

# Curriculum Vitae

Prof. dr. Ernst C. Wit

Professor of Statistics and Data Science

21 May, 2021

- Prof. Dr. Ernst Wit  
Institute of Computing, Director  
Università della Svizzera italiana  
Via G. Buffi 13  
6900 Lugano  
Switzerland

Honorary appointment:  
Bernoulli Institute  
Rijksuniversiteit Groningen  
PO Box 407, 9700 AK Groningen  
The Netherlands

*Home address:*  
Via delle Coste 2  
6933 Muzzano  
Switzerland

- Doctorate: May 1997 (Philosophy, Pennsylvania State University), June 2000 (Statistics, University of Chicago).
- Other details:

Email: wite@usi.ch  
Website: <https://www.rug.nl/staff/e.c.wit/>  
Telephone: +41 (0)58 666 4952  
DOB: 5 April, 1972

## 1 Employment

### 1.1 Current employment

Institute of Computing, Università della Svizzera italiana

- Director (2021 – )

- Full professor of Statistics and Data Science (permanent)

## 1.2 Activities

- University related activities
  - Director of the Institute of Computing
  - Head of Data Science (CI, USI) (2018 – )
  - Director of the Master in Computational Science (USI)
- International activities
  - Scientific advisor, Ministry of Internal Affairs, The Netherlands (since 2014)
  - Chair of a Europe-wide EU COST Action (CA15109) for a network of European Scientists working on Statistical Network Science (Since 2015).
  - Associate editor *Biometrics* (since 2014), *Statistical applications in genetics and microbiology* (since 2012). Reviewer for many journals.

## 1.3 Employment record

- *1 June, 2018 – current*, Full Professor of Statistics and Data Science, 1 fte, permanent Institute of Computing, Università della Svizzera italiana.
- *1 June, 2008 – 1 June, 2018*, Full Professor of Statistics and Probability, 1 fte, permanent Johann Bernoulli Institute, University of Groningen.  
Chair of Johann Bernoulli Institute, consisting of 32 fte permanent staff.  
Management of Statistics and Probability Unit, consisting of 3.6 fte permanent staff  
Supervision of 15 PhD students, 2 postdocs, 1 instructor, 40+ BSc/Master students.
- *1 January, 2006 – 31 May, 2008*, Full Professor of Biometrics, 1 fte, permanent Department of Mathematics and Statistics, Lancaster University.  
Director of the Medical Statistics Unit, consisting of 20+ research staff.  
Supervision of 2 post-docs, 2 Master Students, 2 PhD students.
- *1 July, 2004 – 31 December, 2005*, Reader in Statistics, 1 fte, permanent  
*1 September, 2000 – 30 June, 2004*, Lecturer in Statistics, 1 fte, fixed term  
Department of Statistics, University of Glasgow.  
Supervision of 3 post-docs, 3 BSc students, 4 PhD students.

## 1.4 Master's ('doctoraal')

University of Higher Education: Vrije Universiteit, Amsterdam

1. MSc Statistics (Mathematics), 30/6/1994
2. MA Philosophy, 30/6/1997
3. MA Philosophy of Science, 31/7/1997

## 1.5 Doctorate

1. PhD Philosophy, “The Ethics of Chance” (Supervisor: Prof. Dr. Joseph J. Kockelmans), Pennsylvania State University, USA, 31/5/1997.
2. PhD Statistics, “The Categorical Imperative: Extendibility Considerations for Statistical Models” (Supervisor: Prof. Peter McCullagh), University of Chicago, USA, 31/6/2000

## 2 Education

### 2.1 Teaching philosophy

My teaching is informed by three principal components: my teacher parents, my experience as a student and my own teaching experiences in different social, cultural and academic backgrounds.

Both my parents were primary school teachers and this fact has made me sensitive to the amount of work and personal commitment that goes into teaching very early on. My parents would come home with scripts to correct, with school grades to enter and with lesson plans to be made. Another not unimportant aspect of a primary school is the very diverse academic qualities of the pupils. The way they resolved it was by focusing their apparent attention to weaker-average students while giving carefully monitored liberties to the better students to work on their own and to help their colleagues. This is an idea that I have carried along with me even at university level.

I have been educated in the Netherlands and the US, both in the humanities and the sciences. This diversity has been inspirational to my learning and teaching. Different socio-cultural contexts present their own parameters for learning and teaching. In the past twenty-five years, my teaching has been tried in many different geographical locations and it has not been left unaffected by these social-cultural interactions. Whereas certain techniques worked extremely well in the USA, they did not necessarily work in the UK or Australia.

When I moved to the USA, I really had to get used to a completely different student-lecturer relationship. Students expected to be taken as individuals rather than as an amorphous class. They wanted more interaction with the lecturer in front of the class-room. The responsibility of learning was as much considered being a responsibility of the lecturer as it was of the students themselves. Even though student-focused teaching is becoming more and more an issue in the Netherlands, in the USA it was pushed to its extreme. There are good reasons for student-focused teaching. Stevens (1992) expresses the idea that humanism in learning seeks ways to empower individuals to direct their own learning. This encourages a deep approach to learning. American students, who expected a lot from their lecturer, also expected more from themselves. Participation in course work was higher than it is in the Netherlands. Before returning to Europe, I taught for a short while as a lecturer at the University of New South Wales in Sydney. Sydney is a multicultural city and that is reflected in the student population. There were many first and second generation students from Southeast Asia. It was particularly that group of students that performed very well in the classes I taught. They were industrious and social, and as a result pulled the other students along with them. The style of teaching they seemed to respond to best was a more top-down approach, combined with sufficient openness to student interaction. When I came to UK, I had to adjust again. It was particularly striking how students disliked speaking in public. In a little study I performed, 74% of the students found public speaking intimidating and 87% did not want to fail in front of the lecturer.

When I moved to the Netherlands in 2008, I have found my international background increasingly useful. I now feel able to handle an increasingly diverse background rather effortlessly. This was useful as I had to focus on various other aspects. I succeeded in introducing a new statistics tracks both in the Bachelor and the Master programme in Mathematics, as well as expanding service teaching to a number of programmes (Biology, Computer Science, Artificial Intelligence, Engineering), even including the Graduate School (“Refresher Course in Statistics”) and the Honours College (“Figures and facts: statistics in the news”, “Taking chances with the sciences”).

Since moving to Switzerland, I became the director of the new Data Science Master (part of the Computation Science master), which is an interdisciplinary master to teach high-level quantitative skills to students from various national and disciplinary backgrounds. Although it is perhaps too early to say something definite at this early stage, this environment seems to resemble the Australian experience: ambitious students that work hard and that look for interaction with their peers and instructor in order to excel. It already has made me adjust the course material, by including additional challenges.

## 2.2 Professionalization

During my Master degree (VU, 1994) I have obtained a didactics degree. Furthermore, while teaching in the US (Pennsylvania State University, University of Chicago) I have attended several continuing education courses on teaching. When I was appointed in Glasgow as a lecturer, I followed a two-year University Teaching Qualification course. As part of this course I prepared a teaching portfolio and obtained UTQ degree. In 2013 I updated my teaching portfolio and submitted it with additional teaching references to obtain a Dutch BKO degree.

## 2.3 Teaching

In Switzerland, I am teaching four Master level courses:

- Introduction to Data Science (6 ECTS)
- Network science and graphical models (6 ECTS)
- Introduction to Computational Science (3 ECTS)
- Extensions of the linear model (3 ECTS)

## 3 Research

### 3.1 Brief summary of research over last five years

**Networks** are remarkable models for a large variety of real world processes. Infections, traffic flow, causal chains, societal relations, gene regulation and signaling and many other processes can be described by means of a network. However, fundamental questions for many of these networks remain only partially answered: (i) what is the structure of these networks, (ii) what is the dynamic kinetics of the process and finally (iii) what drives the structure of these networks. My group deals with these questions on the basis of often limited amounts of data. I have set up a research group with currently 4 PhD students, 1 post-doc and 1 master student on statistical network

science, particularly dynamic networks. With my background in high-dimensional genomic data (as evidence by my 2004 book on the statistical analysis of microarray data), I became fascinated by the problem of modelling and inferring complex systems from limited amount of data. Although I am inspired by biological systems, because of their complexity and persistence, I do consider other systems as well, such as social networks and ocean currents. I am currently the chair and instigator of European COST Action (CA15109) on European Cooperation on Statistics for Network Data Science, bringing together some 200 research groups from 33 countries within Europe working on statistical network science.

Since 2014 I have been working as the expert consultant for the **Ministry of Internal Affairs** in the Netherlands to give advise on a number of projects, ranging from introducing a safe form of electronic voting, detecting election fraud and providing time-saving sampling tools to the Central Election Body (Kiesraad) in case of referendums.

### 3.2 Recent (Inter)national activities

### 3.3 Institutional activities

- Chair of the Board, Johann Bernoulli Institute for Mathematics and Computer Science (2015–2018)
- Head of Management Team Mathematics (2015–2018)
- Tenure Track coach, Johann Bernoulli Institute (2016–2018)
- Chair of Promotion Committee (BC1), Faculty of Science and Engineering (2014–2018)
- Member of RuG Scientific Integrity Committee (2017–2018)
- Member of Programme Committee Mathematics (2010–2018)

#### 3.3.1 Recent service to research community

- President BMS-ANed, Dutch Society of Biostatisticians (2017–2018)
- Member Management Team NWO Stochastics Cluster, STAR (2016–2018)
- Member Commissie Onderzoek Platform Wiskunde Nederland PWN (2015–2018)
- Member of Scientific Advisory Board EPSRC project EP/L020319/1: “Computational inference of biopathway dynamics and structures,” 2014-2018.
- Director of the International Biometrics Society, representing Europe (2014-2016).
- President of the *Bernoulli Society*, European Region (2012-2014).
- Chair of the Editorial Board of the Dutch Mathematics Platform (PWN) (2014-2016).
- Chair of National Accreditation Committee, NVAO, Master of Statistics, University of Leiden (2015)
- Member of Editorial Advisory Board of the International Biometrics Society (2013-2016) and of the *Journal of Applied Statistics* (2011-2016).

- Chair of the Programme Committee (Applied) Mathematics, University of Groningen (2014 – 2017)

### 3.3.2 Recent editorial work

- Guest editor JRSS-C, special issue “Applied Network Science” (2016).
- Guest editor *Statistica Neerlandica*, special issue “All models are wrong...” (2012).
- Associate editor *Biostatistics* (2006-2009).
- Editor of the *JRSS-B Read Papers* (2006-2008).
- Associate editor *JRSS-C* (2001-2005).

### 3.3.3 Recent research related activities

- Invited as visiting scholar to the Isaac Newton Institute, University of Cambridge, “Statistical Theory and Methods for Complex, High-Dimensional Data” programme (7 January - 27 June 2008) and “Theoretical foundations for statistical network analysis” (11 July – 21 December, 2016).
- Invited to the Mathematical Institute, National University of Singapore “Meeting the Challenges of High Dimension: Statistical Methodology, Theory and Applications” (13 Aug - 26 Oct 2012) and “Networks in Biological Sciences” (1 June – 31 July, 2015).
- Honorary Secretary of the *Research Committee* of the *Royal Statistical Society* (2006-2008), Member of RSS Research Committee (2003-2008)
- Organizer of several large (100+ participants) international workshops:
  - International Workshop on Statistical Modelling, 2-7 July 2017.
  - “All models are wrong...”, 14-16 March 2011,
  - “High-dimensional inference and complex data”, 23-25 November 2009, Groningen;

## 3.4 Ph.D. and postdoctoral supervision

Being a scientist is as much about obtaining scientific results as it is about communicating those results. Teaching and supervision of students (Bachelor, Master and PhD) and postdocs is one, and very integral, part of this process. Below I list the PhD students I have supervised over the years.

- (Current, funded by USI) Igor Artico, “Longitudinal network models.”
- (Current, funded by USI) Giacomo Ceoldo, “Extensions of the Stochastic Actor-oriented model.”
- (Current, funded by Ministry of Education) Spyros Balafas, “Statistical modelling and inference of the dynamics of multivariate ordinal processes.”

- (Current, funded by NWO) Francisco Richter Mendoza, “Simultaneous estimation and selection of species diversification models”
- (PhD, January 2018) Pariya Behrouzi, “Detection and analysis of high-dimensional genetic incompatibilities”
- (PhD, July 2017) Hassan Pazira, “High-dimensional Variable Selection for GLMs and Survival Models.”
- (PhD, May 2017) Seyed Mahdi Mahmoudi, “Statistical inference of causal and ordinary differential equation models.”
- (PhD, May 2017) Mirko Signorelli, “Inferring Community-driven structure in complex networks”
- (PhD, April 2017) Danilo Pellin, “Stochastic modelling of dynamic systems in biology.”
- (PhD, July 2016) Nazia Gill, “Generalized Linear Modelling for Biometrical Sciences” (HEC)
- (PhD, June 2016) Saverio Ranciati, “Statistical modelling of spatio-temporal dependencies in NGS data”
- (PhD, April 2015) Abdolreza Mohammadi: “Model uncertainty in network inference” (NWO/STAR)
- (PhD, June 2014) Ivan Vujacic: “ODE inference of genetic networks”.
- (PhD, March 2014) Lotsi Anani: “Statistical inference of biological networks”.
- (PhD, April 2012) Antonio Abbruzzo, “Graphical models for estimating dynamic networks”.
- (PhD, August 2007) Vilda Purutcuoglu, “Bayesian methods for gene network analysis”
- Other PhD supervision: Matthey Sperrin (Lancaster), Vasilis Giagos (Lancaster), Ximin Zhu (Glasgow), Luigi Palla (Glasgow/Bologna), Elisa Grilli (Glasgow/Bologna), Angela Recchia (Glasgow/Bari).

Post-doctoral supervision:

- (2018-2021) Fentaw Abegaz, “Multiscale modelling of state transitions in the host-microbiome-brain network.” (NWO – Complexity in Health & Nutrition)
- (2011-2014) Javier Gonzalez, “Inference for Energy Metabolism and Ageing.” (NWO Energy Metabolism and Ageing – SBC)
- (2010-2016) Fentaw Abegaz, “Copula-based inference of conditional independence graphs.”
- (2006-2008) Yongxiang Fang, “A lifetime of attrition: post-genomic analyses of ecological and evolutionary processes in nematode-vertebrate systems”.
- (2005-2008) Angela Recchia, ‘Stochastic Modelling and Statistical Inference of Gene Regulatory Pathways: Integrating Multiple Sources of Data”.
- (2003-2007) Raya Khanin, “DNA microarray data analysis and modelling: an integrated approach.”
- (2002-2004) David Bakewell, “Hypothesis testing in microarray experiments.”
- (2001-2004) John McClure, “Statistics for microarray: design, modelling and inference”.

## 4 Scholarships, grants and prizes

### 4.1 Large grants

- NWO, 2017-2021, “Multiscale modelling of state transitions in the host-microbiome-brain network,” € 267,228. Dutch National Science Foundation (Co-PI with B. Bakker, UMCG).
- H2020 COST, 2015-2020, “European Cooperation on Statistics for Network Data Science” (Action CA15109), € 585,000. Horizon2020, Cooperation in Science and Technology.
- NWO-MPE, 2015-2019, “Simultaneous estimation and selection of species diversification models”, € 200,000. Dutch National Science Foundation.
- NWO STAR, 2011–2015, “Network modelling with noisy ODEs using Gaussian Process priors”, € 90,312. Dutch National Science Foundation.
- Workpackage leader, *2010 – 2015*, Systems Biology Centre for Energy Metabolism and Ageing (SBC-EMA), Groningen, € 190,000. Dutch National Science Foundation.
- Principal Investigator, *January 2008 – 31 May 2008*, “Data mining: A Large Scale Re-analysis of Designed Microarray Experiments”, NE/F001355/1, £168,000, Natural Environment Research Council.
- Principal Investigator, *April 2006 – March 2008*, “A lifetime of attrition: post-genomic analyses of ecological and evolutionary processes in nematode-vertebrate systems”, NE/D000602/1, £150,000, Natural Environment Research Council.
- Principal Investigator, *September 2005 – August 2008*, “Stochastic Modelling and Statistical Inference of Gene Regulatory Pathways: Integrating Multiple Sources of Data”, £204,395, Engineering and Physical Sciences Research Council.
- Principal Investigator, *February 2003 – February 2007*, “DNA microarray data analysis and modelling: an integrated approach,” £218,728, Biotechnology and Biological Sciences Research Council and Engineering and Physical Sciences Research Council.
- Co-applicant, *February 2003 – February 2005*, “Functional genomics of nutrient transport in Arabidopsis: a bioinformatics approach,” £87,306, Biotechnology and Biological Sciences Research Council, with Dr Anna Amtmann, IBLS, Glasgow.

### 4.2 Small grants

- STAR Workshop Grant, 2017, “International Workshop on Statistical Modelling – Groningen, 2-7 July, 2017”, € 5,000. Dutch National Science Foundation.
- STAR Workshop Grant, 2017, “SEMSTAT – Eindhoven, 7-10 March, 2017”, € 5,000. Dutch National Science Foundation.
- STAR Workshop Grant, 2011, “All models are wrong...”, € 5,000. Dutch National Science Foundation.
- Principal Investigator (Value In People award holder – 2003-2004), Wellcome Trust, £22,853.



- Principal Investigator, *November 2001 – January 2004*, “Discovering the frontiers of statistical bioinformatics,” £14,180, Engineering and Physical Sciences Research Council.
- Co-applicant, *September 2002*, “Ph.D. Summer School: Mathematical, Computational and Statistical Modelling of Biological Systems,” £14,000, *Mathfit Programme*, Engineering and Physical Sciences Research Council, with Dr Ela Hunt, Computer Science, Glasgow.

### 4.3 Awards and Scholarships

- (2012-2013) *Best Dutch Biostatistics Paper*, by Dutch Biostatistics Society (BMS-ANed), with F. Abegaz.
- (2004-5) *Teacher Mobility Grant*, University of Glasgow, University of Bologna.
- (1994-97) *Fulbright Fellowship*, US government.
- (1994-97) Several *smaller grants*: Dittmer Grant (Dittmer Fund), De Bussy Grant (De Bussy Stichting), VU-Fonds Grant (Vrije Universiteit, Amsterdam), VSB Grant (VSB Bank).

## 5 Publications

### 5.1 International (refereed) journals

1. SN Wood, **EC Wit**, M Fasiolo, PJ Green (2021) “COVID-19 and the difficulty of inferring epidemiological parameters from clinical data” *The Lancet Infectious Diseases*, 21(1), 27–8 DOI:[https://doi.org/10.1016/S1473-3099\(20\)30437-0](https://doi.org/10.1016/S1473-3099(20)30437-0).
2. Artico, I., Smolyarenko, I., Vinciotti, V., **Wit, E. C.** (2020). “How rare are power-law networks really?”. *Proceedings of the Royal Society A*, 476(2241), 20190742.
3. R Užupytė, EC Wit (2020) “Test for triadic closure and triadic protection in temporal relational event data”, *Social Network Analysis and Mining*, 10(1), 1-12.
4. S Ranciati, EC Wit, C Viroli (2020) “Bayesian smooth-and-match inference for ordinary differential equations models linear in the parameters”, *Statistica Neerlandica*, 74(2), 125-144.
5. EC Wit, L Augugliaro, H Pazira, J González, F Abegaz (2020), “Sparse relative risk regression models”, *Biostatistics* 21 (2), e131-e147.
6. F Richter, B Haegeman, RS Etienne, EC Wit (2020), “Introducing a general class of species diversification models for phylogenetic trees”, *Statistica Neerlandica*, 74(3), 261-274, <https://doi.org/10.1111/stan.12205>.
7. W Kruijer, P Behrouzi, D Bustos-Korts, MX Rodríguez-Álvarez, SM Mahmoudi, Brian Yandell, **EC Wit**, FA van Eeuwijk (2020), “Reconstruction of networks with direct and indirect genetic effects”, *Genetics*, 214 (4), 781-807.
8. S de Vos, S Patten, **EC Wit**, EH Bos, KJ Wardenaar, P de Jonge (2020) “Subtyping psychological distress in the population: a semi-parametric network approach”, *Epidemiology and psychiatric sciences*, 29.

9. Signorelli, M., **Wit, E. C.** (2020). “Model-based clustering for populations of networks”. *Statistical Modelling*, 20(1), 9-29.
10. Ranciati, S., Vinciotti, V., **Wit, E. C.** (2020). “Identifying overlapping terrorist cells from the Noordin Top actor–event network”. *Annals of Applied Statistics*, 14(3), 1516-1534.
11. D Pellin, L Biasco, A Aiuti, MC Di Serio, **EC Wit** (2019), “Penalized inference of the hematopoietic cell differentiation network via high-dimensional clonal tracking”, *Applied Network Science*, 4(1), 115.
12. K Kamphorst, BC Oosterloo, AM Vlieger, NB Rutten, CM Bunkers, **EC Wit**, RM van Elburg (2019) “Antibiotic Treatment in the First Week of Life Impacts the Growth Trajectory in the First Year of Life in Term Infants,” *Journal of pediatric gastroenterology and nutrition*, 69 (1), 131-136.
13. S de Vos, S Patten, **EC Wit**, EH Bos, KJ Wardenaar, P de Jonge (2019), “Subtyping psychological distress in the population: a semi-parametric network approach,” *Epidemiology and psychiatric sciences*, 1-8.
14. A Abbruzzo, I Vujacic, AM Mineo, **EC Wit** (2019), “Selecting the tuning parameter in penalized Gaussian graphical models,” *Statistics and Computing* 29 (3), 559-569
15. NP Gill, L D’Arrigo, **EC Wit** (2019), “Comparison of Postoperative Fever and Effectiveness of Percutaneous Nephrolithotomy (PCNL) Versus Retrograde Intrarenal Surgery (RIRS) for the Treatment of Renal Stones,” *SN Comprehensive Clinical Medicine*, 1 (3), 154-159.
16. N Demetrashvili, N Smidt, H Snieder, ER Van Den Heuvel, **EC Wit** (2019) “Variance components models for analysis of big family data of health outcomes in the lifelines cohort study” *Twin Research and Human Genetics*, 22 (1), 4-13
17. P Behrouzi, **EC Wit** (2019) “Detecting epistatic selection with partially observed genotype data by using copula graphical models,” *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 68(1), 141–160.
18. SM Mahmoudi, **EC Wit** (2018) “Estimating Causal Effects from Nonparanormal Observational Data,” *The international journal of biostatistics*, 14 (2)
19. **EC Wit**, L Augugliaro, H Pazira, J González, F Abegaz (2018) “Sparse relative risk regression models,” *Biostatistics*, DOI: 10.1093/biostatistics/kxy060
20. P Behrouzi, **EC Wit** (2018) “De novo construction of polyploid linkage maps using discrete graphical models,” *Bioinformatics*, <https://doi.org/10.1093/bioinformatics/bty777>.
21. H Pazira, L Augugliaro, **EC Wit** (2018) “Extended differential geometric LARS for high-dimensional GLMs with general dispersion parameter,” *Statistics and Computing* 28 (4), 753-774
22. BMS Arani, M Mahmoudi, L Lahti, J González, **EC Wit** (2018) “Stability estimation of autoregulated genes under Michaelis-Menten-type kinetics,” *Physical Review E* 97 (6), 062407
23. **EC Wit** (2018) “Big data and biostatistics: The death of the asymptotic Valhalla,” *Statistics & Probability Letters* 136, 30-33

24. A Litsios, AD Ortega, **EC Wit**, M Heinemann (2018) “Metabolic-flux dependent regulation of microbial physiology,” *Current opinion in microbiology* 42, 71-78.
25. S Ranciati, C Viroli, **EC Wit** (2017) “Mixture model with multiple allocations for clustering spatially correlated observations in the analysis of ChIP-Seq data,” *Biometrical Journal*, 59(6), 1301-1316.
26. A Papagiannakis, B Niebel, **E Wit**, M Heinemann (2017) “A CDK-independent metabolic oscillator orchestrates the budding yeast cell cycle,” *FEBS JOURNAL*, 284, 54-54.
27. de Vos, S., Wardenaar, K. J., Bos, E. H., **Wit, E. C.**, Bouwmans, M. E., de Jonge, P. (2017). “An investigation of emotion dynamics in major depressive disorder patients and healthy persons using sparse longitudinal networks.” *PloS one*, 12(6), e0178586.
28. Mohammadi, A., Abegaz, F., Heuvel, E., **Wit, E. C.** (2017). “Bayesian modelling of Dupuytren disease by using Gaussian copula graphical models.” *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 66(3), 629-645.
29. Purutcuoglu, V., Agraz, M., **Wit, E.** (2017). “Bernstein approximations in glasso-based estimation of biological networks.” *Canadian Journal of Statistics*, 45(1), 62-76.
30. Papagiannakis, A., Niebel, B., **Wit, E. C.**, Heinemann, M. (2017). “Autonomous Metabolic Oscillations Robustly Gate the Early and Late Cell Cycle.” *Molecular cell*, 65(2), 285-295.
31. Gill, N. P., Bos, E. H., **Wit, E. C.**, de Jonge, P. (2017). “The association between positive and negative affect at the inter-and intra-individual level.” *Personality and Individual Differences*, 105, 252-256.
32. Pazira, H., Augugliaro, L., **Wit, E.C.** (2017), “Extended differential geometric LARS for high-dimensional GLMs with general dispersion parameter.” *Statistics and Computing*. Online available.
33. Lotsi, A., **Wit, E.** (2017). “Network estimation in State Space Models with L1-regularization constraint.” *Afrika Statistika*, 12(2), 1251-1271.
34. Scala, S., et al. (2016). “Clonal tracking of engineered human hematopoiesis through integration sites analysis.” *Human Gene Therapy* 27(11), pp. A19-A20.
35. Demetrashvili, N., **Wit, E. C.**, van den Heuvel, E. R. (2016). “Confidence intervals for intraclass correlation coefficients in variance components models.” *Statistical methods in medical research*, 25(5), 2359-2376.
36. Signorelli, M., Vinciotti, V., **Wit, E. C.** (2016). NEAT: an efficient network enrichment analysis test. *BMC bioinformatics*, 17(1), 352.
37. Augugliaro, L., Mineo, A. M., **Wit, E. C.** (2016). “A differential-geometric approach to generalized linear models with grouped predictors.” *Biometrika*, 103(3), 563-577.
38. Augugliaro, L., Mineo, A. M., **Wit, E. C.** (2016). “ $\ell_1$ -Penalized Methods in High-Dimensional Gaussian Markov Random Fields.” *Computational Network Analysis with R: Applications in Biology, Medicine and Chemistry*, 7.

39. Biasco, et al. (2016). “In vivo tracking of human hematopoiesis reveals patterns of clonal dynamics during early and steady-state reconstitution phases.” *Cell Stem Cell*, 19(1), 107-119.
40. V Vinciotti, **EC Wit**, R Jansen, EJCN de Geus, BWJH Penninx, DI Boomsma, PAC’t Hoen (2016), “Consistency of biological networks inferred from microarray and sequencing data”, *BMC bioinformatics* 17 (1), 1.
41. V Vinciotti, L Augugliaro, A Abbruzzo, **EC Wit** (2016), “Model selection for factorial Gaussian graphical models with an application to dynamic regulatory networks”, *Statistical applications in genetics and molecular biology*, 15 (3), 193-212.
42. I Vujacic, SM Mahmoudi, **EC Wit** (2016), “Generalized Tikhonov regularization in estimation of ordinary differential equations models”, *Stat* 5 (1), 132-143.
43. I Vujacic, A Abbruzzo, **E Wit** (2015), “A computationally fast alternative to cross-validation in penalized Gaussian graphical models”, *Journal of Statistical Computation and Simulation*, 85 (18), 3628-3640
44. F Abegaz, **E Wit** (2015), “Copula Gaussian graphical models with penalized ascent Monte Carlo EM algorithm”, *Statistica Neerlandica* 69 (4), 419-441.
45. I Vujacic, I Dattner, J González, **E Wit** (2015), “Time-course window estimator for ordinary differential equations linear in the parameters” *Statistics and Computing* 25 (6), 1057-1070
46. S de Vos, KJ Wardenaar, EH Bos, **EC Wit**, P de Jonge (2015), “Decomposing the heterogeneity of depression at the person-, symptom-, and time-level: latent variable models versus multimode principal component analysis”, *BMC medical research methodology* 15 (1), 1.
47. P Pechlivanoglou, F Abegaz, MJ Postma, **E Wit** (2015), “An alternative parameterization of Bayesian logistic hierarchical models for mixed treatment comparisons”, *Pharmaceutical statistics*, 14 (4), 322-331.
48. **EC Wit**, A Abbruzzo (2015), “Inferring slowly-changing dynamic gene-regulatory networks”, *BMC bioinformatics*, 16 (Suppl 6), S5.
49. S Ranciati, C Viroli, **E Wit** (2015), “Spatio-temporal model for multiple ChIP-seq experiments”, *Statistical applications in genetics and molecular biology*, 14 (2), 211-219.
50. **EC Wit** and A. Abbruzzo (2015), “Factorial graphical models for dynamic networks”, *Network Science*, 3 (01), 37-57.
51. L Augugliaro, AM Mineo, **EC Wit** (2014), “dglars: An R Package to Estimate Sparse Generalized Linear Models”, *Journal of Statistical Software*, 59 (1), 1-40.
52. DHEW Huberts, J González, SS Lee, A Litsios, G Hubmann, **EC Wit**, M. Heinemann (014), “Calorie restriction does not elicit a robust extension of replicative lifespan in *Saccharomyces cerevisiae*”, *Proceedings of the National Academy of Sciences*, 111 (32), 11727-11731.
53. Gonzalez, J., Vujacic, I., **Wit, E.** (2014) “Reproducing kernel Hilbert space 802 based estimation of systems of ordinary differential equations.” *Pattern Recognit. Lett.*, **45**, 26–32.

54. Demestashvili, N, Van den Heuvel, ER, **Wit, E**, (2014) “Probability genotype imputation method and integrated weighted adaptive lasso for QTL identification”, *BMC Genetics*, 14 (1), 125.
55. F Abegaz, **E Wit**, (2013) “Sparse time series chain graphical models for reconstructing genetic networks”, *Biostatistics* 14 (3), 586-599.
56. Y Bao, V Vinciotti, **E Wit**, P AC’t Hoen, (2013) “Accounting for immunoprecipitation efficiencies in the statistical analysis of ChIP-seq data”, *BMC bioinformatics* 14 (1), 169.
57. A Mohammadi, MR Salehi-Rad, **EC Wit**, (2013) “Using mixture of Gamma distributions for Bayesian analysis in an M/G/1 queue with optional second service”, *Computational Statistics*, 1-18.
58. J Gonzalez, I Vujacic, **E Wit**, (2013) “Inferring latent gene regulatory network kinetics”, *Statistical applications in genetics and molecular biology* 12 (1), 109-127.
59. Luigi Augugliaro, Angelo M. Mineo, **EC Wit** (2013) “Differential geometric least angle regression: a differential geometric approach to sparse generalized linear models”, (DOI: 10.1111/rssb.12000), *Journal of the Royal Statistical Society: Series B* (Statistical Methodology), Volume 75, Issue 3, pages 471–498, June 2013.
60. V. Purutcuoglu, **E.C. Wit** (2012), “Estimating network kinetics of the MAPK/ERK pathway using biochemical data”, *Mathematical Problems in Engineering*, vol. 2012, Article ID 752631, 34 pages, 2012. doi:10.1155/2012/752631.
61. Gonzalez, J., Vujacic, I., **Wit, E**, (2012) “A new statistical framework to infer gene regulatory networks with hidden transcription factors”, *Statistical Applications in Genetics and Molecular Biology*, accepted for publication.
62. E. Ayyildiz, V. Purutcuoglu Gazi, **E Wit** (2012) “A short note on resolving singularity problem in covariance matrices,” *International Journal of Statistics and Probability*, 1(2).
63. **Wit, E**, Romeijn, JW, Van den Heuvel, ER, (2012) “‘All models are wrong...’: an introduction to model uncertainty,” *Statistica Neerlandica*, 66(3), p.5-21.
64. **Wit, E** and D. Bakewell, (2012) “Borrowing strength: a likelihood ratio test for related sparse signals,” *Bioinformatics*, 28(15): 1980-1989 (doi: 10.1093/bioinformatics/bts316).
65. Mohammadi, A. and Salehi-Rad, MR and **Wit, EC** (2012), Using mixture of Gamma distributions for Bayesian analysis in an M/G/1 queue with optional second service, *Computational Statistics*, DOI: 10.1007/s00180-012-0323-3.
66. **E.C. Wit** (2012), Review: Learning and Inference in Computational Systems Biology, *Bio-metrics* 68, 335.
67. Sperrin, M., Jaki, T., **Wit, E**. (2010) “Probabilistic relabelling strategies for the label switching problem in Bayesian mixture models”, *Statistics and Computing*, 20(3), 357–366.
68. Sawle, A.D., **Wit, E.**, Whale, G. and Cossins, A.R. (2010), “An information-rich, alternative, chemicals testing strategy using a high definition toxicogenomics and zebrafish (*Danio rerio*) embryos, *Toxicological Sciences*, 1096-6080.

69. Friel N, Pettitt AN, Reeves R, **Wit, E.** (2009) “Bayesian Inference in Hidden Markov Random Fields for Binary Data Defined on Large Lattices”, *Journal of Computational and Graphical Statistics*, 18(2):243-261.
70. Purutcuoglu, **Wit, E.** (2008) “Bayesian inference for the MAPK/ERK pathway by considering the dependency of the kinetic parameters”, *Bayesian Analysis*, 3(4):851-86.
71. Recchia, A, **Wit, E.**, Vinciotti, V., et al. (2008) “Computational inference of replication and transcription activator regulator activity in herpesvirus from gene expression data”, *IET Systems Biology*, 2(6):385-396.
72. Evans, H; Mello, LV; Fang, YX, **Wit, E.**, et al. (2008) “Microarray analysis of gender- and parasite-specific gene transcription in *Strongyloides ratti*”, *International Journal for Parasitology*, 38(11):1329-1341.
73. Martin, F. L., German, M. J., **Wit, E.**, Fearn, T., Ragavan, N. and Pollock, H (2007) “Identifying variables responsible for clustering in discriminant analysis of data from IR microspectroscopy of a biological sample,” *Journal of Computational Biology*, 14(9):1176-1184.
74. Purutcuoglu, V., **Wit, E** (2007) “FGX: A Frequentist Gene Expression Index,” *Biostatistics*, 8(2):433-437.
75. Khanin, R, Vinciotti, V, Mersinias, V, Smith, CP, **Wit, E** (2007) “Statistical reconstruction of transcription factor activity using Michaelis-Menten kinetics,” *Biometrics*, 63(3):816–823.
76. Khanin, R and **Wit, E** (2006) “How scale-free are gene networks?”, *J. of Computational Biology*, 13(3):810–8.
77. Khanin, R, Vinciotti, **Wit, E** (2006) “Reconstructing repressor protein levels from expression of gene targets in *E. Coli*,” *PNAS*, 103(49):18592-6.
78. V. Purutcuoglu and **E. Wit** (2006) “Exact and Approximate Stochastic Simulations of the MAPK Pathway and Comparisons of Simulations Results.” *Journal of Integrative Bioinformatics*, 3(2):38.
79. Flück, M, Daepf, C, Schmutz, S, Hoppeler, H, **Wit, E** (2005) “Transcriptional profiling of skeletal muscle plasticity: the underestimated influence of shifts in gene expression and of technical limitations,” *J Appl Physiol*, 99(2): 397 - 413.
80. **Wit, E**, Nobile, A, Khanin, R, (2005) “Near-optimal designs for dual-channel microarray studies,” *Applied Statistics*, 54(5):817-30.
81. Dennis, JL, Hvidsten, TR, **Wit, E**, Komorowski, J, Bell, AK, Downie, I, Mooney, J, Verbeke, C, Bellamy, C, Keith, WN, Oien, KA (2005) “Markers of Adenocarcinoma characteristic of the site of origin: development of a diagnostic algorithm,” *Clinical Cancer Research*, 11(10):3766-72.
82. Khanin, R and **Wit, E** (2005) “Design of large time-course microarray experiments with two channels,” *Applied Bioinformatics* 4(4):253-61.
83. Vinciotti, V, Khanin, R, D’Alimonte, D, Liu, X, Cattini, N, Hotchkiss, G, Bucca, G, de Jesus, O, Rasaiyaah, J, Smith, CP, Kellam, P and **Wit, E** “An experimental evaluation of a loop versus a reference designs for two-channel microarrays,” *Bioinformatics*, **21**:492-501.

84. Bakewell, D, **Wit, E** (2005) “Weighted analysis of microarray gene expression using maximum likelihood,” *Bioinformatics*, **21**:723-9.
85. McClure, JD, **Wit, E** (2003) “Post-normalization quality assessment visualization of microarray data,” *Comparative and Functional Genomics*, November, 2003.
86. **Wit, E** (2003) “Who wants to be... The Use of a Personal Response System in Statistics Teaching,” *MSOR Connections*, **3**:2, pp. 14–20.
87. **Wit, E**, McClure, JD (2003) “Statistical Adjustment of Signal Censoring in Gene Expression Experiments,” *Bioinformatics*, 19:9.
88. Dennis, JL, Vass, JK, **Wit, E**, Keith, WN, Oien, KA (2002) “Identification from public data of molecular markers of adenocarcinoma characteristic of the site of origin,” *Cancer Research*, **62**:5999-6005.
89. Haas, M, **Wit, E** (2000) “Etiologies and outcome of acute renal insufficiency in older adults,” with M. Haas, *The Am. J. of Kidney Diseases*, **35**, No. 3, pp. 433-47.
90. Haas, M, **Wit, E** (1999) “Smooth muscle-specific actin levels in renal transplant recipients,” with M. Haas, *The Am. J. of Kidney Diseases*, **34**, No. 1, pp. 69-84.
91. **Wit, E** (1999) “Kant and the limits of civil obedience,” *Kant-Studien*, Band 90, Heft 3, pp. 285-305.

## 5.2 Books or contributions to books

1. **Wit, E.**, Vinciotti V. and Purutcuoglu, V. (2013) “Statistics for biological networks: How to infer networks from data,” Chapman-Hall/CRC Press.
2. Khanin, R., **Wit, E.** (2007) “Construction of Malaria Gene Expression Network Using Partial Correlations” in **Methods of Microarray Data Analysis V**, Editors McConnell, P., Lin, S. M., Hurban, P., Springer: New York.
3. **Wit, E.**, Purutcuoglu, V., O’Donovan, L., Zhu, X. (2006) “Gaining weights... and feeling good about it” in *Microarray Technology and Cancer Gene Profiling*, Editor S. Mocellin, Springer, New York, 2006.
4. **Wit, E**, Khanin, R (2006) “Integrating statistical approaches in experimental design and data analysis,” In: *Encyclopedia on Genetics, Genomics, Proteomics and Bioinformatics*, Vol.4, *Bioinformatics*. John Wiley & Sons.
5. **Wit, E** and McClure, JD (2004) *Statistics for Microarrays; Design, Analysis and Inference*, Chichester: John Wiley & Sons.
6. **Wit, E**, McCullagh, P (2001) “The Extendibility of Statistical Models,” in *Algebraic methods in Statistics*, AMS Contemporary Mathematics Series.

### 5.3 Proceedings

1. Abbruzzo, A. and **Wit, EC** (2012), Factorial Graphical Lasso and Slowly Changing Graphical Models for Estimating Dynamic Networks, *46th Scientific meeting of the Italian Statistical Society*.
2. Fang, Y.X., **Wit, E.**, “Test the overall significance of p-values by using joint tail probability of ordered p-values as test statistic”, Advanced Data Mining and Applications, *Proceedings 4th International Conference, ADMA 2008*, pp.435-43, 2008.
3. Bakewell, DJG; **Wit, E.**, “A global statistical test for improved detection of gene activity”, BMC Systems Biology, Vol.1,P10, 2007.
4. Purutcuoglu, V.; **Wit, E.**, “Bayesian inference of the kinetic parameters of a realistic MAPK/ERK pathway”, BMC Systems Biology, Vol.1, P19, 2007.
5. **Wit, E**, Thomson, N (2005) “Bayesian modelling of gene networks with topological constraints”, *Proceedings of the International Workshop on Statistical Modelling*, Sydney.
6. **Wit, E**, Van der Laan, M (2003) “Error Control in Multiple Testing using a Mixture Model Setting,” *Conference Proceedings Internal Biometrics Society Meeting*, Italian Region, September 9-12, 2003.
7. **Wit, E**, Friel, N (2003) “Hidden Markov Modelling of Genomic Interactions,” *Bulletin of the International Statistical Institute*, 54th session, August 2003.
8. **Wit, E** (2002) “Statistical modelling of gene expression data,” *2002 ASA Proceedings*, August 2002.

## 6 Invitations to scientific meetings and conferences

Invited talks only (excluding departmental seminars):

- “Dynamic Networks in Modern Statistics,” RSS Journal Webinar, 9 December 2020.
- “Covid-19 and the perils of inferring epidemiological parameters from clinical data,” CO-COCO meeting, Munich, 10 July 2020.
- “Estimating flow networks via systems of noisy differential equations,” COSTNET meeting, Bilbao, 9 October 2019.
- “Statistical learning of epistasis, genetic maps and microbial networks via graphical models,” BMS-ANed meeting, Utrecht, 16 May 2019.
- “Discussion of *Functional and complex data* by Laura M. Sangalli”, 19 February, 2019.
- “Stochastic network modelling of evolutionary tree,” SIS Palermo, 20 June 2018.
- “Network Inference in Genomics,” COSTNET Meeting, Palma de Mallorca, 26 October 2017.
- “Statistics for Biological Networks,” Emerging Topics in Biological Networks and Systems Biology Symposium SCAS, Uppsala, Sweden, 11 October 2017.



- “Reconstruction of Biological Networks,” Eurandom SAM, 10th edition, 20 September 2017.
- “Network inference in Genomics,” CLADAG Conference, Milano, Italy, 14 September 2017.
- “ODE network inference in genomics,” SIS Conference, Florence, Italy, 28 June 2017.
- “Beyond (generalized linear) models,” Peter McCullagh Symposium, Chicago USA, 7 June 2017.
- “Estimation of dynamic networks with differential equations,” Royal Statistical Society, Emerging Application Section, London, UK, 8 May 2017.
- “COSTNET, Networks and Detecting Epistatic Selection,” CMStatistics, Seville, Spain, 10 December 2016.
- “Network inference in Genomics,” Theoretical foundations for statistical network analysis, Isaac Newton Institute, Cambridge, UK, 24 August 2016.
- “God playing dice: stochastic species diversification models,” Mathematics of Planet Earth, CWI, Amsterdam, 20 January 2016.
- “Exponential Random Graphical Models,” CMStatistics, London, UK, 14 December 2015.
- “Short Course: Network Modelling,” ECAS, Muenchen, DE, 30 September - 2 October 2015.
- “Networks: between measures and data,” Keynote, 12th Applied Statistics Conference, Slovenia, 22 September 2015.
- “Inference of genomic network dynamics with non-linear ODEs,” IMS, Singapore, 11 June 2015.
- “Exponential Random Graphical Models,” European Meeting of Statisticians, Amsterdam NL, 9 July 2015.
- “Big Networks and Data,” STAR Outreach, Eindhoven, NL, 12 December 2014.
- “Sparse high-dimensional graphical models,” ERCIM, Pisa, Italy, 7 December 2014.
- “DgCox: a differential geometric approach for high-dimensional Cox proportional hazard models”, CIBB, Cambridge, UK, 27 June 2014.
- “Model selection in graphical models,” Royal Statistical Society, General Application Section, 22 May 2014.
- “SHORT COURSE: Modelling genomic Networks”, Norwegian Winter School, Geilo, Norway, 20-24 January 2014.
- “Network inference via Birth-Death MCMC”, MCMSki (ISBA), Chamonix, France, 8 January 2014.
- “Sparse Graphs in Genomics”, CIBB, Nice, 21 June 2013.
- “Statistical Network Science”, Colorado State University Invited Honorary Lecturer, Fort Collins, CO, USA, 14-25 May 2013.

- “Sparse graphs in genomics”, *Challenges for Integrated analysis of Omics datasets* in conjunction with EMGM (European Mathematical Genetics Meeting), 27 April 2013.
- “Sparse Graphs (from noisy data, obviously)”, Meeting the Challenges of High Dimension: Statistical Methodology, Theory and Applications Workshop, IMS Singapore, 4 October 2012.
- “Colourful sparse dynamic genomic networks”, Optimising Information Retrieval from Biological Data, Sheffield, 3 April 2012
- “Futility of models in science: about the Higgs boson, Fukushima and Lehmann Brothers”, Chances in Sciences Workshop, Lorentz Centre, Leiden, 26 October 2011.
- “Sparse Coloured Graphs for Gene Network Models”, BIO-SI workshop, Rennes, 19 October 2011.
- “Sparse model-based network inference using Gaussian graphical models”, Biometric Conference, Italian region, Garganno, 21 June 2011.
- “PhD Short Course: Optimal design of microarray experiments”, Amagro, Ciudad-Real, Spain, 7-10 June 2011.
- “PhD Short course: Statistical Network Modelling”, Hilversum, Netherlands, 23-25 May 2011.
- “Model uncertainty and replication problems in designing microarray experiments,” Dutch National Academy of Sciences (KNAW), Amsterdam, 28 April 2011.
- “Sparse modelling and inference of dynamic genetic networks”, Royal Society, Kavli Centre Bucinhamshire, 28 March 2011.
- “Short Course: Statistics for Networks,” International Biometrics Society meeting, Florianopolis, Brazil, 2-5 December, 2010.
- “Sparse model-based network inference using Gaussian graphical models”, invited talk, LASR meeting, Leeds, 6 July 2010.
- “Looking for sparse genetic needles in high-dimensional haystacks”, invited talk, Nederlands Mathematisch Congres, Utrecht, 23 April 2010.
- “Living in a sparse world”, invited talk, NDNS meeting, Eindhoven, 12 April 2010.
- “War on Error”, invited talk, Stat-OR Dag, Amsterdam, 1 April 2010.
- “Modelling networks: top-down or bottom-up”, invited talk, GeneSys meeting, Warwick, 22 September 2009.
- “Mixed modelling ideas for microarray data”, invited talk, CLADAG, Catania, Italy, 9-11 September 2009.
- “How statistics conquered genetics (or vice versa)”, invited talk, Nederlands Mathematisch Congres, Groningen, The Netherlands, 14 April 2009.
- “Reverse engineering pathway dynamics from microarray data”, invited talk, IBS-EMR Conference, Istanbul, Turkey, 13 May 2009.

- “Muddling or modelling your way through normalization?”, CAMDA, Vienna, Austria, 5 December 2008.
- “Nesting and other replication issues in two-channel microarray designs”, invited talk, International Biometric Conference, 17 July 2008.
- “High-dimensional inference in bioinformatics and genomics,” Newton Institute, *Future Directions in High-dimensional Data Analysis: New Methodologies, New Data Types and New Applications*, Cambridge, 24 June 2008.
- “From genomes to systems and ‘some’ statistics in-between”, invited talk, From Genomes to Systems Conference, Manchester, UK, 19 March, 2008.
- “Modelling transcription activation using microarray data”, invited talk, 6th workshop: Statistical Methods for Post-genomic Data”, Rennes, France, 31 January 2008.
- “Random effects modelling for multivariate data from cDNA microarrays”, invited talk, CLADAG, Macerata, Italy, 13 September 2007.
- “Statistics for Microarrays,” invited short course, Ankara, 15 August 2007.
- “Microarray study design,” invited talk, *NUGO microarray data analysis course*, Maastricht, Netherlands, 2-5 July 2007.
- “Reverse engineering pathway dynamics from microarray data”, invited talk, *International Workshop Omics: Assembling System(s) Biology*, Lugano, Switzerland, 24-8 June 2007.
- “Microarray experiments: linear mixed-effect models for unusual designs”, invited tutorial, *NERC Microarray and Gene Expression Workshop*, Liverpool, 14-7 May 2007.
- “Modelling transcription activation using microarray data,” invited talk, *Statistical Bioinformatics & Stochastic Systems Biology*, Newcastle, 2-3 April 2007.
- “statistics for microarrays,” invited tutorial, *BioSysBio Conference*, Manchester, 10 January, 2007.
- “Design for microarray experiments,” invited talk, *RSS Conference*, 10-14 September, 2006, Belfast, UK.
- “Optimal design for microarrays,” invited talk, *Design Workshop*, 8-10 September, 2006, Southampton, UK.
- invited talk, *IMS Workshop in Probability*, 30 July-4 Aug, 2006, Rio de Janeiro, Brazil.
- “Statistics for Microarrays: a One Day Tour,” invited Short Course, *International Workshop on Statistical Modelling*, 2 July, 2006, Galway, Ireland.
- “Multivariate Analysis in Bioinformatics,” Master Course, 29 May - 2 June, 2006, Department of Statistics, University of Padova, Italy. “Statistical Analysis of Genetic and Gene Expression Data,” MolPAGE training, March 20-24, 2006, University of Pavia, Italy.
- Invited talk, Workshop on Experimental Design, Friday 10th March 2006, BioScope-IT, Ghent, Belgium.

- “Design of Microarray Experiments,” invited talk, *5th VIB Microarray Users Group Meeting*, 16-18 November 2005, Ghent, Belgium.
- “Inferring transcription factor activity from gene expression data,” *Data Fusion Meeting*, 6-8 September 2005, London, UK.
- “Decision making and modelling in genomics,” invited talk, *25th European Meeting of Statisticians*, 24-28 July, 2005.
- “Statistical Bioinformatics,” invited speaker, *European Young Statisticians Training Camp*, 18-23 July, 2005.
- “Hierarchical network modelling with architectural constraints,” invited talk, *Recent Advances in Biostatistics, Bioinformatics and Markov Chain Monte Carlo*, University of New South Wales, Sydney, 6-7 July 2005.
- “Experimental Design and Differentially Expressed Genes,” *ESF Training Course: Microarray Gene Expression Analysis: Power and Potential of Standardisation*, 23-7 May 2005, Trondheim, Norway.
- “From experimental design to biological networks”, *Intelligent Data Analysis*, 18-20 May 2005, Leiden, Netherlands.
- “Classification in high-dimensional spaces with microarrays in mind,” invited talk, *Statistics Day*, 11 April, 2005, University of Rotterdam.
- “Robust optimal designs of microarray experiments using simulated annealing,” invited talk, *DEINDE workshop*, 29-31 March 2005, Turin, Italy.
- “The Role of Statistics in Genomics,” invited talk, *RCUK Genomics Showcase*, 16 November 2004, Brussel, Belgium.
- “Optimal design of microarray experiments,” invited talk, *BBSRC Microarray Workshop, Methods of analysis and interpretation of microarray data*, 20-1 September 2004, Rothamsted Research, Harpenden, U.K.
- “Statistics for Microarrays: Design, Analysis and Inference”: 2-day workshop, Department of Epidemiology and Medical Statistics, University of Verona.
- “How not to analyze microarray data,” invited talk, *Statistical Microarray Workshop*, University of Singapore, Singapore, January 2004.
- “Error control in multiple testing using a mixture model setting,” invited talk, *International Biometrics Society Conference*, Marina di Massa, Italy, 11 Sept 2003.
- “Statistical Microarray Analysis Workshop,” *International Biometrics Society Conference*, Marina di Massa, Italy, 9-10 Sept 2003.
- “Hidden Markov Models for Gene Expression Analysis,” *Joint Statistical Meeting*, San Francisco, USA, 5 Aug 2003.
- “Can We Make Statistics Count in Bioinformatics,” 8 May, 2003, Royal Statistical Society, Local North-East Group, Durham.

- “Hidden Markov Modelling of Genomic Expression Interactions” 22 February 2003, Statistical Microarray Workshop, MaPhySto, University of Aarhus, Danmark.
- “Can We Make Statistics Count in Bioinformatics,” 13 February, 2003, Royal Statistical Society, Local Group Aberdeen.
- “Hidden Markov Models for Genomic Interactions,” 15 January 2003, Seminar at Computational Biology Seminars, University of Glasgow.
- “Bayesian Hierarchical Models in Microarray Studies,” invited talk, *BIOSS Annual lecture*, Edinburgh, 18 November, 2002.
- “Hierarchical Models for Gene Expression Analysis,” invited talk, *Workshop on Statistical Aspects of Microarray Data*, Aarhus University, Denmark, February 20-22, 2003.
- “Dynamic Analysis of Time Course Gene Expression,” invited talk, at *Mining Biomedical Data Session of Joint Statistical Meeting*, New York, August 11-15, 2002.
- “Experimental Design of Microarray Studies,” *Biologist Meets Statistician Meeting*, (Stratagene), European Bioinformatics Institute, Hixton, May 2002.
- “Correcting for Truncation effects and the Use of Background Information in Microarrays,” Array Meeting, UMIST, February 14, 2002.
- “The Use of Statistics in Microarray Studies,” at *Microarray Technologies Summit & Exposition*, Princeton Marriott, New Jersey USA, September 24-25, 2001.