

A new database for genome-wide RNA-chromatin interactome

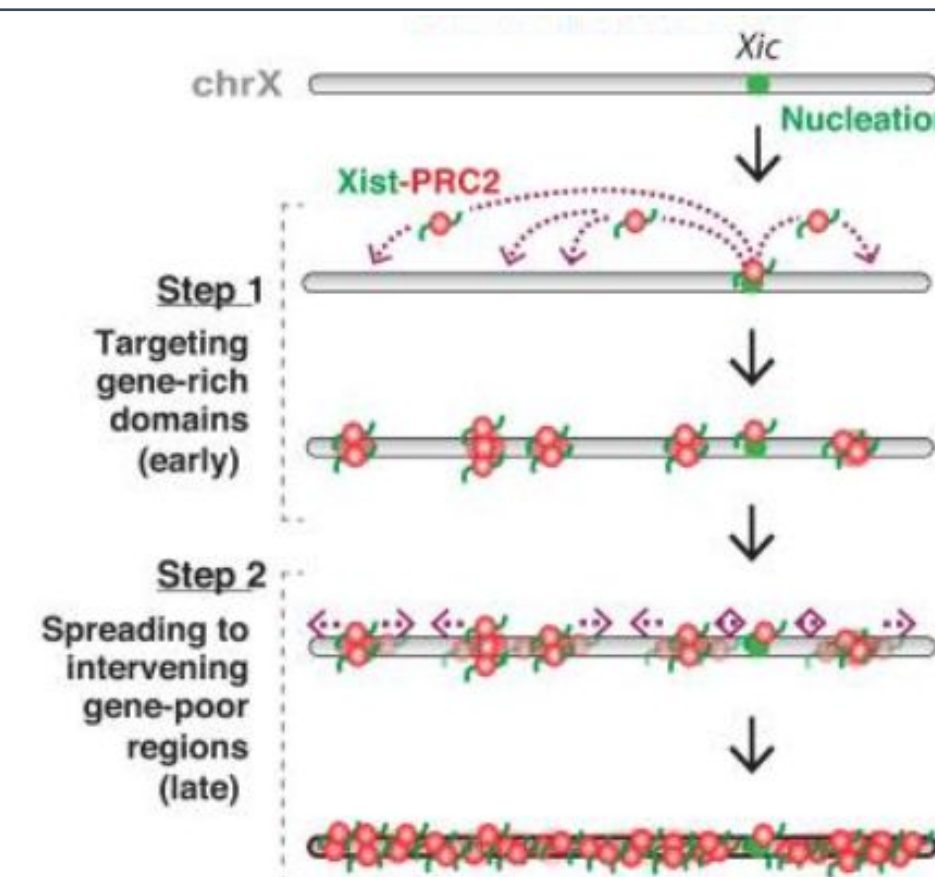
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Introduction

There is a large amount of evidence that non-coding RNAs may participate in many processes of cell life, in particular, in transcriptional regulation processes, chromatin remodeling, and chromatin architecture maintenance. For the present various techniques have been developed to determine genome-wide localisation of both specific RNAs (**one-vs-all**) and all RNAs on chromatin (**all-vs-all**).



Matthew Simon, et all, Nature, 2013

Results

Our resource “**RNA-Chrom**” (<http://rnachrom.bioinf.fbb.msu.ru/>) not only stores RNA-chromatin data, but also provides analytical capabilities for quick and convenient comparative analysis of interactions: single RNA, RNA classes (Fig. 1).

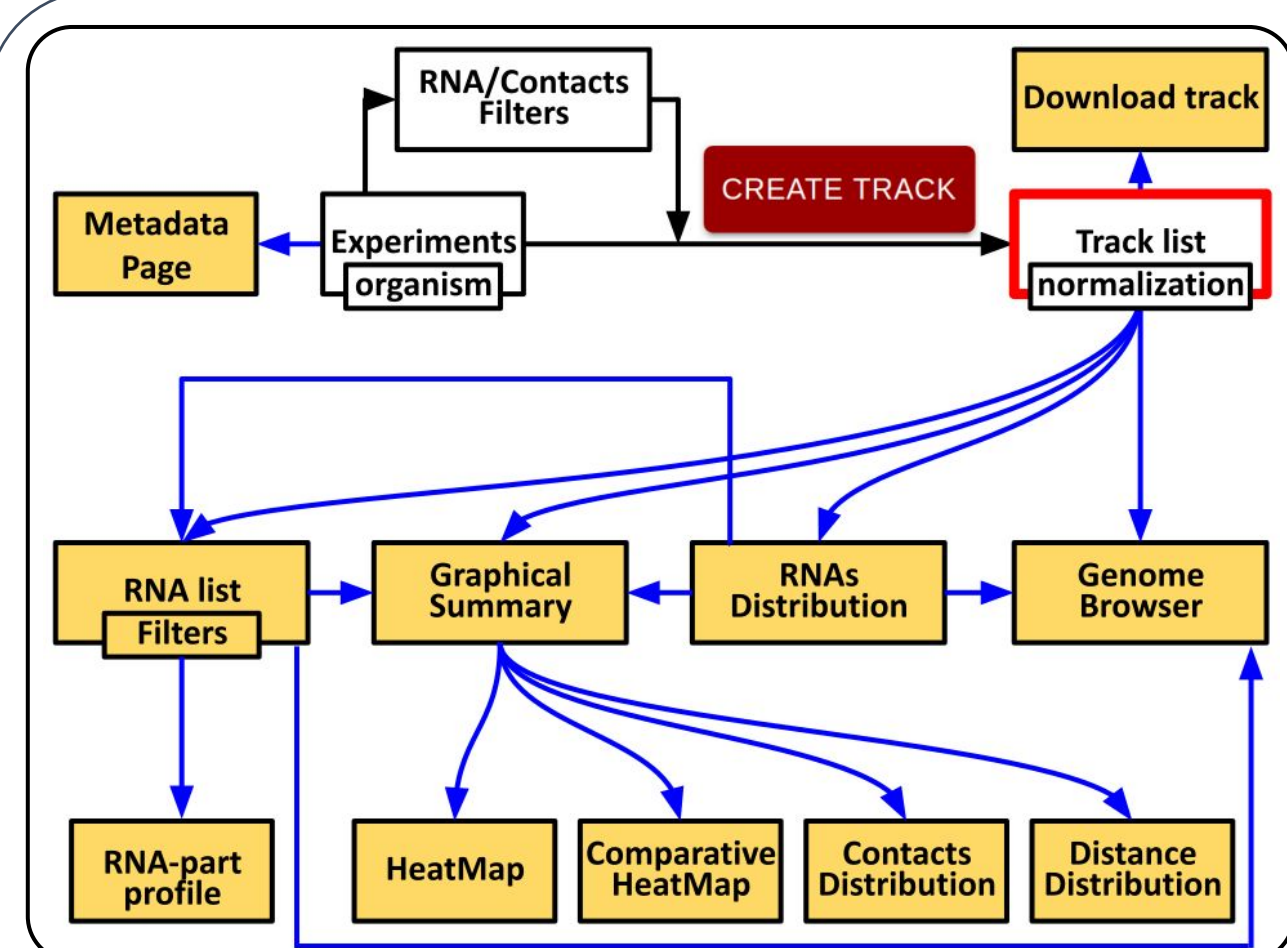


Fig. 1: Analysis Workflow.

Metadata information:		RNAs distribution:		
Name	Description	Gene types	RNAs in the dataset	Annotated RNAs
Dataset ID	12	Xrna	41138	50000
Organism	Mus musculus	protein_coding	20281	21843
Tissue	Mouse oligodendrocyte progenitor cells	lncRNA	8689	9959
Cell type	mES R08 cells	pseudogene_P1	5412	10002
Data type	All vs all	scRNA	2139	8321
Method	RADICL	TEC	2668	3238
Genome version	mm10	lRNA	1259	4755
Reference	Bonetti A., Agostini F., Suzuki A.M., Hashimoto K., Pascarella G., Gimenez J., et al. "RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions". Nat. Commun. 2020; 11:1018. DOI: 10.1038/s41467-020-14337-6. PMID: 32094342			
GEO	GSM3852760, GSM3852761, GSM3852762, GSM3852763, GSM3852764, GSM3852765			
		pseudogene_TP2	233	300
		pseudogene_TU2	203	272
		misc RNA	151	562

Fig. 2: Metadata.

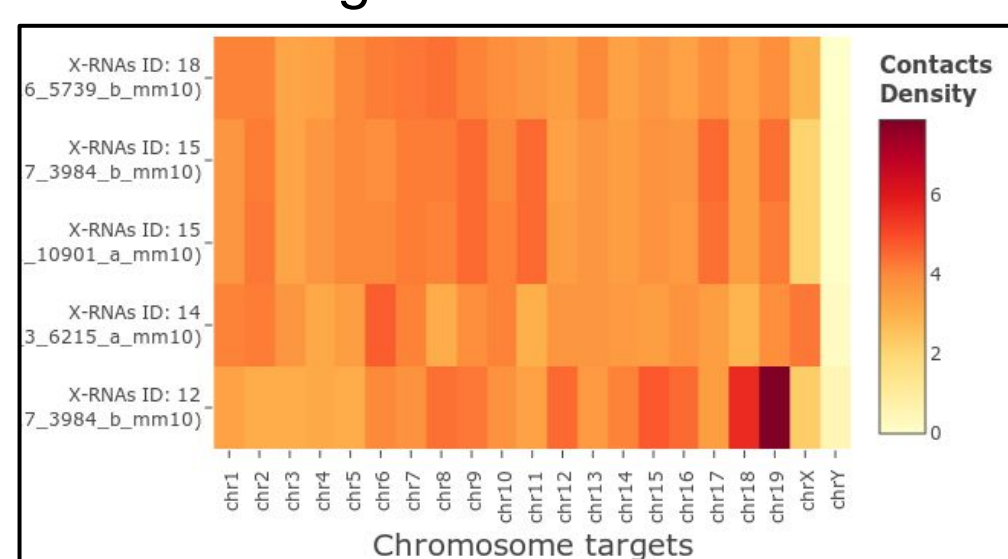


Fig. 3: A heat map that displays contacts density distribution over chromosomes for selected RNAs

RNA-Chrom database: Tracks

START ANALYSIS

ABOUT

DATA LIST

Data: 6 selected

One vs all

All vs all

Mus musculus

ID	Cell Type	Data type	Method	Extra information
<input type="checkbox"/> 10	ES cells	All vs all	GRID	None
<input checked="" type="checkbox"/> 12	mES R08 cells	All vs all	RADICL	1% formaldehyde
<input checked="" type="checkbox"/> 13	mES R08 cells	All vs all	RADICL	2% formaldehyde
<input checked="" type="checkbox"/> 14	mES R08 cells	All vs all	RADICL	Actinomycin D
<input checked="" type="checkbox"/> 15	mES R08 cells	All vs all	RADICL	Proteinase K
<input checked="" type="checkbox"/> 17	mOPC R08 cells	All vs all	RADICL	Proteinase K
<input checked="" type="checkbox"/> 18	mOPC R08 cells	All vs all	RADICL	1% formaldehyde
<input type="checkbox"/> 5	ES cells	One vs all	RAP	pSM33-0hr-Xist

Track name

X-RNAs

CREATE TRACK

RNA Filter

chr1:10000-23000; chrX

Select genes

Xrna

QUARTILES

THRESHOLD

Number of contacts:

☐ Upper quartile: Q4

☐ Second & Third: Q2+Q3

☐ Lower quartile: Q1

It is important:

between "RNA Filter" and "Contacts Filter", a logical AND is implied, while a logical OR is inside each of them !!

Contacts Filter

chrY:1234-777234; chr5

☐ Upstream 5-50kb

☒ Upstream 0-5kb

☒ Gene Body regions

☐ Downstream 0-5kb

☐ Downstream 5-50kb

☐ Gene deserts

Track list: 1 selected

General information

RNA Filter

Contacts Filter

Track name	Organism	Dataset ID	Locus	Contacts threshold	Genes	Locus	Gene Body	Up 0-5kb	Down 0-5kb	Up 5-50kb	Down 5-50kb	Gene deserts
<input checked="" type="checkbox"/> X-RNAs	Mus musculus	12, 13, 14, 15, 17, 18			Xrna		all genes	all genes				

GRAPHICAL SUMMARY

RNA LIST

GENOME BROWSER

RNAs DISTRIBUTION