**Announcement**:

 Short Course: **“Introduction to the statistical analysis of genome-wide association studies”**

 Course Dates: **4-8 July 2017**

 Course Location: Department of Genomics of Common Disease, Imperial College, London, UK

 Course Leader: Dr Inga Prokopenko

Course Lecturers: Dr Krista Fischer (Tartu, Estonia), Dr Marika Kaakinen (London, UK), Dr Reedik Mägi (Tartu, Estonia), Prof Andrew Morris (Oxford and Liverpool, UK) , Dr Inga Prokopenko (London, UK)

 Attendance fee: (pound sterling) £850 academic /£1250 non-academic rate to include course registration fee, lunch, 5 nights’ accommodation (extra nights can be booked at own expense). If paid in full BEFORE 15 May 2017, a discount of £100 will be applied.

 Fellowships: A limited number of the European Society of Human Genetics (ESHG) -funded scholarships are available for young scientists in training from European countries. Preference will be given to ESHG members and researchers from countries which are disadvantaged economically, although scholarships are not limited to these groups. Scholarships will cover the full attendance fee only. **Deadline for applications for Fellowships**: 20 April 2017.

 Application information:

<http://www.imperial.ac.uk/school-public-health/study/short-courses/genomic-studies/>

 Audience: Geneticists facing the need to analyse from small to large-scale human genotyping data in relation to their effect on common human traits and diseases. Scientists and students in training aiming to undertake SNP-based association analyses, genome-wide association studies and their meta-analyses. Researchers willing to understand better the statistical approaches and analytical procedures for the genetic association studies.

 Applicants’ background: Applicants should understand basic genetic principles such as modes of inheritance, DNA and gene structure, SNPs and other genetic variants, principles of crossing over and recombination, concepts of heritability and penetrance. Additionally, knowledge of basic statistical tests and some command line scripting skills would be an advantage.

 Course content: This course will enable you to analyse large-scale genetic data using standard analytical approaches and freely available software tools. The course will cover statistical background for association studies; primer on scripting in the most frequently used computational environments, design and analysis of such studies, interpretation of the results. Each topic will be covered by a lecture, followed by a practical exercise, which will include use of the state-of-art software tools and example datasets. Practical exercises will be tailored to illustrate the ideas discussed during lectures and will be accompanied by discussion of the results.

 Topics covered:

         Introduction to statistics for geneticists

         Introduction to Linux and R

         Genome-wise association studies (GWAS)

         Quality Control (QC) for GWAS

         Association analysis

         Population structure

         Imputation of GWAS

         Meta-analysis of GWAS

         Analysis of rare variants

         Genetic risk scores

         Mendelian Randomization

**Three guest lectures** will be given by renowned scientists in the field of human genetics.

There will be no need to bring own laptop or data. Computers will be available at the venue; datasets will be designed and provided for each analytical exercise.

 Applicationsand all accompanying documentation should be submitted to the Course Administrator using email: gcdshort.courses@imperial.ac.uk

Application documents:

         Application form

         A curriculum vitae (résumé) in English, including work and research experience

         A letter of motivation in English (max. 500 words)

         A signed letter of recommendation from a supervisor

 Please refer to our website

<http://www.imperial.ac.uk/school-public-health/study/short-courses/genomic-studies/> or the attached flyer and application form for more details.

 Join our Facebook group “Analytical approaches in genetics and omics” <https://www.facebook.com/groups/1727397860834196/> to stay in contact, generate discussions and have updates from us.

 Follow us on twitter [@StatGenImperial](https://twitter.com/StatGenImperial)

We hope to see you in London soon!