Report from participation in the course:

Analysis of Next Generation Sequence Data Course For Complex and Mendelian Traits at Max Delbrück Center for Molecular Medicine,

Berlin, Germany, June 23-27, 2014,

by Piotr Stawiński

The *Analysis of Next Generation Sequence Data Course For Complex and Mendelian Traits* course emphasized teaching of both theory and application of various methods to analyze next generation sequence (NGS) data.

Paweł Gaj, an experienced researcher and MSc. Piotr Stawiński, IT specialist, members of the Bioinformatics Group led by Dr Radosław Zagożdżon, participated in the course under the Task T2.3 – the Know-how sharing and promotion.

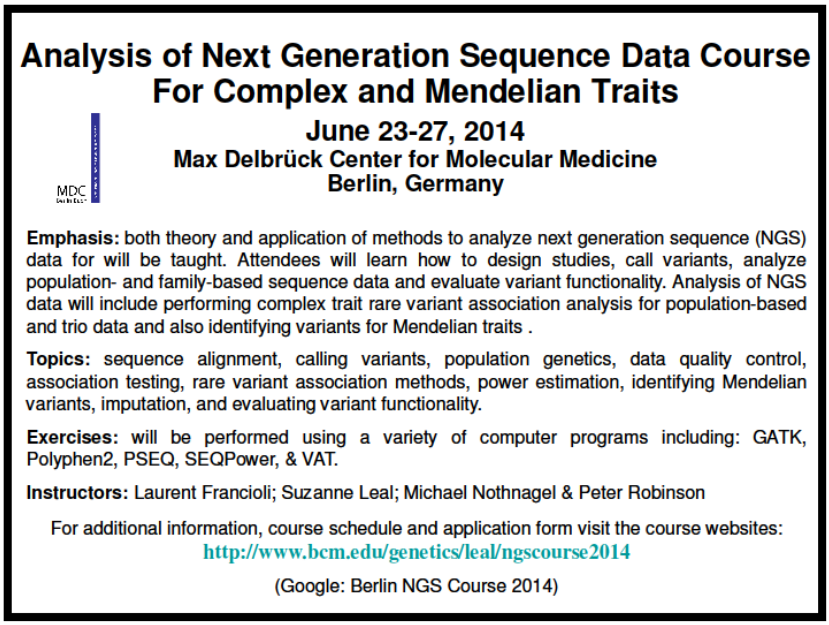
Figure 1. The course participahts. Paweł Gaj and Piotr Stawiński are marked with white arrows

The attendees were learning how to design studies, call variants, analyze population- and family-based sequence data and evaluate variant functionality. Analysis of NGS data included performing complex trait rare variants, as well as (to certain extent) common variants association analysis for population-based and trio data. It also covered identifying variants for Mendelian traits.

Specific topics of the course included: sequence alignment, calling variants, population genetics, data quality control, association testing, rare variant association methods, power estimation, identifying Mendelian variants, imputation, and evaluating variant functionality. Exercises were conducted using variety of computer programs including: GATK, Polyphen2, PSEQ, SEQPower, & VAT.

In this context, particularly valuable was the top notch experience of the instructors (Michael Nothnagel and Suzanne Leal) in programming in commonly used R-project environment and other popular programming languages.

Instructors: Laurent Francioli; Suzanne Leal; Michael Nothnagel & Peter Robinson



Analysis of Next Generation Sequence Data Course For Complex and Mendelian Traits

June 23-27, 2014

Max Delbrück Center for Molecular Medicine
Berlin, Germany

Emphasis: both theory and application of methods to analyze next generation sequence (NGS) data for will be taught. Attendees will learn how to design studies, call variants, analyze population- and family-based sequence data and evaluate variant functionality. Analysis of NGS data will include performing complex trait rare variant association analysis for population-based and trio data and also identifying variants for Mendelian traits .

Topics: sequence alignment, calling variants, population genetics, data quality control, association testing, rare variant association methods, power estimation, identifying Mendelian variants, imputation, and evaluating variant functionality.

Exercises: will be performed using a variety of computer programs including: GATK, Polyphen2, PSEQ, SEQPower, & VAT.

Instructors: Laurent Francioli; Suzanne Leal; Michael Nothnagel & Peter Robinson

For additional information, course schedule and application form visit the course websites:
http://www.bcm.edu/genetics/leal/ngscourse2014

(Google: Berlin NGS Course 2014)

Figure 2. The course flyer

MDC MAX-DELBRÜCK CENTRUM FÜR MOLEKULARE MEDIZIN BERLIN-BUCH

BCM Baylor College of Medicine

CERTIFICATE OF COMPLETION

THIS IS TO CERTIFY THAT

PIOTR STAWINSKI

HAS COMPLETED THE

NEXT GENERATION SEQUENCE DATA COURSE

AT THE MAX DELBRÜCK CENTER FOR MOLECULAR MEDICINE

BERLIN, GERMANY

JUNE 23-27, 2014

THIS COURSE IS OFFERED THROUGH A COLLABORATION BETWEEN THE BAYLOR COLLEGE OF MEDICINE, HOUSTON, TEXAS, USA, AND THE MAX DELBRÜCK CENTRUM, BERLIN, GERMANY

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MICHAEL NOTHNAGEL
PROFESSOR
COLOGNE CENTER FOR GENOMICS
UNIVERSITY OF COLOGNE
COLOGNE, GERMANY

Figure 3. Piotr Stawiński certificate of completion