de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

MDC MAX DELBRÜCK CENTER FOR MOLECULAR MEDICINE IN THE HELMHOLTZ ASSOCIATION
BIMSB — THE BERLIN INSTITUTE FOR MEDICAL SYSTEMS BIOLOGY

RBC: BIMSB

RNA Bioinformatics Center: The Berlin Institute for Medical Systems Biology

Fkz 031A538C

Bora Uyar, Dilmurat Yusuf*, Ricardo Wurmus, Dan Munteanu, Lorenzo Calviello, Altuna Akalin, Nikolaus Rajewsky, Uwe Ohler
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.**

de.NBI services

	Service	Description	Stats until April '17
Data-bases	Galaxy Server	Galaxy server at MDC	82 unique users (UU)
	doRiNA	A database of RNA interactions	15680 UU
	circBase	A database to explore and discover circular RNAs	34215 UU
RNA (Seq) Tools	RCAS	RNA-centric annotation system	652 downloads (Ds)
	NASTIseq	identifies cis-Natural Antisense Transcripts from RNA-seq data	417 Ds
	RiboTaper	Ribo-Seq analysis pipeline	1257 Ds
miRNA Tools	PIPmiR	identifies novel plant miRNA genes from deep sequencing data	586 Ds
	PicTar	Web resource for microRNA targets	66158 UU
	miRDeep	microRNA detection tool in deep sequencing data	5644 Ds
	miReduce	discovers motifs in mRNAs and correlates with gene expression changes	34 Ds
RBP Tools	PARalyzer	PAR-CLIP sequencing analysis	1201 Ds
	micro-MUMMIE	microRNA target-site prediction in PAR-CLIP data	*added later*
	cERMIT	finds optimal motifs in high-throughput ChIP or RIP datasets	*added later*

General information on the project

- **No. of staff paid from de.NBI grant:** 2
- **Other staff involved:** 2

Progress report

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

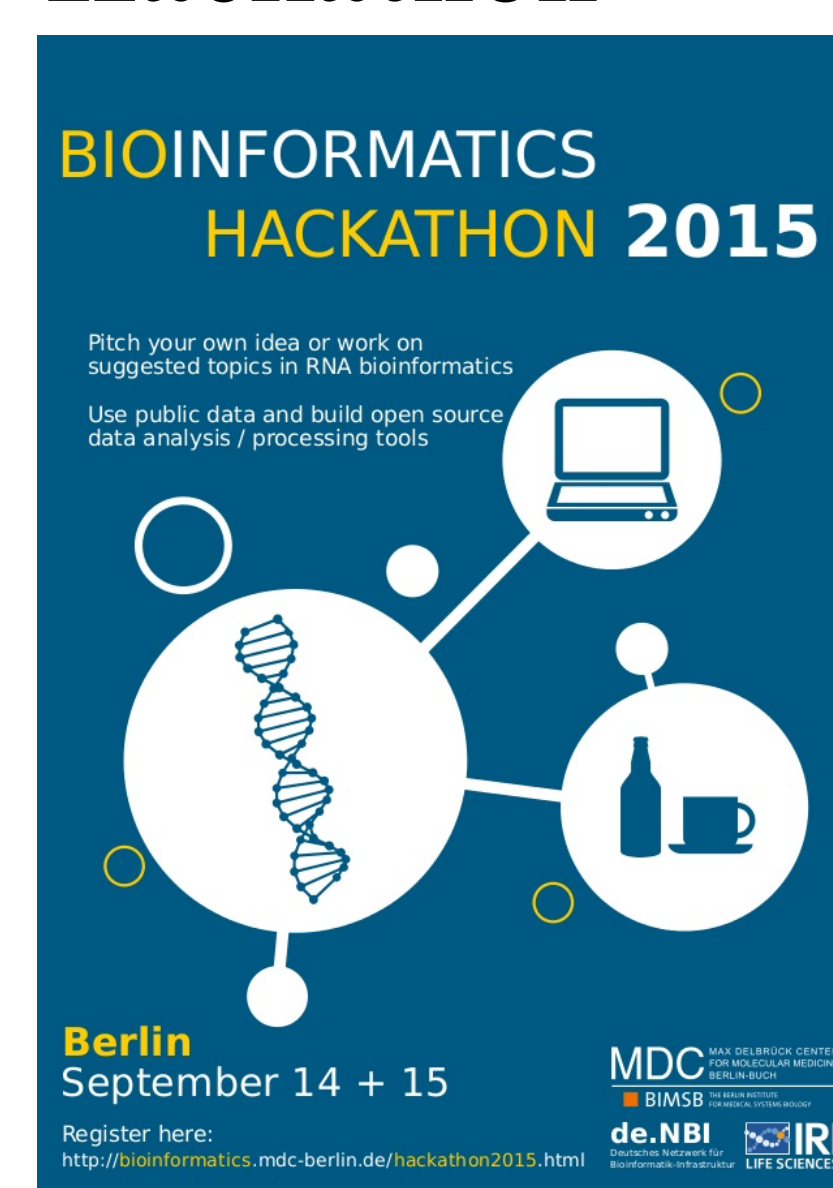Bioconductor — OPEN SOURCE SOFTWARE FOR BIOINFORMATICS   WEB SERVICE   Guix   docker

◦ Organised three **summer schools**
◦ Organised a bioinformatics **hackathon**
◦ Organised three **Galaxy Workshops**
◦ Participated in deNBI related events

de.NBI Training and education

Summer schools (Total: 60 participants)

Bioinformatics **Hackathon**

15 participants

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

Total: 55 participants

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

GEFÖRDERT VOM — Bundesministerium für Bildung und Forschung   PTJ Projektträger Jülich Forschungszentrum Jülich   www.denbi.de