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

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Short description of the project

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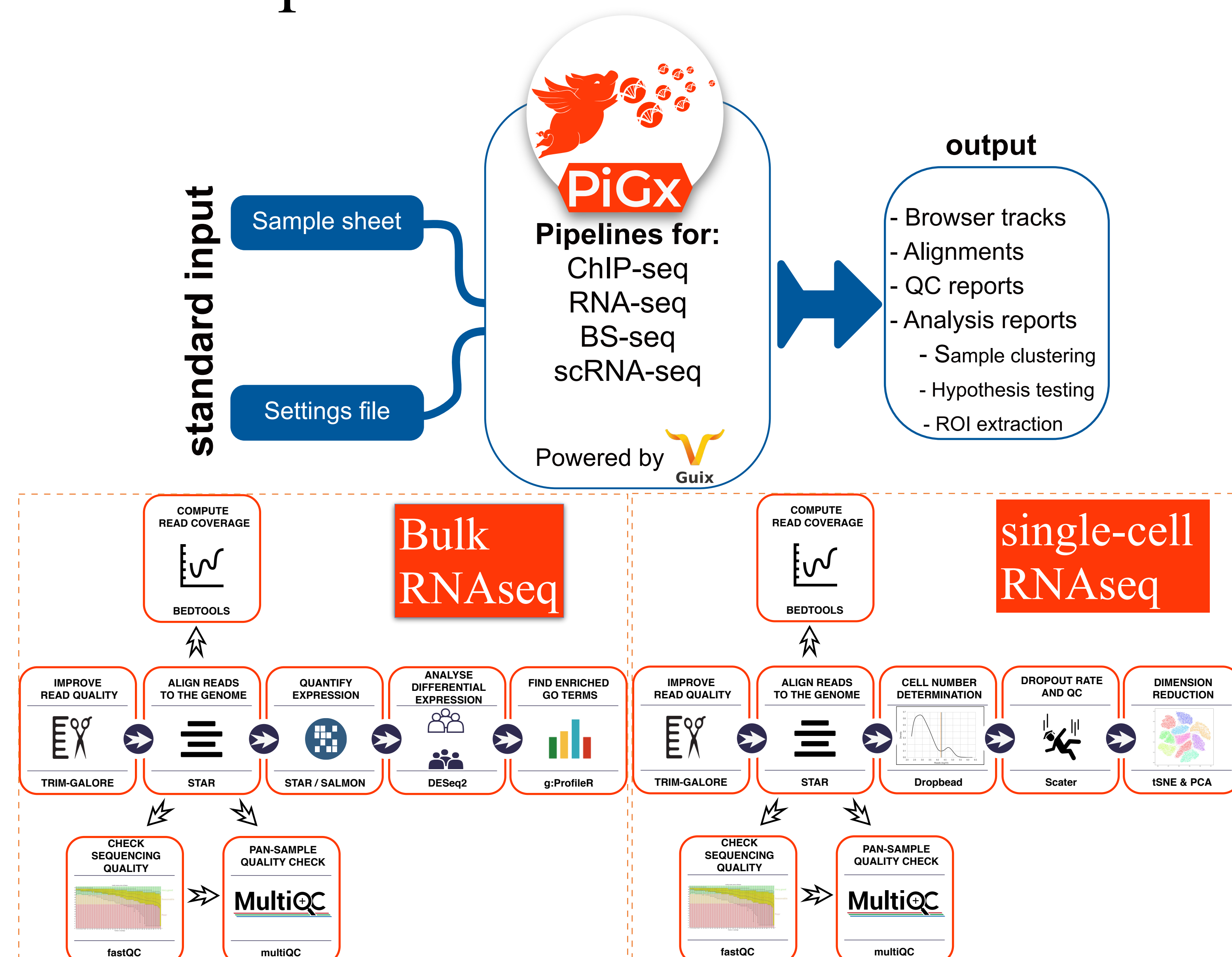
de.NBI services

	Service	Description
Data-bases	Galaxy Server	Galaxy server at MDC
	doRiNA	A database of RNA interactions
	circBase	A database to explore and discover circular RNAs
RNA (Seq) Tools	PiGx	RNAseq and single-cell RNA-seq pipelines
	RCAS	RNA-centric annotation system
	NASTIseq	identifies cis-Natural Antisense Transcripts from RNA-seq data
	RiboTaper	Ribo-Seq analysis pipeline
miRNA Tools	PIPmiR	identifies novel plant miRNA genes from deep sequencing data
	PicTar	Web resource for microRNA targets
	miRDeep	microRNA detection tool in deep sequencing data
	miReduce	discovers motifs in mRNAs and correlates with gene expression changes
RBP Tools	PARalyzer	PAR-CLIP sequencing analysis
	micro-MUMMIE	microRNA target-site prediction in PAR-CLIP data
	cERMIT	finds optimal motifs in high-throughput ChIP or RIP datasets

General information on the project

- **No. of staff paid from de.NBI grant:** 2
- **Other staff involved:** 3

Progress report

Developed and Maintained Software

standard input — Sample sheet, Settings file

PiGx Pipelines for: ChIP-seq, RNA-seq, BS-seq, scRNA-seq — Powered by Guix

output:
- Browser tracks
- Alignments
- QC reports
- Analysis reports
  - Sample clustering
  - Hypothesis testing
  - ROI extraction

Bulk RNAseq: COMPUTE READ COVERAGE — BEDTOOLS; IMPROVE READ QUALITY — TRIM-GALORE; ALIGN READS TO THE GENOME — STAR; QUANTIFY EXPRESSION — STAR / SALMON; ANALYSE DIFFERENTIAL EXPRESSION — DESeq2; FIND ENRICHED GO TERMS — g:ProfileR; CHECK SEQUENCING QUALITY — fastQC; PAN-SAMPLE QUALITY CHECK — MultiQC (multiQC)

single-cell RNAseq: COMPUTE READ COVERAGE — BEDTOOLS; IMPROVE READ QUALITY — TRIM-GALORE; ALIGN READS TO THE GENOME — STAR; CELL NUMBER DETERMINATION — Dropseq; DROPOUT RATE AND QC — Scater; DIMENSION REDUCTION — tSNE & PCA; CHECK SEQUENCING QUALITY — fastQC; PAN-SAMPLE QUALITY CHECK — MultiQC (multiQC)

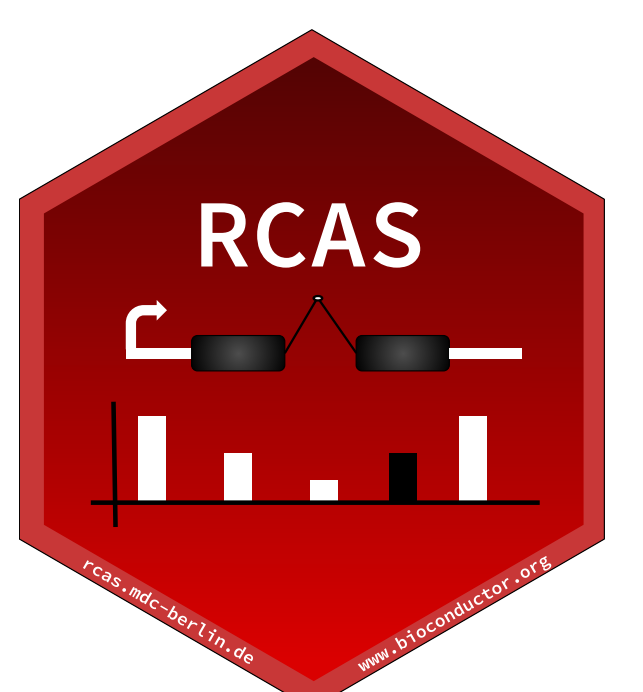**http://bioinformatics.mdc-berlin.de/pigx/**

PiGx pipelines are being used in Epigenomics and Epitranscriptomics QC group (EpiQC) as part of the FDA's SEQC2 Study.

Local Galaxy Server at MDC
> 100 Total Users

Galaxy

RCAS: RNA-Centric Annotation System

~ 120 monthly downloads on Bioconductor
- Packaged using Conda, Guix, and available on the local Galaxy Server

RCAS

doRiNA database of RNA interactions

doRiNA

de.NBI Training and education

Provided one-on-one **mentorships** and **consultations**

Selected Publications

Wyler, Emanuel, **Vedran Franke** et al. 2019. "Single-Cell RNA-Sequencing of Herpes Simplex Virus 1-Infected Cells Connects NRF2 Activation to an Antiviral Program." *Nature Communications* 10 (1): 4878.

Müthel, Stefanie, **Bora Uyar** et al. 2019. "The Conserved Histone Chaperone LIN-53 Is Required for Normal Lifespan and Maintenance of Muscle Integrity in Caenorhabditis Elegans." *Aging Cell* 18 (6): e13012.