WebMeta, a web-based platform for the annotation and visualization of mRNA modifications

User Interface:
Figure 1a shows the interface for WebMeta, 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 WebMeta to perform analysis. Sample dataset can be downloaded in the links provided as seen in Figure 1b.

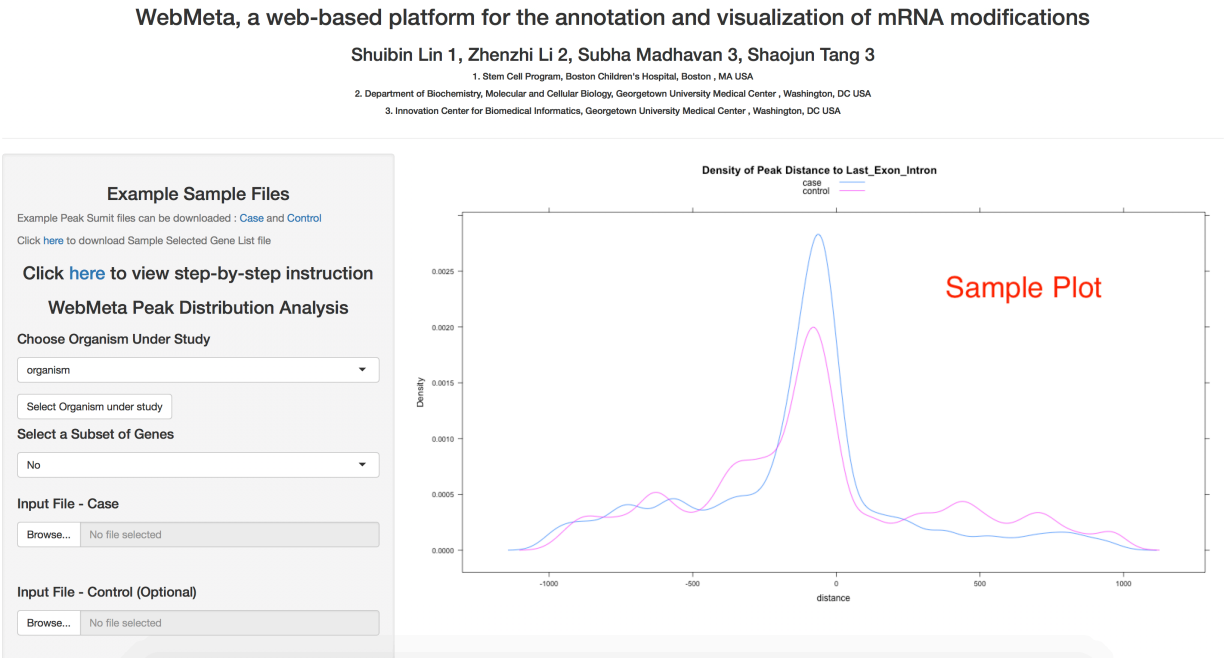

Figure 1a. Screenshot of WebMeta User Interface

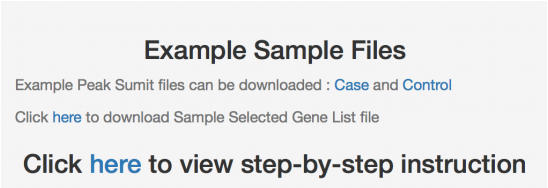

Figure 1b. Sample data download link

Step 1 organism selection:
The first step of the analysis is to select organism of experimentation. WebMeta 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 WebMeta to load necessary genome annotation reference file.

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.

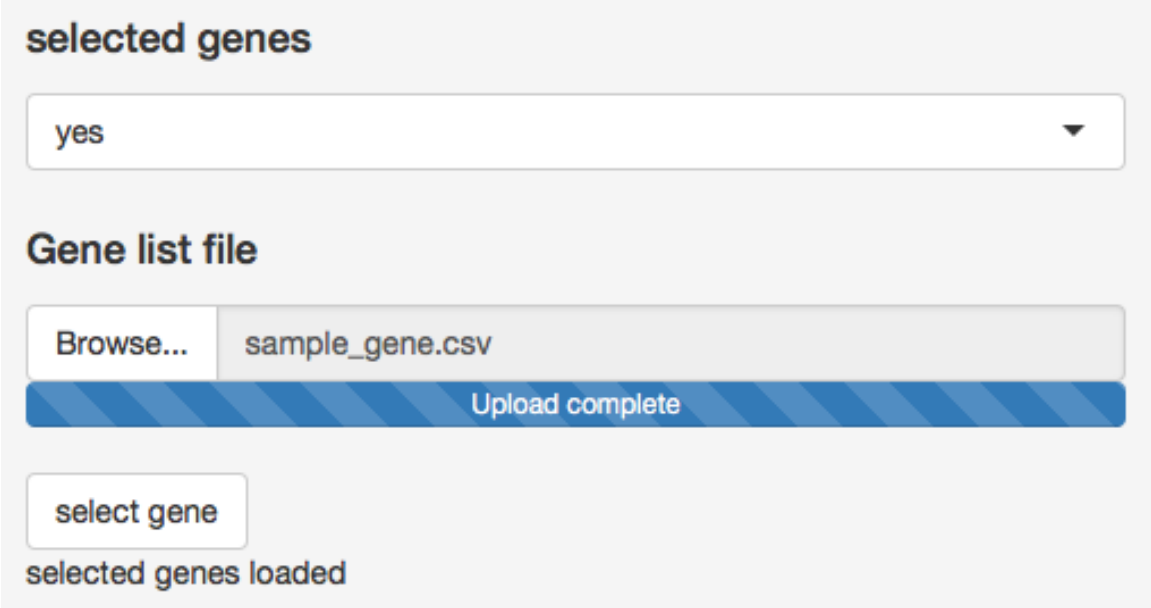

Figure 3. Uploading gene list

Step 4 Peak file(s) upload and analysis selection:
WebMeta 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, user selected analysis (see Analysis Methods, Figure 4a) 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)

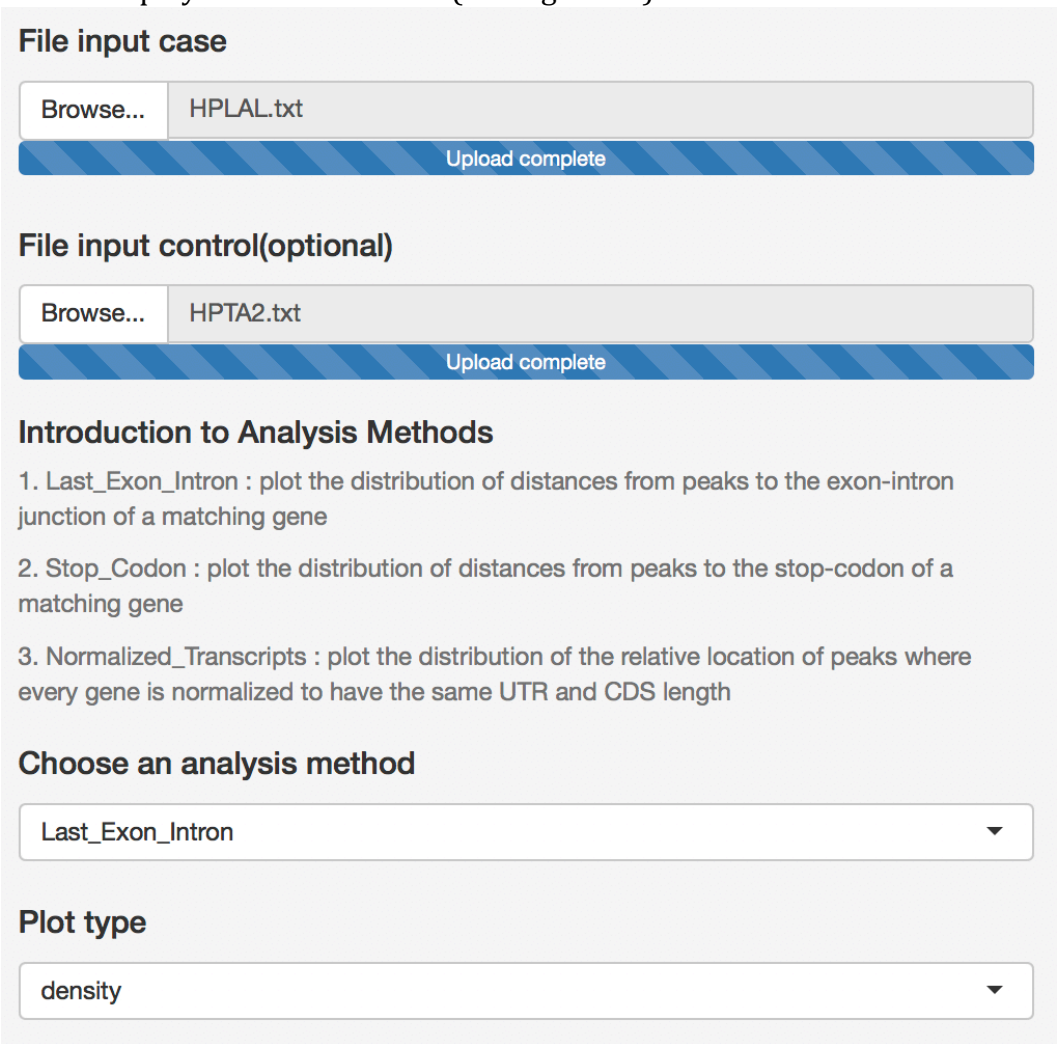

Figure 4a. Peak file(s) upload.

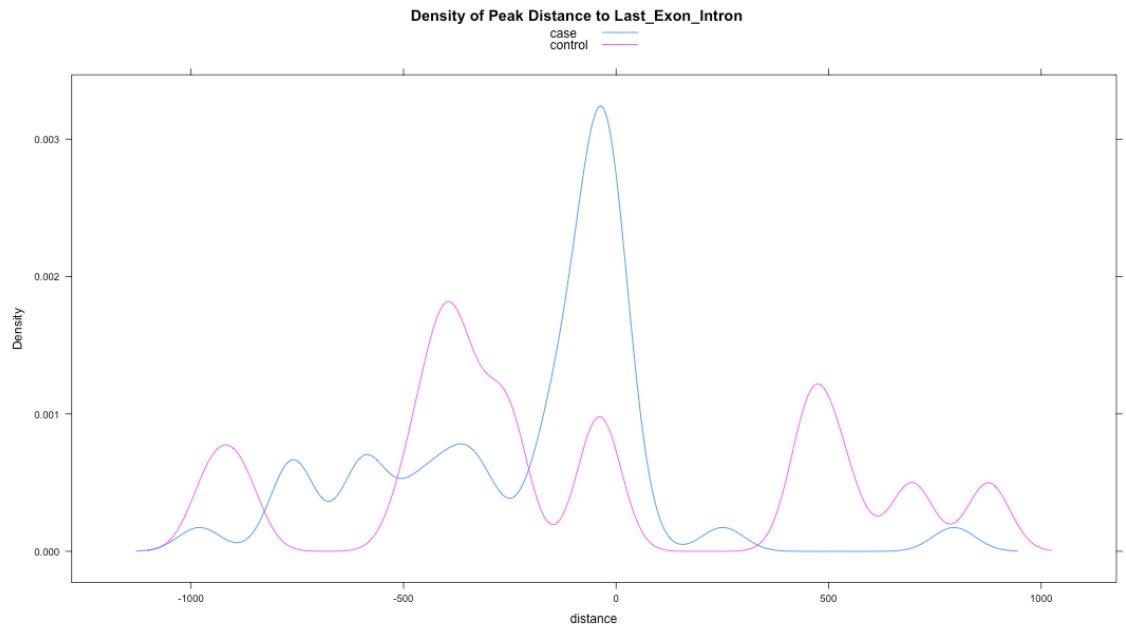

Figure 4b. Density plot of peaks

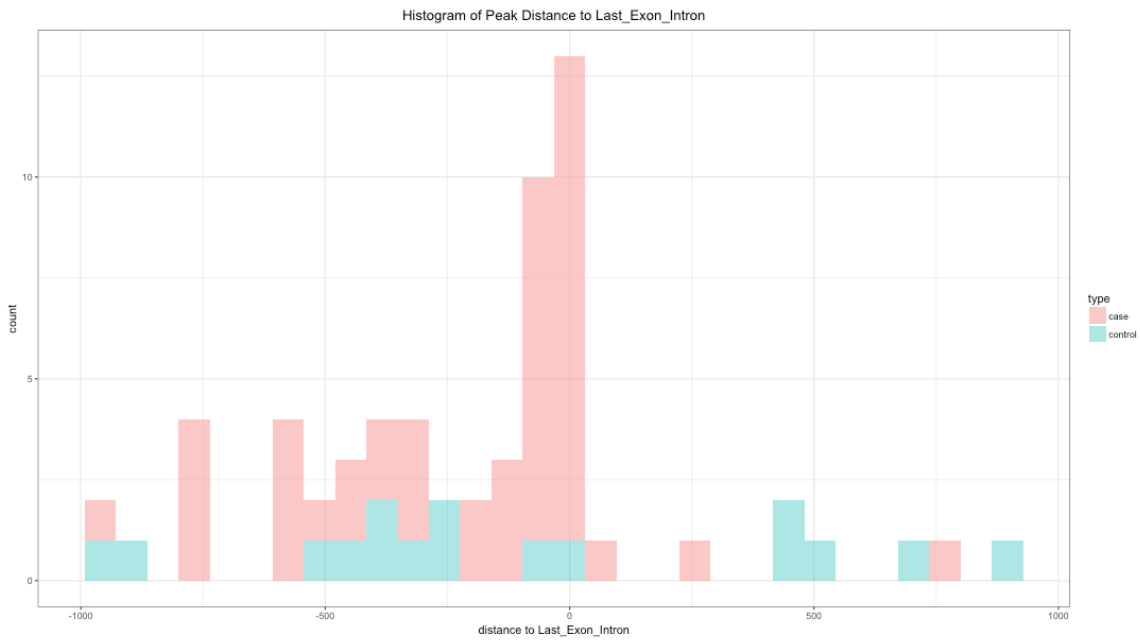

Figure 4c. Histogram of peaks