

## Online Platform for RNA - Protein Interaction Analysis (OPRIA) Instruction

### User Interface:

Figure 1a shows the interface for OPRIA, parameter selection and file upload section is on the left side whereas figure display will be on the right side. User ought to follow step-wise instruction below to effectively use OPRIA to perform analysis. Sample dataset can be downloaded in the links provided as seen in Figure 1b.

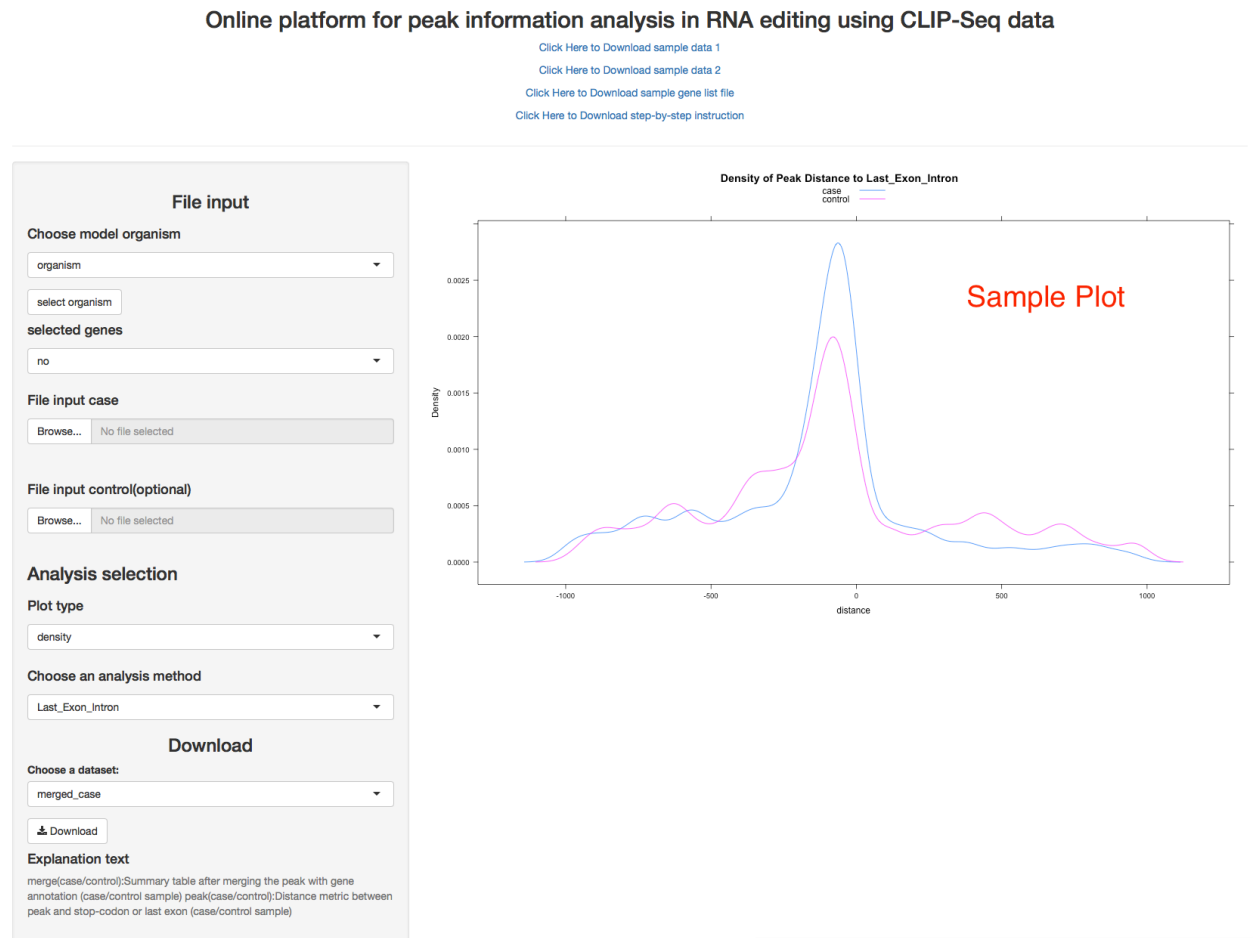


Figure 1a. Screenshot of OPRIA User Interface

[Click Here to Download sample data 1](#)

[Click Here to Download sample data 2](#)

[Click Here to Download sample gene list file](#)

[Click Here to Download step-by-step instruction](#)

Figure 1b. Sample data download link

Step 1 organism selection:

The first step of the analysis is to select organism of experimentation. OPRIA currently supports human hg19 and mouse mm10. After selecting organism from the dropdown menu, press “select organism” and wait for “hg19 selected” or “mm10 selected” before proceeding to the next step as shown in Figure 2. This step allows OPRIA to load necessary genome annotation reference file.



**Choose model organism**

hg19 ▼

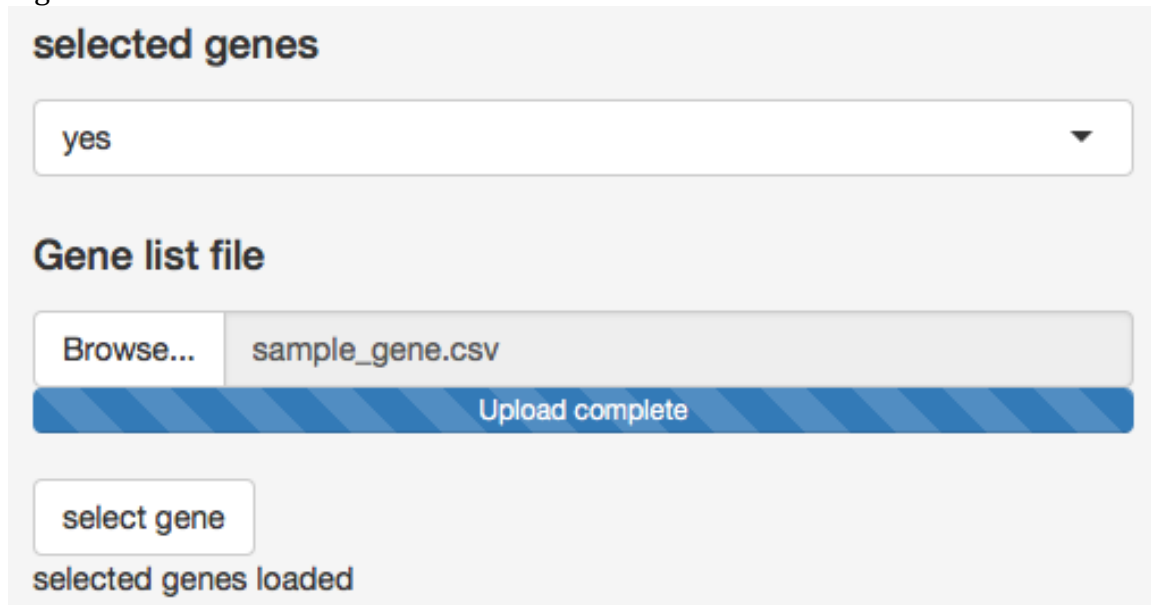
select organism

hg19 selected

Figure 2. Organism selection

Step 2 uploading gene list:

If user wish to perform analysis only on specific genes, an optional gene in csv format which the first column should be official gene symbols. After selecting “yes” on “selected genes” dropdown menu, user can upload the csv file and click the “select gene” button. Wait for “selected gene loaded” before next step as seen in Figure 3.



**selected genes**

yes ▼

**Gene list file**

Browse... sample\_gene.csv

Upload complete

select gene

selected genes loaded

Figure 3. Uploading gene list

Step 4 Peak file(s) upload and analysis selection:

OPRIA allows users to load up to two txt format peak files (Figure 4a), which the first four columns should be “chr”, “start”, “end” and “summit” information. Once the peak files are uploaded, analysis will be performed.

The default analysis type is “Last\_Exon\_Intron”, which computes peaks’ distance to the last exon and intron junction of each annotated gene. User can choose “Stop\_Codon” to compute peaks’ distance to the stop codons of annotated genes or “Normalized\_Transcripts” to show peaks’ normalized position on transcripts.

The default plot type is density plot, which the vertical axis displays relative density of the peaks (Figure 4c). User can also select histogram, which absolute peak count will be displayed on vertical axis (see Figure 4c)

The screenshot displays the OPRIA web interface with the following sections:

- File input case**: A file upload area showing a button labeled "Browse...", a text field containing "HPLAL.txt", and a blue progress bar at the bottom with the text "Upload complete".
- File input control(optional)**: A second file upload area showing a button labeled "Browse...", a text field containing "HPTA2.txt", and a blue progress bar at the bottom with the text "Upload complete".
- Analysis selection**: A section containing two dropdown menus:
  - Plot type**: A dropdown menu with "density" selected and a downward arrow on the right.
  - Choose an analysis method**: A dropdown menu with "Last\_Exon\_Intron" selected and a downward arrow on the right.

Figure 4a. Peak file(s) upload.

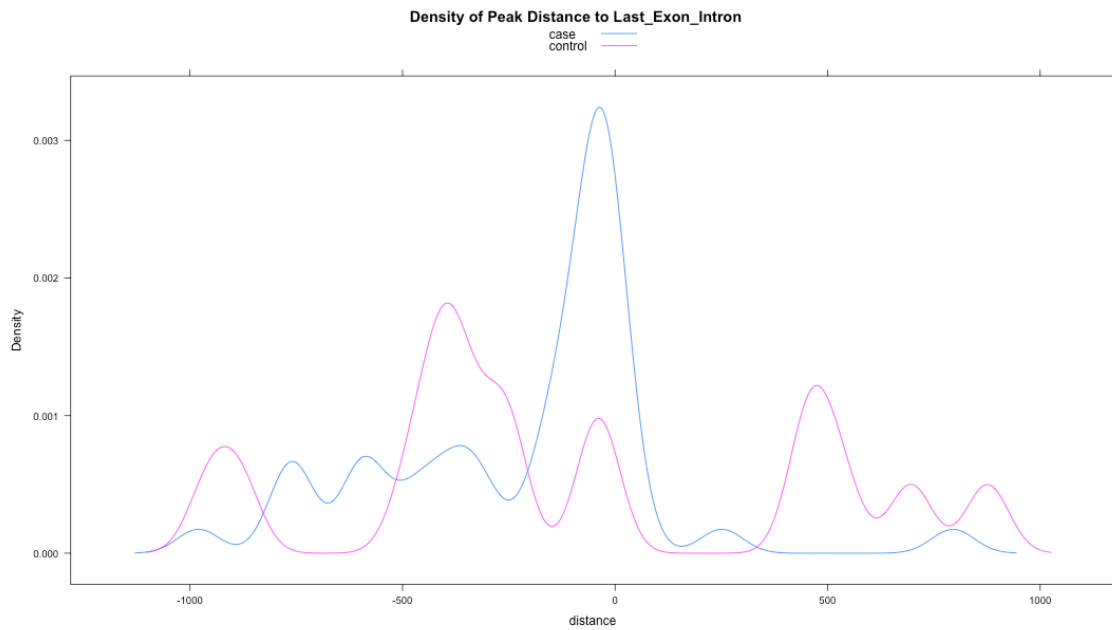


Figure 4b. Density plot of peaks

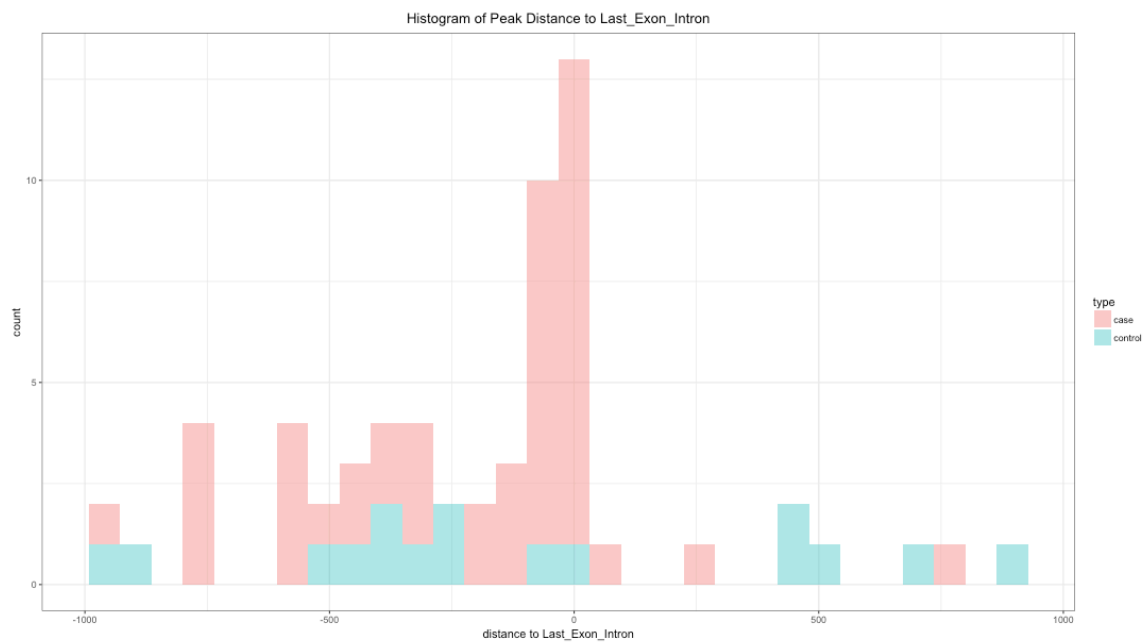


Figure 4c. Histogram of peaks