Organised by: MIPT MOSCOW INSTITUTE OF PHYSICS AND TECHNOLOGY Supported by: PolyKnomics GENOMENAL

Introduction to quantitative genetics

Fall semester 2021, a course taught online

Quantitative genetics is the study of the genetic basis underlying phenotypic variation among individuals in natural and managed populations, with a focus on complex traits that are under control of multiple genetic and environmental factors. With the developed countries moving towards precision medicine and agriculture, it becomes increasingly clear that the quantitative genetics approach is fundamental to an understanding of the dynamics of evolutionary change, and of methods for animal and plant improvement and alleviation of complex disease. This course provides an introduction to quantitative genetics.

Aim of the course: Provide participants with understanding of classical and novel quantitative genetics models and methods through self-learning, hands-on learning and problem solving.

By the end of the course, the participants should be able to:

- Formulate and apply laws governing genes in populations and families
- Solve typical statistical genetic problems, such as estimating heritability and associations
- Describe the limits of genetic and genomic prediction and selection
- Critically read manuscripts reporting results of genome-wide association studies

Target group: MSci and PhD candidates, although others can also apply

Prerequisites: Good command of English, basic knowledge of genetics and statistics. A personal computer with internet connection.

Duration of the course and workload: From end-September to mid-December 2021, with an average of 4 hours per week (including self-study). Overall, you are expected to spend about 48 hours on this course.

Location: online

Dates and time: Starting at the end of September, each week, 1.5 hour of online class and 1.5 hour of online seminar (optional). The participants will also spend about 2-2.5 hour on a self-study. **THE EXACT DAY/TIME INFORMATION WILL BE ADDED AS SOON AS WE KNOW THE SCHEDULE.**

Organisers: Moscow Institute of Physics and Technology, School of Medical and Biological Physics, Department of Bioinformatics and Systems Biology; and Vavilov Institute of General Genetics, Russian Academy of Sciences. The course is supported by PolyKnomics BV (Netherlands) and Genomenal.

Principal educator: Prof. Dr. Yurii Aulchenko, Head, Laboratory of Theoretical and Applied Functional Genomics, Novosibirsk State University; Chief Scientist, PolyKnomics, The Netherlands.

How to apply: The deadline for application is on Wed, Sept 15, 2021, at 23:59 Central European Time. To apply, please send PDF files with your CV, one recommendation letter, and a motivation letter, to the email statgenomicslab@gmail.com. All documents should be submitted in English. Please use the email subject “Models and methods of human quantitative genetics - application from YOUR NAME”. In the body of the email, please indicate if, in case you are admitted to the course, you intend to take the group track (see below “organisation of the course”). If not indicated, in case you are admitted, we will assign you to the “core track”. Please name the PDF files: as: LastName_FirstName_CV, LastName_FirstName_RL, Last Name_FirstName_ML. Note that we accept recommendation letters from anyone (this does not need to be a professor!), who can explain why you should attend this course. Please supply a motivation letter of approximately one A4 page length or less. In the motivation letter, specifically indicate: why are you applying for this course? Do you have a sufficient background to follow the course? How much time do you plan to spend for the course? Given your other obligations, why do you think you will be able to dedicate necessary time to the course? How do you plan to use the knowledge obtained in the course? Will you use this knowledge in the coming year? Five years? How will you use this knowledge?

Extended information

Target group:

MSci and PhD candidates, although prospective participants from other levels can also apply. The core (see below “organisation of the course” for definition of the “core” and “group track”) course is limited to 50 participants (of which about 25 places are booked for the internal participants from the Department of Bioinformatics and Systems Biology, MIPT), while the group track is limited to 20 participants (of which about 10 places are booked for the internal participants).

Prerequisites:

Official language of the course is English and you are supposed to have a working knowledge of English to understand the course texts, videos and to communicate with other course participants.

You have a basic knowledge of genetics (e.g. genes, alleles, Mendel’s laws) and mathematics, including basic probability (e.g. independent events, mutually exclusive events, Bayes theorem) and statistics (e.g. distributions, hypothesis testing).

You will need a personal laptop and good internet connection. For computations, you will need statistical computing software, such as R or Python/SciPy.

Duration of the course and workload:

Throughout the fall semester, from mid-September to mid-December 2021, with an average of 3 hours per week. This will include ~12 (online) lecture hours, ~12-16 hours of self study and ~12 optional hours of seminars.

Educators:
prof. dr. Yurii Aulchenko; Yakov Tsepilov, PhD; Arina Nostaeva, MSci; TBA

Course topics:
- Genes in populations. What is a genetic population? Populations of very large size: Hardy-Weinberg equilibrium, Wahlund’s effect, inbreeding, selection. Genes in populations of realistic size: inbreeding and genetic drift.
- Genetics of complex traits. Polygenic model of Fisher, heritability, threshold liability model, prediction of quantitative traits from the phenotypes of relatives.
- Understanding biology through genetics. Locus identification through genome-wide association studies (GWAS). Genomic prediction of complex traits. From locus to function: *in-silico* analysis allows formulation of functional hypotheses via investigation of large-scale functional genomics data (post-GWAS analyses). Analysis of GWAS summary statistics.

Support resources:
- MOOC “From disease to genes and back” (Coursera platform)
- D. Falconer, Introduction to quantitative genetics
- Course slides, texts, and exercises at Perusall.com

Organization of the course:
The course is organised online according to flipped classroom methodology. The “core track” of the course, which is obligatory for all participants, consists of about 12 weekly blocks. Each week, you will spend 45-90 minutes on a self-study of a predefined set of topics. These topics will then be discussed in an online session (40-50 minutes) with the course teacher.

COMPULSORY: In case you choose a “group track”,you will also participate in a weekly seminar. A seminar will consist of 45 minutes of online work in groups of 4-5 participants to solve specific problems. Then you will present the solutions to the seminar leaders and other course participants during a joint session (25-30 minutes). For the seminars you will be organised into “green” and “red” subtracks. The participants with less background in mathematics and genetics are recommended to take the green subtrack.

COMPULSORY: For those who are willing to dedicate more time to the course, it will also be possible to take project assignments. The project works are not an obligatory part of the course, and you are free to choose whether to participate or not.

COMPULSORY: We may organise invited lectures on a range of topics. These additional lectures will be planned no more often than once every two weeks. These lectures are not an obligatory part of the course, and you are free to attend or not.

Last year (fall semester 2020), the list of invited speakers and topics included

- “Combined analysis of single cell RNA-Seq and ATAC-Seq data reveals regulatory toggles operating in native and iPS-derived retina” by prof. Michel Georges, director, GIGA Institute of University of Liege, Belgium
- “The Human Glycome Project – What did we learn from the analysis of the first 150,000 people” by prof. Gordan Lauc, Director of the Human Glycome Project, University of Zagreb Faculty of Pharmacy and Biochemistry & Genos Glycoscience Research Laboratory, Zagreb, Croatia
- “Application of quantitative genetics in dogs, copper toxicosis in Labrador retrievers” by dr. Hille Fieten, University of Utrecht, the Netherlands
- “Main steps in preparing a good presentation” by dr. Marianna Bevova, Director of the GIGA Doctoral School for Health Sciences, University of Liège, Belgium
- “Reproducible research in practice”, a workshop by dr. Lennart Karssen, Chief technical Officer of PolyKnomics BV, the Netherlands
- “Variant annotation and effect prediction”, by dr. Vasily Ramensky, National Medical Research Center for Therapy and Preventive Medicine, Russia