



# CSCDA 2010, Leuven, 25-27 August 2010

## Program

### Wednesday, 25 August 2010

*Short intro courses : Keynote speakers*

**13.15 - 15.00:** Design and analysis of GWAs using SNPs

David Evans, Department of Social Medicine, University of Bristol, UK

**15.00 – 15.45 :** coffee break

**15.45 - 18.00 :** Design and Analysis of GWAs using CNVs

Christophe Lambert, Golden Helix, USA

### Thursday, 26 August 2010

*State of the art on "interaction analysis" : Keynote speakers*

**08.30 - 09.30 :** Gene-gene interactions

Jason Moore, Department of Computer Science, University of New Hampshire, USA

**09.30 - 10.30 :** The link between insertion/deletion and SNPs with their implications

Madan Babu, MRC Laboratory of Molecular Biology, University of Cambridge, UK

**10.30 – 11.00 :** Coffee break

**11.00 - 12.00 :** Gene-environment interactions in human diseases

Nilanjan Chatterjee, Division of Cancer Epidemiology & Genetics, NIH/NCI, USA

**12.00 – 13.30 :** lunch

**13.30 - 15.30 :** Participants' case studies with discussions from the speakers

Moderator : Marylyn Ritchie, Department of Molecular Physiology & Biophysics, Vanderbilt University, USA

C2 Karolien Bettens, Nathalie Brouwers, Ana Gil, Helen Van Miegroet, Sebastiaan Engelborghs ,  
Peter P. De Deyn , Rik Vandenberghe , Kristel Slegers and Christine Van Broeckhoven  
*Indepth genetic analysis of CLU in Alzheimer's disease*

C3 Sarah Bonneux, Erik Fransen, Els Van Eyken, Lut Van Laer, Guy Van Camp  
*Analyses of rare variants in the mitochondrial genome contributing to Age-Related Hearing Impairment*

C4 Vincent Botta, Pierre Geurts, Louis Wehenkel  
*Trees inside trees for genome wide association studies*

C5 Cesar Boulosa, Daniel Rico, Inigo Landa, Lucia Inglada-Perez, Mercedes Robledo, Alfonso Valencia  
*Comparison of Epistasis Detection Methods and Application to a Real Dataset*

C6 Tom Cattaert, Jestinah M. Mahachie John, François Van Lishout, and Kristel Van Steen  
*Alternative Risk Cell Definitions Based on Ranking Improve Performance of Model-Based Multifactor Dimensionality Reduction for Epistasis Detection*

C7 Isabelle Cleynen, Jestinah M. Mahachie John, Liesbet Henckaerts, Wouter Van Moerkercke, Paul Rutgeerts, Kristel Van Steen, and Severine Vermeire  
*Molecular reclassification of Crohn's disease by cluster analysis of genetic variants*

C14 Jestinah M. Mahachie John, Tom Cattaert, François Van Lishout and Kristel Van Steen  
*A Detailed View on Model-Based Multifactor Dimensionality Reduction with Quantitative Traits for Detecting Gene-Gene Interactions: Different Ways of Adjusting For Lower-Order Effects*

C15 Gaëlle Marenne, Stephen J Chanock, Montserrat Garcia-Closas, Luis Perez-Jurado, Benjamin Rodriguez-Santiago, Guillermo Pita, Daniel Rico, Alfonso Valencia, Kevin Jacobs, David G. Pisano, Ramon Diaz-Uriarte, Julie Earl, Nathaniel Rothman, Debra Silverman, Manolis Kogevinas, Emmanuelle Genin, Francisco X. Real, Nuria Malats  
*CNV Association Analysis Using Continuous Measurement Replicates the Association Between GSTM1 Deletion And Bladder Cancer*

C17 Olga E. M. Savenije, Jestinah M. Mahachie John, Marjan Kerkhof, Dirkje S. Postma, Kristel Van Steen, Gerard H. Koppelman  
*Genetic epistasis in the IL1RL1 pathway and wheezing phenotypes: multinomial MB-MDR analyses*

C19 Victor Urrea, M. Luz Calle, Nuria Malats  
*Feature Selection Using Random Forest. Application to the Study of Genetic Component of Bladder Cancer*

**15.30 – 16.00** : coffee break

**16.00 – 16.45** : Short summary presentation of afternoon session

Moderator : Marylyn Ritchie, Department of Molecular Physiology & Biophysics, Vanderbilt University, USA

**16.45 – 17.30** : Case study : It's all in genes; the genetics of Inflammatory Bowel Disease

Severine Vermeire, Gastroenterology Department, University Hospital Leuven, Belgium

## Friday, 27 August 2010

*State of the art on "-omics integration"*

**08.30 - 09.30** : From genome to proteome

Ivo Gut, CNAG – Centro Nacional de Análisis Genómico, Spain

**09.30 - 10.30** : The model organism as a system :integrating -omics data sets

Peter Van der Spek, Department of bioinformatics, Erasmus University Medical center, The Netherlands

**10.30- 11.00** : coffee break

**11.00 - 12.00** : Pathway analysis of genome-wide data

Peter Holmans, Department of Psychological Medicine, School of Medicine, Cardiff University, UK

**12.00 – 13.30** : Lunch

**13.30 - 15.30** : Participants' case studies with discussions from the speakers

Moderator : Lude Franke, University of Groningen, The Netherlands

C1 P. Antal, P. Marx, A. Millinghoffer, G. Hullam, I. Ungvary, Cs. Szalai, A. Falus  
*Bayesian fusion of heterogeneous signs for biomarker and pathway discovery*

C8 Susan L. M. Coort, Thomas Kelder, Martijn P. van Iersel, Robert Kleemann, Chris T. A. Evelo  
*Integrated omics analysis, using PathVisio, to investigate the development of insulin resistance*

C9 Lizzy De Lobel, Lutgarde Thijs, Tatiana Kouznetsova, Jan Staessen, Kristel Van Steen  
*A Family-based Association Test to Detect Gene-Gene Interactions in the Presence of Linkage*

C10 Wendimagegn Ghidey, Marian Beekman, Eline Slagboom, Bart Mertens, Jeanine Houwing-Duistermaat  
*A Method for Simultaneous Analysis of Multiple Molecular and Phenotypic Parameters Predicting Longevity Within Families*

C11 S. H. Heisterkamp  
*Directed Acyclic Graphs using the Linear Mixed model algorithm*

C12 Jeroen R. Huyghe, Guy Van Camp, Kristel Van Steen  
*Elucidating the Molecular Etiology of Asthma using Genome-Wide Association Study Pathway Analysis*

C13 Iris C. R. M. Kolder, Pieter G. Postema, Maarten P. Van den Berg, Marcel M. A. Mannens, J. Peter Van Tintelen, Freek Van den Heuvel, Arthur A. Wilde, Connie R. Bezzina, Michael W. T. Tanck  
*Linkage Analyses in a Large Dutch Kindred*

C16 Antoni Picornell, Stephen J Chanock, Montserrat Garcia-Closas, Guillermo Pita, Daniel Rico, Alfonso Valencia, Kevin Jacobs, David G. Pisano, Nathaniel Rothman, Debra Silverman, Manolis Kogevinas, Maria L. Calle, Francisco X. Real, Nuria Malats  
*Genome-Wide Prognosis Study in Bladder Cancer*

C18 Isabelle Schrauwen, Erik Fransen, Megan Ealy, Ayda Khalfallah, Saber Masmoudi, Richard J. H. Smith, Guy Van Camp

*Metaanalysis of Association Data in Otosclerosis*

C21 A. Wienecke-Baldacchino, M. Heinäniemi, C. Carlberg

*Biological Reasoning by massive Data Integration*

C20 Julie Van der Zee, Tim Van Langenhove, Gernot Kleinberger, Kristel Slegers, Marc Cruts, Christine Van Broeckhoven

*Replication of genome-wide association findings on frontotemporal lobar degeneration in a Flanders-Belgian sample: TMEM106B a first risk factor for frontotemporal lobar degeneration*

**15.30 – 16.00** : coffee break

**16.00 - 16.45** : Short summary presentation of afternoon session

Moderator : Lude Franke, University of Groningen, The Netherlands

**16.45 – 17.30** : Case study : molecular genetics of neurodegenerative brain diseases

Christine Van Broeckhoven, Neurodegenerative Brain Disease Group, VIB and University of Antwerp, Belgium