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

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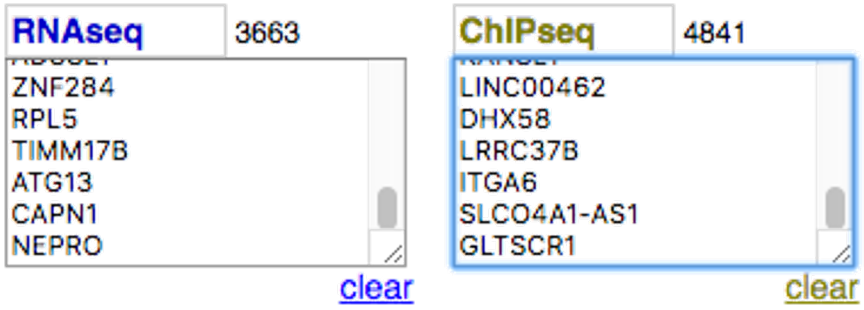
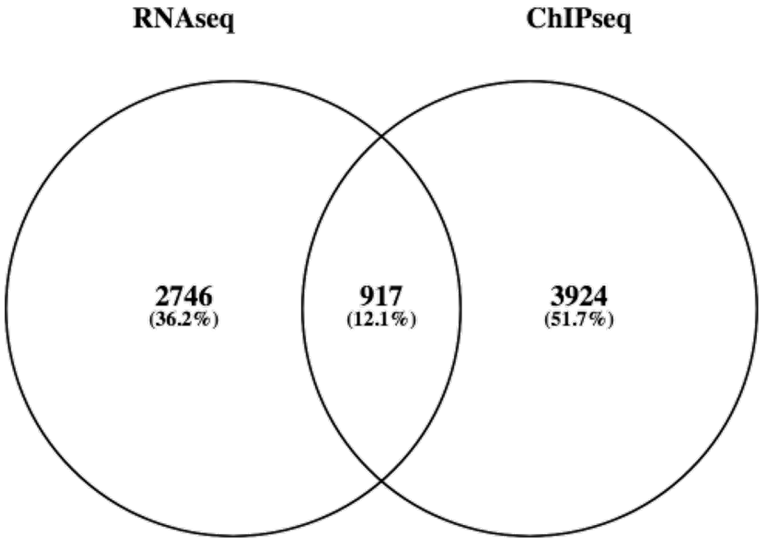
Exercise 1

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

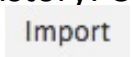
2.
   - Click on the button  and select “Saved Histories”
   - In the table of histories, click on the history named “RNA-seq data analysis”
   - Datasets from this history appears on the history panel
   - Click on the button  of the dataset named « SARTools DESeq2 tables »
   - Click right on the file 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 

- Select history: Correlation
- Click on 

- Go back to the main page by clicking on "Analyzed data" (top menu)

4.

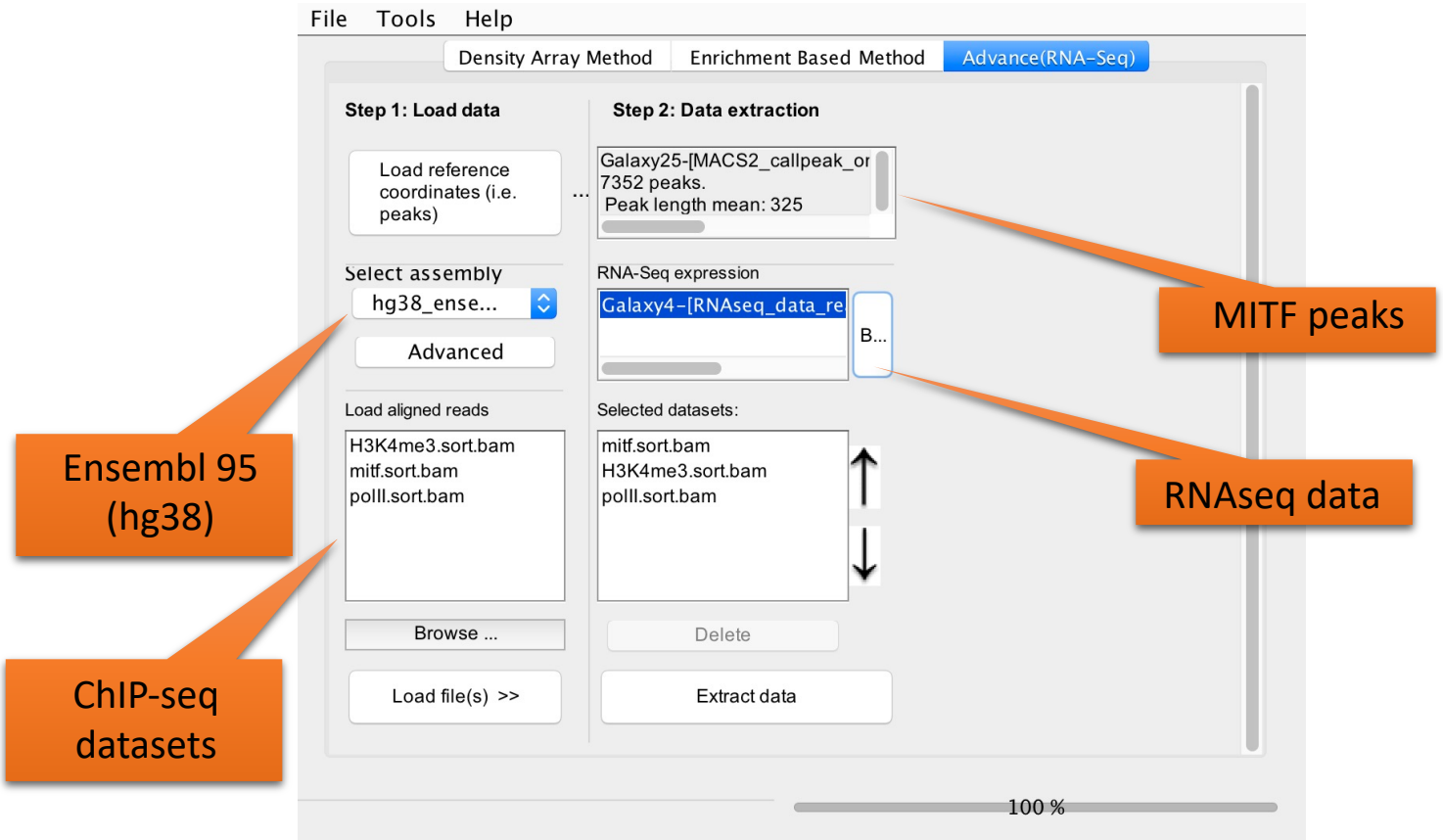
- Search for "**cut**" in the search field (tool panel)
- Click on the name of the tool "Cut columns from a table »
- Fill in the parameters:
  - **Cut columns: C1, C13**
  - **From:** Data_normalization_annotation.txt

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

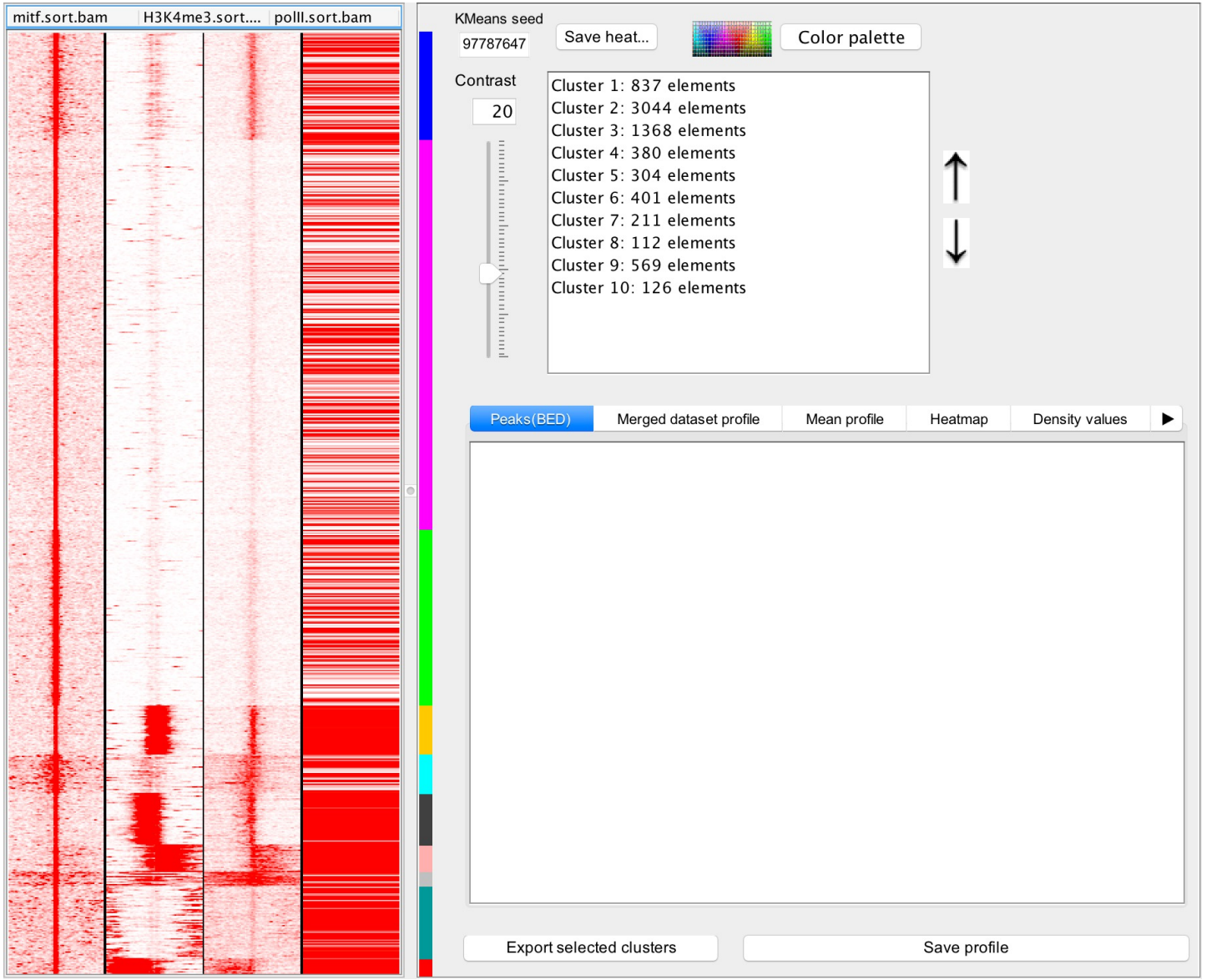
- 2.
  - Download MITF peaks (Output of MACS2 peak summits - BED) -> Use it as reference coordinates in seqMINER



Exercise 2

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

Exercise 2


mitf.sort.bam
H3K4me3.sort....
polII.sort.bam
KMeans seed
97787647
Save heat...
Color palette
Contrast
20
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
Peaks(BED)
Merged dataset profile
Mean profile
Heatmap
Density values
Export selected clusters
Save profile