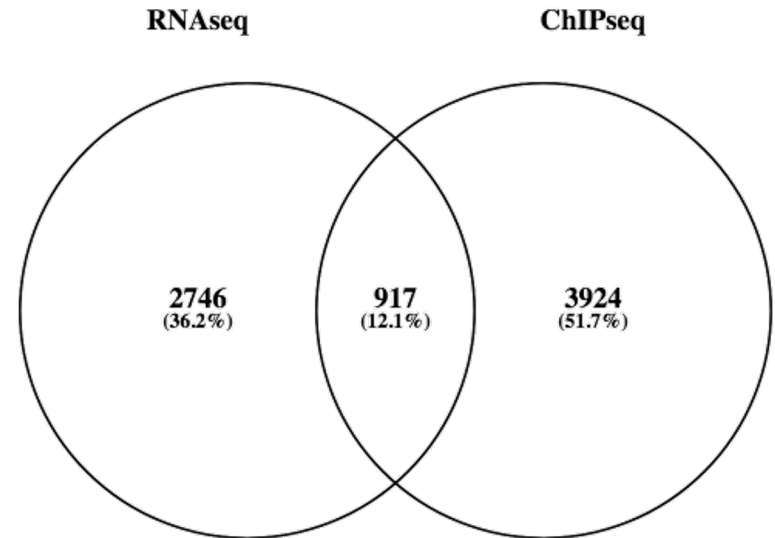
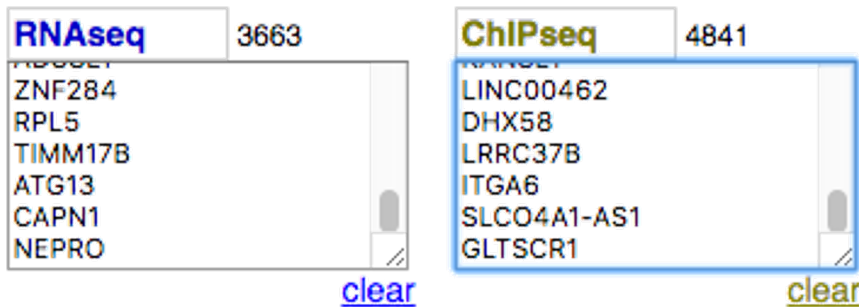


Correlation of RNA-seq and ChIP-seq data (answer to questions)

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Exercise 1


- 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.







Exercise 2

To generate the file with RNA-seq data for seqMINER:

1.

- Click on the button  and select “create new”
- Click on the history name “Unnamed history”, erase “Unnamed history”, enter “Correlation” and press enter



2.

- Click on the button  and select “Saved Histories”
- In the table of histories, click on the history named “RNA-seq data analysis”
- Datasets from this history appears on the history panel
- Click on the button  of the dataset named « SARTools DESeq2 tables »
- Click right on the file named « siMitfvssiLuc.complete.txt » and download it.
- Switch to your history named « Correlation »
 - Click on the button  and select “Saved Histories”
 - In the table of histories, click on the history named “Correlation”
- Import the file to Galaxy by clicking on the button  and drag and drop the file from your computer to the Galaxy window. Type: tabular, Genome: hg38.

Exercise 2

- Search for “**RNAseqDataAnnotation**” in the search field (tool panel)
- Click on the name of the tool
- Fill in the parameters:
 1. **Select file** : the file siMitfvssiLuc.complete.txt you generated with SARTools
 2. **Select the species for your data**: Homo Sapiens
 3. **Ensembl version?** Version 95


3.

- Click on Shared Data (top menu) and select “Data Libraries”
- Click on “NGS data analysis training ” > “Correlation”
- Select Data_normalization_annotation.txt (tick the box beside dataset name)
- Click on the button  to History
- Select history: Correlation
- Click on 
- Go back to the main page by clicking on “Analyzed data” (top menu)

4.

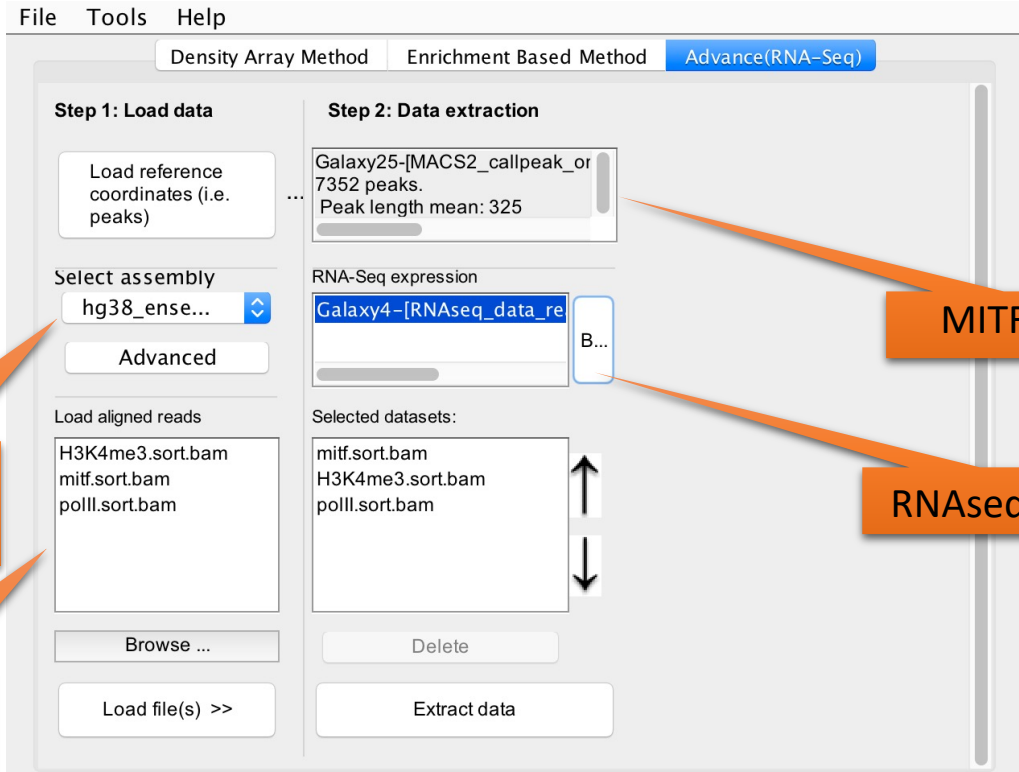
- Search for “**cut**” in the search field (tool panel)
- Click on the name of the tool “Cut columns from a table »
- Fill in the parameters:
 - **Cut columns: C1, C13**
 - **From:** Data_normalization_annotation.txt

Exercise 2

- Search for “**compute**” in the search field (tool panel)
- Click on the name of the tool “Compute an expression on every row »
- Fill in the parameters:
 - **Add expression:** $c2/50$
 - **as a new column to:** Cut on data 1
- Search for “**cut**” in the search field (tool panel)
- Click on the name of the tool “Cut columns from a table »
- Fill in the parameters:
 - **Cut columns:** **C1, C3**
 - **From:** Compute on data 2
- Download the dataset
 - Click on the name of the dataset: Cut on data 3
 - Click on  to download the file

Exercise 2

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



Ensembl 95 (hg38)

ChIP-seq datasets

MITF peaks

RNAseq data

Exercise 2

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

Exercise 2

The image shows a software interface for analyzing genomic data. On the left, there are three vertical heatmaps labeled 'mitf.sort.bam', 'H3K4me3.sort....', and 'poll.sort.bam'. The heatmaps display red intensity patterns across a vertical axis. To the right of the heatmaps is a vertical color bar with segments in blue, magenta, green, yellow, cyan, black, grey, and teal. The main interface area on the right contains the following elements:

- KMeans seed:** 97787647
- Save heat...:** A button to save the heatmap.
- Color palette:** A button to change the color scheme, with a small color palette icon next to it.
- Contrast:** A slider set to 20.
- Cluster list:** A list of 10 clusters with their respective element counts:
 - Cluster 1: 837 elements
 - Cluster 2: 3044 elements
 - Cluster 3: 1368 elements
 - Cluster 4: 380 elements
 - Cluster 5: 304 elements
 - Cluster 6: 401 elements
 - Cluster 7: 211 elements
 - Cluster 8: 112 elements
 - Cluster 9: 569 elements
 - Cluster 10: 126 elements
- Navigation:** Up and down arrow buttons next to the cluster list.
- View options:** A row of tabs: 'Peaks(BED)' (selected), 'Merged dataset profile', 'Mean profile', 'Heatmap', and 'Density values'.
- Export options:** 'Export selected clusters' and 'Save profile' buttons at the bottom.