

Curriculum Vitae

Prof. Dr. E. C. Wit

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- Prof. Dr. Ernst Wit
Johann Bernoulli Institute
Rijksuniversiteit Groningen
PO Box 407, 9700 AK Groningen
- Doctorate: May 1997 (Philosophy), June 2000 (Statistics).
- Other details:

Email: E.C.Wit@rug.nl
Website: <http://www.math.rug.nl/~ernst>
Telephone: +31 (0)50 363 5170
Fax: +31 (0)50 363 3800

1 Curriculum vitae

1.1 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

1.2 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

1.3 Current employment

Full professor (permanent)

1.4 Employment record

- *1 June, 2008 – current*, Professor of Statistics and Probability, 1 fte, permanent
Johann Bernoulli Institute, University of Groningen.

Management of Statistics and Probability Unit, consisting of 2.0 fte permanent staff
Supervision of 4 PhD students, 2 postdocs, 1 instructor, 6 BSc/Master students.

- *1 January, 2006 – 31 May, 2008*, Chair in Biometrics, 1 fte, permanent
Department of Mathematics and Statistics, Lancaster University.
Managing 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.

1.5 Brief summary of research over last five years

Four years ago I moved to the University of Groningen, where I have set up a research group with 4 PhD students and 2 post-docs to work on “Network Science” in all of its diverse aspects. With my background in high-dimensional genomic data, I was intrigued by several publications in *Science* and *Nature* on the ubiquity of so-called “scale-free networks”. It led me to re-analyze 10 such datasets, in which I found that none of the networks in these papers were really scale-free [20]. This led me to consider more complicated models for genetic networks.

- My PNAS publication [21] explored inferring kinetic parameters in deterministic differential equations measured with noise. The area of ODE inference is vastly unexplored and this is why I am making it one of the focus points of my future research.
- I have worked on single cell dynamic network systems, modelled as a stochastic differential equation. The computational complexities that I encountered in this work, led me to consider computational efficient alternatives.
- I am one of the key scientists of the System Biology Centre at the RuG, involved in Energy Metabolism and Ageing. On the methodological side, this involves developing realistic biological models.

I am currently the coordinator and instigator of an effort to bring together 47 research groups within Europe working on Network Science. I have been the supervisor of 12 PhD students and 7 postdocs. Until 2008 I have led an academic department (Medical Statistics, Lancaster) with 20+ academic (permanent and post-doctoral) staff.

1.6 International activities

- Coordinator of a Europe-wide EU COST application for a network of European Scientists working on Network Science, bringing together 47 research groups.
- Member of Scientific Advisory Board of the BBSRC Genome Analysis Centre (Norwich, UK).
- Invited to the Newton Institute “Statistical Theory and Methods for Complex, High-Dimensional Data” programme, University of Cambridge (7 January - 27 June 2008).
- 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).
- I have worked in academics in USA, UK, Netherlands and Australia.
- Regular guest lecturer at the University of Bologna, University of Palermo (Italy), at the Middle Eastern Technical University (Ankara, Turkey), University of Ciudad Real (Spain).

1.7 Other academic activities

- Associate editor *Statistical applications in genetics and microbiology*, Guest editor *Statistica Neerlandica*.
- 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 (“High-dimensional inference and complex data”, 23-25 November 2009, Groningen; “All models are wrong...”, 14-16 March 2011)

TEACHING AND 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 on a HEC grant) Nazia Gill, “MUSE: Museum User Statistical Evaluation”
- (Current, funded on a Research Council grant: STAR) Abdolreza Mohammadi: “Model uncertainty in network inference”
- (Current, replacement funding by faculty) Ivan Vujacic: “ODE inference of genetic networks”.
- (Current, replacement funding by faculty) 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:

- (Current, funded on a Research Council grant: EMA-SBC) Javier Gonzalez, “Inference for Energy Metabolism and Ageing.”
- (Current, funded on a teaching grant) 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”.

1.8 Scholarships, grants and prizes

Grants

- NWO STAR, 2011–2013, “Network modelling with noisy ODEs using Gaussian Process priors”, € 90,312.
- Workpackage leader, 2010 – 2015, Systems Biology Centre for Energy Metabolism and Ageing (SBC-EMA), Groningen.
- STAR Workshop Grant, 2011, “All models are wrong...”, € 5,000.
- 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.
- Principal Investigator (Value In People award holder – 2003-2004), Wellcome Trust, £22,853.
- 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.
- 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.

Awards and Scholarships

- (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).

1.9 Publications

International (refereed) journals

1. Augugliaro, L, Mineo AM and **E Wit**, (2012) “A differential geometric approach to sparse high-dimensional GLMs”, *Journal of the Royal Statistical Society, Series B*, accepted for publication.
2. Augugliaro, L, Mineo AM and **E Wit**, (2012) “Differential geometric LARS via cyclic coordinate descent method”, *Computational Statistics & Data Analysis*, accepted for publication.
3. V. Purutcuoglu, **E.C. Wit** (2012), “Estimating network kinetics of the MAPK/ERK pathway using biochemical data”, *Mathematical Problems in Engineering*, accepted for publication.
4. 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.
5. 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).
6. **Wit, E**, Romeijn, JW, Van den Heuvel, ER, (2012) “An introduction to model uncertainty,” *Statistica Neerlandica*, 66(3), p.5-21.
7. **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).
8. 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.
9. **E.C. Wit** (2012), Review: Learning and Inference in Computational Systems Biology, *Biometrics* 68, 335.
10. **Wit, E**, Romeijn, JW, Van den Heuvel, ER, (2012) “‘All models are wrong...’: an introduction to model uncertainty,” *Statistica Neerlandica*, Vol 66, no. 3.
11. Sperrin, M., Jaki, T., **Wit, E**. (2011) “Probabilistic relabelling strategies for the label switching problem in Bayesian mixture models”, *Statistics and Computing*, 20(3), 357366.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.

17. 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.
18. Purutcuoglu, V., **Wit, E** (2007) "FGX: A Frequentist Gene Expression Index," *Biostatistics*, 8(2):433-437.
19. 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.
20. Khanin, R and **Wit, E** (2006) "How scale-free are gene networks?" , *J. of Computational Biology*, 13(3):810-8.
21. Khanin, R, Vinciotti, **Wit, E** (2006) "Reconstructing repressor protein levels from expression of gene targets in *E. Coli*," *PNAS*, 103(49):18592-6.
22. 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.
23. 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.
24. **Wit, E**, Nobile, A, Khanin, R, (2005) "Near-optimal designs for dual-channel microarray studies," *Applied Statistics*, 54(5):817-30.
25. 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.
26. Khanin, R and **Wit, E** (2005) "Design of large time-course microarray experiments with two channels," *Applied Bioinformatics* 4(4):253-61.
27. 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.
28. Bakewell, D, **Wit, E** (2005) "Weighted analysis of microarray gene expression using maximum likelihood," *Bioinformatics*, **21**:723-9.
29. McClure, JD, **Wit, E** (2003) "Post-normalization quality assessment visualization of microarray data," *Comparative and Functional Genomics*, November, 2003.
30. **Wit, E** (2003) "Who wants to be... The Use of a Personal Response System in Statistics Teaching," *MSOR Connections*, **3**:2, pp. 14-20.
31. **Wit, E**, McClure, JD (2003) "Statistical Adjustment of Signal Censoring in Gene Expression Experiments," *Bioinformatics*, 19:9.
32. 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.
33. 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.
34. 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.

35. **Wit, E** (1999) “Kant and the limits of civil obedience,” *Kant-Studien*, Band 90, Heft 3, pp. 285-305.

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.

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.

Submitted for publication:

1. Gonzalez, J., Vujacic, I., **Wit, E** “Reproducing Kernel Hilbert space based estimation of systems of ordinary differential equations”, submitted for publication.
2. Gonzalez, J., Vujacic, I., **Wit, E** “A new statistical framework to infer gene regulatory networks with hidden transcription factors”, submitted for publication.
3. **Wit, E**, Abbruzzo, A, “Factorial graphical lasso for dynamic networks”, submitted for publication.
4. **Wit, E**, Abbruzzo, A, “Modelling slowly changing dynamic gene-regulatory networks”, submitted for publication.
5. Demestrashvili, N, Van den Heuvel, ER, **Wit, E**, “Probability genotype imputation method and integrated weighted adaptive lasso for QTL identification”, submitted for publication.
6. Lotsi, A, **Wit, E** “State space modeling of dynamic genetic networks”, submitted for publication.
7. Lotsi, A, **Wit, E** “Network estimation in State Space Model with L1-regularization constraint”, submitted for publication.
8. Abegaz, F, **Wit, E**, “Sparse mixed interaction graphical models applied to the NFL”, submitted for publication.
9. Abegaz, F, **Wit, E**, “Gaussian copula graphical models using EM algorithm with l_1 penalized maximum likelihood applied to breast cancer clinical and genomic data”, submitted for publication.
10. Abegaz, F, **Wit, E**, “Sparse time series chain graph models for reconstructing genetic regulatory networks from gene expression profiles”, submitted for publication.
11. Bao, Y, Vinciotti, **Wit, E** and 't Hoen, P., “Accounting for immunoprecipitation efficiencies in the statistical analysis of ChIP-seq data”.
12. Augugliaro, L, Mineo AM and **E Wit**, “Group dgLARS: A Differential Geometric Approach to Sparse GLMs with Grouped Predictors”.

1.10 Scientific scientific meetings and conferences

Invited talks only, but excluding departmental seminars:

- “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, Denmark.
- “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.