28 September 2017, Bordeaux, France - invited
3. ECML PKDD 2017 (European Conference on **Machine Learning and Principles and Practice of Knowledge Discovery in Databases**) – Workshop on Deep Learning for Precision Medicine: "**Systems Health – challenges and opportunities**", 22 September 2017, Skopje, Macedonia - invited
4. DDTWC 2017 (**Drug Discovery and Therapy** World Congress): "Systems genetics for precision medicine", 10 July 2017, Boston, USA - invited
5. ESHG 2017 persentation in Workshop on "Big Data in Human Genetics" – part of interactive discussion with additional facilitators Bertram Müller-Myhsok, Chloé Azencott, Kathryn Lewis, 29 May 2017, Copenhagen, Denmark – Organizer (as part of ESHG SPC)
6. ICG-2017 - BIT Congress Inc. (ICG-2017 is dedicated to promote **life science and biotech development and accelerate international education exchange and scientific information exchange** in China): "Beyond GWAS - Opportunities and Challenges of Large-Scale Epistasis Screening" , 27 April 2017, Xi'an, China – invited
7. **Max-Planck Section Symposium on Complex Trait Genetics: "Complexity and reductionism in the omics era",** 7 October 2016, Berlin, Germany - invited
8. Advanced summer school courses: **1) "Reductionism and complexity in the omics era", and 2) "Living in a world of interactions", as part of the Summer School "Genomic Medicine – briding research and the clinic" [Portoroz, Slovenia, May 2016]**
9. COST Action BM1204 TRAINING SCHOOL "Statistical Interactions/Interactome" jointly organized with the Belgian Society of Statistics and CSCDA2016 [Antwerp, 2016] - invited
10. In-FLAMES: Reductionism and Complexity in the Omics Era, April 2016, Maastricht, the Netherlands - invited
11. Combined EFISDS & EPC Meeting on Burning issues in pancreatology: "Neostrategies in integrating omics data in pancreatic cancer", 6-7 November 2015, Cluj, Romania - invited
12. 3rd International Symposium on Statistical Genetics (ISSG), "Integromics – boiling the ocean?", Seoul, South Korea, 27-28 2015 – invited keynote speaker
13. Bioinformatics and biostatistics applications in cancer genomics research (BBACGR2015), "Integromics – boiling the ocean?", Doha, Qatar, 26-28 April 2015 – invited keynote speaker
14. Methodological aspects in integromics – ERCIM 2014, 7 December, Pisa,Italy – invited

15. 59. GMDS-Jahrestagung in Göttingen; „Big Data und Forschungsinfrastruktur – Perspektiven für die Medizin", 9 September 2014 (section Epidemiology) - invited
16. Genomic MB-MDR for integrated analysis – IBS2014, Florence, Italy - invited
17. Genomic MB-MDR for rare variant analysis – ERCIM 2013, 14 December, London, UK – invited
18. To interact or not to interact? Dutch Biometry Award celebration (DBA2013), Leiden, the Netherlands, 2013. - invited
19. Biological interpretation of data in the context of GWAI studies – CFE-ERCIM 2012, Oviedo, Spain - invited
20. Explaining genetic heritability by interaction analysis? PHOEBE-P3G-BBMRI conference, Brussels, Belgium, 2009. - invited
21. Unified framework for epistasis detection in (un)relateds, ESHG 2009, Vienna, Austria
22. Some perspectives on family-based GWAs, 55. Biom. Kolloquium 2009, Hannover, Germany, 2009. – invited
23. Perspectives on genomewide association screening in the light of epistasis, Scientific Symposium - New methodology for multi-factorial disease genetics, Malmö, Sweden, 2008.- invited
24. Genomic screening in family based association testing using the same data set and the multiple testing problem, 5th annual Hawaii international conference on statistics, mathematics and related fields, Honolulu, Hawaii, USA, 2006.
25. Genomic screening in family based association testing using the same data set and the multiple testing problem, 14th annual meeting of IGES, Park City, USA, 2005.
26. Genomic screening in family based association testing and the multiple testing problem, 3rd EMR-IBS conference, Greece, 2005.
27. Multicollinearity in prognostic factor analyses using the EORTC QLQ-C30: Identification and impact on model selection ISCB 2000, Italy, 2000.
28. Sensitivity Analysis of Longitudinal Binary Quality of Life Data with Dropout: An example using the EORTC QLQ-C30; ISCB-GMDS 99, Germany, 1999.

Selection of other oral presentations in life sciences (as presenter):

Since 1998, I have had the chance to talk about my work and to present my work and that of my team at many "local" events, such as a series of seminars or scientific meetings (other than mainstream international conferences) in Belgium or abroad. 100% of them were by invitation.

29. BIOMINA seminar series: **"From biomarker discovery to clinicatl trials in precision medicine",** February 2019, Antwerp, Belgium - invited
30. EORTC general assembly: "Stratified medicine and translational science within large scale randomized trials", Nov 2018 , Brussels EORTC Head Quarters– invited
31. EORTC Stats Club: **"Translational Systemics: From understanding to utility"**, 11 September 2018 , Brussels EORTC Head Quarters– invited
32. Benelux Personalized Medicine Forum (PMF), "**Translational Systemics for Precision Medicine**", 12-13 June 2018, Utrecht, the Netherlands – invited
33. 'Green and live sciences' group workshop (DFG project "Scaling problems in statistics"), "**Precision Medicine: from the individual to populations and back again**", 22-25 May 2018 - invited
34. Mini-symposium for thesis defense at Institute Pasteur: "**Systems Health for Precision Medicine**", 2 October 2017, Paris, France - invited

35. Complex Genetics Seminar series at KU Leuven (CME): "**Beyond GWAS - Opportunities and Challenges of Large-Scale Epistasis Screenin**g", 8 June 2017, Leuven, Belgium - invited
36. **EDT - Biochemistry, Molecular & Cellular Biology** (MBCB); Interuniversity PhD Student Day: " Beyond GWAS - Opportunities and Challenges of Large-Scale Epistasis Screening", 11 May 2017, Liege, Belgium – invited
37. **Inaugural lecture at KULeuven** (CME): "Through the looking-glass - Interactions revealed!", 25 October 2016, Leuven, Belgium
38. IRIBHM Thursday Seminar: "Complexity and reductionism in the omics era", June 16th 2016, Bruxelles (ULB) Université libre de Bruxelles – invited
39. ETH Zurich Machine learning and computational biology seminar: "Alice in wonderland. Interactions revealed!?", 13 October 2016, Basel, Switzerland - invited
40. **ETH Zurich seminar series: "Believing in the Impossible "Complex" Human Genetics**", 13 October 2016, Basel, Switzerland –invited
41. ByteMAL - Bioinformatics for Young international researchers Expo: Maastricht-Aachen- Liège: "Alice in Wonderland – Interactions Revealed?!", 27 September 2016, Liège, Belgium – invited
42. COST Action BM1204 TRAINING SCHOOL "Statistical Interactions/Interactome" jointly organized with the Belgian Society of Statistics and CSCDA2016 [Antwerp, 2016]
43. Advanced summer school courses: 1) "Reductionism and complexity in the omics era", and 2) "Living in a world of interactions", as part of the Summer School "Genomic Medicine – briding research and the clinic" [Portoroz, Slovenia, May 2016]
44. TÉLÉVIE meeting: "Neostrategies in integrating omics data in pancreatic cancer", Gembloux, Belgium, December 2015 - invited
45. GIGA-Cancer seminar series, "Integromics: integrating multiple omics data sets", Liège, Belgium, 18 October 2015 – invited
46. MaCSBio, "Unraveling genetic components in complex biological phenomena – opportunities for collaboration", Maastricht, the Netherlands, 18 September 2015 - invited
47. Colloquiem Medical Informatics – ETH Zurich: "Unraveling genetic components in complex biological phenomena; A Space-Time Odyssey", Zurich, Switzerland, 18 2015 – invited
48. **VIB Inflammation Research Center - Ghent seminar series: "INTEGROMICS – bridging the gap between machine learning and statistics", Ghent, Belgium, 14 November 2014 - invited**
49. IB2 Student Days: "Methodological aspects in Integromics : integrating multiple omics datasets", ULB-VUB, Brussels, Belgium, 18 October 2014 - invited
50. 2nd MLPM Summer School: "Methodological aspects in integromics", Paris, France, 11-19 September 2014 - invited
51. CME seminar series: "From Statistical to Biological Interactions - A Rare Variant's Perspective", KUL, Leuven, Belgium, 20 June 2014 - invited
52. Seminar series department of Genetics and Genomics, Institut Pasteur – Paris – From statistical to biological interactions – a rare variant's perspective, Paris, France, 17 April 2014 - invited
53. Guest speaker within "Research Training Grant of the German Research Foundation on Scaling Problems in Statistics" – contact person: Heike Bickeböller – Chair, dept of genetic epidemiology, University of Göttingen, Germany. Funding period: 2015-2019 - invited

54. EDGE meeting on "epistasis dectection in genetic epidemiology": From statistical to biological interactions – a rare variant's perspective, Key West, Florida, USA, 6 February 2014 - invited
55. GIGA-DAY 2014: From statistical to biological interactions – a rare variant's perspective, Liege, Belgium, 27 January 2014 - invited
56. Meeting on "data integration for the study of bladder cancer": Statistical omics integration in complex disease analysis, Paris, France, 6 December 2013- invited
57. EU COST Pancreas BM1204 work group meetings: "Omics integration", Madrid, Spain, 28-29 November 2013 (WG2 leader; kick-off meeting)
58. Biostatistics Seminar Series: As above, so below – human complex disease (gen)-omics. Boston University, Boston, USA, 31 October 2013 – invited
59. 1st MLPM Summer School: "Scientific Communications", Tübingen, Germany, 23-27 septembre, 2013 – invited
60. GIGA Systems Biology and Chemical Biology: presenting "bioinformatics and statistical genetics", 1 July 2013, GIGA-R, Liege, Belgium
61. Institute of Clinical Molecular Biology (IKMB) Seminar Series: As above, so below – human complex disease (gen-)omics. Kiel, Germany, August 2013 - invited
62. Center for Systems Genomics Seminar Series: As above, so below – human complex disease (gen-)omics. Penn State, USA, February 2013 - invited
63. Seminar Series Department of Epidemiology, Biostatistics and HTA, Department of Human Genetics: To interact or not to interact – a tale of two visions. Radboud. University Nijmegen Medical Centre, 5 November 2012 - invited
64. Bladder Cancer Consortium Meeting: Perspectives on statistical omics-integration in complex disease analysis.CNIO, Madrid, Spain, 9 October 2012 - invited
65. CNIO workshop: To interact or not to interact – a tale of two vision. CNIO, Madrid, Spain, September 2012 - invited
66. IIBDGC meeting: epistasis and clustering analytic groups – state of the art (discussant; E Gusareva and B Maus: presenters). 18-19 February 2012, Barcelona, Spain.
67. CNIO seminar series: Data integration for GWAIs: practical considerations. CNIO, Madrid, Spain, 21 February 2012 – invited
68. Perspectives on statistical –omics integration in complex disease analysis, Epidem&OMICS workshop, CNIO, Madrid, 2011 - invited
69. Got genetic heritability lost in a world of interactions? University of Maastricht, MAASTRO, the Netherlands, 2011 - invited
70. MBMDR-2.6.2: an efficient software to identify significant gene-gene or gene-environment interactions, PSIMEx Workshop: Interactions and Pathways. 28 March - 1 April 2011 - EMBL-EBI, Hinxton, UK (author responsible; presentor: F Van Lishout)
71. Got genetic heritability lost in a world of interactions? University of Munich, Munich, Germany, 2010 - invited
72. Perspectives on Large-Scale Multi-Stage Family-Based Association Studies, UMCG Seminar Series, Groningen, the Netherlands, 2010 - invited
73. From data to statistical analysis: Explaining genetic heritability by interaction analysis, INSERM, Paris, France, 2009 - invited
74. Multifactor dimensionality reduction methods: coping with epistasis, Montefiore seminar series (joint presentation with Tom Cattaert) ULg, Liège, Belgium, 2009 - invited
75. Interaction analysis in the context of GWAs, UMCG Seminar Series, Groningen, the Netherlands, 2009 - invited

76. Screening strategies to detect genetic interactions and subphenotypes in (un)-related individuals, University Hospital Ghent, Medical Genetics, Ghent, Belgium, 2009 - invited
77. MB-MDR based screening strategies to detect high-order genetic interactions in (un)-related individuals, Institut für Medizinische Biometrie und Statistik, Universitaet zu Lübeck, Lübeck, Germany, 2009 - invited
78. MB-MDR based screening strategies to detect high-order genetic interactions in (un)-related individuals, University of Nantes (BIL seminar series) Nantes, France, 2008 - invited
79. The challenges of detecting epistatic patterns in genomic association studies, Klinikum Grosshadern, Germany, 2008 - invited
80. MB-MDR based screening strategies to detect high-order genetic interactions in (un-)related individuals, Institute of Epidemiology - Helmholtz Zentrum München (German Research Center for Environmental Health, Neuherberg) Germany, 2008 - invited
81. FAM-MDR, a novel screening method to detect epistasis in genetic association studies (Bio-Informatique Ligérienne) Nantes, France, 2008 - invited
82. MB-MDR based screening strategies to detect high-order genetic interactions in (un-)related individuals, Imperial College, London, UK, 2008 - invited
83. MB-MDR based screening to detect high-order genetic interaction in (un-) related individuals, BBC 2008, Maastricht, the Netherlands, 2008 - invited
84. MB-MDR based screening strategies to detect high-order genetic interactions in (un-)related individuals, NCIO, Madrid, Spain, 2008 - invited
85. MB-MDR based screening strategies to detect high-order genetic interactions in (un-)related individuals, Helmholtz Zentrum München, Munich, Germany, 2008 - invited
86. Unravelling the mysteries of genetic interactions
    – The semi-parametric way? –, ERS- GA^{2}LEN Research Seminar : "Post Genome Respiratory Epidemiology II: An Interdisciplinary Challenge", Cernay, France, 2008 - invited
87. Statistical Challenges in Genomewide Association Analysis, ERS- GA^{2}LEN Research Seminar : "Post Genome Respiratory Epidemiology II: An Interdisciplinary Challenge", Cernay, France, 2008 - invited
88. FAM-MDR: A family-based multifactor dimensionality reduction technique to detect gene-gene interactions, Harvard School of Public Health, Boston, USA - invited
89. Detecting high-order interactions – the semi-parametric way?, Universitat Politècnica de Catalunya (UPC) Barcelona, Spain, 2008 - invited
90. Statistical challenges in genomewide association analysis, Universitat de Vic, Vic, Spain, 2008 - invited
91. A statistical genetics research club …, VIB Technology Park Ghent, Ghent, Belgium, 2008 - invited
92. Power in statistical genetics and statistical significance; Part II: Evaluating power in genomewide association studies, Complex Genetics Meeting Seminar – Statistical Genetics Research Club, UZ Gasthuisberg, Leuven, Belgium, 2008 - invited
93. Power in statistical genetics and statistical significance; Part I: What it involves and does not involve (Peter Konings and Kristel Van Steen) Complex Genetics Meeting Seminar – Statistical Genetics Research Club, UZ Gasthuisberg, Leuven, Belgium, 2008 - invited
94. Statistical perspective on genomewide screening, Kick-off Meeting - Statistical Genetics Research Club, Montefiore, ULg, Liège, Belgium, 2008 - invited

95. True or false – when the number of SNPs grows, Mc Master University, Hamilton, USA, 2008 - invited
96. Invitation by Prof Dr Judah Denburg to attend AllerGen's 3rd annual research conference in Alberta Canada – discussant panel member as former GA^{2}LEN affiliate and scientific collaborator with birth cohorts work package, 2008. - invited
97. Unravelling the mysteries of genetic interactions – a statistical challenge, Liège, Belgium, 2007 - invited
98. Unravelling the mysteries of genetic interactions – a statistical perspective (Invited Speaker) Lausanne, Switzerland, 2007 - invited
99. Are we ready for genomewide association analysis? Quality of Life Unit Mediterranean Institute of Hematology (IME) (Invited Speaker) Rome, Italy, 2007. - invited
100. Genomic Complex, simplex, complexity and simplicity in statistical genetics (Invited speaker) Oncologisch Zorgprogramma UZ Ghent (Invited Speaker) UZ Ghent, Belgium, 2007 - invited
101. Perspectives on genomic association screening, Invited Seminar, UCL, Louvain-la-Neuve, Belgium, 2007. - invited
102. Are we ready? Invited Speaker, UMC, Utrecht, The Netherlands, 2007 - invited
103. Perspectives on genomic screening, Invited Seminar, ESAT - KUL, Leuven, Belgium, 2007. - invited
104. Statistical Consulting for the Clinic (Provisional title; Invited Speaker) UZ Ghent Biostatistics Workshop, Ghent, Belgium, 2007. - invited
105. Topics in Genetic Association Analysis (Invited Speaker) UCL, Belgium, 2007.
106. When the number of SNPs grows too large, Universitat Politècnica de Catalunya (UPC) Barcelona, Spain, 2006. - invited
107. When the number of SNPs grows, part II, Seminar Series on Complex Genetics, University Hospital Gasthuisberg Leuven, Belgium, 2006. - invited
108. When the number of SNPs grows, part I, Seminar Series on Complex Genetics, University Hospital Gasthuisberg Leuven, Belgium, 2006. - invited
109. Genomewide association screening using family-based association tests, Seminar at the faculty of Medicine at UZ Gasthuisberg (Afdeling Hypertensie en Cardiovasculaire Revalidatie) Leuven, Belgium, 2006. - invited
110. Genomic screening methodology for common diseases and complex traits, Organon, Oss, the Netherlands, 2006. - invited
111. Perspective on genomic screening in families, Invited Seminar, ESAT - KUL, Leuven, Belgium, 2006. - invited
112. Genomic Screening in Family Based Association Testing using the same Data, Invited research stay with talk at the Institute Municipal d'Investigacio Medica (IMIM) Barcelona, Spain, 2006. - invited
113. Genomic screening in family based association testing using the same data set and the multiple testing problem, IAP Workshop V on "Flexible statistical analysis adapted to complex data structures", UCL, Louvain-la-Neuve, Belgium, 2006. - invited
114. Genomic screening in family based association testing using the same data set and the multiple testing problem, Seminars in econometrics and statistics (invited speaker) Faculty of econometrics and applied economics, University Center for Statistics, KULeuven, Leuven, Belgium, 2006. - invited
115. Key concepts in genetic epidemiology, Seminars in epidemiology and clinical trials (invited speaker) Working group on epidemiology and center for clinical pharmacology, UZ St Rafael, Leuven, Belgium, 2006. - invited
116. Genomic screening methodology for common diseases and complex traits, CMGG Invited Seminars, University Hospital Ghent, Belgium, 2006. - invited

117. Genomic screening methodology for common diseases and complex traits, Seminar Series on Complex Genetics (Invited Speaker) Department of Psychiatry, University Hospital Gasthuisberg Leuven, Belgium, 2006. - invited
118. Genomic screening in family based association studies, Channing Laboratory FBAT seminar series, Harvard Medical School, USA, 2004. - invited
119. Genomic screening in family based association testing using PBAT, Invited talk at the department of molecular genetics (UA) organized by VIB-UA, Belgium, 2004. - invited
120. Exhaustive allelic transmission disequilibrium tests based on TDT, Channing Laboratory FBAT seminar series, Harvard Medical School, USA, 2004.
121. Statistical methods in psychiatric genetics, Pychiatric Biostatistics Seminar Series, Harvard School of Public Health, USA, 2003. - invited
122. Comparing DNA sequences using generalized estimating equations and pseudo-likelihood, Hasselt University Seminar Series, Belgium, 2002. - invited
123. Genetic associations using the multivariate Dale model, 3 Country Corner (3CC) Meeting, Belgium, 2002. - invited
124. The multivariate Dale model and genetic associations, Channing Laboratory FBAT seminar series, Harvard Medical School, USA, 2002. - invited
125. The multivariate Dale model and genetic associations, invited talk at Department of Epidemiology, Harvard School of Public Health, USA, 2002. - invited
126. An introduction into the genetic vocabulary (Part 1-4) Research forum Hasselt University, Belgium, 2001. - invited
127. The omnipresence of missingness in statistical genetics. Research forum Hasselt University- tUL, Belgium, 2001. - invited
128. Multiple imputation in practice, Research forum Hasselt University, Belgium, 2000. - invited
129. Analyzing longitudinal quality of life data with dropout; a macro oriented approach (Part 1-4) EORTC Seminar Series, Belgium, 1999. - invited
130. Estimation of genetic distances using statistical distance measures, University of Newcastle - school of mathematics and statistics, UK, 1998. – invited

Selection of poster presentations at international conferences in life sciences – as first or responsible author:

131. Capturing fine-level structure using unsupervised clustering method with multiple data types – ByteMal 2016 (author responsible)
132. A novel unsupervised clustering approach with multiple data types to reveal fine-level structure – ESHG2016 (author responsible)
133. Iterative pruning method of unsupervised clustering for categorical data – ICGH 2016 (author responsible)
134. Detecting Patient Subgroups Using Reduced Set Of Disease-Related Markers With Iterative Pruning Principal Component Analysis (IPPCA) – IGES2015 (author responsible)
135. Gene-based replication strategy and meta-analysis in the context of epistasis: application for Alzheimer's disease - Functional Genomics & Predictive Medicine Conference 2015 (author responsible)
136. LD-based haplotype encoding scheme with iterative pruning principal component analysis –HGM 2014 (author responsible)
137. A novel integrated framework for large scale association analysis - HGM 2014 (author responsible)
138. Genomewide epistasis screening for Alzheimer's disease – ACMG Phoenix 2013 (author responsible)

139. Identification of asthma-related trans-acting epistatic eQTL using Model-Based Multifactor Dimensionality Reduction - Annual Society of Human Genetics Annual Meeting 2013, Boston, USA (author responsible)
140. Genome-wide environmental interaction analysis using multidimensional data reduction principles to identify asthma pharmacogenetic loci in relation to corticosteroid therapy – Annual Society of Human Genetics Annual Meeting 2013, Boston, USA (author responsible)
141. Replication of large-scale epistasis studies: an example on ankylosing spondylitis – International Genetic Epidemiology Society (IGES) 2013, Chicago, USA (author responsible).
142. Application of mixed polygenic model to control for cryptic/genuine - abstract accepted for poster presentation at HGM 2012, Sydney, Australia (author responsible)
143. A robustness study of parametric and non-parametric tests in modelbased multifactor dimensionality reduction for epistasis detection - abstract accepted for poster presentation at HGM 2012, Sydney, Australia (author responsible)
144. Making sense of epistasic findings from different methodologies- abstract accepted for poster presentation at HGM 2012, Sydney, Australia
145. The impact of genotyping error on power and type-I error of quantitative trait genetic association studies – EMGM 2011, London, United Kingdom (author responsible)
146. Comparison of MB-MDR to BOOST and RAPID for detecting epistasis in unrelated - 6th EMR-IBS, Crete, Greece (author responsible)
147. Genome-wide epistasis screening for asthma associated traits – submitted for ISM2011 / Joint Statistical Meetings, Miami Beach, Florida USA (author responsible)
148. A detailed view on model-based multifactor dimensionality reduction with quantitative traits for detecting gene-gene interactions: different ways of adjusting for lower-order effects - Human Genetics Meeting 2011, Dubai, United Arab Emirates (author responsible)
149. A detailed view on model-based multifactor dimensionality reduction with quantitative traits for detecting gene-gene interactions: different ways of adjusting for lower-order effects – ESHG 2011, Amsterdam, the Netherlands (author responsible)
150. A robustness study to investigate the performance of parametric and non-parametric tests used in Model-Based Multifactor Dimensionality Reduction Epistasis Detection. International Genetics Epidemiology Society (IGES), Heidelberg, Germany, September 18-20, 2011.(author responsible)
151. Comparison Of Different Methods For Detecting Gene-Gene Interactions In Case-Control Data, IGES 2011 Heidelberg, Germany, 19 September 2011 (author responsible)
152. A detailed view on model-based multifactor dimensionality reduction with quantitative traits for detecting gene-gene interactions: different ways of adjusting for lower-order effects, HGM2011, Dubai, UAE (author responsible)
153. Got heritability lost in a world of interactions? HGM2011, Dubai, UAE
154. Using mixed models with a mixture of normal distributions for the random residual effect leads to a fast and powerful genomewide association test, IBC, Florianopolis, Brasil, 2010 (author responsible)
155. A detailed view on model-based multifactor dimensionality reduction with quantitative traits for detecting gene-gene interactions: different ways of adjusting for lower-order effects, IBC, Florianopolis, Brasil, 2010 (author responsible)

156. Model-Based Multifactor Dimensionality Reduction for detecting gene-gene interactions in case-control data in the absence and presence of noise, ASHG, Washington, USA, 2010
157. Elucidating the molecular etiology of asthma using genome-wide association study pathway analysis, ASHG, Washington , USA, 2010 (author responsible)
158. Model-Based Multifactor Dimensionality Reduction for detecting gene-gene interactions in case-control data in the absence and presence of noise, IGES, Boston, USA, 2010
159. Model-Based Multifactor Dimensionality Reduction to detect epistasis for quantitative traits in the presence of error-free and noisy data , IGES, Boston, USA, 2010 (author responsible)
160. Alternative risk cell definitions based on ranking improve performance of model-based multifactor dimensionality reduction for epistasis detection, IGES, Boston, USA, 2010 (author responsible)
161. A detailed view on several Model-Based Multifactor Dimensionality Reduction methods for detecting gene-gene interactions in case-control data in the absence and presence of noise, ECCB, Ghent, Belgium, 2010 (author responsible)
162. Model-Based Multifactor Dimensionality Reduction to detect epistasis for quantitative traits in the presence of error-free and noisy data, ECCB, Ghent, Belgium, 2010 (author responsible)
163. A family-based association test to detect gene-gene interactions in the presence of linkage (responsible author) IGES, Hawaii, 2009
164. Epistasis detection using MB-MDR, guided by prior biological knowledge (author responsible) IGES, Hawaii, 2009
165. Selecting multiple epistatic models using MB-MDR (responsible author). ASHG Annual Meeting, Hawaii, 2009
166. Selecting multiple epistatic models using MB-MDR (author responsible) BVS annual meeting, Lommel, Belgium, 2009
167. FAM-MDR: a novel multifactor dimensionality reduction method for interactions. UK-MEG2008, Barcelona, Spain, 2008.
168. MB-MDR based screening to detect high-order genetic interactions in (un-) related individuals. BBC2008, Maastricht, the Netherlands, 2008.
169. FAM-MDR: A flexible method of multifactor dimensionality reduction for high-order genetic interaction in related individuals, ASHG Annual Meeting, USA, 2008.
170. Genomic screening methodology for common diseases and complex traits, accepted poster at the Third Seattle Symposium in Biostatistics – statistical genetics and genomics, Washington, USA, 2005.
171. Genomic screening in family-based association testing, IGES Annual Meeting, the Netherlands, 2004.
172. The Multivariate Dale Model and Genetic Associations, ASHG Annual Meeting, USA, 2002.
173. Merits of the Multivariate Dale Model in Genetic Association Studies, IGES Annual Meeting, USA, 2002.
174. Merits of the multivariate Dale model in genetic association studies, EMGM, UK, 2002.
175. The omnipresence of missingness in statistical genetics – an equivalence test to compare DNA sequences, 1st Dutch-Belgian Biometric Conference (BBC2001) Belgium, 2001.
176. Introduction of the Multivariate Dale Model in Genetic Association Studies, ASHG Annual Meeting, USA, 2001.

d) Publications (including those for doctorate or study)

Available on ORBi

e) Scientific networking

<u>IN/ OUT:</u>

See Sections **III.4. a)** "organizational talent", **III.4. b)** "team spirit", **III.4. c)** "networking"

f) Participation to scientific groups or organizations

<u>Membership of scientific organizations:</u>

- Elected Scientific Program Committee Member for the European Society of Human Genetics (ESHG) (2014-2018)
- Elected member Board of Directors of the International Genetic Epidemiology Society (IGES) (2013-2016)
- Ambassador for Belgium & member of the International Genetic Epidemiology Society (IGES) (-2016)
- Elected board member of the Belgian Statistical Society (SBS-BVS) (2007-2009; 2010-2012; 2013-2015)
- Member of the Human Genome Organisation (HUGO) (-2017)
- Member of the International Genetic Epidemiology Society (-2017)
- Member of the International Biometrics Society (IBS) - 2011
- Member of the Quetelet Society (-2015)
- Member of the American Society of Human Genetics (ASHG) (-2015)
- Member of the Statistical Modeling Society (SMS) - 2013
- Member of the Belgian Society of Human Genetics (BeSHG) - 2013
- Member of the European Society of Human Genetics (ESHG) -2018

<u>Participation in committees with respect to research:</u>

In 2013-2018 (a selection)

- **ITN Marie Curie MLFPM 2018: 1 of 3 members of the Network Coordination Team, responsible for for instance monitoring organisation of summer schools and closing conferences, monitoring conduction of secondments, organisation of shorter training events (Online Seminar, ESR treat).**
- EU COST CA15120 Open Multiscale Systems Medicine (OpenMultiMed); MC member and WG 2 Co-leader (2016+)
- Expert evaluator In Trans-Domain-Proposals (COST open calls) (start: 2014)
- Expert evaluator for European Research Council (ERC); peer reviewer of scientific proposals submitted to the ERC Consolidator Grant 2016 Call for Proposals.
- Organising committee of team's conferences: short course and mini-conference in Liège "Capital selecta in complex disease analysis", CSCDA2014
- Elected SPC member for the European Society of Human Genetics (ESHG) (4 years, starting 2014)

- EU COST Pancreas BM1204 member of the management committee, steering committee, Belgian node representative and WG2 leader on "omics integration"
- EU Marie Curie ITN "Machine learning for personalized medicine", Belgian node leader, gender officer and member of the advisory board (since 2013)
- Organising committee of team's conferences: short course and mini-conference in Liège "Capital selecta in complex disease analysis", CSCDA2014 (CSCDA2016 was replaced by a Training School on Interactions)
- FWO interdisciplinary committee, "foreign expert" – since 1 Jan 2010, till 31 December 2015
- Participation in discussion group to create a new Thematic Research Unit on BioMedical Engineering Research (B-MER) (initiative taker: Lies Geris)
- Participation in the Statistical Analysis (sub-)Group(s) of the International Genetics IBD Consortium, in particular the groups on "interactions" and "molecular reclassification" (group leader: 2012+)
- Proposed Statistical Genetics member in the Scientific Committee of ESHG
- IGES ambassador for Belgium

In 2010-2012

- AERES expert evaluator for INSERM UNIT Florence Demenais (13 December 2012)
- Award committee member for the Dutch Biometry Award (2012)
- **Advisory committee ZAP/BOF Genetic neuroepidemiology for tenure track position of Kristel Sleegers (UA)**
- Programme committee of international scientific meetings (e.g., ISMB2010, BENELEARN 2012)
- Local scientific organizing committee of the Annual Meeting of the Belgian Statistical Society (BSS 2012)
- Organising committee of team's conferences: short course and mini-conference in Liège "Capital selecta in complex disease analysis", CSCDA2010, CSCDA2012
- Initiator of the Statistical Genetics Research Club, which aims to bring together people from different backgrounds, within Life Sciences, so as to stimulate discussions and provide a nutrient pool for growing novel and cutting-edge ideas in the field if statistical genetics and beyond.
- IGES ambassador for Belgium
- Elected board member of the Belgian Statistical Society
- FWO interdisciplinary expert panel (since 1 Jan 2010)

In 2008-2009

- IGES ambassador for Belgium
- Elected board member of the Belgian Statistical Society
- FRIA jury mathematics (2009)
- Organising committee: e.g., short course and mini-conference in Liège "Aspects in statistical genetics" (2008), BBC09
- Programme committees:
  - 18th annual Belgian-Dutch Conference on Machine Learning: BENELEARN 2009
  - Second International Workshop on Machine Learning in Systems Biology, MLSB08, Brussels (Belgium)
  - ECCB08, Cagliari – Sardinia (Italy)

- 17th annual Belgian-Dutch Conference on Machine Learning: BENELEARN 2008, Spa (Belgium)
- Steering committee member: ERBM workshop (Electronic Recognition of Bio-Molecules) Liège, Belgium

Prior to 2008 (a selection)

- Elected board member of the Belgian Statistical Society (since 2007)
- SBS/BVS Meeting 2002 – member of the scientific committee
- Member of the user committee for the project: "Het biotechnologisch potentieel in Belgium" (2000-2003) - DWTC (federale diensten wetenschapsbeleid) / IWT.
- Local organizing committee: European Mathematical Genetics Meeting, 13-15 April 2000, Diepenbeek, Belgium. (Ann. Hum. Genet. 2000, 64: 455-477)

Participation in task forces or follow-up meetings with respect to research:

- GIGA-R Medical Genomics Director (since 1 Jan 2016) / GIGA-R Systems Biology and Chemical Biology (SB&CB) Director (1 Jan 2014-31 Dec 2015)
- Follow-up activities related to the "Swiss Institute of Bioinformatics meets ULg" event, 15-16 December 2015, Lausanne. In particular, several follow-up meetings took place involving Prof Dr Murielle Bochud to establish a link between our groups and institutes, hereby facilitating exchange of researchers (PhD students / post-docs).
- ELIXIR – contact point in Liège (Wallonia) towards a national project proposal under the general coordination of Yves Van de Peer. Project successfully submitted in 2015
- Working group participant (WGs on 1. Registries, 2. Diagnosis) in the context of a novel Multi-Stakeholder Platform on Pancreatic Cancer (Kick-off meeting at EU Parliament on 12 November 2014; Chair: MEP Philippe De Backer)
- Connector between the Maastricht Center for Systems Biology (https://macsbio.maastrichtuniversity.nl/) and GIGA-R SB&CB, promoting inter-university research in systems biology (since January 2015).
- Initiator of two Global Research Working Groups: 1) Mixed Models for NGS and 2) Population/Patient Stratification in Omics (since January 2015).
- Work group leader for the International IBD Genetics Consortium on 1) "Reclassification of Crohn's disease and Ulcerative Colitis based on genetic marker data" (with Isabelle Cleynen) and 2) Epistasis
- Thematic research unit B-MER member (Biomedical Engineering Research) – since September 2014
- Representing COST EUPancreas at "Multi stakeholder platform on pancreatic cancer – EU Parliament (kick-off meeting 12 November 2014)
- UniGR Community "Systems biology and systems analysis in the Greater Region" (via UniGR community website – since 2014)
- Honorary member and participating scientist in the IUAP BeMGI (Belgian Medical Genomics Initiative) – since 2014
- EDGE (Epistasis Detection in Genetic Epidemiology) USA expert group – since February 2014
- Member of the thesis advisory committee of Iryna Nikolayeva (Institut Pasteur, Paris, France) in the context of building a future EU SYNERGY network on "integromics", involving Kiel (Germany), Madrid (Spain) and Oslo (Norway).
- "Big data handling in kernel methods" – joint collaboration between the teams of K Van Steen (ULg) and H Bickebӧller (University of Gӧttingen)

- Task force on omics involvement in population/patient stratification (STRATOMIX) – joint collaboration between the teams of K Van Steen (ULg), Inke König (Kiel), Anavaj Sakubanthai (Paris), Luisa Pereira (Porto), Dave Fardo (Lexington, USA), Ed Silverman (Boston, USA).
- Participation in the Statistical Analysis (sub-)Group(s) of the International Genetics IBD Consortium, in particular the groups on "interactions" and "molecular reclassification"
- EU ITN Marie Curie Action – node leader (since 2013)
- EU COST Pancreas BM1204 – node and WG leader (since December 2012)
- Participation in the Spanish Biostatical Network an opportunity given by the Spanish Ministry of Science and Innovation.
- Participation in the Harvard alumni scientific network.
- Member of the Interuniversity Attraction Pole (IAP – Phase VI): BioMAGNet on Bioinformatics and Modelling – from Genomes to Networks (2007-2011)
- Member of the FP7 PASCAL2 Network of Excellence Pattern Analysis, Statistical Modelling and Computational Learning (IST/ICT Programme of the European Community, IST-2007-216886 (since 2008)
- Member of the Interuniversity Attraction Pole (IAP – Phase VI): Statistical analysis of association and dependence in complex data (2007)
- Member of the Interuniversity Attraction Pole (IAP – Phase V): Statistical analysis of association and dependence in complex data (2006)

See also Sections
III.4. b) "team spirit" and **III.4. c)** "networking"

g) Obtained grants / scientific contracts

Obtained or under submission (obtained grants for organization of events and travel grants are not listed):

> Not submitting a project proposal will never lead to additional funding ... As competition increases, I see it essential to submit several project proposals, but quality prevails above quantity. Most national project proposals that I submit are coordinated by me. For the majority of European projects in which I am involved, I mainly play the role of "partner by invitation".

Year of submission	Type	Title / Description	Function	Funding	Status
2018	H2020-MSCA-ITN-2018 (ETN)	MLFPM: Machine learning frontiers in precision medicine	Partner node leader (coordinator : Karsten Borgwardt ETH Zurich)	Staff and operational costs	Accepted
2018	TÉLÉVIE	Molecular drivers and markers of pancreatic cancer initiation and progression: a translational and multidisciplinary approach (continuation of TELEVIE 2016 grant)	Co-applicant	Staff and operational costs	Accepted
2017	WELBIO – SGR (RENEWAL)	2-DESTinCT: DEtecting STastistical INteractions in Complex Traits (follow-up to DEST*in*CT)	Promotor	Staff and operational costs	Accepted
2016	FNRS-CDR	SysMedPC	Promotor	Operational costs (sequencing)	Accepted
2016	TÉLÉVIE	Molecular drivers and markers of pancreatic cancer initiation and	Co-applicant	Post-doc	Accepted

		progression: a translational and multidisciplinary approach (promotor: Ingrid Struman, ULg – GIGA)			
2015	WELBIO - SGR	DESTinCT: DEtecting STastistical INteractions in Complex Traits	Promotor	Staff and operational costs	Accepted
2015	TÉLÉVIE	PDAC-xome: Exome Sequencing in Pancreatic Ductal AdenoCarcinoma	Promotor	Operational costs	Accepted (reduced budget – no human resources)
2014	HORIZON2020	PAncreas Cancer risK: INtegratinG data towards a predictive model (acronym: PACK-Ing)	Partner (promotor: Nuria Malats, Spain)	Staff and operational costs	First stage proposal – accepted; Full proposal not accepted
2012	FP7-PEOPLE-2012-Marie Curie Initial Training Network	Machine Learning for Personalized Medicine	Partner (representing ULg) + Students' dean Promotor: Karsten Borgwardt, Max Planck, Tübingen, Germany)	Phd student exchange within the consortium	Accepted
2012	FNRS projet de recherche	Robust Machine Learning Forests in Network Construction for Integrative Omics Analyse	Promotor	Post-doc (2 years), doctoral student (4 years), and functioning budget	Accepted
2012	Zwaartekracht programma van NWO	Genen, omgevingsfactoren en inflammatore darmziekten; een "kip-en eiprobleem" (Gen-omgeving interactie in	Partner		Accepted

		het ontstaan en ziektebeloop van IBD)			
2012	COST (2nd stage proposal)	An integrated European platform for pancreas cancer research: from basic to clinical and public health interventions for a rare disease	Partner Promotor: Nuria Malats (CNIO, Madrid, Spain)	Travels, training, stages, workshops, conferences	Accepted
2012	ARC2012	Molecular dissection of inherited predisposition to inflammatory bowel disease (IBD-ULG)	Partner	Staff member (total budget: 1250000 EURO)	Accepted (reduced budget)
2010	FNRS projet de recherche	Integrated complex traits epistasis kit	Promotor	Post-doc (2 years), doctoral student (4 years), and functioning budget	Accepted
2010	Mandat de post-doctorat à l'ULg pour chercheur étranger	Associations génétique des taux d'IgE dans des échantillons de populations et de familles mis en commun.	Group Leader	Post-doc	Accepted
2007	Crédit de démarrage R.CFRA.0141	Association génétique des taux d'IgE spécifiques totaux et sériques dans des échantillons de populations caucasiennes et de familles mis en commun	Principal Investigator	88 000 EURO	Accepted
2007	Beques de recerca per a professors/res i investigadors/res	Strategies for the identification of genetic	Host Institute: University of Vic, Spain	2 250 EURO / month	Accepted (Only 3 out of 4 months were taken

	visitants a catalunya (piv 2007) - núm. expedient: 2007 piv 10018	variability associated with complex phenotypes.			up, in order to be able to fullfill the new commitments made at ULg)
2007	FWO onderzoeksproject G.0.410.08.N.10	Development of prevalence and determinants of asthma, COPD and allergies among adults in Flanders ; a follow-up study of the European Community Respiratory Health Survey (ECRHS)	Co-promotor (Promotor: Joost Weyler, UA, Antwerp, Belgium)	2008: 27000 EURO 2009: 22000 EURO 2010: 22000 EURO 2011: 10000 EURO	Accepted

For a complete list of submitted projects, see **Appendix 2 (success rate ~ 30% for local funding agencies; ~20 % for other funding schemes)**

h) Self-study time

<u>During study/research leaves:</u>

- Institut Pasteur, Paris, France (October 2017). Topic : Translational Systemics in practice (invited by Benno Schwikowski).
- Harvard University, Boston, USA (July 2017). Topic: Replication and Translating Statistical Interactions (Mark Vidal Lab - brainstorming) / Network Medicine for Patient Stratification (Amitabh Sharma lab – brainstorming)
- ETH Zurich (October 2016). Topic: personalized networks (invited by Karsten Borgwardt lab)
- Harvard School of Public Health, Boston, USA (May 2015 / October 2013 / April 2013 / November 2011 / November 2010 / November 2009 / October 2008). Topics: Network medicine / Omics integration / Population stratification / Meta-analytic approaches and missing data in GWAIs / Asthma genetics / Epistasis screening in genome-wide association studies / Using phenotypes in family members in genetic association testing.
- Short Term Scientific Mission (STMS), COST Action BM1204 "An integrated European platform for pancreas cancer research: from basic science to clinical and public health interventions for a rare disease. Topic 1: Integromics research in pancreatic cancer: garbage in, garbage out" (January 2015 – 1 week) / Topic 2: DNA/RNA seq data integration (April 2016 – 1 week)
- Institut Pasteur, Systems Biology (February 2015). Topic: Comparative and competing interaction tools for network analysis
- Penn State, Center for Systems Genomics, State College, USA (April 2013). Topic: Interactions versus integromics
- Seoul National University, South Korea (February 2013). Topic: Biological and statistical interactions
- Institut national de la santé et de la recherché médicale (INSERM / Florence Demenais) in Paris, France (July, November 2009). Topic: jointly testing of groups of markers; setting out a strategy for new project proposals.
- Departament de Biologia de Sistemes, Universitat de Vic, Barcelona, Spain (December 2008 – January 2009, February 2010). Topic: Incorporating machine learning techniques in the search for epistatic effects.
- Departament de Biologia de Sistemes, Universitat de Vic, Barcelona, Spain (May – June 2008). Topic: Genetic interactions – methodological developments for large-scale screening.
- Municipal Institute of Medical Research (IMIM) Barcelona, Spain, 2007 and 2006 (invited by Dr M Kogevinas). Topics: Missing SNPs in candidate genes / Non-parametric techniques to detect epistasis in ECRHS II data set.
- Department of biostatistics, HSPH, Boston, USA, 2005 and 2002 (invited by Dr N Laird). Topics: Optimalization of FBAT screening methodology / Research on the use of the Dale model in genetic association studies.

III.4. Additional competences

a) Competence 1: Organizational talent

Organization of conferences, study days, work shops:

> I consider achieving visibility as an important component of research. This includes the communication of research results, whether preliminary or final, at international conferences, but also during smaller national and international scientific meetings, allowing for a higher degree of interaction and discussion.

	Speaker	Affiliation	Date	Location	Description
Mini-workshop	Peter van der Spek /Chloe Azencott/ Emmanuelle Génin	EMC Rotterdam, The Netherlands Mines ParisTech, France / INSERM Brest, France	/8-9/2018	ULg	Invited jury members of thesis defense Ramouna Fouladi
Mini-workshop	Anavaj Sakuntabhai / Peter van der Spek / Luisa Pereira	Institut Pasteur, Paris, France/ EMC Rotterdam, the Netherlands/ Porto University, Porto, Portugal	06/10/2017	ULg	Invited jury members of thesis defense Kridsadakorn Chaichoompu
Mini-workshop	Monika Stoll / Benno Schwikowski	University of Münster, Germany / Institut Pasteur, Paris, France	04/07/2016	ULg	Invited jury members of thesis defense Kirill Bessonov

Mini-workshop	Inke König / Peter Van der Spek	Universität zu Lübeck, Germany / Erasmus MC, Rotterdam, The Netherlands	14/06/2016	ULg	Invited jury members of thesis defense François Van Lishout
Training School of COST Action BM1204 (WG2) / CSCDA2016	http://eupancreas.com/meetings-events		27-29 April 2016	Antwerp, Belgium	Training school organized by WG2 on "omics integration", as part of BM1204. Co-sponsored by the Belgian Society of Statistics.
Medical Genomics seminar – section BIO3	Maggie Wang	University of Hong Kong	26 April 2016	Liege, Belgium	A fast and powerful W-test for pairwise epistasis testing
Workshop: Omics Integration in PDAC	http://eupancreas.com/meetings-events		1 July 2015	Barcelona, Spain	"Cancer genomics and personalised medicine workshop: focus on pancreas cancer" Organized by WG2 on "omics integration" as part of BM1204. Local organizer: Nuria Lopez-Bigas
Conference with short course : Capita Selecta in Complex Disease Analysis (CSCDA2014) COST WP2 Meeting	http://www.statgen.ulg.ac.be/CSCDA2014/cscda2014.html		24-26/11/2014	Liège, ULg - GIGA	3rd Edition of biennial Conference organized by ULg, in collaboration with 1 extra French-speaking university in Wallonia/Brussels and 2 universities in Flanders. This edition part focusses on pancreatic cancer and is organized in conjunction with

					the Annual Meeting of the COST Action BM1204. The short course is seen as an extra deliverable for the COST Action BM1204, WG2 (Omics Integration; coordinator: K Van Steen)
SB&CB seminar – section BIO3	Gaëlle Marenne	Wellcome Trust Sanger Institute, Human Genetics Programme, UK	27/6/2014	GIGA	The importance of allele-specificity in complex disease analysis
SB&CB seminar – section BIO3	Fabian Tibaldi	GlaxoSmithKline Biologicals – biostat expert leader	11/6/ 2014	GIGA	TBA
BIO3 seminar series @ GIGA	BIO3 Team members (F Van Lishout, F Gadaleta, K Bessonov, K Chaichoompu, R Fouladi, S Pineda)		9 , 23 , 28 , 5 June, 17 June, 27 June 2014	GIGA	Bridging the gap between research and practical applications / consulting
SB&CB seminar – section BIO3	Jelle Goeman	Radboud University Medical Center in Nijmegen, the Netherlands	16 /5/ 2014	GIGA	Flexible multiple testing corrections
Workshop	Nuria Lopez-Bigas/ Yves Moreau / Simon Forbes / Claude Chelala	University Pompeu Fabra, Spain / KU Leuven University, Belgium /	14/2/2014	Heidelberg	This training workshop is organized by WG2 (omics integration) of the EU COST Action on pancreatic cancer. Coordinator of WG2: K Van Steen

		Wellcome Trust Sanger Institute, UK/ Barts Cancer Institute, UK			
	Florian Frommlet	Medical University of Vienna / Center for Medical Statistics, Informatics, and Intelligent Systems (Section for Medical Statistics)	17/5/2013	ULg	Optimal selection procedures in GWAs
Mini-workshop	Florence Demenais / Marylyn Ritchie / Nuria Malats	INSERM U794, CEPH, Paris, France / Penn State Biochemistry and Molecular Biology, USA/ CNIO Madrid, Spain	20/12/2012	ULg	Invited jury members of thesis defense Jestinah M Mahachie John
	Silvia Pineda	Genetic and Molecular Epide-miology Group Human Cancer Genetics Programme (CNIO)	30-6/06/2012	ULg	Start of joint phd and research projects ULg/CNIO. Research visit to StatGen Montefiore, GIGA-R and CHU on omics integration in bladder cancer

Conference with short course : **Capita Selecta in** **Complex Disease** **Analysis (CSCDA2012)**	www.statgen.ulg.ac.be		30/05-1/06/2012	Liège	2nd Edition of biennial Conference organized by ULg, in collaboration with 1 extra French-speaking university in Wallonia/Brussels and 2 universities in Flanders
	Stijn Vansteelandt	Ghent University - Department of Applied Mathematics and Computer Science	20/04/2012	ULg	Gene-environment interactions
	Georgi Nalbantov	Maastricht University	04/11/2011	ULg	Data integration based on similarity matrices
	Bärbel Maus	Maastricht Univer-sity - Department of Methodology and Statistics	23/09/2011	ULg	Optimal experimental designs for functional magnetic resonance imaging
COMED FP7 kick-off meeting			21/06/2011	Brussels, Belgium	
Workshop: "UA meets ULg"	K Van Steen (moderator)	Montefiore, ULg, Belgium	02/02/2011	ULg	Joint meeting of UA, CHU and Montefiore research teams: exploring common grounds. UA contact point: Prof Joost Weyler
	Jean-Charles Lambert	Institut Pasteur de Lille, France	28/01/2011	ULg	Genetics of Alzheimer's disease
Conference with short course : **Capita Selecta in** **Complex Disease** **Analysis (CSCDA2010)**	www.statgen.be		25-27/08/2010	Leuven City, Belgium	1st Edition of biennial Conference organized by ULg, in collaboration with 1 extra French-speaking university in

					Wallonia/Brussels and 2 universities in Flanders
	Rudy Parker	Golden Helix, Inc, USA	24/08/2010	ULg / GIGA	Golden Helix features for CNV GWAS and Imputation efforts
	P Konings	ESAT, Leuven, Belgium	28/05/2010	ULg	Fast computing in R and beyond
	K Van Steen	Montefiore, ULg, Belgium	12/05/2009	KUL	Evaluation of the Statistical Genetics Research Club : Research and Discussion
	B Müller-Myhsok	Max-Planck-Institute of Psychiatry, Munich, Germany	02/07/2009	ULg	Novel techniques in statistical genetics
	Y Aulchencko	Erasmus MC Rotterdam, the Netherlands	23/03/2009	ULg	Pedigree-based association testing
Summer Sabbatical at Montefiore – Ulg (Belgium)	A Ziegler	Universitaet zu Luebeck, Luebeck, Germany	21/11/2008	ULg	Gene-gene and gene-environment interactions
	L-C Tranchevent	ESAT, KUL, Leuven, Belgium	18/11/2008	ULg	Gene prioritization (involves bioinformatics students ULg about ENDEAVOUR)
Conference with short course: Statistics in Genetics	www.statgen.be		15-18/09/2008	ULg	Co-organized by K Van Steen (Montefiore) and G Haesbroeck (Département de mathématique) Subsides aux écoles doctorales thématiques (département des Sciences de la Vie ;

					département des sciences biomédicales et précliniques ; département d'astrophys, géophysique et océanographie ; département des sciences de la santé)
	G de Cooman	SYSTeMS Research Group, UG, Ghent, Belgium	12 /08/2008	ULg	Trying to be more honest about probabilistic modelling : a case study involving Markov chains
	H Van Maldeghem	Pure mathematics and computer science, UG, Ghent, Belgium	18/04/2008	ULg	From real estate denomination to pure mathematics and back to real life
Kick-off Meeting Statistical Genetics Research Club (www.statgen.be)	K Van Steen (Montefiore) and G Haesbroeck (Département de mathématique / Statistique mathématique)		08/04/2008	ULg	**Setting goals and aims** This research club aims to bring together people from different backgrounds, within Life Sciences, so as to stimulate discussions and provide a nutrient pool for growing novel and cutting-edge ideas in the field of statistical genetics. **Achieving the goals** ▪ by organizing introductory sessions to establish a common language ▪ by hosting seminars with state-to-the-art approaches

					▪ by reading, presenting and discussing key papers, from conception of ideas to current common practice, to "grow" into a problem area **Club House** ▪ Institut Montefiore / Bioinformatique (at ULg) ▪ Services de Statistique de l'Institut de Mathématique (at ULg)
Short course	Lecturers N Laird and C Lange (Harvard School of Public Health, USA) and tutorial responsible A Murphy (Harvard School of Public Health, USA)		11-13/09/2006	Ghent University, Belgium	Specialized course "Family-Based Genetic Association Testing". Organized within the context of "Continuing Education at Ghent University". Focus: FBAT/PBAT methodology and related software. Organization: combining lectures and computer tutorials with hands on data analyses.
Short course	Joe Terwilliger (Columbia University, USA) and John Blangero, Laura Almassy (Texas Biomedical Research Institute, USA)		2002	LUC, Diepenbeek Belgium	Specialized course on Linkage Analysis

Legend: italic = scheduled future events

b) Competence 2: Team spirit

<u>Scientific consulting ULg (2008-present):</u>

Contact	Institution	Start	Topic
Grégoire Noël	ULg - Functional and evolutionary entomology	2016	Bee classification (using in-house developed molecular reclassification techniques for complex diseases)
Agnès Noël	GIGA Cancer	2016	Integrative analysis in age-related macular degeneration
Vincent Castronovo/ Andrei Turtoi/Akeila Bellahcène	GIGA Cancer – Institut de Pathologie	2015	Metastases research
Marcela Chavez/Ingrid Struman	CHU Centre Intégr´d'Oncologie du CHU, Liege	2014	Oncostatistics
Masendu Kalenga	Neonatal Intensive Care Unit, Ulg, CHR Citadelle	2014	Longitudinal study of inflammatory mediators in prematurely born infants, which will include analysis of causality among various factors
Bernard Peers	GIGA – development	2014	RNA-seq analyses
Florence Schleich	Ulg / CHU- Respiratory Medicine	2014	Biostatistical analysis
Renaud Louis / Christophe Desmet /	Ulg / CHU- Respiratory Medicine	2013	Subphenotyping IBD patients (projet IIBDGC)
Franck Trolliet	Primatology Research Group Ulg, Behavioral Biology Unit	2012	Spatial statistics
Eric Salmon / Christophe Phillips	Cyclotron and memory centre – CHU, Liège	2014 2011	Collaboration in FNRS post-doctoral mandate submitted January 2014 (promotor: Christophe Phillips) The genetics of Alzheimer's disease
Fréderic Farnir / Tom Druet	GIGA-R	2010	Non-parametrics in epistasis mapping / Genomic selection models for complex diseases in humans – imputation strategies (with Prof S Vermeire – KU Leuven)
Liesbet Geris	Ulg – Département d'aéro-spatiale et mécanique	2010	Component based, Network and Integrative approaches in bone tissue engineering
Damien Ernst	Ulg – Institut Montefiore	2010	Random Rotations to find your way in the Random Jungle

Edouard Louis	Ulg – Département des sciences cliniques	2010	Genetics of inflammatory bowel disease in the light of the International IBD Genetics Consortium
Michel Georges	Ulg – Département de productions animales / GIGA-R : Génomique animale	2013	Finding IRF8 targets Omics analyses of healthy controls Sex-specific genomic IBD analysis
		2010	Strategies with medical applications for the identification of gene-gene and gene-environment interactions and multiple causal variants with complex phenotypes.
Vincent Bours	Ulg – Département des sciences biomédicales et précliniques / GIGA-R : Génétique générale et humaine	2014	RNA-seq analysis methodologies; compatability of RNA-seq and ChiP-seq analysis results (with Claire Josse and Stéphan Wenric)
		2010	Strategies with medical applications for the identification of gene-gene and gene-environment interactions and multiple causal variants with complex phenotypes.

Scientific consulting for other Belgian institutions:

Contact	Institution	Start	Topic	Status	Public.
Ann Gils	KU Leuven, Therapeutic and Diagnostic Antibodies – Dept of Pharmaceutical and Pharmacological Sciences	2016	Multivariate data analyse; Data mining	Ongoing	
Hilde Peeters	UZ Leuven Gasthuisberg Belgium	2015	Family-base genomic analysis / Modern genetic epidemiology	Ongoing	

Paul Coucke	UZ Gent Belgium	2015	Various topics in human genetics: advice on study design and analysis	Ongoing	
Li Zhe	UZ Leuven Gasthuisberg Belgium	2015	Foxp3(+) Regulatory T-cell Subsets and Foxp3(-) Type 1 Regulatory-like T Cells	Finished	x
Ina Callebaut	UZ Leuven Gasthuisberg Belgium	2014	Clinial Trials statistics	Finished	
Bart Lemmens	UZ Leuven Gasthuisberg Belgium	2014	Multilevel modeling	Finished	
Eveline Hoefkens	UZ Leuven Gasthuisberg Belgium	2013	Functional role of Crohn disease risk alleles involved in microbial sensing	Finished	x
Fimoneen Haerynck	UZ Ghent	2013	Genetic variation in toll-like receptor pathway	Finished	x
Thomas Billiet	UZ Leuven Gasthuisberg Belgium	2012	Familial aggregation in the response to anti-TNF in inflammatory bowel disease patients	Finished	x
Magali De Bruyn / Marc Ferrante	UZ Leuven Gasthuisberg Belgium	2012	Optimal test development via ROC analysis	Finished	x
Filip Baert	H Hart Kliniek Roeselare	2012	Gastro-enterology Stomach, Intestinal and Kidney Disorders	Finished	
Jurgen del Favero	Multiplicom	2011	Trisomy non-invasive statistical test	Finished – paid consult	
Bart Loeys / Lut Van Laer	Universiteit Antwerpen Medische Genetica	2014 / 2011	NGS analysis pipeline / Marfan syndrome	Ongoing	
Ann Gils	Laboratory for Pharmaceuti-cal Biology KULeuven	2013 – 2014 / 2011	CIFs / Pharmacokinetic/Pharmacody namic modeling of anti-TNF therapeutics	Finished	x
Gert Van Assche	UZ Gasthuisberg Leuven Belgium	2011	Predicting clinical response to anti-TNF therapy	Finished	x
Clementine Perrier	UZ Leuven Gasthuisberg Belgium	2011	Mouse model analysis	Finished	x

Niels Vande Casteele	KUL Laboratory for Pharmaceuti-cal Biology	2011	TAXIT	Finished	x
Mira Wouters	KUL Translational Research Center for Gastrointestina l Disorders	2011	Inflammatory Bowel Syndrome (IBS)	Finished	x
Lucia Marquez	UZ Leuven Gasthuisberg Belgium	2011	Effects of haptoglobin polymorphisms and deficiency on susceptibility to inflammatory bowel disease and on severity of murine colitis	Finished	x
Katrijn op de Beeck	UZ Leuven Klinische Biologie Immunologie	2011	Heterogeneous nuclear ribonucleoproteins as targets of autoantibodies in systemic rheumatic diseases	Finished	x
Yvan Vandenplas	Univerisitair Kinderzieken-huis Brussel Belgium	2010	Domperidone study	Finished	x
Gigi Veereman	BESPGHAN (Belgian Society for Paediatric Gastroentero-logy Hepatology and Nutrition)	2010	Belgian Pediatric data base statistical analysis	Finished – paid consult	x
Christine Breynaert	UZ Leuven Gasthuisberg Belgium	2010	Tolaribility of shortened infliximab infusion times	Finished	x
David Drobne	UZ Leuven Gasthuisberg Belgium	2010	Infliximab combo project	Finished	x
Christoph Metaldis	UZ Leuven Gasthuisberg – Belgium	2010	Genetic association studies with clinical and histological outcomes in nephrology	Finished	
Liesbeth Viaene	UZ Leuven Gasthuisberg – Belgium	2010	Long-term evolution of serum and urine parameters for patients in peritoneal dialysis	Finished	x
Hilde Peeters	UZ Leuven Gasthuisberg – Belgium	2010	Suitable family-based association screening techniques	Finished	

Greet Van Den Berghe / Ilse Vanhore-beek	UZ Leuven Gasthuisberg – Belgium	2010	Disturbances in energy metabolism and the control of inflammatory responses in critical illness: role of genetic predisposition Mitochondrial DNA analyses for subgroup identification	Finished	
Sylvie Seeuws	UZ Gent – Belgium	2010	Pros and cons of WHAP analysis	Finished	
Hans Vermeesch	UZ Gent – Belgium	2009	Dealing with X-inactivation in genetic	Finished	
JM Kaufman	UZ Gent – Belgium	2009	Follow-up on genetic screening for osteoporosis in men; confirmation sought in Swedish population	Finished	
Vanessa Vermeirs-sen	VIB UG – Belgium	2009	Converting learning module networks for microarray expression data to general human complex disease applications	Finished	
Lotte Moens	VIB UA – Belgium	2009	X-MDR epistasis screening and interaction graphs	Finished	x
Nathalie Vermeulen	UZ Leuven Gasthuisberg – Belgium	2009	Protoarray data analysis	Finished	x
Philip Gevaert	UZ Gent – Belgium	2008	Anti-IL5 analysis	Finished	x
Claus Bachert	UZ Gent – Belgium	2008	IgE association study	Finished	x
Nicholas Van Bruaene	UZ Gent – Belgium	2008	Sinusitis cohort sampling design and analysis	Finished	
Daan De Maeseneer / Simon Van Belle	UZ Gent – Belgium	2008	Data base construction of national breast cancer data Quality of Life analysis in breast cancer patients	Finished	x
Filomeen Haerynck	UZ Gent – Belgium	2008	Extensive genetic analysis on pseudonoma: main effects and interaction analyses	Finished En cours	x
Maaike Alaerts	VIB UA – Belgium	2008	FBAT analysis and X-MDR epistasis screening	Finished	x
Ingrid Arijs	UZ Leuven Gasthuisberg – Belgium	2008	Support in statistical analysis of microarray data in inflame-matory bowel disease patients	Finished	x

Isabelle Cleynen	UZ Leuven Gasthuisberg – Belgium	2008	Epistasis and multi-locus analysis in Crohn's disease The power of the X-chromosome (former contact person Isabel Verstreken)	Finished Help in start-up	
Herma Fidder	UZ Leuven Gasthuisberg – Belgium	2008	Immortal time bias	Finished	x
Matthias Jürgens	UZ Leuven Gasthuisberg – Belgium	2008	CRP profile analysis	Finished	x
Liesbet Henckaerts	UZ Leuven Gasthuisberg – Belgium	2007	Genetic risk profiling and prediction of disease course in Crohns disease patients	Finished	x
Marc Ferrante	UZ Leuven Gasthuisberg – Belgium	2007	Serological marker in inflammatory bowel disease	Finished	x
Marie Joossens	UZ Leuven Gasthuisberg – Belgium	2006	Bacterial gut flora: analysis	Finished	x
Johannes Ruige	UZ Gent – Belgium	2006	Genetic association study for type I diabetes	Finished	
Patricia Crabbe	UZ Gent – Belgium	2006	Optimal marker selection for genetic association studies in families	Finished	
Mario Van Poucke	UG – Belgium	2006	PNRP polymorphisms associated with PRNP mRNA expression in blood in Belgian sheep population	Finished	
Sofie Bekaert	Bioscope-IT/ UG, Belgium	2006	Experimental designs and formulation of requirements to set up a biostatistical platform service bridging university and university hospital	Finished	
Youri Taes	UZ Gent – Belgium	2005	Variance components analysis of SIBLOS data	Finished	x
Jacques Vanobber-gen	UZ Gent – Belgium	2005	Oral hygiene of elderly people in long-term care institutions	Finished	
Jan Hellemans	UZ Gent – Belgium	2005	Statistical approaches to labo-ratory 105alibration problems	Finished	
Sofie Joossens	UZ Leuven Gasthuisberg – Belgium	2005	Month of birth and Crohn's disease	Finished	x
Marieke Pierik	UZ Leuven Gasthuisberg – Belgium (currently in	2004	How to make sense of mixed families when inflammatory bowel disease is involved?	Finished	x

Sofie Joossens	UZ Leuven Gasthuisberg – Belgium	2004	Pancreatic autoantibodies in inflammatory bowel disease	Finished	x
Maastricht University)					
Liesbeth Bruckers (former co-coordinator consult Uhasselt)	TIBOTEC-VIRCO // HIS// DWTC// OECD	2000 - 2003	HIV longitudinal analysis// Evaluation of the Belgian Health Interview Survey 1997 // New sampling strategies for health surveys and non-response analysis// Belgian statistical representative; mapping biotech activities in Belgium for policy makers	Finished	

Legend: x = paper available or to be expected

Scientific consulting other countries:

Contact	Institution	Start	Topic	Status	Public.	Country
Damian Roqueiro / Karsten Borgward	ETH Zurich: machine learning and computational biology	2015	Optimized epistasis detection (COPD)	Ongoing	x	Germany
Inke König	Institut für Medizinische Biometrie und Statistik Universität zu Lübeck, Lübeck	2015	Implementation and interpretation of GammaMaxT in MB-MDR on real-life genome-wide data	Ongoing	x	Germany
Chih-Mei Hettler-Chen	Charité	2014	Bridging the gap between the environment and genetics	Effective start: Easter 2014	(special issue on enviro-integromics)	Germany
Heike Bickeböller	Department of Genetic Epide-miology – University of Göttingen	2014	Kernel methods in association testing	Effective start: Easter 2014 – site visit by post-doc of BIO3 team completed		Germany

Tom Hemming Karlsen	Norwegian PSC Research Center	2014	HLA region infrastructure	Ongoing	x	Norway
Anavaj Sakuntabhai	Institut Pasteur, Genomes and Genetics	2014 2012	Finding fine population substructure GWAI of malaria	Ongoing Started up after Easter 2012 - ongoing	x (first joint authorr: K Bessonov)	France
Andre Franke	Institute of Clinical Molecular Biology Christian-Albrechts-University of Kiel	2012	GWAI of psoriasis	Practical applica-tion to methods paper		Germany
Emmanuelle Génin	Inserm U946 Fondation Jean Dausset - CEPH	2011	The stability of PCs in population stratification assessment	Ongoing	x	France
Jean-Charles Lambert	Institut Pasteur de Lille	2011	GWA epistasis screening in Alzheimer's patients	Start-up in April 2011 – ongoing	x	France
Angela Brand	Institute for Public Health Genomics (IPHG) Cluster of Genetics & Cell Biology Faculty of Health, Medicine and Life Sciences Maastricht University	2011	Omics Integration for Personalized Medicine – incorporating "dynamics"	Kick-off meeting Decem-ber 2011 ongoing	x (EU COST BM1204 publ.)	The Netherlands
Olga Savenije	University Medical Center Groningen – The Netherlands	2010	Epistasis analysis on latent class membership categorical variables using MB-	ongoing	x	The Netherlands

			MDR methodology			
Matthias Riemen-schneider	Universitäts-klinikum des Saarlandes	2010	Family-based association testing of mental health-related phenotypes	First contacts made		Germany
Thomas Ochsenkühn	Klinikum Großhadern, Munich	2010	Retrospective cohort analysis on the effects and side effects of immunomodulator therapy in the context of inflammatory bowel disease	paid consult	x	Germany (K Van Steen invited as principal statistician of the study)
Lude Franke	University Medical Center Groningen	2009	Application of MB-MDR to expression trait values	ongoing		The Netherlands
Harold Snieder	University Medical Center Groningen – The Netherlands	2008	Statistical analysis of genetic data in twins using FBAT and MDR methodology	ongoing	x	The Netherlands
Fabian Schnitzler	Klinikum Grosshadern, Munich, Germany (formerly: UZ Gasthuisberg – Belgium)	2008	Pregnancy and the effect of IBD treatment regimens	finished	x	Germany

Legend: x = paper available or to be expected

Social service / Consulting (< 2005):

E.g,
- ZOL: multivariate data analyses
- TIBOTEC –VIRCO: HIV longitudinal data analysis
- OESO /OECD: Mapping biotech activities in Belgium to adjust current policies
- HIS: Evaluation of the Health Interview Survey 1997
- DWTC: Non-response analysis and new sampling strategies

c) Competence 3: Networking

> Being smart and being eager to learn is not enough to score high on a career ladder. This is true not only for jobs in the private sector, but also for research/teaching positions. Apart from performance and productivity, establishing and maintaining a network of influential people, cooperation and sharing, are important when further developing my career. Several of them have written **support letters** for me in the past (e.g.; full professor promotion; see **Appendix 3**).

Personally established network:

Contact	Institution	Start	Topic	Additional info	Country
In Europe					
Chris Aertsens	ILFARO - Solution Focused Coaching, Training and Consultancy	2017	Team coaching	Organisatie-ontwikkeling en communicatie	Belgium
Peter Jacobs	ThermoFisher Scientific	2016	Biofluids	Clinical Business Developer	Belgium
Denis Horgan	European Alliance for Personalised Medicine (EAPM)	2015	Facilitating Pancreatic Cancer Research in Europe	Executive Director	Belgium
Philippe De Backer	European Parliament (MEP)	2014	Multi-stakeholder Platform on Pancreatic Cancer	Initiative taker to create EU opportunities to combat pancreatic cancer (links to activities of KVS in COST Action BM1204)	Belgium
Yvan Saeys	VIB Ghent; Inflammation Research Center	2014	Machine learning meeting statistics	Group leader in search for active topics in human genetics	Belgium

Cornélie Terlez	EUCOPE	2014	European confederationof pharmaceutical entrepeneurs AISBL / legal aspacts (patents, etc.)	Communications Officer	Belgium
Jeroen Raes	Systems Biology VUB / KUL	2014	The gut flora	Contact person for Infect-ERA follow-up projects with Institut Pasteur, Paris, France Gateway to MetaHIT consortium (P Bork)	Belgium
Niko Speybroeck	Institut de recherche santé et société -UCL	2014	Malaria ; Conditional inference trees; Spatial statistics	Expert biostatistics in FWO Interdisciplinary committee	Belgium
Stéphane Schurmans	Functional Genetics Laboratory / GIGA	2014	Alzheimer disease : knocking out identified interacting genes in AlzD		Belgium
Luc Bijnens / Tine Casneuf	J&J pharma	2014	Bioinformatics data applications	Janssen Pharmaceutica - Biometrics and Clinical Informatics / Bioinformatics and Systems Biology	Belgium
Fabian Tibaldi	GSK	2014	Clinical biostatistics	Contact person to set up exchange programs between ULg students and big pharma	Belgium
Paul Coucke	Ghent University – dept of medical genetics	2014	Genetic causes of Hypermobility		Belgium
Veronique Feys	BELSPO	2014	Establishing research networks in Belgium	Contact person for IUAP programs	Belgium
Coen Corneels	EORTC	2014	BIO3 statistical collaborative	Representative of EORTC Brussels:	Belgium

			projects (research / education) + Pancreatic cancer research (EU COST Pancreas)	contact person for collaborations with -) CRP of GI group -) Head of stats department -) chairman of Pancreatic Task Froce of the GI group (JL Van Laethem)	
Paul Rietjens	Foreign Affairs, Foreigh Trade and Development Cooperation	2013		Director General of Legal Affairs	Belgium
Dirk Van Dyck	University of Antwerp	2012		Lead to Emmanuel Gustin, Principal scientist at Tibotec.j&j / Annie Cuyt at Department of Mathematics and Computer Science - University of Antwerp	Belgium
Fernando Ulloa Montoya	GSK	2012	part I: Development of a predictive Companion Diagnostic assay in the ongoing MAGE-A3 Phase III clinical studies – classification methodologies development part II: Better understanding ASCI mode of action through integration of different type of markers		Belgium
Léon Van Rompay	UTERON Pharma	2012		Chairman	Belgium
Andrew Bottomley	EORTC	2012	Quality of Life Genomics		Belgium

Stijn Van-steelandt	Ghent University	2012	Semi-parametric testing for gene-gene or gene-environment interactions	Creation of WG on DTR (dynamic treatment regimen) in Belgium	Belgium
Herman Van Oyen/ Sylviane De Viron	Scientific Insitute of Public Health/ Jules Bordet Instituut	2012	Genetic pathways influencing smoking cessation		Belgium
Jan Ramon		2012	Integrative nomograms	Lead to FuturICT	Belgium
Geert De Meyer	Bayer Bio-Science N.V. – Zwijnaarde	2011		Head Biometrics	Belgium
Margo Hagendo-rens	University of Antwerp	2011	Kindergen. & neonatologie		Belgium
Marc Zabeau	Ugent Tech Transfer	2010	Integration of biological network approaches	General manager	Belgium
Joost Weyler	University of Antwerp	2010	Epidemiology of asthma		Belgium
Yves vande Peer	VIB UGent	2009	Integrating bioinformatics interaction tools to detect epistasis in predictive models		Belgium
Geoffrey Henno	Per4mant Solutions	2009	Sales activities for Life Science supply and service companies, catalyzing the exchange of knowledge, ideas and technological expertise.	General manager	Belgium
Guy Van Camp	University of Antwerp, Belgium	2009	CIDR grant on Genome-wide Association Analysis of otosclerose		Belgium
Wouter Van Gool /Mark Veugelers	VIB RUG, Ghent	2008	Introduction of Statistical Genetics approaches in emerging technologies of life sciences	Integration Manager VIB	Belgium
Gert De Cooman	SYSTeMS research group RUG, Ghent	2008	Probabilistic 112odeling versus imprecise		Belgium

			probability 113odeling: pros and cons in genetic screening		
Claus Bachert	University Hospital Ghent	2005	Common and differential properties of upper and lower airways disorders, in different ethnic groups	Preparation to NIH grant applications (e.g., in collaboration with Dr De Yun – University of Singapore)	Belgium
Séverine Vermeire / Paul Rutgeerts	UZ Gasthuis-berg, Leuven	2000	Real-life data problems leading to biometric applications and methodological developments in the context of IBD	Lead to consortium IBD Genetics International	Belgium
Bob Vlietinck	KUL, Leuven	1999	Statistical Genetics and Complex Disease Analysis	Emeritus	Belgium
Andrew Bottomley	E.O.R.T.C. (European Organisa-tion for Research and Treatment of Cancer) Brussels	1998	Quality of Life data in oncology	Directeur du centre QoL	Belgium
Adrian Geismaier		2014	webstudio	IT consultant / Project manager	Denmark
Jukka Tuomi	FIRPA	2016	Research Director; President of FIRPA	Engineering design and production; Advanced production methods	Finland
Lars Rogge		2014	Immunology of Ankylosing Spondylitis	Head of Immuno-regulation Unit and CNRS URA 1961 - Department of Immunology	France
Anavaj and Laura team		2013 2012	Population stratification software development and application HyperCube		France

			Investigating omics links between malaria and inflammatory diseases		
Jean-Charles Lambert	Institut Pasteur de Lille	2011	Genetics of Alzheimer's disease: in search for evidence of epistasis		France
Sophie Lebre	INSERM UMR 915	2009	Inferring changes in regulartory network structures from gene expression data		France
Florence Demenais	INSERM U794	2005	An integrated view on how to make sense of GWAs	Lead to GABRIEL consortium/ EU FP COMed consortium core member	France
Francine Kauffmann	Institut National de la Santé et de la Recherche Medicale (INSERM), France	2005	European studies of air pollution effects		France
Anita Schweiger	Rs Media GmbH	2014	Medical writer	Connected to EU Multistakeholder Platform on Pancreatic Cancer	Germany
Chih-Mei Hettler-Chen	Institute of Social Medicine, Epidemio-logy and Health Economics, Charité Universitätsme dizin, Berlin	2014	Bridging the gap between the environment and genetics; Searching for opportunities to add on as a partner in follow-up grants for MeDALL (expires 2014)	Connected to EU Birth cohorts (Thomas Keil) and to MeDALL (Mechanisms of the Development of ALLergy)	Germany
Silke Szymczak	Institute of Clinical Molecuarl Biology; Christian-Albrechts-	2014	Integromics	Connections with NIH via Joan Bailey-Wilson	Germany

	University of Kiel				
Andre Franke	Institute of Clinical Molecular Biology, Kiel University (CAU)	2013	Genomic networks charachterizing psoriasis		Germany
Stephan Weidinger	University Medical Center Schleswig-Holstein, Campus Kiel	2013	Subphenotyping using molecular data and beyond		Germany
Florian Frommlet	LMU Munich	2012			Germany
Thomas Ochsen-kühn	Klinikum Großhadern Munich	2010	Inflammatory bowel disease	Assisten to the Medical Director	Germany
Andreas Ziegler	Universitaet zu Luebeck	2009	Statist. approaches to genetic epidemiology	EU FP COMed consortium core member	Germany
Bertram Müller-Myhsok	Max-Planck-Institute of Psychiatry, Munich	2009	Computational complexity issues of whole-genome analysis of epistasis Epistasis adjusted for population stratification (2011) Coding in epistasis analysis (2013)		Germany
Stephan Weidinger	Technische Universitaet Muenchen	2009	Optimal strategies for GWAs and allergy related phenotypes	Lead to CORA	Germany
Anne-Laure Boulesteix	University of Munich (formerly: Sylvia Lawry Centre for MS Research)	2008	SNP-SNP interact-tions in genome-wide association studies Handling rare variants in genetic association screening or disease prediction / random forests for correlated data (2010)		Germany

			Random forests for interaction detection (2012)		
Thomas Keill	Klinik für Pädiatrie MS. Pneumolo-gie und Immunolo-gie Berlin	2005	GA^{2}LEN and follow-up European birth cohort projects		Germany
Michael Rossbach	University of Bonn	2004	Integrating stem cell knowledge in disentangling the genetic basis of human complex diseases	EU FP COMed consortium core member	Germany
George Patrinos	University of Patras	2017	Population pharmacogenomics	European Medicines Agency; Golden Helix Foundation	Greece
Fabio Efficace		2016	Quality of Life	Head, Health Outcomes Research Unit Chairman, Working Party Quality of Life GIMEMA (Italian Group for Adult Hematologic Diseases)	Italy
Giovanni Malerba	University Verona	2008	IgE in Verona families	Lead GEIRD study (PI: Roberto De Marco)	Italy
Giovanna Albertini	University Bologna	2008	IgE in Coner Study Bologna		Italy
Fabio Efficace	Mediterranean Institute of Hemato-logy Rome	2004	Quality of Life		Italy
Folkert Asselbergs		2014	Exome sequence data and analysis - portal to the Netherlands Biobanks	Associate Professor of Cardiology University Medical Center Utrecht, the Netherlands Adjunct Assistant	The Netherlands

				Professor of Community and Family Medicine in Epidemiology, Dartmouth Medical School	
Jelle Goeman	Radboud University Nijmegen	2014	Multiple testing for omics data	Professor in Biostatistics	The Netherlands
Leon de Windt	Maastricht University	2012	Omics integration in practice	Cardio as example to showcase particular WPs of FP7 project proposal (submitted 2011). Continue the work of COMED I coordinated in the context of aforementioned FP7 proposal.	The Netherlands
Sita Vermeulen team	Radboud University Nijmegen Medical Centre/ Department of Epidem., Biostatistics and HTA	2012	Multivariate Genetic Association Studies		The Netherlands
Gerhard Zielhuis / Alejandro Arias Vásquez	Radboud University Nijmegen Medical Centre/ Depart-ments of Psychiatry & Human Genetics	2012	Machine learning in interaction detection		The Netherlands
Behrooz Z. Alizadeh	University Medical Center Groningen,	2012	Model-based clustering for patient stratification		The Netherlands
Rinse Weersma	Groningen University	2012	GWAIs – an example on RA		The Netherlands
Matty Weijenberg	Maastricht University	2012	Mechanisms of adult-attained height and cancer		The Netherlands

			risk: the role of early-life exposure to energy restriction and genetic variation		
Charlotte Onland-Moret	Division Julius Center, Clinical Epidemiology UMC Utrecht	2011	Omics integration		The Netherlands
Chris Evelo / Lars Eijssen	Maastricht University - BIGCAT	2011	QC in microarray analysis Omics integration		The Netherlands
Philippe Lambin / Georgi Nalbantov	Maastricht University	2010	Applications in cardiovascular disease	Directeur Medical de la MAASTRO CLINIC	The Netherlands
Paul Volders	Maastricht University	2010	Synergy between the mathematical and clinical aspects of cardiovascular systems biology	Group de travaille élu réprésentatif au ESC Council on Basic Cardiovascular Science.	The Netherlands
Ronald Westra	Maastricht University	2010	Setting up exchange program in bioinformatics (First meeting: 11/6/2010 in Maastricht)	director Biomathematics & Bioinformatics DKE-Mathematics	The Netherlands
Olga Savenije / Marieke Bouzen	University Medical Center Groningen	2010	Epistasis analysis on latent class membership in asthmatics	Lead to PIAMA Study data	The Netherlands
Marieke Pierik	Maastricht University	2009	Genetics of inflammatory bowel disease		The Netherlands
Andrew Stubbs	Erasmus MC Rotterdam	2009	Data analysis of alternative splicing microarrays Interpretation and analysis of exon array analysis		The Netherlands
Lude Franke	University Medical Center Groningen	2009	Integrated analysis Co-expression networks		The Netherlands
Aaron Isaacs	Erasmus MC Rotterdam	2008	Co-author on text book "A Roadmap		The Netherlands

			to Genetic Association Studies: A user-oriented approach"		
Harold Snieder	University Medical Center Groningen	2008	Statistical analysis of genetic data in twins		The Netherlands
Clara Elbers	University Medical Center Utrecht	2007	Genome-wide pathway analyis for complex disease analysis		The Netherlands
Siem Heister-kamp	RUG University of Groningen	2006	Pharmacogenomics	Senior Principal Statistician at Organon/part of Schering Plough Research Institute, Dep. of Research and Quantitative Sciences	The Netherlands
Yurii Aulchencko	Erasmus MC Rotterdam	2005	Family-based genetic association screening		The Netherlands
Peter van der Spek	Erasmus MC Rotterdam	2002	Bioinformatics in Medicine	Director dept Bioinformatics and founder Organon bioinfor-matics group	The Netherlands
Tom Hemming Karlsen		2014	HLA-ILT4 binding scores		Norway
Marek Kowalski	Medical University of Lodz	2007	Genetics of IgE using family-based design	GA^{2}LEN partner and data provider	Poland
Inge Breznik	National education institute Slovenia	2016	Networking and Collaboration through Music	Senior consultant for music education	Slovenia
Tanja Kunej	University of Ljubljana	2016	Proteomics integration with BIO3's integromics work (miRNA, etc)	Dept of animal science: biotechnical faculty	Slovenia
Alenka Franko	University Medical Center Ljubljana	2016	GxE interactions	Assistent Professor	Slovenia
Tamara Lah Turnsek	National Institute of Biology	2016	Cell-cell interactions	Director NIB; Chairman of the science and technology council	Slovenia

Eric Duell	Cancer Epidemiology Research Program Bellvitge Biomedical Research Institute (IDIBELL) Catalan Institute of Oncology (ICO)	2012	Interaction studies – the E part in Gene-Environment interaction studies	Unit of Nutrition, Environment and Cancer	Spain
Guadalupe Gómez Melis	UPC (Universitat Politècnica de Catalunya) Barcelona	2009	Erasmus exchange program with Montefiore Spanish Biostatistical Network	Contrat bilateral entre UPC et ULg pour les années académiques 2008-2013 Lifelong Learning programme: ERASMUS (signé en 2009)	Spain
Nuria Malats	CNIO (Centro Nacional de Investigacione s Oncoló-gicas) Madrid	2006	Association tests and software for CNV analysis MB-MDR bladder cancer proof of concept Testing LeMoNe on bladder cancer data Omics integration in bladder cancer (2012)	EU FP COMed consortium core member	Spain
Malu Calle	University of Vic, Vic	2006	Biostatistical statistical genetics: developments of MDR based methodologies Erasmus exchange program with Montefiore	« Contrat bilateral » between University of Vic and ULg 2008-2013 Lifelong Learning programme: ERASMUS (signed in 2009)	Spain
Manolis Kogevinas	Institut Municipal d'Investiga-ció Mèdica	2006	Genetics and epidemiology of asthma related	Lead to ECRHS and SAPALDIA studies	Spain

	(IMIM-Hospital del Mar), Barcelona		phenotypes: data mining		
Nuria Perez	Fundacio de Lluita con-tra la SIDA / Universitat Politecnica de Catalunya, Barcelona	2005	Practical and theoretical concerns related to data below detection limits		Spain
Ivo Gut	Centre Nacional de Análisis Genómico, Barcelona	2010	Liaison activities between Barcelona (Spain) and Paris (France)	EU FP COMed consortium core member	Spain
Yudi Pawitan	Karolinska Institutet	2013	Novel methods to detect interactions	Department of Medical Epidemiology and Biostatistics	Sweden
Charles Steward	Congenica	2017	Clinical genomics		UK
Steve Coldicott	Precision Medicine Forum	2017	Facilitating global collaboration about Precision Medicine		UK
Tony Fletcher	London School of Hygiene and Tropical Medicine	2012	Omics integration in practice – Case study: Cancer	Bladder Cancer Consortium	UK
Ahmad Tariq	Royal Devon and Exeter NHS Foundation Trust	2012	Genetics of serious adverse drug reactions		UK
Chris Haley	MRC Human Genetics	2009	Getting ready for genomewide epistatic association screening	EU FP COMed consortium core member Collective effort to obtain funding for an extensive collaboration between MRC nd ULg on epistasis	UK
Madan Babu	University of Cambridge	2009	Structural alterations and single nucleotide changes to better understand epistatic events		UK

Petra Wark	Imperial College former University of Wagenin-gen in the Netherlands	2001	Addressing different aspects of the rela-tionship between risk factors and molecular alterations in tumour tissue: multivariate and hierarchical latent variable models		UK
Erik Melen	Karolinska Institutet, Stockholm	2005	Evaluation of power-ful methodologies to detect gene-gene interactions using asthma-related phenotypes	Gateway to the BAMSE study	Sweden
Juni Palmgren	Medical Epidemiology and Biostatistics Karolinska Institutet	2005	PHOEBE Biobanking in Europe Platform initiation	Directeur du Wallenberg Consortium North (WCN) Bioinformatics platform	Sweden
Murielle Bochud	Swiss School of Public Health, University of Lausanne	2006	Genetic epidemiology of cardiovascular risk factors		Switzerland
Outside Europe					
Maggie Wang	University of Hong Kong	2016	Interactions via test statistc aggregation; Developing a "best of all worls" interaction detection tool	Center for Clinical Research and Biostatistics – gateway to Asian efforts on Pancreatic Cancer Omics Research	China
Serkey Suchkov	I.M. Sechenov First Moscow State Medical University	2017	Personalized / translational medicine	School for Pharmacy; Secretary General, United Cultural Convention Cambridge, UK	Russia

Ruslan Ludannyy	Federal budget institution of science central research institute for epidemiology	2015	Molecular diagnostics and epidemiology		Russia
Youngja Hwang Park	Korea University Sejong Campus	2016	Pharmaceutical research		South Korea
Taesung Park	Seoul National University	2013	Epistasis, omics integration	Bioinformatics and Biostatistics – Key lab in Asia	South Korea
Jin-Young Jang	Seoul National University Hospital	2013	Pancreas biomarker discovery	Coordinator of pancreas multicenter activities in Asia	South Korea
Junghyun Namkung	SK Telecom	2013	Biomarker discovery using integrative omics	Healthcare / Bioinformatics	South Korea
Michael Rossbach	Genome Institute of Singapore	2011	Business development in Liège / Asia	Office of Business Development	Singapore
Peter Linsley	Elsevier	2017	Science & Technology Books	Acquisitions Editor	USA
Kimberley Glass	Channing Division of Network Medicine, Boston	2015	Message passing algorithms		USA
Micheal Cho	Channing Division of Network Medicine, Boston	2015	Integrative genomics		USA
Ruth Loos	Mount Sinai Hospital	2014	Application of in-house DNA-sequence analysis techniques on real-life data (part of GIANT consortium)	Director of the Genetics of Obesity and Related Metabolic Traits Program, in the Charles R. Bronfman Institute of Personalized Medicine	USA
Richard Duerr	University of Pittsburg	2012	Subphenotyping via omics exploitation	Inflammatory Bowel Disease Genetic Chaire de récherche Co-Directeur et directeur	USA

				scientifique Directeur, UPMC Inflammatory Bowel Disease	
Jose Costa	Yale Medical Group	2012	Omics integration – Bladder Cancer Consortium		USA
Nilufer Ertekin-Taner	o Clinic Dept of Neuro-science	2012	Genetics of Alzheimer's disease: in search for evidence of epistasis		USA
Tasha Fingerlin	University of Colorado Denver	2011	Gene-environment interactions (collaborative methodological effort with key players in and outside Europe)	Depts. of Epidemiology and Biostatistics & Informatics Colorado School of Public Health	USA
Peter Kraft	HSPH – Harvard University	2010	Gene-environment interactions (collaborative methodological effort with key players in and outside Europe)	Department of Epidemiology	USA
Channing Laboratory	Harvard Medical School – Harvard University	2010	Pharmacogenetics Effects of endotoxins and fungi on asthma MB-MDR asthma related phenotypes using a variety of cis- and trans-variants The investigation of in cis and trans effects using MB-MDR methodologies (2011)	Contacts : Kelan Tantisira Gus Litonjua Benjamin Raby	USA
HSPH Alums Network	Harvard University	2009		Initiative of the Harvard School of Public Health Postdoctoral Association (PDA) to create a network	USA

				of HSPH post-doctoral alumni	
Winston Hide	HSPH, Harvard University	2009	Biological network systems	Second affiliation: SA National Bioinfor-matics Insitute, University of Western Cape near Cape Town, South Africa To date: in the UK	USA
Chris Huttenhouwer	HSPH, Harvard University	2009	Computational Biology and Bioinformatics for large collections of genomic data		USA
Marylyn Ritchie	Vanderbilt University (to date: Penn State)	2008	MDR and MB-MDR developments	Envisaging post-doctoral exchanges in the future	USA
Fernando Martinez	Arizona Respirato-ry Center, University of Arizona, Tuscon	2008	Clinical interpretation on asthma data from 3 networks: CAMP, CARE nd ACRN Epistasis screening on aforementioned Share Consortium data	Access to dbGaP SNP Health Association Resource (SHARe) Asthma Resource Project (SHARP) [request #4361-1 approuvé : 2009]	USA
Todd Edwards	Vanderbilt University (formerly Miami Institute of Human Genomics)	2008	MDR extensions	Gateway to AFDS (Amish Family Diabetes Study) Gateway to Parkinson's disease data	USA
Benjamin Raby	HMS, Harvard University	2003	CAMP: Childhood Asthma Management Program	Longitudinal measures of asthma phenotypes	USA

<u>6th Framework European Programme: Network of Excellence GA^{2}LEN:</u>

My position in the European Network GA2LEN has allowed me to obtain a better view on the general functioning of networks on an international scale, on European regulations, on the different layers of a network, on why every single unit within a network is important in order to guarantee a global success.

My responsibilities during the period 2005-2007:

- Specific management activities as a project manager for the University Ghent (e.g, managing official incoming and outgoing documents and contracts)
- Involvement in global non-scientific work packages such as structural integration, training and education, exchange programs, …
- Involvement in scientific work packages, offering statistical insights and expertise, as well as a global view on IP in Europe:
  o Draft project proposals for GA^{2}LEN sustainability:
    ▪ FP7 (European 7th Framework Programme)
    ▪ Crédit de démarrage ULg: R.CFRA.0141
  o Assistance in questionnaire development issues based on experience at the EORTC (European Organization of Research and Treatment of Cancer) data management center
  o Honorary researcher in (bio-)statistics (the analysis of multi-center cohort data) and genetic linkage and association studies
    ▪ co-author of submitted publication
    ▪ research stays at partner's institutions to assist in data analysis
    ▪ jointly developing gene-gene interaction methodology
    ▪ jointly developing strategies to deal with informative missing marker information
  o Setting up a collaborative effort to use family-based genetic association tests on multiple IgE measurements (Crédit de démarrage ULg: R.CFRA.0141)

<u>BIOSTATNET:</u>

I have commited myself to participate in the Complementary Action: "Building Up A Biostatistics National Network (Formación De Una Red Nacional De Bioestadística)" with Professor Carmen Mª Cadarso Suarez (Universidad de Santiago de Compostela) as principal investigator and Guadalupe Gómez Melis (Universitat Politècnica de Catalunya) as principal investigator of the node Catalunya-Bcn in the ***Subprogram of Complementary Actions for Non-oriented Fundamental Research Projects, Type B: Officially-approved actions of technical-scientific character, networks*** (Subprograma de Acciones Complementarias a Proyectos de Investigación Fundamental no orientada, Modalidad B: Acciones concertadas de carácter scientífico-técnico, redes). This is part of the **Third Call of the Program of Fundamental Research Projects for the VIth National I+D+I Plan 2008-2011** (Tercera Convocatoria del Programa de Proyectos de Investigación Fundamental del VI Plan Nacional de I+D+i 2008-2011).

TranSYS: Bringing together industry and academia for patients' benefits:

Consortium composition and set-up
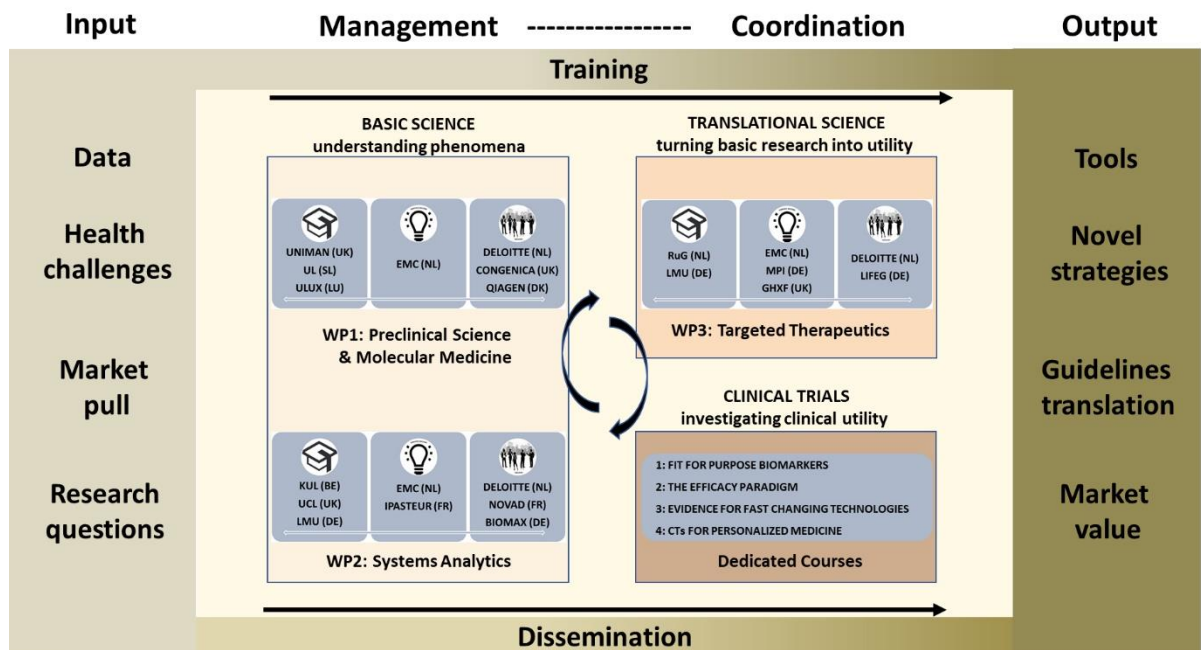
Abstract

In order to put Europe at the forefront of precision medicine, giving less weight to economic sales increases and more weight to which patients to target to achieve the best medical results, paradigm shifts are needed. These should be characterized by significant scientific multifaceted knowledge and a scientific spirit that allows bridging different primary interests, cultures and work flows, hereby representing the important check-points in the R&D process of bench-to-bedside science. Our ETN aims to induce such paradigm shifts by bringing together leaders in Preclinical Science & Molecular Medicine, Systems Analytics, and Targeted Therapeutics, both from academia and the private sector, with the aim to induce a highly-trained workforce of next generation scientists, with the right mind-set, knowledge and skills, at the interface of Translational and Systems Medicine.

d) Competence 4: "Woman of enterprise"

Founding a new SME:

- I was co-founder, co-owner and scientific director of the SME StepGen, cvba, from January 2006 till January 2009. During this period, StepGen was acknowledged as a spin-off of the Ghent University and as an official Collaborating Centre to GA^{2}LEN.
- In the meantime the first efforts have been made to set up a new company (StepGen^{NG}) or more formal consultancy unig under the auspices of ULg and in collaboration with Dr Michael Rossbach (Singapore Human Genome Center). A business plan has been worked out. The consultancy charter which served as a basis can be downloaded from www.montefiore.ulg.ac/~kvansteen.

See also **III.2. f)** Know-how "creating a culture of innovation".

e) Competence 5: Critical attitude

> - Since 2014 I am an expert evaluator for COST EU Trans-domain projects, depending on time availability.
> - In 2016, I accepted an invitation from the European Research Council (ERC) to participate in the peer review of the scientific proposals submitted to the ERC Consolidator Grant "2016 Call for Proposals". My name was recommended by a group of experts in my field of research. This group was chaired by Patrick Couvreur.
> - Since 2017 I am a member of the Editorial Board of "Genomics & Informatics"
> -

Referee jobs for scientific journals include:

- Allergy (editorial board)
- American Journal of Human Genetics
- American Journal of Respiratory and Critical Care Medicine
- American Journal of Epidemiology
- Applied Statistics.
- Australian, New Zealand Journal of Statistics
- BioData Mining
- Bioinformatics
- Biometrical Journal
- Biometrics
- BMC Genetics
- BMC Bioinformatics
- Briefings in Bioinformatics
- Clinical Endocrinology
- Computer methods and programs in biomedicine
- Emerging Themes in Epidemiology
- European Journal of Epidemiology

- European Journal of Human Genetics
- Genomics and Informatics (editorial board)
- Human Genetics
- Human Heredity
- Human Mutation
- Hypertension (statistical genetics statistical consulting editor)
- Journal of Allergy and Clinical Immunology
- Journal of Clinical Bioinformatics
- Journal of clinical pathology and forensic medicine
- New England Journal of Medicine
- Nucleic Acids Research
- PAI
- Respiratory Medicine
- Statistical Applications in Genetics and Molecular Biology Statistics in Medicine
- Statistics in Medicine (associate editor)

Referee jobs for funding agencies include:

- Interdisciplinary expert evaluator for ERC (ERC2016 open calls)
- Expert evaluator of bioinformatics call within WIV-ISP (Belgium)
- AERES – evaluation of INSERM unit U 946
- Interdisciplinary expert evaluator for Trans-Domain-Proposals (COST open calls, since 2014)
- Alzheimer's Association International Research Grant Program
- Admission to PhD or post-doc programs in Africa, Australia, Canada, Switzerland, UK
- ATIP-Avenir - to evaluate projects from young scientists that wish to start their own independent laboratory; commissions organized by CNRS and INSERM France (commitment from 2014 onwards)
- Czech Science Foundation – main public funding agency in the Czech Republic supporting all areas of basic scientific research (commitment from 2014 onwards)
- Dutch Biometry Award
- Estonian Science Foundation (ETF)
- FP7 systems biology
- FWO Vlaanderen (Fonds Wetenschappelijk Onderzoek) / FNRS (Fonds de la Recherche Scientifique)
- Icelandic Research Fund for Graduate Students
- Israel Science Foundation - grant proposal no 1190/06-75.6
- "Prijs Ontwikkelingssamenwerking" (external academic referee)

f) Competence 6: Communicative and listening comprehension

Apart from teaching and student coaching activities (e.g., responsible for the well-being of VLIR students at Hasselt University during 1999-2003), I have made several contributions to the dissemination of science, using different channels, including:

- StepGen CVBA (as a member of BioFlanders).
- UZ Ghent consultant (via a customer oriented approach highlighting the potential of available data).
- BioScope-IT involvement (participation in work shops and bridging the gap between industry and academia).
- GA^{2}LEN (involvement in work package on dissemination).

III.5. Miscellaneous	

a) Computer skills

- Statistical / Computing environments: extensive use of biostatistical software including SAS, SPlus and R, Gauss, STATA, SPSS; Developed skills in several genetic software environments, including FBAT and PBAT, Golden Helix, Genehunter, MEGA2 (Manipulation Environment for Genetic Analyses), …
- Programming: Pascal, Perl
- Applications: LaTex, common Windows database, various spreadsheet and presentation software
- Operating systems: Windows, UNIX/Linux

b) Beta testing

for a variety of software packages, including

- MDR related software, MB-MDR
- Golden Helix – PBAT modules
- Biofilter

c) Language proficiencies

- Dutch: 1st language (CEFR level C2)
- English: 2nd language (C2)
- French: 3rd language (in practice: 4th language; B1)
- German: 4th language (in practice: 3rd language; C1)
- 3rd cycle educational training: Russian elementary knowledge, LBC-NVK Sint-Niklaas 1991-1993 (CEFR level A1)

d) Breaking down boundaries

Professional evaluation based on the "Interpretation Manual for Communication Styles Technology" developed by Paul Mok, has revealed that I have developed a communication style which allows me to excel in:

- **planning,**
- **scope development,**
- **strategic thinking and planning,**
- **creativity.**

APPENDIX 1 :

Research infrastructure and scientific animation

a) Internal and external evaluation about implemented research infrastructure at BIO3

<u>Scientific advisory board evaluation of GIGA-Systems Biology & Chemical Biology:</u>

Statistical genetics (K Van Steen)

The group's research interest is in developing bio-statistical techniques and their applications in the fields of human genetics, genetic epidemiology and public health.

The group's publication record is impressive, containing several papers in the top forums and many papers where Van Steen is the main PI. The performance is outstanding, in particular given that the group is young and the PI is in the process of consolidating her group.

The success brings with it the biggest challenge of the group, of how to manage the growth and avoid the PI becoming a full-time manager. The PI reported on innovative management methods, and the strategy is clear and focused, giving faith that the outcome of the challenge will probably be positive.

The SAB particularly welcomed the open and active attitude of the group towards collaboration, actively seeking opportunities and establishing links useful for both recruitment, funding, and research opportunities. This attitude should be encouraged and rewarded in other groups as well. Note that seeking of opportunities does not imply diversification of the research agenda; a clear and focused but dynamic strategy helps there.

In summary, this is a young group with outstanding merits and potential, a worthwhile investment in any research centre.

Reviewers in the 2013 evaluation: charles.pineau@inserm.fr, samuel.kaski@aalto.fi,olaf.wolkenhauer@uni-rostock.de, philippe.minard@upsud.fr, ruddy.wattiez@umons.ac.be

<u>Evaluation team management and research organization as perceived by GIGA:</u>

Sujet: Congratulations !!!
De : Louis Wehenkel <L.Wehenkel@ulg.ac.be>
Date : 2/07/2013 20:39
Pour : Kristel Van Steen <kristel.VanSteen@ulg.ac.be>

Dear Kristel,

This is just to let you know that in my opinion you did really a great job for this TRU evaluation.

I think that your presentation is an EXAMPLE of professional thinking about how to focus and manage research, and I can say that many others were indeed impressed as well about this.

Best wishes,

Louis

Louis Wehenkel : at that time Director of GIGA-R Systems Biology and Chemical Biology

b) PhD student evaluation – progress during PhD training

The following questions are based on an existing questionnaire from Bristol and have been test-run by me in the ITN MLPM for which I was *student dean*. They are now part of the BIO3 team repository.

SELF-EVALUATION FORM
GAINING INFORMATION AND KNOWLEDGE

1	I am very uncertain about how to find information in a library	1 2 3 4 5	I am able to find the precise information I need in a library quickly and efficiently
2	I do not have an effective method of recording information I have gained from reading	1 2 3 4 5	I am able to record information gained from my reading which is easily accessible when I need it
3	I do not have an effective method for recording information presented by tutors in teaching sessions	1 2 3 4 5	I am able to record information gained from tutors in teaching sessions which is easily accessible when I need it
4	I find it difficult to summarise the salient points of what I have found out	1 2 3 4 5	I am able effectively to summarise the central points of the information I have
5	I find it difficult to remember key points and arguments I need for exams, essays, etc.	1 2 3 4 5	I never have difficulty remembering the information and arguments I need for exams and essays etc.

SELF-EVALUATION FORM
PROBLEM SOLVING

1	I find it very difficult to identify the important constituent parts of a problem	1 2 3 4 5	I am confident that I can focus immediately on what is important about a problem
2	I rarely see the causes and effects which exist in any but the simplest problems	1 2 3 4 5	I am able to suggest likely causes and effects in complex problems I am presented with
3	I am often confused about what is relevant and irrelevant with dealing with topics that are unfamiliar to me	1 2 3 4 5	I quickly identify what is relevant in any new topic area
4	I often find it difficult to use the information I have to reach conclusions	1 2 3 4 5	I am confident in my ability to produce and defend the conclusions I reach based on my own research
5	I rarely see how problems links to other issues and situations	1 2 3 4 5	I am quick to see how problems link to other issues and situations
6	I find I very difficult to distinguish what is unique in a problem form what is similar to other issues and situations	1 2 3 4 5	I am usually able to identify the unique features of a problem as well as those that are similar to other issues and situations
7	I use information from very few sources to generate my conclusions / solutions	1 2 3 4 5	I am confident in bringing a diverse range of evidence and experience to bear when solving problems
8	I rarely question authoritative views on a topic	1 2 3 4 5	I am always ready to challenge received wisdom on any given topic

SELF-EVALUATION FORM
COMMUNICATION

1	I hardly ever give an opinion in an academic discussion	1 2 3 4 5	I am always ready and willing to give my views
2	I find it very difficult to put over anything more than a simple argument in academic discussion	1 2 3 4 5	I am confident of my ability to present complex arguments in academic discussion
3	I rarely challenge the views of others in discussion	1 2 3 4 5	I frequently challenge others to substantiate their views in discussion
4	I am very unskilled in questioning others in order to get them to clarify what they are saying	1 2 3 4 5	Questioning others so that they are able to be clear about the points they are making is one of the skills I am proudest of
5	I am not confident about making a formal presentation	1 2 3 4 5	I am confident of my ability to give an interesting formal presentation
6	I usually find it difficult to express complex thoughts in writing	1 2 3 4 5	Others often compliment me on the quality of my written work
7	I do not really know how to present an argument in essay form	1 2 3 4 5	I am confident of my ability to put forward complex arguments in essay form
8	I am unsure what is appropriate or inappropriate language for essays	1 2 3 4 5	I instinctively use the right kind of language when writing an essay
9	I am not confident of how to use information I have researched to support points I make in an essay	1 2 3 4 5	I am able to use the information I have researched both to support points I want to make and as a material to criticise

SELF-EVALUATION FORM
PERSONAL EFFECTIVENESS

1	I often feel I have too much work to do	1 2 3 4 5	I cope well with the workload I have
2	I find it hard to decide what is important	1 2 3 4 5	I have no difficulty prioritizing my workload
3	There is never enough time to do well all the things I need to do	1 2 3 4 5	I know how to plan my time so that I achieve what I have to do
4	I rarely ask for help or support when I am overwhelmed	1 2 3 4 5	I frequently seek the support of others to help me manage my workload
5	I rarely offer comments to others about their performance	1 2 3 4 5	I am always ready to offer constructive feedback if it is sought
6	I do not like my peers criticizing me	1 2 3 4 5	I welcome feedback from others to help me learn and develop
7	When members of a group I am in are in conflict I make it a point not to get involved	1 2 3 4 5	I see myself as a competent mediator in group conflict
8	I believe that little good arises from conflict	1 2 3 4 5	I believe that most conflicts can enable us to learn and develop if handled positively
9	I don't really work well as part of a group	1 2 3 4 5	I can work effectively as part of a group
10	I don't really like sharing my knowledge and skill with others	1 2 3 4 5	I believe that by sharing their learning all group members learn and develop more effectively
11	I rarely set myself clear objectives	1 2 3 4 5	I usually set myself clear objectives for all important task
12	I rarely give any thought to what went wrong or right in the past	1 2 3 4 5	I often reflect on events I have been involved in order to learn and develop
13	I am often confused about ethical and moral issues	1 2 3 4 5	I am clear about where I stand on most moral and ethical issues
14	I often find it difficult to defend my moral and ethical views	1 2 3 4 5	I welcome challenges to my moral and ethical views
15	I am unable to make accurate assessments of my own strengths and weaknesses	1 2 3 4 5	I can make accurate judgements about my strengths and weaknesses
16	My assessment of the strengths and weaknesses of others is usually inaccurate	1 2 3 4 5	I am usually very accurate in my assessment of other strengths and weaknesses

SELF-EVALUATION
PROGRESS

1	Gaining information and knowledge	I have not made any progress at all since the last evaluation	1 2 3 4 5	I have made good progress since the last evaluation
2	Problem solving	I have not made any progress at all since the last evaluation	1 2 3 4 5	I have made good progress since the last evaluation
3	Personal effectiveness	I have not made any progress at all since the last evaluation	1 2 3 4 5	I have made good progress since the last evaluation
4	Communication	I have not made any progress at all since the last evaluation	1 2 3 4 5	I have made good progress since the last evaluation

c) PhD student evaluation – towards a post-doc position

The following questions are often asked to me when future employers inquire about skills and competences of applicants for post-doc positions. These questions now serve as a guide for BIO3 PhD students.

1. Was X reliable?
2. Was X always on time for meetings, met deadlines without trouble?
3. Was X productive with his/her time?
4. Did his/her project progress at or above the speed you expected?
5. Was X focused and stayed on track?
6. Was X well-organized?
7. Was X able to manage his/her own time and retrieve information/data/results for othis/hers easily?
8. What level of expertise did X reach in his/her area of study?
9. How would X compare to others at the end of their degree in familiarity with concepts, literature, and ability to apply approaches to new problems or datasets?
10. Was his/her work reproducible? Did X keep lab notebooks/script annotations/log files that were sufficient for someone else to re-create his/her work?
11. Did you ever have reason to doubt his/her results or data due to either technical or ethical concerns?
12. How meticulous and detail-oriented was X?
13. Did X have the appropriate insight in application of analyses to real datasets to identify and solve errors?
14. Was X the kind of student to ask very insightful questions, to demonstrate that X understands the big picture of his/her field as well as the methodological details?
15. Did X have any especially creative ideas for his/her project that worked out?
16. Did X seem to love his/her work?
17. Was there one particular aspect that seemed to light X up?
18. Was X a self-starter,
19. self-motivated,
20. independent?

d) Post-doc evaluation – guiding questions

1. Ability to supervise: how would the ability of the candidate to organize, plan and take the lead be rated?
2. Client Service: are clients satisfied with the delivery of the product (i.e., analysis)?
3. Personal Appearance: what impression does the candidate's personal appearance make?
4. Personality Characteristics: how would their ability to get along with others be rated?
5. Growth Potential: does this person have the ability to teach and lead others? Are they able to learn and adapt quickly?
6. Safety & Office Appearance: does this person demonstrate an ability to follow the rules? How well do they look after the equipment or office space they are provided?
7. Attendance: does this person show up for work, or are they routinely absent without permission?
8. Stability, Personality: how stable is this person? How do they deal with pressure? How confident do they appear? How would they describe their predominant mood?
9. Attitude: how willing is this person to carry out instructions and cooperate with you and fellow employees? Are they a team player?
10. Ability to change: is this person able to adapt to changing conditions and learn quickly?
11. Initiative: to what degree does this employee think constructively and take appropriate action? How much supervision does this person require? Are they fair and balanced in decision making?
12. Dependability: how much does this person work conscientiously and in line with instructions? How much do you have to check and verify their work?
13. Quantity of work: is there a satisfactory amount of output? Do they over promise or under deliver? Are they slow or do they work hard and turn out more work than required?
14. Job Knowledge: to what level do they understand all phases of work? Do they excel at the job or do they lack knowledge in the job or certain areas?
15. Quality of work: is there a consistent level of performance in meeting or exceeding quality standards?

APPENDIX 2 :

Complete list of submitted projects as coordinator or invited partner

Year of submission	Type	Title / Description	Function	Funding	Status
2018	H2020-MSCA-ITN-2018 (ETN)	Translational SYStemics: Precision Medicine at the Interface of Translational Research and Systems Medicine (TranSYS)	Coordinator (KU Leuven)	Staff and operational costs	Insufficient Score of 92.6 (will be resubmitted in 2018)
2018	E-Rare-3 JTC 2018	ENSomics: Making sENSe of HSCR associated with Enterocolitis	Partner and WP leader on "Multi-omic integrated approaches to discover the cause of HSCR and HAEC and IBS" (coordinator: Robert Hofstra, Erasmus Medical Center)	Staff and operational costs	Pre-proposal not accepted
2018	H2020-MSCA-ITN-2018 (ETN)	MLFPM: Machine learning frontiers in precision medicine	Partner node leader (coordinator : Karsten Borgwardt ETH Zurich)	Staff and operational costs	Accepted
2018	TÉLÉVIE	Molecular drivers and markers of pancreatic cancer initiation and progression: a translational and multidisciplinary approach (continuation of TELEVIE 2016 grant)	Co-applicant	Staff and operational costs	Pending
2017	ERA-NET / TRANSCAN-2 (Minimally and non-invasive methods for early detection and/or	PaCaDiag: Combining biomarker signatures for a highly accurate diagnosis and prognosis of	Partner / responsible for data integration	Staff and operational costs	Full proposal - not accepted

	progression of cancer)	pancreatic ductal adenocarcinoma (PDAC) from serum sample analysis.			
2017	EOS	Uncovering secrets of diabetes by finding the treasure trove of "hidden" bird genes (CG_Dia)	Partner (with Yves Van de Peer; coordinator: Frans Schuit)	Staff and opertional costs	Not accepted
2017	HDHL-INTIMIC Call for Joint Transnational Research Proposals on "Interrelation of the Intestinal Microbiome, Diet and Health"	F.C. IBS: Low versus high fermentable Carbohydrate diet in Irritable Bowel Syndrome: who may benefit?	WP leader	Staff and operational costs	Full proposal – not accepted
2017	FWO	SPECIAL - Structured Populations in Emerging Cohorts via Interactive AnaLysis	Promotor	Staff and operational costs	Not accepted
2017	FNRS PDR	TRANSPiReS: TRANslational Systemics to Stratify Patients and to assess Risk Scores	Promotor	Staff and operational costs	Rated: excellent; decision: rejection due to lack of funding at FNRS)
2017	WELBIO - SGR	2-DESTinCT: DEtecting STastistical INteractions in Complex Traits (follow-up to DEST*in*CT)	Promotor	Staff and operational costs	Accepted
2016	H2020-MSCA-ITN-2017	Machine learning frontiers in precision medicine MLFPM	Partner node leader (coordinator : Karsten Borgwardt ETH Zurich)	Staff and opertaional costs	Not accepted
2016	HORIZON2020 - SC1-PM-02-2017: New concepts in patient stratification	ORUS: Multi-sources data integration in Ophthalmology Research: towards clinical Use for patient Stratification and management	Partner at coordinating office	Staff and operational costs	First-stage proposal - not accepted
2016	FWO	Data integration to mine the druggable genome to enhance personalized disease management cancer patients with pancreatic ductal adenocarcinoma	Promotor	Staff and operational costs	Not accepted

2016	AARG (Alzheimer's Association Research Grant)	Large-scale assessment of epistasis in late-onset Alzheimer Disease susceptibility using integrated approaches - ADIOMIX	Promotor (with Jean-Claude Twizere and Kristel Sleegers)	Operational costs	LOI not accepted
2016	FNRS-CDR	SysMedPC	Promotor	Operational costs (sequencing)	Accepted
2016	MARIE SKŁODOWSKA-CURIE ACTIONS - COFUND	Crossing border border-region (CBBR)	Committed partner to the CBBR programme (providing training to visiting students)	To be determined (entered the project at later stage)	Not accepted
2016	ARC	Enhancing molecular reclassification and detection of replicable large-scale epistasis susceptibility in Pancreas Ductal Adenocarcinoma – towards integrated interactome maps for PDAC therapeutic targets (IN2PDAC-ULG)	Promotor (with Vincent Bours and Jean-Claude Twizere)	Operational costs	Preproposal - not accepted
2016	TÉLÉVIE	Molecular drivers and markers of pancreatic cancer initiation and progression: a translational and multidisciplinary approach (promotor: Ingrid Struman, ULg – GIGA)	Co-applicant	Post-doc	Accepted
2015	JPI Healthy diet for a Healthy Living	DOMINO: Dietary Optimization of Host-Microbiome Interactions: Targeting the gut-brain axis for healthy living and disease Prevention	Partner	To be determined (entered the project at later stage)	Not accepted
2015	FNRS PDR	P-STRUCCT: Molecualr strata of patients and populations	Promotor	Staff and operational costs	Not accepted
2015	WELBIO - SGR	DESTinCT: DEtecting STastistical INteractions in Complex Traits	Promotor	Staff and operational costs	Accepted
2015	TÉLÉVIE	PDAC-xome: Exome Sequencing in	Promotor	Operational costs	Accepted (reduced budget – no

		Pancreatic Ductal AdenoCarcinoma			human resources)
2014	ARC	Systems biology approaches for deciphering gene regulatory networks in pancreatic cells	Partner (promotor: Bernard Peers)	Staff and operational costs	First stage proposal – not accepted
2014	HORIZON2020	Integrative Systems Biomedicine Study in Systemic Inflammatory Response Syndrome	Partner (promotor: Anavaj Sakubanthai, France)	Staff and operational costs	First stage proposal – Not accepted–
2014	EQUIP 2014 (RW-DGO6) - Projet dans la thématique ESFRI-ELIXIR	Projet GMW - Génomique Médicale en Wallonie promotor: Michel Georges	Partner (promotor: Michel Georges)		Letter of intent - accepted)
2014	Infect-ERA (2nd call)	Genomic Epidemiology and Evolution study of Enterovirus 71 (acronym: EvEnt)	Partner (promotor: Anavaj Sakubanthai, France)	Staff and operational costs	Not accepted
2014	HORIZON2020	PAncreas Cancer risK: INtegratinG data towards a predictive model (acronym: PACK-Ing)	Partner (promotor: Nuria Malats, Spain)	Staff and operational costs	First stage proposal – accepted; Full proposal not accepted
2014	HORIZON2020	Skin barrier in health and disease (acronym: HEALSKIN)	Partner (promotor: Stephan Weidinger, Germany)	Staff and operational costs	Not accepted
2014	HORIZON2020	Fostering advanced Analytical Clinical Environment using Integrated Technologies (acronym: FACE-IT)	Partner (promotor: Peter van der Spek, the Netherlands)	Staff and operational costs	Not accepted
2013	Internal Maastricht University grant proposal "MaCSBIO"	In the context of starting a Systems Biology Institute in Maastricht. Entails three research lines, "Metabolic Pathways", "Phylogenetic Trees", and "Network structure and complexity".	External partner in the context of "strategic alliances" to the project		Not accepted
2013		Advanced model selection issues in statistical genetics	External partner (promotor: Florian Frommlet Center for Medical Statistics, Informatics		Not accepted

			and Intelligent Systems Medical University of Vienna)		
2013	FNRS projet de recherche	Seq-Based Clustering for Association	Promotor	Post-doc for 2 years	Not accepted
2013	FWO onderzoeksproject	Study of the interaction between the intestinal mucosa and microbiota in patients with inflammatory bowel disease	Supplier (copromotor of phd student)		Not accepted (based on 2012 submission, supplemented with microbiome data analysis)
2012	FP7-PEOPLE-2012- Marie Curie Initial Training Network	Machine Learning for Personalized Medicine	Partner (representing ULg) + Students' dean Promotor: Karsten Borgwardt, Max Planck, Tübingen, Germany)	Phd student exchange within the consortium	Accepted
2012	FNRS projet de recherche	Multimodal models of Alzheimer's and Parkinson's diseases evolution: applying multivariate analysis to demographic, clinical, brain imaging, genetic and proteomic data	Co-Applicant	Staff (post-doc) aand operational costs	Not accepted
2012	FNRS projet de recherche	Robust Machine Learning Forests in Network Construction for Integrative Omics Analyse	Promotor	Post-doc (2 years), doctoral student (4 years), and functioning budget	Accepted
2012	FP7 – STREP ICT	Virtual intensive care patient (VIP)	Partner Promotor: Marc Ramon (Department of Computer-science KU Leuven)	Staff support and functioning	Not accepted (based on 2010 submission)
2012	Wetenschappelijk Fonds Willy Gepts (WFWG)	Proton pump inhibitors and gastro-intestinal flora.	Responsible applicant (together with Yvan Vandenplas and Jeroen Raes)	Staff support and functioning	Not accepted

2012	FWO onderzoeksproject	De rol van microrna's binnen inflammatoire darmziekten: an integrated view	Co-promotor Promotor: Paul Rutgeerts	Shared PhD student	Not accepted
2012	Zwaartekracht programma van NWO	Genen, omgevingsfactoren en inflammatore darmziekten; een "kip-en eiprobleem" (Gen-omgeving interactie in het ontstaan en ziektebeloop van IBD)	Partner		Accepted
2012	COST (2nd stage proposal)	An integrated European platform for pancreas cancer research: from basic to clinical and public health interventions for a rare disease	Partner Promotor: Nuria Malats (CNIO, Madrid, Spain)	Travels, training, stages, workshops, conferences	Accepted
2012	ARC2012	Molecular dissection of inherited predisposition to inflammatory bowel disease (IBD-ULG)	Partner	Staff member (total budget: 1250000 EURO)	Accepted (reduced budget)
2011	FNRS projet de recherche	Developing novel omics integration methods to enhance prediction of complex disease traits	Promotor	Staff and functioning	Not accepted
2011	FP7-HEALTH-2012-INNOVATION-1	COMID: Development of statistical tools to integrate multi-omics data for improved diagnostics of complex diseases	Promotor		Not accepted
2011	FP7 – HEALTH. 2012.1.2-1	PANACEA: Development of tools and guidelines to biopharmaceutical treatment of chronic inflammatory diseases through innovative patient stratification and therapeutic drug monitoring	Partner (promotor: Prof Dr A Gils – KUL, Belgium)		Not accepted
2011	FP7-HEALTH-2012-INNOVATION-1	IMPLUCE: Integrated Profiling in Ulcerative Colitis and Crohn's disease in European patients	Partner (promotor: Prof. Paul Savelkoul PhD VU University medical center, Amsterdam)		Not accepted

2011	HEALTH. 2012.2.1.1-1-B	IBD-PROT: Proteomic/Peptidomic technology applied for the development of a friendly to use platform targeting highly analytical diagnostic investigation of Inflammatory Bowel Diseases	Partner (promotor: Maria Gazouli, PhD, University of Athens)		Not accepted
2010	FNRS projet de recherche	Integrated complex traits epistasis kit	Promotor	Post-doc (2 years), doctoral student (4 years), and functioning budget	Accepted
2010	FNRS projet de recherche	Optimizing and developing robust gene-gene interaction detection methods using random rotations of the database	Promotor	Staff and operational costs	Not accepted
2010	Mandat de post-doctorat à l'ULg pour chercheur étranger	Associations génétique des taux d'IgE dans des échantillons de populations et de familles mis en commun.	Group Leader	Post-doc	Accepted
2009	ARC2010	Strategies with medical applications for the identification of gene-gene and gene-environment interactions and multiple causal variants with complex phenotypes.	Promotor	Staff and operating costs	Not accepted in last phase
2007	Crédit de démarrage R.CFRA.0141	Association génétique des taux d'IgE spécifiques totaux et sériques dans des échantillons de populations caucasiennes et de familles mis en commun	Principal Investigator	88 000 EURO	Accepted
2007	Beques de recerca per a professors/res i investigadors/res visitants a catalunya (piv 2007) - núm. expedient: 2007 piv 10018	Strategies for the identification of genetic variability associated with complex phenotypes.	Host Institute: University of Vic, Spain	2 250 EURO / month	Accepted (Only 3 out of 4 months were taken up, in order to be able to fullfill the new commitments made at ULg)

2007	FWO onderzoeksproject G.0.410.08.N.10	Development of prevalence and determinants of asthma, COPD and allergies among adults in Flanders ; a follow-up study of the European Community Respiratory Health Survey (ECRHS)	Co-promotor (Promotor: Joost Weyler, UA, Antwerp, Belgium)	2008: 27000 EURO 2009: 22000 EURO 2010: 22000 EURO 2011: 10000 EURO	Accepted

APPENDIX 3:

Letters of support – level of full professor

a) Max Planck, Munich, Germany

**Max-Planck-Institut
für Psychiatrie**
Deutsche Forschungsanstalt für Psychiatrie

Letter of reference for Prof. Dr. Dr. Kristel van Steen

It is with utmost pleasure that I am writing this letter of recommendation for Prof. Dr. Dr. Kristel Van Steen in support of her application for full professorship.

I have known Kristel for some eight years by now, collaborating with her at first in the field of the analysis of gene-gene interactions, which has now grown into a more general theory and application framework for the analysis of interactions across and between –omics strata. She has always impressed me with her extremely deep knowledge and understanding of the subjects at hand coupled with a very clear sense of the needs of real data analysis.

At the same time she is extremely good at dealing with people, be those students or colleagues, a combination not very often found at all. We are jointly serving as students' deans on our EU-funded ITN network on machine learning in personalized medicine.

Her CV is clearly excellent, she has written and continues to write many and very first class publications, reaching into the very highest journals in doing so. This happens both in the areas of original research as well as reviews and guidelines, which again emphasizes the dual strength and focus on both depth and capturing real life needs, something absolutely necessary to make applications of her research a success. The absolute number, impacts and statistics about her publications are clearly first rate, she has spoken at many conferences, again showing her ability to clearly also communicate her research and her grant support also has been continuous and growing.

In the research world in our disciplines she is in the highest regards, having served and still serving in a variety of very important functions in the relevant societies both at the national, European and international level.

In summary her research strengths, her capabilities both in the theoretical foundations and the applicational aspects of the work, her outstanding skills with people, her networking capabilities and her highest esteem in the community make her a perfect candidate for a full professorship.

Please do not hesitate to contact me, should you require more information.

Munich, May 26, 2016

Prof. Dr. Bertram Müller-Myhsok

Head, Statistical Genetics Group,
Max Planck Institute of Psychiatry, Munich, Germany &
Adjunct Professor of Human Genetics,
Technical University of Munich, Germany &
Chair of Statistical Genetics,
Institute of Translational Medicine, University of Liverpool, UK

b) CNIO, Madrid, Spain

June 16, 2016

Re/ Letter of reference for Prof. Dr. Dr. Kristel van Steen

To whom it may concern,

As head of the Genetic and Molecular Epidemiology Group at the Spanish National Cancer Research Centre (CNIO), Madrid, Spain, and Chair of the EUPancreas COST Action BM1204, I am absolutely delighted to write a strong letter to support Prof. Dr. Dr. Kristel van Steen for her application for a full professorship.

I know Kristel for over ten years through several European collaborative studies on bladder and pancreas cancer, as well as training courses, PhD thesis committees, and conferences. In the last 5 years we shared a PhD student (Sílvia Pineda) who defended her doctoral thesis last October and is now in UCSF, USA, for a postdoc. This PhD process let us explore the new area of integration of omics data mainly embedded in the epidemiology studies of bladder cancer. During these years we have dissected and characterized the heterogeneity of different sets of omics data, we have analysed them by using appropriate statistical and bioinformatics tools and we have developed new analytical strategies to integrate omics with non-omics information into the epidemiological models. This is an innovative and competitive field and we took the challenge to guide a PhD student in state-of-the art analytical strategies. Two articles derived from this project have been already published in Human Heredity (PMID: 26201698) and PLoS Genetics (PMID: 26646822), and an additional paper is under review in Genetic Epidemiology.

Kristel has also directed the work of other students in this area and has importantly innovated in methods and tools that are being applied extensively by the scientific community. Her research is at the forefront of the integromics field at the international level. With Kristel, I had the chance to enter in this rich scientific setting that allowed us to get involved in deep and excited discussions on the assets and limitations of the application of integromics approaches in biomedical sciences. In this regard, we have published several methodological contributions in the field. I am aware that Kristel is very active in establishing this kind of collaboration with European, American, and Asian groups.

Kristel is member of the Steering and Management Committees of the EUPancreas COSt Action BM1204 " *An integrated European platform for pancreas cancer research: from basic science to clinical and public health interventions for a rare disease*" that has over 250 multidiciplinry members from 22 EU countries. Kristel has also coordinated the Working Group 2 of the Action on pancreas cancer omics data generation and analysis. She has also organized conferences, workshops and training schools. Kristel has a long teaching experience and has showed very strong teaching skills in the training schools she led on cutting-edge topics in the field. It is a luxury having her as teacher.

Without question, Kristel is developing a first class research in the areas of statistics and "omics" data integration. In this regard, she has done crucial contributions impacting

46/150

the advancement of the field through publications in high profile journals as her CV shows. Kristel combines the abilities of intellectual strength and creativity with exceptional communication skills. Her teaching abilities, presentation and public speaking skills are simply outstanding. She always stimulates discussion and shares her knowledge with others.

In summary, there is no doubt that Prof. Dr. Dr. Kristel van Steen is making innovative and high-impact contributions to science, thus, I strongly recommend Kristel for her application for a full professorship without hesitation and with enthusiasm.

If you have any question, please do not hesitate to contact me.

Sincerely,

Núria Malats, MD, PhD
Head of the Genetic and Molecural Epidemiology Group
Human Cancer Genetics Programme
Spanish national Cancer Research Centre (CNIO)
Melchor Fernández Almagro, 3
28029-Madrid, España
Tel +34 912246900, Fax +34 912246980
e-mail nuria@cnio.es
www.cnio.es

c) University of Pennsylvania, USA

Jason H. Moore, PhD
Edward Rose Professor of Informatics

Director, Institute for Biomedical Informatics
Director, Division of Informatics
Senior Associate Dean for Informatics

May 30, 2016

RE: Reference letter for Kristel van Steen, Ph.D.

To whom it may concern,

It is with great pleasure that I write this letter in support of Kristel van Steen in her application for full professorship. I have known Kristel for more than five years through interactions at scientific conferences. I have followed her work on novel statistical and computational methods for the detection and characterization of gene-gene interactions in population-based studies of common human diseases. She is global leader in this area and has contributed numerous widely used methods such as model-based multifactor dimensionality reduction (MB-MDR). Her most recent work on this method includes its extension to the analysis of rare variants. This is timely given the broad interest in high-throughput DNA sequencing. There is no question that her work will continue to receive recognition as we transition into an era of human genetics that will be dominated by bioinformatics and genetic analysis using quantitative methods. She has positioned herself to have a huge impact as we begin to focus more intensely on understanding genetic architecture and the biological relevance of genetic risk factors.

I have reviewed her CV and am extremely impressed with her productivity and impact. She has been an author or co-author on more than 125 peer-reviewed journal publications. This is stellar productivity for someone at her career stage. Also, according to Google Scholar, she has an H-index of more than 40 with at least 75 publications that have been cited more than 10 times. There is no questions that her work gets noticed and cited. In addition to her methodological work, she is clearly highly collaborative. She has participated in a number of co-authored publications where it is clear that she made an important contribution to the data analysis. These accomplishments would qualify her for any full professorship in the United States including my home institution of the University of Pennsylvania.

In summary, I give Kristel my absolute highest recommendation for a full professorship. She is highly qualified for this honor by all criteria. Please don't hesitate to contact me if you have questions about her qualifications.

Sincerely,

Jason H. Moore, Ph.D.
Director, Penn Institute for Biomedical Informatics
Senior Associate Dean for Informatics