

# Simon Rogers PhD

## PERSONAL DETAILS

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**Full Name** Simon David Rogers  
**Date of Birth** 14th October 1979  
**Nationality** British  
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**Marital Status** Single  
**Driving License** Full, clean

## ACADEMIC QUALIFICATIONS

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2001 to 2004     **PhD**                    Machine Learning Techniques for Microarray Analysis.  
Dept. of Engineering Mathematics, University of Bristol, under the supervision of Dr. C. Campbell.  
1997 to 2001     **MEng (1st Class)** Electrical and Electronic Engineering, University of Bristol.

## EMPLOYMENT HISTORY

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July 2009 to date     •     Lecturer (equivalent to Assistant Professor in US), Department of Computing Science, University of Glasgow.  
2008 to July 2009     •     Research Associate on EPSRC grant EP/E052029/1, Inference Research Group, Department of Computing Science, University of Glasgow.  
2005 to 2008             •     Research Associate on EPSRC grant EP/C010620/1, Bioinformatics Research Centre, University of Glasgow.  
2004 to 2005            •     Machine learning consultant for Mosaiques Diagnostics and Therapeutics GmbH.  
2001 to 2004            •     Lab. Demonstrator and Tutor, Department of Engineering Mathematics, University of Bristol.

## ACADEMIC PRIZES

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- Presentation prize at University of Bristol Faculty of Engineering Spring Research conference with talk entitled “Estimating Sample Complexity of Gene Expression Data” (2002).
- Sander Prize for best exam results in Electrical and Electronic Engineering at the University of Bristol (2001).

## PROFESSIONAL MEMBERSHIPS

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- Fellow of the Royal Statistical Society

PUBLICATIONS

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- 2010 • Protein Interaction Detection in Sentences via Gaussian Processes: A preliminary evaluation. T. Polajnar, **S. Rogers** and M. Girolami. *International Journal of Data Mining and Bioinformatics*. To appear.
- 2009 • Classification of Protein Interaction Sentences via Gaussian Processes. T. Polajnar, **S. Rogers** and M. Girolami. *Lecture Notes in Bioinformatics, Proceedings of the 4th IAPR International Conference - Pattern Recognition in Bioinformatics* pp 282–292
- Semi-Parametric analysis of Multi-Rater data. **S. Rogers**, M. Girolami and T Polajnar. *Statistics and computing*. To appear. *Impact factor 1.136*
- Infinite factorization of multiple non-parametric views. **S. Rogers**, A. Klami, J. Sinkkonen, M. Girolami and S. Kaski. *Machine Learning*, under review. *Impact factor 1.742*
- Probabilistic assignment of formulas to mass peaks in metabolomics experiments. **S. Rogers**, R. Scheltema, M. Girolami and R. Breitling. *Bioinformatics*, 25(4):512-518. *Impact factor 5.039*
- 2008 • Investigating the correspondence between transcriptomic and proteomic expression profiles using coupled cluster models. **S. Rogers**, M. Girolami, W. Kolch, K. Waters, T Liu, B. Thrall, H.S. Wiley. *Bioinformatics*, 24(24):2894-2900. *Impact factor 5.039*
- 2007 • Multi-class semi-supervised learning with  $\epsilon$ -truncated multinomial probit Gaussian processes. **S. Rogers** and M. Girolami. *Journal of Machine Learning Research, Workshop and conference proceedings* 1:17–32.
- Bayesian model-based inference of transcription factor activity. **S. Rogers**, R. Khanin and M. Girolami. *BMC Bioinformatics*, 8(Suppl. 2) - **12 citations**.
- 2006 • Variational Multinomial Regression with Gaussian Process Priors. M. Girolami and **S. Rogers** *Neural Computation* 18(8):1790-1817 - **27 citations**.
- Identification of Prognostic Signatures in Breast Cancer Microarray Data using Bayesian Techniques. L. Carrivick, **S. Rogers**, J. Clark, C. Campbell, M. Girolami and C. Cooper. *Journal of The Royal Society Interface* 3(8):367-381- **8 citations**.
- 2005 • Disease Diagnosis from Capillary Electrophoresis: Mass Spectrometry. **S. Rogers**, M. Girolami, W. Krebs and H. Mischak. *Proceedings of the International Conference on Advances in Pattern Recognition, Bath 2005* - **1 citation**.
- Hierarchic Bayesian Models for Kernel Learning. M. Girolami and **S. Rogers**. *22nd International Conference on Machine Learning (ICML 2005)* - **18 citations**.
- A Bayesian Regression Approach to the Inference of Regulatory Networks from Gene Expression Data. **S. Rogers** and M. Girolami. *Bioinformatics* 21(14):3131-3137 - **32 citations**.
- The Latent Process Decomposition of DNA Microarray Data. **S. Rogers**, M. Girolami, C. Campbell and R. Breitling. *IEEE Transactions on Computational Biology and Bioinformatics*. 2:143-156 - **17 citations**.
- 2004 • Prognostic Classification of Relapsing Favourable Histology Wilms Tumour Using cDNA Microarray Expression Profiling and Support Vector Machines. R. Williams, S. Hing, B. Greer, C. Whiteford, J. Wei, R. Natrajan, A. Kelsey, **S. Rogers**, C. Campbell, K. Pritchard-Jones and J. Khan. *Genes Chromosomes and Cancer* 41:65-79 2004 - **26 citations**.
- 2003 • Estimating Dataset Size Requirements for Classifying DNA Microarray Data. S Mukherjee, P. Tamayo, **S. Rogers**, R. Rifkin, A. Engel, C. Campbell, T. Golub and J. Mesirov. *Journal of Computational Biology* 10(2):119-142 2003. - **95 citations**.
- Expression Profiling Targeting Chromosomes for Tumour Classification and Prediction of Clinical Behaviour. Y. Lu, D. Williamson, R. Wang, B. Summersgill, S. Rodriguez, **S. Rogers**, K. Pritchard-Jones, C. Campbell and J. Shipley. *Genes Chromosomes and Cancer* 38:207-214 2003 - **16 citations**.

## BOOK CHAPTERS

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- 2004 • Class Prediction with Microarray Datasets. **S. Rogers**, R. Williams and C. Campbell. Chapter in *Bioinformatics using Computational Intelligence Paradigms*. Springer-Verlag 2004. - **3 citations**.

## BOOKS

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- 2009 • A First Course in Machine Learning, M. Girolami and S. Rogers - Chapman and Hall/CRC. *Due February 2010*.

## WORKSHOP PRESENTATIONS

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- 2009 • Mathematical and Statistical Aspects of Molecular Biology (MASAMB), Imperial College.
- 2008 • NIPS workshop on Computational Biology, Whistler BC.  
• NIPS workshop on Learning from Multiple Sources, Whistler BC.  
• MASAMB, Glasgow.
- 2007 • Probabilistic Models in Networks and Pathways, University of Sheffield.
- 2006 • MASAMB, University College Dublin.  
• Probabilistic Models in Systems Biology, Helsinki.

## INVITED SEMINARS

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- University of Strathclyde Institute for Advanced Studies, Complex Networks across the Natural and Technological Sciences, 23rd January 2009.
- Helsinki University of Technology seminar series, 24th April 2008.
- Satellite meeting on Learning and Inference of dynamical systems at JOBIM, Lille, 3rd July 2008.
- Imperial College Centre for Bioinformatics seminar series, 2nd July 2008.
- University of Bristol Intelligent Systems seminar series, 29th November 2007.
- University of Sheffield Computational Biology seminar series, 3rd November 2006.
- Glasgow Systems Biology workshop, 2nd May 2006.
- University of St. Andrews evolution, genes and genomics seminar series, 6th March 2006.
- University of Glasgow Bioinformatics Research seminar series, June 2004.

## TUTORIALS

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- 2009 • Pattern Recognition in Bioinformatics (PRIB 09, Sheffield, UK) - *Combining -Omic datasets*

## REVIEWING

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### JOURNALS:

- PLoS One.
- PLoS Computational Biology.
- Bioinformatics (OUP).
- BMC Bioinformatics.
- IEEE Transactions (Neural Networks, Pattern Analysis and Machine Intelligence, Information Technology in Biomedicine, Signal Processing).
- International Journal of Applied Intelligence.

### CONFERENCES:

- European Conference on Computational Biology (ECCB).
- International Conference on Machine Learning (ICML).
- Neural Information Processing Systems (NIPS).
- IEEE Conference on Control Applications.

### FUNDING COUNCILS:

- Wellcome Trust.
- BBSRC.
- Science Council of New Zealand.
- ZonMw - Netherlands Council for Health Research and Development.

### EDITORIAL BOARD MEMBERSHIP:

August 2009 to date.     •     PLoS One.

## WORKSHOP ORGANISATION

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- 2008
  - Learning in Computational Systems Biology (LICSB).
  - Mathematical and Statistical Aspects of Molecular Biology (MASAMB). **80+ attendees.**
- 2007
  - Practical Inference Methods for Mechanistic Systems Modelling (PIMMS).

## PROGRAMME COMMITTEE MEMBERSHIP

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- 2009
  - 4th International Conference on Pattern Recognition in Bioinformatics, Sheffield UK.

## PROFESSIONAL COLLABORATIONS

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- Member of EU funded PASCAL II network of excellence.
- Member of EU funded PASCAL network of excellence.

## FUNDING

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- 2009
  - Summer studentship funding awarded "MMI IN IR: Developing a reconfigurable architecture to support the testing of models of multimodal interactions for searching and browsing on mobile devices" with Dr. Leif Azzopardi and Prof. Roderick Murray-Smith, Department of Computing Science, University of Glasgow.
- 2008
  - Awarded GBP 800 for visit to the group of Prof. Samuel Kaski through the PASCAL2 short visit program.
  - The Synthesis of Probabilistic Prediction and Mechanistic Modelling within a Computational and Systems Biology Context - EPSRC [EP/E052029/1] *Named Researcher*
- 2005
  - Stochastic Modelling and Statistical Inference of Gene Regulatory Pathways: Integrating Multiple Sources of Data - EPSRC [EP/C010620/1] *Named Researcher*
  - Funded GBP 12,500 by Mosaiques Diagnostics and Therapeutics to undertake 5 months of consultancy work on predictive models for kidney disease diagnosis.

## TEACHING

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### LECTURING:

- 2009
  - Designed and taught masters level course in Systems Biology for the Faculty of Biomedical and Life Sciences, University of Glasgow.
- 2008
  - Designed and taught Research Readings in Computing Science (Machine Learning) for the Department of Computing Science, University of Glasgow.
  - Designed and taught General readings in Computer Science (Bioinformatics) for the Department of Computing Science, University of Glasgow.
- 2007
  - Designed and taught Research Readings in Computing Science (Machine Learning) for the Department of Computing Science, University of Glasgow.
  - Guest lecturer for masters level Machine Learning course, University of Glasgow.
- 2004
  - Laboratory and examples class demonstrator, University of Bristol.

### SUPERVISION:

- 2009
  - Computing Science Level 4 project - Kush Mishra: "Coupled analysis of mRNA and protein profiles".

- 2006 • Advanced Masters project - Matthew Tolan: "Bayesian Inference of Transcriptional Single Input Motifs".

#### PHD ASSESSMENT

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- 2008 • Acted as pre-examiner for Mr. Markus Harva, Helsinki University of Technology. *Algorithms for Approximate Bayesian Inference with Applications to Astronomical Data Analysis*.

#### DEPARTMENTAL RESPONSIBILITIES

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- Computing Science Library Representative.
- Seminar organiser for Bioinformatics Research Centre, Department of Computing Science, University of Glasgow.
- Seminar organiser for Inference Research Center, Department of Computing Science, University of Glasgow.
- Web-master for Inference Research Center, Department of Computing Science, University of Glasgow.

#### REFERENCES

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**Dr. C. Campbell**

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University of Bristol,  
Queens Building, University Walk,  
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