

RNA-seq and ChIP-seq data integration

(answer to questions)

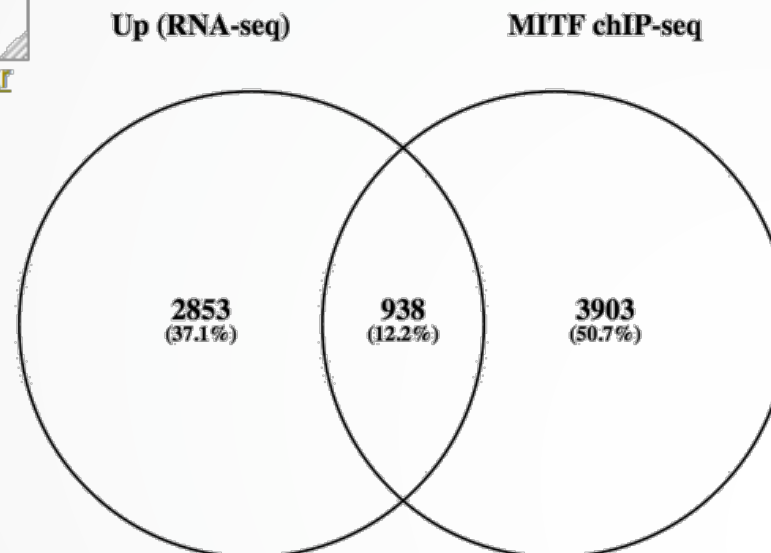
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Exercise

- 1.
 - Retrieve Gene symbols of up-regulated genes (use the file siMitfvssiLuc.up.txt you annotated with BioMart)
 - Download the annotated peaks (dataset generated with HOMER). Use the Gene Name column.

Up (RNA-seq) 3791	MITF chIP-seq 4841
COX20P2	PBRM1
MCRS1	SIM2
HERC4	FAM183A
RP11-39C10.1	SNRNP200
CEP85L	PPP4R1-AS1

[clear](#) [clear](#)



Exercise

- 2.
 - Download MITF peaks (Output of MACS2 narrow peaks) -> Use it as reference coordinates in seqMINER
 - Go to seqMINER

Exercise

File Tools Help

Density Array Method Enrichment Based Method **Advance(RNA-Seq)**

Step 1: Load data

Load reference coordinates (i.e. peaks) ...

Select assembly
hg38_ense... ▾

Advanced

Load aligned reads

mitf.sort.bam
H3K4me3.sort.bam
polII.sort.bam

Browse ...

Load file(s) >>

Step 2: Data extraction

Galaxy29-[MACS2_callpeak_or 7745 peaks.
Peak length mean: 172

RNA-Seq expression

RNAseq_seqMINER.txt

B...

Selected datasets:

mitf.sort.bam
H3K4me3.sort.bam
polII.sort.bam

Delete

Extract data

100%

Ensembl 85 (hg38)

ChIP-seq datasets

MITF peaks

RNAseq data

Exercise

