Emil Rehnberg

CONTACT INFORMATION

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CITIZENSHIP

Swedish and Finnish

EDUCATION

Stockholm University, Stockholm, SWEDEN

Magister Scientae, Mathematical Statistics, May 2009

- Thesis Topic: *Evaluation of a multipoint method for imputing genotypes using HapMap III*
- Supervisors: Juni Palmgren Keith Humphreys Monica Leu
- Area of Study: Biostatistics (genetics)

PROFESSIONAL / ACADEMIC EXPERIENCE

Division of Epigenomics National Cancer Centre, Tsukiji, Tokyo, Japan

Biostatistician **February 2012 to Present**

- Statistical consultant for researchers (Geneticists, Medical doctors).
- Researcher
- Bioinformatician

Department of Medical Epidemiology and Biostatistics Karolinska Institutet, Solna, Stockholm, Sweden

Biostatistician **December 2009 to January 2012 (currently on leave)**

- Statistical consultant for multiple research projects.
- Statistical consultant for PhD-students. Project planning, analysis, data management, methods.
- Teaching assistant in biostatistic courses.

Research Assistant **June 2009 to December 2009**
Collaborators: Juni Palmgren, Keith Humphreys and Monica Leu

- Imputation of genotypes for NordicDB
  - Responsible for imputation of genotype data, genome-wide for NordicDB, which is a nordic database for genome-wide genetic information from controls (genotypes and allele frequences).
  - Paper: NordicDB: a Nordic pool and portal for genome-wide control data, European Journal of Human Genetics , (28 July 2010)

Matteakuten, Stockholm, Sweden

Math teacher **September 2007 to January 2008**

- Employed as a math teacher at upper secondary school level. (As extra work during university studies)

SUBMITTED JOURNAL PUBLICATIONS

Scott RA et al. Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nat Genet.* 2012 Aug 12

DIAGRAM consortium Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nat Genet.* 2012 Aug 12

Manning AK et al. A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nat Genet.* 2012 May 13

Stolk L et al. Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. *Nat Genet.* 2012 Jan 22

Smedby KE et. al. GWAS of Follicular Lymphoma Reveals Allelic Heterogeneity at 6p21.32 and Suggests Shared Genetic Susceptibility with Diffuse Large B-cell Lymphoma. *PLoS Genetics* 2011 April.

Monica Leu, Keith Humphreys, Ida Surakka, Emil Rehnberg, .. Juni Palmgren, Samuli Ripatti. NordicDB: A Nordic pool and portal for genome-wide control data. *European Journal of Human Genetics.* 2010 December.

Emil Rehnberg. Evaluation of a multipoint method for imputing genotypes using HapMap III. Masters thesis, Karolinska Institutet, Department of Medical Epidemiology and Biostatistics, 2009.

Teaching Experience

Department of Medical Epidemiology and Biostatistics, Solna, Stockholm, Sweden

Teaching Assistant **December 2009 to May 2011**

- Master's Programme in Biomedicine, Biostatistics course
  - Teaching assistant for pen & paper exercises and computer labs. Descriptive, univariate, multivariate analysis, logistic regression.
- Bachelor's Programme in Biomedicine, Biostatistics course
  - R and R-commander introduction lecture.
  - Teaching assistant for pen & paper exercises and computer labs.
- Biostatistics for Molecular Oncology course.
  - Statistical consulting for group discussions. Descriptive stats and survival analysis in R.
  - Teaching assistant for pen & paper exercises and computer labs.

Professional activities

The Swedish Society for Medical Statistics - 2011

- Board member
- Website manager

Expertise

Mathematics:

- Applied mathematics, linear algebra, multivariate analysis

Statistics/Biostatistics:

- Epidemiology, descriptive statistics, multivariate analysis, analysis of cathegorical data, stochastic processes, probability theory, survival analysis, prediction, principal component analysis, hierarchical clustering, supervised classification, motif analysis.

Software Skills

Programming:

- Bash shell scripting, parallell computing, R, SAS.
- Exposure to: Pascal, Scheme, HTML, Python, C#, Fortran, C, Ruby.

Applications:

- PLINK, multiple UNIX-based genetic software.

Productivity Applications:

- TEX, Vim

Operating systems:

- Ubuntu, Microsoft Windows family, Apple OS X and other UNIX variants.

COURSES

Workshops / Lectures

- RegStat 2011 - Extensions to Epidemiological Designs in Register-Based Research.
- ENGAGE IT-Course and Statistical Workshop: Tools for data analysis and management in complex traits genetic studies.
- Age Period-Cohort Modelling.
- Essentials of descriptive cancer epidemiology.

Courses

- PDC Summer School - Introduction to High-Performance Computing.
- Epidemiological theory in a statistical framework.

LANGUAGE SKILLS Swedish, English, Japanese (elementary)