

# RBC - BIMSB

## de.NBI – German Network for Bioinformatics Infrastructure RNA Bioinformatics Center: The Berlin Institute for Medical Systems Biology

Bora Uyar, Dilmurat Yusuf\*, Ricardo Wurmus, Dan Munteanu, Uwe Ohler, Nikolaus Rajewsky, Altuna Akalin  
The Berlin Institute for Medical Systems Biology, Max-Delbrueck Center for Molecular Medicine, Berlin, Germany

\*Current affiliation: Bioinformatics Group, Department of Computer Science, Albert-Ludwigs-University Freiburg, Freiburg, Germany

### Short description of the project

We offer tools, services and training for the analysis of **RNA-binding proteins** and **post-transcriptional regulation**.

### Contributions

- Developed and maintained tools & databases made accessible via many channels



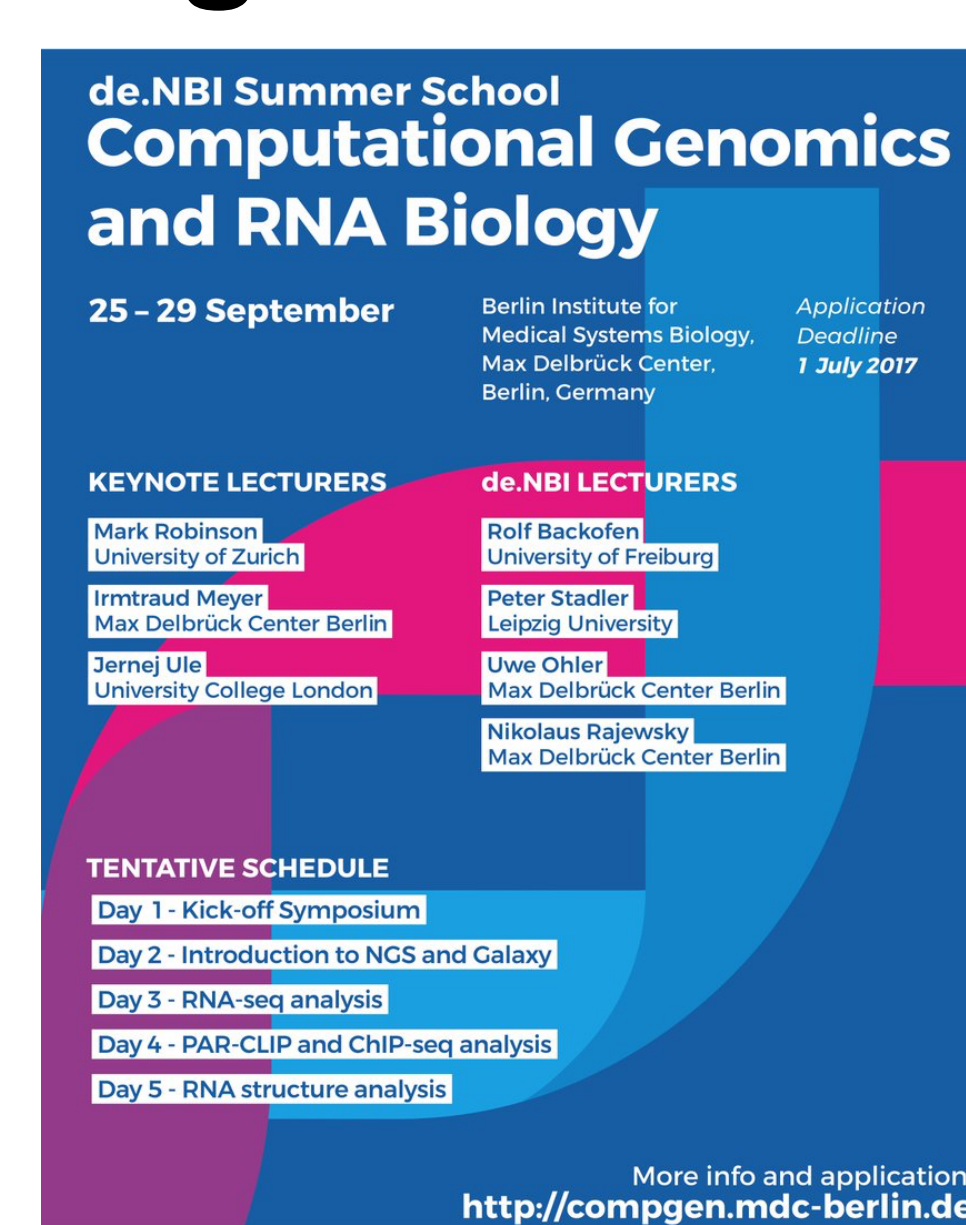
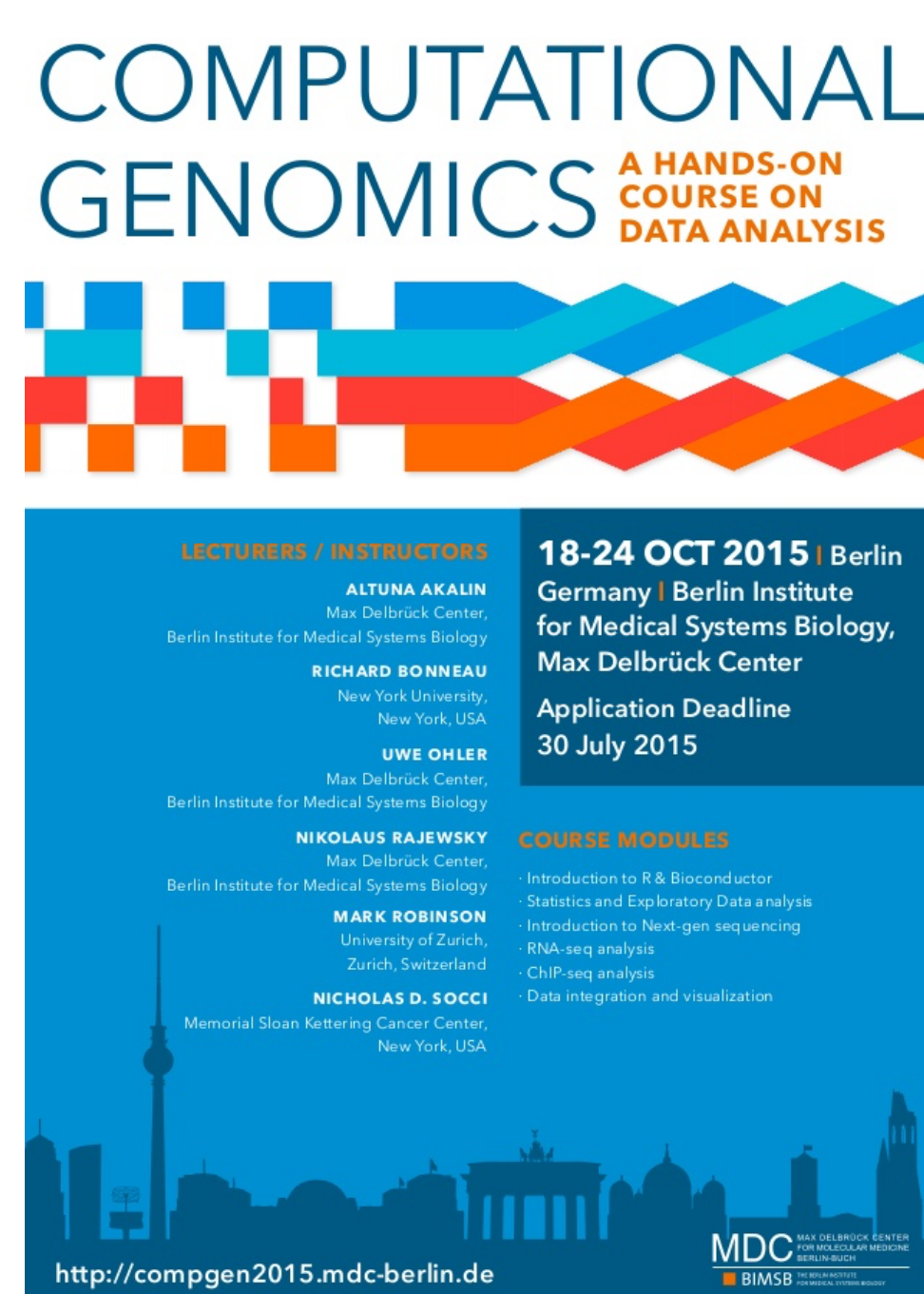
- Organised three summer schools
- Organised a bioinformatics hackathon in Berlin
- Organised three Galaxy Workshops
- Participated in deNBI related events

### Tools & Services

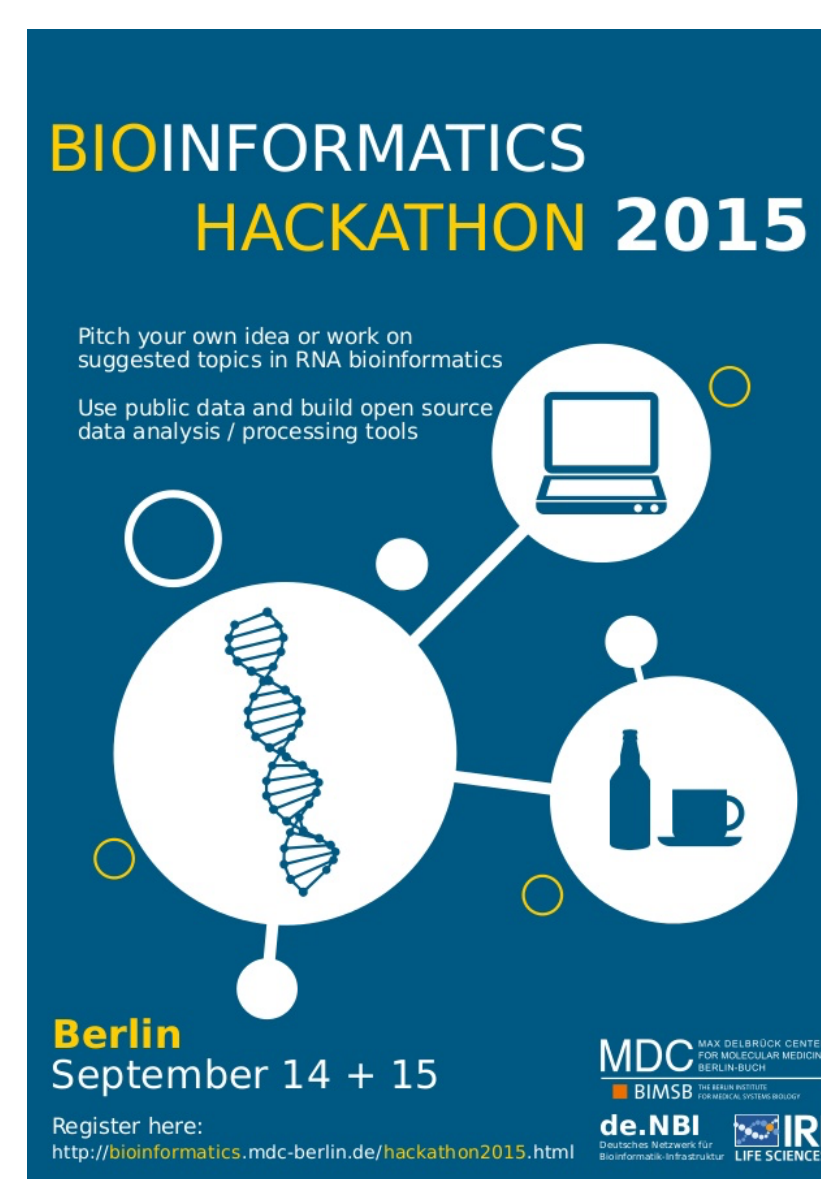
Tool or Service	Description
Galaxy Server	Galaxy server with 92 users from MDC
PicTar	A web resource for microRNA targets
doRiNA	A database of RNA interactions in post-transcriptional regulation
circBase	A database to explore public circRNA datasets and discover circRNAs in RNA-seq data
RCAS	RNA-centric annotation system for transcriptome-wide regions of interest
RiboTaper	Ribosome Profiling (Ribo-seq) analysis pipeline
miRDeep	microRNA detection tool in deep sequencing data
miReduce	discovers motifs in mRNAs which explain changes in gene expression, for example upon perturbation of miRNA expression
PIPMiR	identifies novel plant miRNA genes from a combination of deep sequencing data and genomic features
cERMIT	finds optimal motifs in high-throughput ChIP or RIP datasets
NASTIseq	identification of cis-Natural Antisense Transcripts using strand specific RNA-seq data
PARalyzer	PAR-CLIP sequencing analysis data pipeline
microMUMMIE	microRNA target-site prediction in PAR-CLIP data

### Training & Education

#### Summer schools: computational genomics



#### Bioinformatics Hackathon



Also, offered **three workshops** for RNA-seq analysis using **Galaxy**



### Plans for the next year

- Will continue maintaining the already developed tools/services
- Will make a major update to doRiNA
  - Integrate with the new meta-analysis functionality of RCAS
  - Publish the updated database
- Keep supporting the Galaxy users
- Organise more training workshops for Galaxy
  - ChIP-seq analysis, variant calling
  - Integrate more tools/workflows
  - Expand the user base

### Selected Publications

- Calviello, Lorenzo, Neelanjan Mukherjee, Emanuel Wyler, Henrik Zauber, Antje Hirsekorn, Matthias Selbach, Markus Landthaler, Benedikt Obermayer, and Uwe Ohler. 2015. "Detecting Actively Translated Open Reading Frames in Ribosome Profiling Data." Nature Methods 13 (2). Nature Research: 165–70.
- Uyar, Bora, Dilmurat Yusuf, Ricardo Wurmus, Nikolaus Rajewsky, Uwe Ohler, and Altuna Akalin. 2017. "RCAS: An RNA Centric Annotation System for Transcriptome-Wide Regions of Interest." Nucleic Acids Research, February. doi:10.1093/nar/gkx120.
- Blin K, Dieterich C, Wurmus R, Nikolaus Rajewsky, Markus Landthaler, Akalin A. DoRiNA 2.0—upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. Nucleic Acid Research , 2014

