Cancer Bioinformatics Workshop Programme

Day One: Thursday, 2nd September, 2010

11.30 Registration opens (CRI)

12.00-13.00 Lunch (CRI)

13.00-15.00 Session 1 (Main Lecture Theatre, CRI)
Themed session: signalling networks. Session chair: Colin Campbell

13.00-13.05 **Welcome**

13.05-13.30 **T1A**: *Towards Evidential Inference of Signalling Pathway Topologies*, Mark Girolami (University of Glasgow, UK)

13.30-14.00 **T1B**: *Data-driven characterization of Receptor Tyrosine Kinase signalling networks in breast cancer subtypes,* S. Mukherjee, B.T.J. Hennessey, Y. Lu, S.M. Hill, M. Muller, P. T. Ram, P.T. Spellman, T.P. Speed, J.W. Gray and G.B. Mills (University of Warwick, UK; University of Texas M. D. Anderson Cancer Center, USA; Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, USA; Walter and Eliza Hall Institute of Medical Research, Australia; UC Berkeley, Berkeley, USA)

14.00-14.30 **T1C**: *Uncovering signalling differences between primary and transformed hepatocytes using cell-specific logic-based pathway models*, Julio Saez-Rodriguez (Harvard Medical School and MIT, USA)

14.30-15.00 **T1D**: *Oncogenic network identification from genomic data*, Lodewyk Wessels (NKI Netherlands)

15.00-15.30 Coffee Break (CRI)

15.30-16.30 Session 2 (Main Lecture Theatre, CRI)
General session. Session chair: Mark Girolami

15.30-16.00 **T2A***: Identification of copy number alterations in tumor genomes using next-generation sequencing data,* Peter Park (Harvard University, USA)

16.00-16.30 **T2B**: *Gene expression state space models and cell fate transitions*, John Quackenbush (Dana-Farber Cancer Institute and Harvard School of Public Health, USA)

16.30-17.30 Poster Spotlights, Group PA1-PA15 (Main Lecture Theatre, CRI)

PA1 *Gains in Power from Structured Two-Sample Tests of Means on Graphs*, Laurent Jacob, Pierre Neuvial and Sandrine Dudoit (Department of Statistics, UC Berkeley)

PA2 *Human Tissue, High Throughput Technology and Informatics: A novel approach enabling decision making in Oncology and Drug Discovery*, Garry Beran, Tim French, Chris Womack, Neil Gray, Sally Luke, Ellen Brown, Jim Growcott (AstraZeneca UK, Oncology Bioscience and Discovery Information)

PA3 *Prediction of Chemotherapy Outcomes by Optimal Gene Subsets Selected by Dynamic Programming*, R. Natowicz C. Moraes Pataro R. Incitti M. Costa A. Cela T. Souza A. Padua Braga R. Rouzier (Université Paris-Est ESIEE - Département d'informatique, France)

PA4 *A tool to rank genes on the basis of their oncoantigenic potential*, Cristina Della Beffa, Francesca Cordero, Stefania Lanzardo, Laura Conti, Guido Forni, Raffaele A. Calogero (Molecular

Biotechnology Center, University of Torino and Department of Computer Science, University of Torino, Torino, Italy).

PA5 *Untangling Cancer Transcriptomics Sources for Biomarker Analysis*, Massimiliano Orsini, Antonella Travaglione, Enrico Capobianco (CRS4 Bioinformatics, Polaris Science and Technology Park, Pula, Italy)

PA6 *Reducing variability caused by the algorithmic choice of pre-processing raw microarray data*, Salih Tuna and Mahesan Niranjan (Wellcome Trust Sanger Institute and University of Southampton, UK)

PA7 *Stepwise Classifier for Heterogeneous Genomic data*, Askar Wubulikasimu and Mark van de Wiel (Free University of Amsterdam Medical Center, Amsterdam, Netherlands)

PA8 *Multi-regime models for the association between DNA copy number and gene expression*, Gwenael G.R. Leday, Mark A. van de Wiel and Aad W. van der Vaart (VU University, Amsterdam, Netherlands)

PA9 *Intra-experiment variation in Illumina BeadChip data*, Robert R. Kitchen, Vicky S. Sabine, J. Michael Dixon, John MS. Bartlett and Andrew H. Sims (University of Edinburgh, UK)

PA10 *Computational interaction analysis for the redox reaction pathway*, Dhondalay G. K., Lemetre C., Barnett A., Lancashire L. J., Ellis I.O., Martin S, Ball G. R. (John Van Geest Cancer Research Centre, Nottingham, UK)

PA11 *COSMIC: Annotating whole-genome resequencing experiments in the catalogue of somatic mutations in cancer*, SA Forbes, N Bindal, D Beare, A Menzies, S Bamford, C Cole, E Dawson, R Shepherd, M Jia, CY Kok, K Leung, T Webb, J Teague, P Cambell, MR Stratton and PA Futreal (The Cancer Genome Project, Wellcome Trust Sanger Institute, UK).

PA12 *Development of a MicroRNA Target Prediction Tool using Profile Hidden Markov Models*, Anastasis Oulas, Panayiota Poirazi and Ioannis Iliopoulos (Division of Medical Sciences, University of Crete Medical School, Greece and Institute of Molecular Biology and Biotechnology-FORTH, Heraklion, Crete, Greece)

PA13 *Identifying Structural Rearrangements via Local Assembly of Next-Generation Sequence Data*, John Marshall, Adam Butler, Jon Teague, Michael R. Stratton, P. Andrew Futreal, and Peter J. Campbell (Cancer Genome Project, Wellcome Trust Sanger Institute, Hinxton, UK).

PA14 *Ranking of microRNA target prediction scores by Pareto front analysis*, Sudhakar Sahoo, Andreas A. Albrecht (Queen's University Belfast, Centre for Cancer Research and Cell Biology, Belfast, UK)

PA15 *Identifying low-prevalence single-base somatic mutations in tumor from next-generation sequencing data*, Karen Messer, Juan Rodriguez-Flores, Kelly Frazer, Olivier Harismendy (Moores UCSD Cancer Center, University of California, San Diego USA)

17.30-19.00 Poster Session, group A (adjacent to Main Lecture Theatre, refreshments available)

Standard delegates:

19.00-19.30 Transfer to Homerton College

19.30-21.00 Dinner in Homerton College (Great Hall)

Invited speakers:

19.00 onwards, transfer to restaurant*: De Luca Cucina*, 83 Regent Street, Cambridge for dinner 7.30pm onwards.

Day Two (Friday 3rd September)

09.00-10.30 Session 3 (Main Lecture Theatre, CRI)
General session. Session chair: Christina Leslie

09.00-09.30 **T3A***: Estimating Rearrangement Evolution in Cancer with Massively Parallel Paired End Sequencing*, Chris D Greenman, Erin Pleasance, Scott Newmann, P. Andy Futreal, Mike Stratton, Paul Edwards, Peter Campbell (Cancer Genome Project Wellcome Trust Sanger Institute, UK)

09.30-10.00 **T3B**: *CHASM: Cancer-specific high throughput analysis of somatic mutations,* Rachel Karchin (John Hopkins University, USA)

10.00-10.30 **T3C**: *Integrating genetic and gene expression evidence into genome-wide association analysis of gene sets,* Sayan Mukherjee (Duke University, USA)

10.30-11.00 Coffee Break

11.00-13.00 Session 4 (Main Lecture Theatre, CRI)
Themed session: copy number alterations. Session chair: Florian Markowetz

11.00-11.20 **T4A**: *Differential regulation of gene expression by copy-number alterations in cancer sub-types*, Yinyin Yuan, Oscar M. Rueda, Christina Curtis, Florian Markowetz (Cancer Research UK Cambridge Research Institute, Cambridge, UK and Department of Oncology, University of Cambridge, UK)

11.20-11.40 **T4B**: *Fast joint segmentation of multiple array CGH profiles for detecting frequent copy number variations*, Kevin Bleakley and Jean-Philippe Vert (School of Mines, ParisTech, Paris, France)

11.40-12.00 **T4C**: *An algorithm to detect copy number aberrations in cancer genomes of tumour specimens*, Arief Gusnanto, Stefano Berri, Henry M. Wood and Pamela Rabbitts (Department of Statistics and Leeds Institute of Molecular Medicine, University of Leeds, Leeds, UK).

12.00-12.20 **T4D**: *A random coefficients model for regional co-expression associated with DNA copy number aberrations*, Wessel N. van Wieringen, Johannes Berkhof, Mark A. van de Wiel (VU University, Amsterdam, The Netherlands)

12.20-12.40 **T4E**: *Spatial clustering of array CGH features in combination with hierarchical multiple testing*. Mark A. van de Wiel with Kyung In Kim and Etienne Roquain (VU University Medical Center, VU University, Amsterdam, The Netherlands and Biometric Research Branch, Division of Cancer Treatment and Diagnosis, NCI, Rockville, USA and UPMC Univ Paris 06, Paris, France)

12.40-13.00 **T4F**: *Finite-state transducers for inferring tumour evolution from copy number variation profiles*, Charlotte Ng, Roland Schwarz, Susanna Cooke, James Brenton, Florian Markowetz (CRUK Cambridge Research Institute and Department of Oncology, University of Cambridge, UK)

13.00-14.00 Lunch (CRI)

14.00-16.00 Session 5 (Main Lecture Theatre, CRI)
Themed session: application studies in breast cancer. Session chair: Colin Campbell

14.00-14.30 **T5A**: *Towards a systems-level view of breast cancer through the integrated analysis of 1000 tumour genomes and transcriptomes*, Christina Curtis (University of Cambridge and Cancer Research UK Cambridge Research Institute, UK)

14.30-15.00 **T5B**: *Developing a substitution calling algorithm to analyse breast cancer exomes by next generation sequencing*, D. Jones, P. J. Stephens, I. Varela, P. Tarpey, K. Raine, D. D. Galappaththige, M. Jia, L. Mudie, C. Latimer, A. Butler, J.Teague, M. R. Stratton, P. A. Futreal, P. J. Campbell (Cancer Genome Project, Wellcome Trust Sanger Institute, Cambridge, UK)

15.00-15.30 **T5C**: *Joint SNP analysis using a breast cancer GWAS Data Set*, Xia Jiang, Gregory F. Cooper (University of Pittsburgh, USA)

15.30-16.00 **T5D**: *A comprehensive analysis combining network inference and pathway analysis for treatment response in basal breast cancer*, Marine Jeanmougin, Mickael Guedj, Christophe Ambroise (Statistics and Genome laboratory, University of Evry, France; Department of Biostatistics, Pharnext, Paris, France).

16.00-16.30 Coffee Break (CRI)

16.30-17.30 Poster spotlights, Group PB1-PB15 (Main Lecture Theatre, CRI, chair: Colin Campbell)

PB1 *Feature Extraction on Breast Cancer Signatures* Jonathan Taminau, Cosmin Lazar, Stijn Meganck, Ann Nowe (Computational Modeling Lab (CoMo), Vrije Universiteit Brussel, Pleinlaan 2, 1050 Brussels, Belgium)

PB2 *Integrating Affymetrix and Illumina gene expression data for meta-analysis of breast cancer microarray studies*, Arran K. Turnbull, Alexey A. Larionov, J. Michael Dixon, Andrew H. Sims (Applied Bioinformatics of Cancer Group, Breakthrough Research Unit, Edinburgh Cancer Research Centre, Edinburgh, UK)

PB3 *Pathway activation patterns reveal novel breast cancer subgroups*, Esteban Czwan, Roland Eils, Benedikt Brors (Theoretical Bioinformatics, German Cancer Research Center, Heidelberg, Germany)

PB4 *A Bayesian Clustering Analysis of Breast Cancer Gene Expression*, Richard S. Savage, Sinéad Aherne, Padraig Doolan, Colin Clarke, Martin Clynes, David L. Wild (Systems Biology Centre, University of Warwick, UK and National Institute for Cellular Biotechnology, Dublin City University, Ireland)

PB5 *Allele-specific copy number analysis of breast carcinomas*, Peter Van Loo, Silje H. Nordgard, Ole Christian Lingjærde, Hege G. Russnes, Inga H. Rye, Wei Sun, Victor J. Weigman, Peter Marynen, Anders Zetterberg, Bjørn Naume, Charles M. Perou, Anne-Lise Børresen-Dale, Vessela N. Kristensen (Department of Genetics Institute for Cancer Research, Rikshospitalet-Radiumhospitalet, Oslo, Norway)

PB6 *Artificial neural networks in the prediction of lymphatic vascular invasion in primary breast cancer*, Dhondalay G. K., Lemetre C., Barnett A., Lancashire L. J., Caldas C., Ellis I. O., Ball G. R. (John Van Geest Cancer Research Centre, Nottingham Trent University, Nottingham, UK)

PB7 *Cell Lineage-Specific DNA Methylation Differentiates Tumour Subtypes in Breast Cancer*, Duncan Sproul, Jayne Culley, Jacqueline Dickson, Colm Nestor, Richard R. Meehan, Bernard Ramsahoye and Andrew H Sims (Breakthrough Research Unit and Edinburgh Cancer Research Centre, University of Edinburgh, UK)

PB8 *High PTP4A3 phosphatase expression correlates with metastatic risk in uveal melanoma patients*, Cécile Laurent, Fabien Valet, Nathalie Planque, Licia Silvieri, Selma Maacha, Philippe Hupe, Corine Plancher, Cécile Reyes, Benoit Albaud, Audrey Rapinat, David Gentien, Jérôme Couturier, Xavier Sastre-Garau, Laurence Desjardins, Sergio Roman-Roman, Bernard Asselain Sophie Piperno-Neumann, Emmanuel Barillot and Simon Saule (Institut Curie, Paris, France).

PB9 *Spectral bi-clustering reveals survival related gene sets for head and neck squamous cell carcinoma*, G. Kalna, J.K. Thurlow and B.W. Ozanne, (The Beatson Institute for Cancer Research, Glasgow, Scotland, UK)

PB10 *Uncovering biological signals involved in bladder cancers with Independent Component Analysis*, Anne Biton, Andrei Zinovyev, Yves Allory, Emmanuel Barillot and Francois Radvanyi (Institut Curie, Centre de Recherche, with INSERM Paris and Mines ParisTech, France)

PB11 *Identifying transcriptional pathway signatures to predict MEK addiction and response to selumetinib (AZD6244)*, Jonathan Dry, Tim French and Paul Smith (Cancer Bioscience (Bioinformatics), AstraZeneca UK).

PB12 *Artificial Neural Network Algorithm for Interaction Network Inference in Genomic Array Studies*, Christophe Lemetre, Lee James Lancashire, Graham Roy Ball (Nottingham Trent University, UK)

PB13 *Lymphoma Diagnosis Based on Automated Analysis of Flow Cytometry*, DataHabil Zare, Ali Bashashati, Andrew Weng, Randy Gascoyne, Arvind Gupta, Ryan Brinkman (University of British Columbia and BC Cancer Agency, Canada)

PB14 *Integrated analysis of miRNA and mRNA expression profiling as a tool to identify prognostic markers and associated pathways*, Francesca Buffa, Carme Camps, Laura Winchester, Harriet Gee, Helen Sheldon, Marian Taylor, Adrian L. Harris, Jiannis Ragoussis (Weatherall Institute of Molecular Medicine and Wellcome Trust Centre for Human Genetics, University of Oxford, UK)

PB15 *A ranking stability indicator in bioinformatics*, G. Jurman, S. Riccadonna, R. Visintainer, G. Guzzetta, C. Furlanello (Fondazione Bruno Kessler, Italy)

17.30-19.00 Poster Session, Group B (adjacent to main lecture theatre, refreshments available)

19.00-19.30 Transfer to Homerton College

19.30-21.00 Dinner in Homerton College (Great Hall)

21.00-22.30 Discussion Forum A in Homerton College (Boulind Suite, Mary Allan Building)

This is an informal opportunity to debate the future direction of the subject. To provide a structure, Professor Carlos Caldas (Cambridge Research Institute) will give a short presentation addressing key questions in data analysis from the viewpoint of a cancer researcher. Thereafter he will be joined in the discussion by members of a panel and the audience.

Day Three (Saturday 4th September)

09.00-10.40 Session 6 (Main Lecture Theatre, CRI)
Themed session: data integration. Session chair: Mark Girolami

09.00-09.30 **T6A**: *Learning and retrieval from multiple sources,* Sami Kaski (Helsinki University of Technology, Finland)

09.30-10.00 **T6B**: *CONEXIC: An Integrated Approach to Uncover Drivers of Cancer*, Dana Pe'er (Columbia University, USA)

10.00-10.20 **T6C**: *Biomarkers Discovery in Breast Cancer by Interactome -Transcriptome Integration*, Maxime Garcia, Olivier Stahl, Pascal Finetti, Daniel Birnbaum, François Bertucci, Ghislain Bidaut (Inserm, CRCM, Integrative Bioinformatics, Marseille, France)

10.20-10.40 **T6D**: *An integrated analysis of molecular aberrations in NCI-60 cell lines*, Chen-Hsiang Yeang, Shyh-Dar Li, Tatsuaki Tagami (Institute of Statistical Science, Academia Sinica, Taipei, Taiwan and Ontario Institute of Cancer Research, Toronto, Canada)

10.40-11.10 Coffee Break (CRI)

11.10-13.00 Session 7 (Main Lecture Theatre, CRI)
General session. Session chair: Florian Markowetz

11.10-11.40 **T7A**: *The Importance of Reproducible Research in High-Throughput Biology: Case Studies in Forensic Bioinformatics*, Keith Baggerly (MD Anderson Cancer Center, USA)

11.40-12.10 **T7B***: Inferring transcriptional and microRNA-mediated regulatory programs in glioblastoma*, Christina Leslie （Sloan Kettering Cancer Center, New York, USA)

12.10-12.40 **T7C**: *Revealing cancer mutations using deep sequencing*, Olivier Elemento (Cornell, USA)

12.40-13.00 **T7D**: *Non-Negative Matrix Factorisation finds Connections in Complex Data*, Clare M. Lee, Desmond J. Higham, J. Keith Vass, and Daniel Crowther (University of Strathclyde and Translational Medicine Research Collaboration, University of Dundee, UK and Translational Medicine Research Collaboration, Pizer Inc.)

13.00-14.00 Lunch (CRI)

14.00 End of Workshop for international (non-UK) attendees

14.00-15.00 Discussion Forum B for UK-based cancer bioinformatics researchers (main lecture theatre, CRI, chair: Colin Campbell)

This is an informal opportunity for UK-based cancer bioinformatics researchers to discuss issues such as collaborative arrangements and networking, conjoint bids, the future direction of the subject, arrangement of future meetings or workshops and any other topics of interest to the audience.

Workshop Sponsors:

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