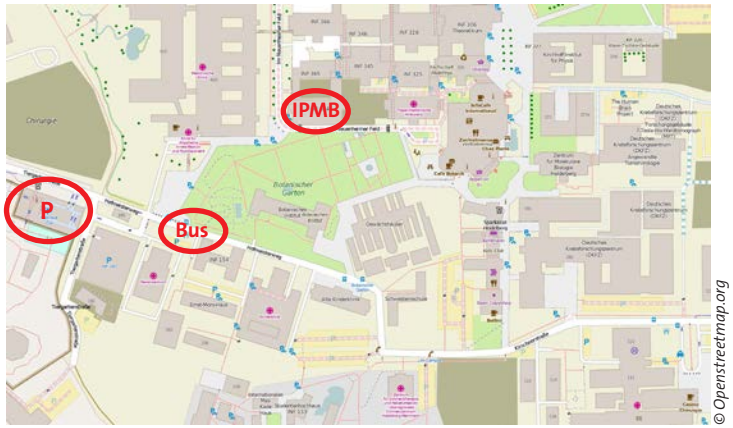
dkfz.
German Cancer Consortium
Core center Heidelberg

LOCATION

IPMB (Institute for Pharmacy and Molecular Biotechnology)
Im Neuenheimer Feld 364
5th Floor, Room N° 542
69120 Heidelberg



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DIRECTIONS

By car:
Coming from highway (A656), follow signs to Clinic/Campus Neuenheimer Feld and turn left at 3rd traffic light after the bridge following the signs „Zoo, Kopfklinik“. Parking isavailable at the Zoo.

By train/public transport:
Take Bus 31/32 (direction “Sportzentrum”) and exit at “medizinische Klinik”.

SUPPORTERS

EMBL

UNIVERSITÄT HEIDELBERG ZUKUNFT SEIT 1386

Bundesministerium für Bildung und Forschung

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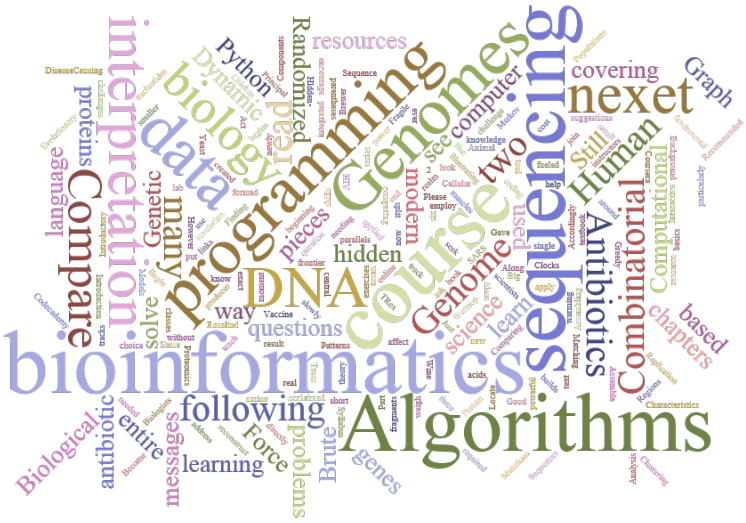

Joint Workshop of HD-HuB and DKTK School of Oncology

BIOINFORMATICS

October 7th and 8th, 2015, 9am - 5pm

Data Interpretation for Next Generation Sequencing Data

Dear Colleagues,

Modern cancer research highly benefits from technologies at high throughput level. This results in rapidly increasing amounts of data output and various data types. Education in translational cancer research therefore has to impart skills in bioinformatics and knowledge of available bioinformatics resources in order to enable young researchers to benefit from the available data.

This workshop offers the unique opportunity to get a profound insight into existing tools for interpretation of Next Generation Sequencing data and to train the newly gained knowledge.

Moreover you will get in touch with colleagues from different partner institutions, thus stimulating scientific exchange and novel collaborations. We cordially invite you to this exciting workshop and look forward to meeting many of you in Heidelberg.

Christof von Kalle

Roland Eils

OCTOBER 7th

Introduction:
Next Generation Sequencing Technology

Data Interpretation:
Whole Genome and Exome Sequencing

Visualization of NGS Data

Hands-on Training:
Whole Genome and Exome Sequencing

Wrap-Up Scientific Lecture:
Results from RNA Seq/Exome Analysis

OCTOBER 8th

Data Interpretation:
RNASeq and Whole Genome Bisulfite Sequencing (WGBS)

Hands-on Training:
RNASeq/WGBS

Wrap-Up Scientific Lecture:
Results from RNASeq/WGBS

WORKSHOP

COURSE DESCRIPTION

The DKTK School of Oncology and the Heidelberg Center for Human Bioinformatics (HD-HuB) from the German Network for Bioinformatics Infrastructure (de.NBI) invite you to a two-day bioinformatics workshop on “Data Interpretation for Next Generation Sequencing Data in Cancer Research”. The course is aimed at researchers working with larger datasets of next-generation sequencing (NGS) data arising from patient tumor samples. It will teach background knowledge on technologies used for data generation and for data analysis. Commonly used tools for data interpretation will be presented and can be applied in hands-on sessions on provided data sets.

The course will combine instructional lectures in the morning, which focus on a specific NGS data type (e.g. Whole Genome, whole exome, methylome, RNAseq ...). The lectures will introduce methods for data generation and tools for analysis. The latter will be demonstrated in interactive course in the afternoon. Each day will be closed by scientific lecture presenting oncology research highlights using methods described in the course.

APPLICATION CRITERIA

The course is targeted at researchers with a background in medicine or biology, who work in oncological projects analyzing large data sets arising from tumor samples and who work together with bioinformatics specialists for data analysis. Basic knowledge in R and command line skills are appreciated but not mandatory. The course is not aimed at bioinformatics specialists.

To apply, please fill out the questionnaire (http://bit.ly/1RnZc5j). Application deadline is August 9th ,2015.

CONTACT

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School of Oncology
German Cancer Consortium
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sigrid.ziegler@nct-heidelberg.de

LECTURERS

Benedikt Brors is a Chemist by training and obtained his PhD in Biochemistry from Düsseldorf University. His division "Applied Bioinformatics" combines methods from informatics, bioinformatics and statistics to understand the development and improve therapy and diagnostics of cancer. His particular expertise is the analysis of next-generation sequencing data, for example whole genome and exome sequencing, epigenetic analyses and RNASeq in translational oncology approaches.

Stefan Fröhling heads the Research Section "Molecular and Cellular Oncology" and serves as Attending Physician in the Department of Translational Oncology at NCT Heidelberg. He has a long-standing interest in identifying genetic abnormalities that define disease subgroups and treatment outcome in patients with cancer. Furthermore, he works to identify new cancer drug targets through a better understanding of the functional dependencies of hematologic and solid-organ malignancies, and to bring targeted approaches and molecularly based patient stratification to clinical trials and patient treatment broadly across tumor types.

LECTURERS

Matthias Schlesner studied Human Biology and obtained his PhD in Biochemistry at the Max Planck Institute of Biochemistry (Martinsried). His research group "Computational Analysis" develops and applies various statistical methods and machine learning techniques to analyze data from next generation sequencing (whole genome, exome and methylome) and microarray experiments. His aim is to better understand cancer biology and to translate these findings back into the clinic.

Carl Herrmann studied Applied Mathematics and obtained his PhD from the University of Marseille (France) in theoretical Physics. His research focus ses on understanding the principles of transcriptional regulation in development and cancer. In particular, he is interested in developing bioinformatics tools to identify and contextualize regulatory elements from whole-genome sequencing data. Moreover, he is interested in influences of the genetic background on the methylome by analysins whole genome bisulfite methylation data.