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Study Coordinating Centre  
Hypertension and Cardiovascular Rehabilitation Unit  
Department of Cardiovascular Diseases  
University of Leuven

## **A 6-day Course on Statistical Genetics**

17-22 July 2006

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*The course consists of two parts:*

- **S.A.G.E. course: *Statistical Analysis for Genetic Epidemiology:***  
*17-20 July*
- **SAS JMP Genetics course:**  
*21-22 July*

### **Attendants**

The course is intended for statisticians, epidemiologists, geneticists, physicians, molecular biologists, public health specialists, MPH students and any scientist involved in a genetic research programme. Level of experience preferred: Master's or Doctoral degree in statistics, biostatistics, epidemiology, public health, medicine, biology or genetics.

### **Organisation**

Dr. Jan A. Staessen, Study Coordinating Centre, Hypertension and Cardiovascular Rehabilitation Unit, Department of Cardiovascular Diseases, University of Leuven.

### **Course venue**

17-20 July: Room GS1, 4th floor, Campus Gasthuisberg, Research Building (Onderwijs en Navorsing).

21-22 July: Room IG2.73, 2nd floor, University Hospital Gasthuisberg.

Both meeting rooms have internet connectivity.

### **Course fee**

400 EUR / 200 EUR (staff K.U.Leuven). The course fee includes registration, lunches, coffee breaks and handouts.

### **Hotel accommodation and travel**

Leuven is a small city, about 20 kms from Brussels. Hotel accommodation is limited. There are frequent and direct trains running between Brussels Airport and Leuven and between Brussels and Leuven.

OMNIA Travel (Ghis Costermans, Parijsstraat 50, 3000 Leuven, tel. +32/16/24.38.21, fax +32/16/24.38.01, email: ghis.costermans@omnia.be) can assist you in booking hotel accommodation and planning your travel.

## **Registration**

*Preregistration is needed.*

Study Coordinating Centre, Hypertension and Cardiovascular Rehabilitation Unit, Department of Cardiovascular Diseases, University of Leuven: Ms. Sandra Covens (sandra.covens@med.kuleuven.be; tel. +32/16/34.71.05) or Mrs. Renilde Wolfs (renilde.wolfs@med.kuleuven.be; tel. +32/16/34.71.04); fax +32/16/34.71.06.

## **Registration deadline**

Registration forms have to be returned before 15 May 2006. We can accommodate about 40 applicants. Applicants will be handled on a first-in first-served base. Please, send us also a short curriculum so that the Faculty are informed about your scientific interests and knowledge of statistics.

# **S.A.G.E. Course: Statistical Analysis for Genetic Epidemiology**

**17-20 July 2006**

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## **Primary course objectives**

- To review the basic principles underlying genetics.
- To learn about the main areas of study in genetic epidemiology: familial aggregation, segregation, cosegregation (linkage analysis) and association.
- To familiarize participants with the statistical techniques specific to genetic epidemiology through the use of the S.A.G.E. software.
- To present each S.A.G.E. program in detail: PEDINFO, FCOR, SEGREG, MARKERINFO, FREQ, GENIBD, RELTEST, SIBPAL, LODPAL, LODLINK, MLOD, DECIPHER, ASSOC, TDTEX, DESPAIR.
- To give the statistical details underlying the methods to those knowledgeable in statistical methodology

## **Course description**

The course presents the software S.A.G.E. (Statistical Applications for Genetic Epidemiology) developed by the Human Genetic Analysis Resource (H.G.A.R.) from the Department of Epidemiology and Biostatistics, at Case Western Reserve University, Cleveland, Ohio.

The development of the software is supported by the National Center for Research Resources (NCRR) of the U.S. National Institutes of Health (NIH). Course topics will include an overview of genetics and statistical genetic techniques. These techniques include familial aggregation, commingling analysis, segregation analysis, IBD (identity-by-descent) allele sharing analysis, model-based linkage analysis, model-free linkage analysis, haplotype analysis, transmission disequilibrium, and allelic association.

Participants will receive a hard copy handout of the slide show at the beginning of the course.

The course will be given in English.

## **Software availability**

All non-profit organizations can have a freely renewable annual license for the S.A.G.E. software. For-profit organizations can request a free one-month license prior to the beginning of the course. Participants are welcome to bring their laptop computers to the course with S.A.G.E. already uploaded (but this is not

mandatory). Instructions on how to register for a software license are available at the S.A.G.E. webpage (<http://darwin.cwru.edu/sage/>). We advise interested participants to obtain the license at least two weeks before the beginning of the course.

## **Course outline**

### *Day 1 – 16 July 2006*

14h00-16h00:                      Guided tour of Leuven.

Each day of the following 4-day S.A.G.E. short course will start at 9 am and end at 5.00 pm, and will consist of four one and a half hour sessions, with half hour breaks in the morning (10.30 am - 11.00 am) and the afternoon (3.00 pm - 3.30 pm), and a one hour lunch break (12.30 pm - 13.30 pm).

### *Day 2 – 17 July 2006*

Basic genetics for statisticians: genetic terminology, modes of inheritance, identity by descent, Hardy-Weinberg equilibrium, polygenic and multifactorial models.

Introduction to S.A.G.E. for completely new users (preparation of data and use of the FUNCTION block).

### *Days 3 and 4 – 18-19 July 2006*

The S.A.G.E. programs, with concentration on the purpose of each, the options available, and the interpretation of the output:

- PEDINFO - pedigree statistics
- FCOR - familial correlations
- SEGREG - segregation models and commingling analysis
- MARKERINFO - Mendelian inconsistencies
- FREQ - allele frequency estimation
- GENIBD - IBD estimation
- RELTEST - relationship testing linkage analysis
- SIBPAL - Haseman-Elston regression linkage tests
- LODPAL - relative pair linkage tests
- LODLINK and MLOD - model based linkage methods
- DECIPHER – haplotype analysis
- ASSOC - association analysis and heritability estimation
- TDTEX - exact transmission disequilibrium tests
- DESPAIR - design of affected sibpair studies

Day 5 – 20 July 2006

Statistical details for those knowledgeable in statistics.

### **Faculty**

Dr. Robert C. Elston is the S.A.G.E. principal investigator and Director of the Division of Genetic and Molecular Epidemiology, Department of Epidemiology and Biostatistics, Case Western Reserve University, Cleveland, Ohio.

For more than 30 years, Dr. Elston has been involved in the development of statistical methods to analyze individual, family and pedigree data for the identification of genes that cause disease, implementing them in computer programs, and applying them in collaborative research with others who collect family data. Dr. Elston has extensive experience in teaching short courses on statistical genetics and genetic epidemiology to a variety of audiences, internationally. He is a world-renowned expert on genetic epidemiology with several hundred publications in peer-reviewed journals. Among other awards, he received the leadership award from the International Genetic Epidemiology Society in 1995, the William Allan Award from the American Society of Human Genetics in 1996, a NIH merit award in 1998, and the Marvin Zeller Leadership Award for Statistical Science from the Harvard University School of Public Health in 2004.

Dr. Courtney Gray-McGuire is Assistant Professor in the Division of Molecular and Genetic Epidemiology at Case Western Reserve University. Dr. Gray-McGuire is involved in all aspects of S.A.G.E. – development, distribution, training and theoretical research.

Mr. Kevin Cartier, who will also be present, is the Project Manager for S.A.G.E.

# SAS JMP Genetics course

21-22 July 2006

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## Course description

This two-day course will begin with an introduction to genetic terminology and JMP software. This will be followed by detailed explanation of several techniques used in the analysis of genetic data, including marker analyses such as Hardy-Weinberg and linkage disequilibrium testing, haplotype estimation, and tagging SNP selection; association testing methods for case-control analyses, the analysis of quantitative traits, and the transmission disequilibrium test (TDT); and model-free linkage analyses including affected sib pair methods, Haseman-Elston regression, and variance components. Instruction will consist of a balance between short lectures on the various analysis methods, instructor-led demonstrations using JMP genetic software, and lab sessions in which students are encouraged to work through analyses and explore the JMP genetics software at their own pace.

## Course outline

Each day of the 2-day SAS short course will start at 9 am and end at 5.00 pm, and will consist of four one and a half hour sessions, with half hour breaks in the morning (10.30 am - 11.00 am) and the afternoon (3.00 pm - 3.30 pm), and a one hour lunch break (12.30 pm - 13.30 pm).

*Day 1 – 21 July 2006*

### Introduction

- Introduction to genetics *Genetic terminology, Mendelian genetics, linkage and recombination.*
- Overview of genetic marker data. *Types of genetic markers, size and scale of modern data sets, common websites.*
- Overview of JMP Genetics software.

### Importing data into JMP Genetics

*Affymetrix SNP CHP, Arlequin, NEXUS, Pedigree formats.*

*Mid-morning break*

### Marker analyses

- Statistical Genetics Basics. *Marker properties, Linkage Disequilibrium.*
- Haploype Analyses. *Haplotype estimation, Tagging SNP selection.*

#### *Lunch*

- Lab: Students work on performing the above analyses.

#### Association testing

- Case-control Association.  *$X^2$  tests (for both single-marker and haplotypes), as well as related issues such as multiple testing.*

#### *Mid-afternoon break*

- Association analyses for quantitative traits *Marker-Trait Association, Haplotype trend regression.*
- Lab: Students work on performing the above analyses.

#### *Day 2 – 22 July 2006*

- Questions from the audience.
- TDT and Quantitative TDT.

#### *Mid-morning break*

- PBAT
- Lab: Students work on performing the above analyses.

#### *Lunch*

#### Model-free Linkage

- Affected Sib-Pairs.
- Haseman-Elston Regression.
- Variance Components.

#### *Mid-afternoon break*

- Lab: Students work on performing the above analyses.
- Final question and answer session.

## Faculty

- Dahlia Nielsen, Research Assistant Professor of Statistics, Bioinformatics Research Center, North Carolina State University, Campus Box 7566, Raleigh NC 27695-7566, U.S.A.  
tel. +1/919/515.2586, fax +1/919/515.7315.
  - Amy Anderson, Senior Fellow in Biostatistics, Bioinformatics Research Center, North Carolina State University, Campus Box 7566, Raleigh NC 27695-7566, U.S.A.  
tel. +1/919/513.3439.
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# REGISTRATION FORM

S.A.G.E. and SAS courses

16 – 22 July 2006

Dr. Jan A. Staessen, Study Coordinating Centre, Hypertension and Cardiovascular Rehabilitation Unit, Department of Molecular and Cardiovascular Research, University of Leuven.

Fax +32/16/34.71.06 (Phone: +32/16/34.71.04)

**To be returned by 15 May 2006**

Mrs.:  Mr.:

Surname: .....

First name: .....

Profession: .....

Mailing address:  private  professional

Invoicing address:  private  professional

*Professional address:* .....

Street and number: .....

Post Code/City: .....

Phone (W): ..... Fax (W): .....

*Private address:* .....

Street and number: .....

Post Code/City: .....Phone (H): .....

*Main reasons for selecting the course:* .....

I shall pay the amount of 400 EUR (200 EUR for staff K.U.Leuven) upon receipt of the confirmation of my nomination and before the beginning of the course.

*In case of cancellation, a 10% fee will be charged. No refund will be given if the cancellation takes places within 10 days prior to the start of the course.*

Date and Place:  
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Signature:  
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