

Correlation of RNA-seq and ChIP-seq data

(answer to questions)

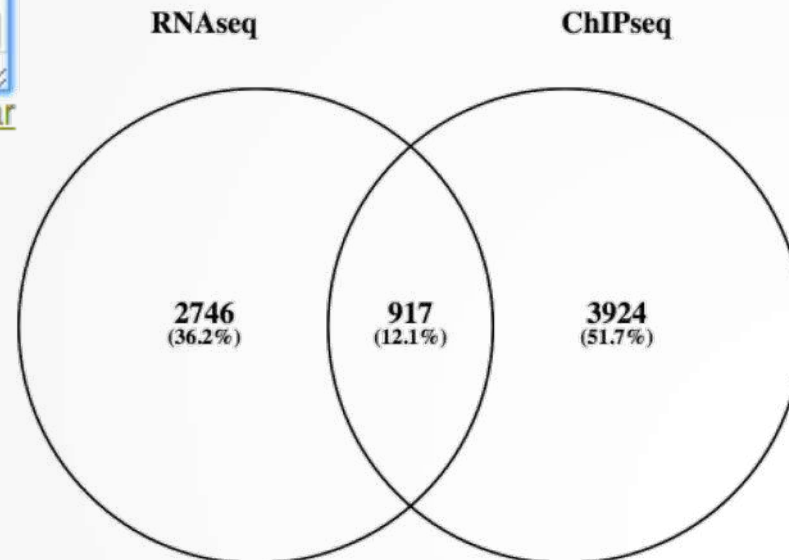
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Exercise

- 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.

RNAseq	3663	ChIPseq	4841
ZNF284		LINC00462	
RPL5		DHX58	
TIMM17B		LRRC37B	
ATG13		ITGA6	
CAPN1		SLCO4A1-AS1	
NEPRO		GLTSCR1	

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



Exercise

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

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
poll.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
poll.sort.bam
Delete
Extract data

Ensembl 95 (hg38)

ChIP-seq datasets

MITF peaks

RNAseq data

100%

Exercise

- Go to Density Array Method (top tabs)
- Click on Extract data
- Click on Clustering

Exercise

