

## ***“GENOMIC DATA ANALYSIS” Course, Moscow, July 2 – 11, 2012***

High-throughput genomics assays have become pervasive in modern biological research. To properly interpret these data, biologists need to have a firm grasp of the appropriate statistical methodology and skill with tools for data handling. A course on “GENOMIC DATA ANALYSIS” will be organized in Moscow from July 2 to July 11, 2012 with partial support from OJSC RUSNANO, Skolkovo Institute of Technology, Health Ministry of the Russian Federation, and InterLabService. This course is regularly held at Cold Spring Harbor Laboratory, and it is among most popular courses at CSHL (CSHL website at <http://www.cshl.edu/>; more information on 33 educational courses within CSHL Meetings and Courses Program at <http://meetings.cshl.edu/courses.html>). The course is designed to build competence in quantitative methods for the analysis of high-throughput molecular biology data using R and Bioconductor, specifically genomic microarray and next-generation sequencing data. Moscow program will be held in English by CSHL instructors and speakers. No translation will be provided. Original curriculum and format of CSHL course will be kept.

**Curriculum** includes the following topics:

- Review of R and introduction to Bioconductor
- Review of statistical methods for genomics
- Microarray technologies
- High-throughput sequencing technologies
- Basic analysis (quality control, normalization)
- Analysis using predefined gene sets
- Cis-regulatory sequence analysis
- Modeling of transcriptional networks
- DNA methylation assays and DNase I footprinting
- Expression profiling by RNA-Seq
- Analysis of ChIP-chip and ChIP-Seq data
- Integration of multiple data types
- Expression QTL analysis

### **Format:**

It is an extremely intensive ten-day course with one day and two evenings-off (Sunday, July 8, Wednesday, July 4<sup>th</sup>, and Saturday, July 7, correspondingly). A working day starts at 8am and continues until late at night. Detailed lectures and presentations by guest speakers in morning and evening will be combined with hands-on computer tutorials in the afternoon. The methods covered in the lectures will be applied to public high-throughput data sets, primarily human, mouse and yeast data. Students will be expected to have a basic familiarity with the R programming language at the start of the course. The students are to work very hard; therefore highly motivated applicants are invited.

Besides lectures and lab exercises, students will spend evening time in scientific and technical discussions which is a perfect way to do networking. Other than that, there will not be much room for leisure time. Absence from classes is not encouraged.

Students will be selected on a competitive basis; application package includes CV, one page essay about current research of the applicant and how it relates to genomic data analysis, and up to two letters of recommendation. Applications should be submitted by E-mail at [gda-course-2012@yandex.ru](mailto:gda-course-2012@yandex.ru) before April 30, 2012.

### **Participation Fee:**

The cost of participation in the course is \$2,000 and includes room and board but not the travel expenses (the cost of this course at CSHL is \$3,535). A limited number of stipends for participants may be available on discretion of course organizers. The number of stipends will increase when/if additional sponsor support for the Course is secured.