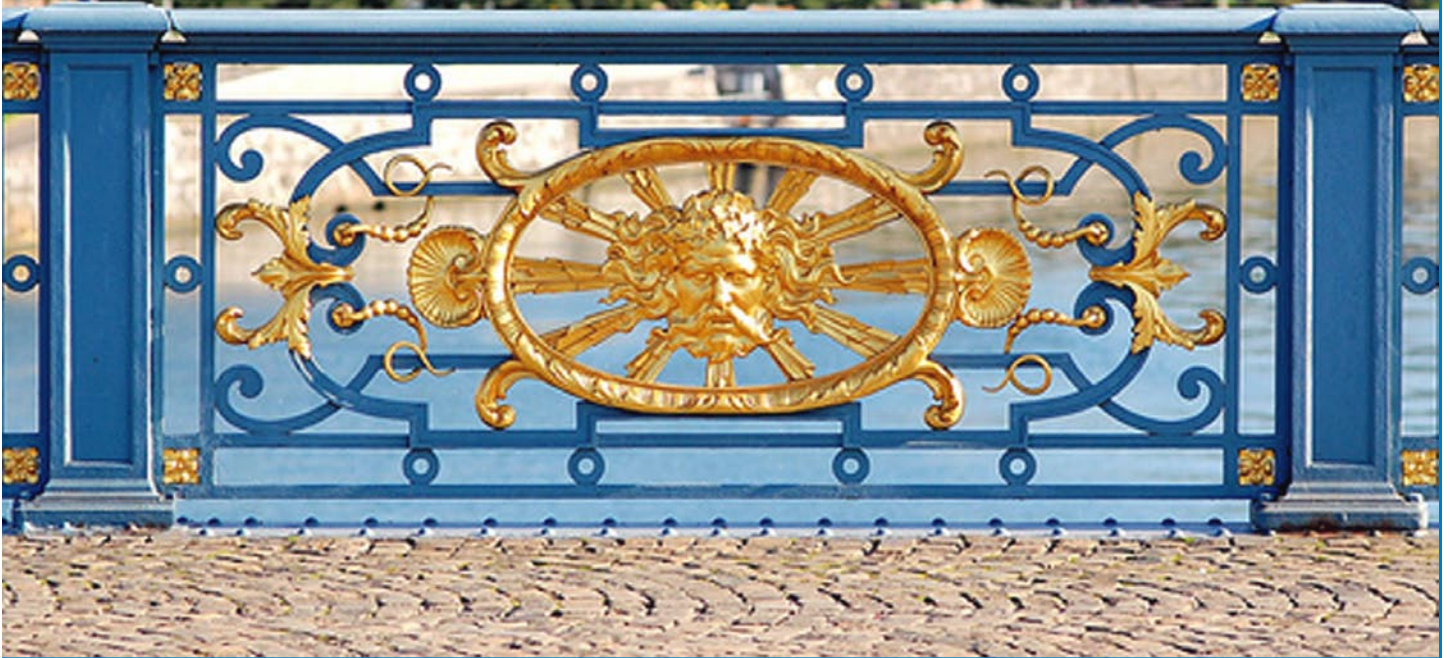


EUROPEAN INSTITUTE IN STATISTICAL GENETICS



August 31 - September 9, 2009

UNIVERSITY of LIÈGE

Liège, Belgium

<http://sisg.biostat.washington.edu>

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**EISG
2009**

Sponsored by:

Université
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DEPARTMENT OF BIostatISTICS
SCHOOL OF PUBLIC HEALTH
UNIVERSITY of WASHINGTON

Administrative Details

General Information

The 2009 European Institute in Statistical Genetics will be held in the “Ampithéâtres de l’Europe” on the Sart Tilman campus of the University of Liège. It is being organized under the auspices of the Centre for Biomedical Integrative Genoproteomics at ULg. Dormitory Accommodation is available on the ULg campus, and hotels in downtown Liège are easily accessible by public transportation. Details about accommodation and travel to Liège are posted on the **Institute website: <http://sisg.biostat.washington.edu>**.

Scholarships

Statistical scholarship assistance may be available to European students: Send a curriculum vitae, a statement of the purpose in attending the Institute, and a letter of support from an academic advisor. These materials should be sent to: EISG, Centre for Biomedical Integrative Genoproteomics, University of Liège; B43, 20 Boulevard de Colonster, 4000-Liège, Belgium, by June 20, 2009.

Applicants should also register for the modules at <http://sisg.biostat.washington.edu>, and check the “Yes” button to the question, “Are you applying for a Summer Institute scholarship?” so that payment will not be required at time of registration.

Registration Deadlines and Fees

Registration fee per module: \$650 (USD); Early-bird rate: \$550 (USD).

Reduced academic and government registration fee per module: \$500 (USD); Early-bird rate: \$400 (USD).

Early-bird deadline is Friday, August 14, 2009.

Registration fees cover course materials and four refreshment breaks per day. Hotel rooms and meals are not included in the tuition fee.

Cancellation policy: A \$100 processing fee will be deducted from refunds requested after August 14, 2009. No refunds will be processed after August 28, 2009.

Payment method: Payment can be made by credit card (VISA, MasterCard, or American Express), purchase order (U.S. companies and organizations only), or by check or money order in U.S. dollars drawn on a U.S. bank. Checks should be made payable to the University of Washington. For wire-transfers, please refer to your Registration Invoice for instructions.

Registration Procedures

You may register online via secure server at: **<http://sisg.biostat.washington.edu>**. Space in each module is limited and will be filled on a first-come, first-served basis.

How to register: Visit the Institute website at: **<http://sisg.biostat.washington.edu>** where you may register and make payment online using VISA, MasterCard, or American Express. If you wish to pay by check, you can print the registration invoice and submit it by mail as directed. You will receive your registration confirmation by email.

Daily Schedule

8:30 am	Registration
9:00 am - 10:00 am	Class Session
10:30 am - 11:00 am	Break
11:00 am - 12:30 pm	Class Session
12:30 pm - 1:30 pm	Lunch (and registration on Wednesday)
1:30 pm - 3:00 pm	Class Session
3:00 pm - 3:30 pm	Break
3:30 pm - 5:00 pm	Class Session
5:00 pm - 6:00 pm	Refreshments (except Friday)

Conference Inquiries

European Institute in Statistical Genetics
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Department of Biostatistics
1705 NE Pacific Street
Box 357232
Seattle, WA 98195-7232

Email: sisg09@u.washington.edu
Phone: +1-206-543-1044; Fax: +1-206-543-3286

Institute website: <http://sisg.biostat.washington.edu>

Instructional Program

Module 1: Population Genetic Data Analysis

Instructors: Dahlia Nielsen and Bruce Weir

Dates: Monday, August 31 - Wednesday, September 2

This module covers estimation of allele and haplotype frequencies, inferences about Hardy-Weinberg and linkage disequilibrium, characterization of population structure, linkage estimation, joint genotype probabilities, and relationship estimation. Includes using public domain software packages, including GDA and PowerMarker.

Module 2: Quantitative Genetics

Instructors: Bill Muir and Bruce Walsh

Dates: Monday, August 31 - Wednesday, September 2

This module covers quantitative trait models, variances and covariances of relatives, estimation of variance components, response to selection, and the effects of mutation.

Module 3: Expression Data Analysis

Instructors: Greg Gibson and John Storey

Dates: Monday, August 31 - Wednesday, September 2

This module provides an overview of technologies and statistical methods for analysis of all types of expression data, including RNA, proteins, and metabolites, obtained by microarrays, mass spectrometry, or sequencing. Sessions cover data normalization, experimental design, statistical modeling and inference (e.g., detecting differential gene expression, ANOVA, multiple testing correction, clustering and classification, network behavior), and expression QTL analysis. Examples are taken from human genetics, model systems, and evolutionary biology. The module includes software demonstrations.

Module 4: QTL Mapping

Instructors: Rebecca Doerge and Zhao-Bang Zeng

Dates: Wednesday, September 2 - Friday, September 4

This module covers linkage map construction, single-marker analyses, multiple and partial regression methods, and interval, composite-interval, and multiple-interval mapping. Model selection and determining significance levels are addressed. Includes using the Windows QTL-Cartographer software package.

Module 5: DNA Evidence

Instructors: John Buckleton and Bruce Weir

Dates: Wednesday, September 2 - Friday, September 4

This module covers statistical and population genetic topics for the interpretation of forensic DNA profiles. Topics addressed include allelic independence, Bayes' theorem and likelihood ratios, genotype probabilities for one and two individuals, effects of relatives and population structure, interpretation of mixtures, low copy number profiles, and paternity index and missing person calculations. Includes using GDA and DNAMix-3 public domain software.

Module 6: Coalescent Theory

Instructors: Gill McVean and Philip Awadalla

Dates: Wednesday, September 2 - Friday, September 4

Sequence variation within populations is important to medical genetics and to the study of evolutionary history. Coalescent models that describe genealogical histories underlying sampled chromosomes in natural populations are central to the analysis of such data. The module covers the derivation and properties of the basic model and its extension to include factors such as recombination, geographical structure, and natural selection; use of the coalescent in analyzing data, considering different statistical approaches to inference in the settings of disease mapping, estimating recombination rates, and detecting recent adaptive evolution; and use of coalescent methodologies in large-scale surveys of genetic variation, such as the HapMap project. Computer programs that can analyze real data and simulate genealogies will be demonstrated and used in computer sessions.

Module 7: Association Mapping

Instructors: Lon Cardon, Dahlia Nielsen and Michel Georges

Dates: Monday, September 7 - Wednesday, September 9

Topics for this module include an introduction to the theory of linkage disequilibrium and mapping, population and family-based association techniques for discrete and quantitative traits, detecting and accounting for population structure, estimating haplotypes from population data, haplotype blocks, and multiple testing issues.

Module 8: R/Bioconductor Workshop

Instructors: Thomas Lumley and Ken Rice

Dates: Monday, September 7 - Wednesday, September 9

This module introduces software for analysis of genetic data in the R statistical environment. Data management in R, programming concepts for R, and standard regression analyses will be discussed. These topics will be followed by analysis more specific to genetic data, including association analysis, and haplotype inference. Use of the extensive collection of genomics packages from the Bioconductor project will be introduced. Finally, the use of R as an interface to other more specialized "legacy" software will be demonstrated.

Module 9: Graphical Models for Genetics

Instructors: Vanessa Didelez and Nuala Sheehan

Dates: Monday, September 7 - Wednesday, September 9

Probabilistic graphical models have their origins in genetic path analysis and provide a natural general framework for expressing and manipulating many important concepts in statistical genetics. Local computational algorithms can be described in this way but complex issues of identification in forensic settings, for example, together with genetic mapping and pedigree uncertainty can all be handled in this content, as can issues of causal inference and identification of regulatory networks.

Faculty

Philip Awadalla, Professor Invité, Faculty of Medicine, University of Montreal, Canada

John S. Buckleton, Principal Scientist, ESR, New Zealand

Lon Cardon, Senior Vice President for Genetics, GlaxoSmithKline plc

Vanessa Didelez, Senior Lecturer in Statistics, University of Bristol, UK

Rebecca W. Doerge, Professor of Statistics, Purdue University, USA

Michel Georges, Professor of Molecular Genetics, Université de Liège, Belgium

Gregory C. Gibson, Professor of Integrative Biology, University of Queensland, AU

Thomas Lumley, Associate Professor of Biostatistics, University of Washington, USA

Gil McVean, Professor of Statistical Genetics, University of Oxford, UK

William M. Muir, Professor of Genetics, Purdue University, USA

Dahlia M. Nielsen, Research Assistant Professor of Genetics, North Carolina State University, USA

Kenneth M. Rice, Assistant Professor of Biostatistics, University of Washington, USA

Nuala Sheehan, Reader in Statistical Genetics, University of Leicester, UK

John Storey, Associate Professor, Lewis-Sigler Institute and Department of Molecular Biology, Princeton University, USA

J. Bruce Walsh, Professor of Ecology and Evolutionary Biology, University of Arizona, USA

Bruce S. Weir, Director, European Institute in Statistical Genetics, Professor and Chair of Biostatistics, University of Washington, USA

Zhao-Bang Zeng, Reynolds Distinguished Professor of Statistics and Genetics, North Carolina State University, USA

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