

1. Bedpe format for visualizing arcs from HiC,HiChIP, ChIA-PET etc data types.

chrom1	start1	end1	chrom2	start2	end2	name	score	FDR	strand1	strand2	samplenumber
chr6	129208449	129204092	chr6	129231289	129240143	NA	210	0.00	.	.	1
chr2	58151949	58157732	chr2	58158964	58165188	NA	150	0.00	.	.	1
chr7	28371327	28377361	chr7	28377868	28386880	NA	135	0.00	.	.	1
chr7	83649999	83657438	chr7	83658517	83662316	NA	132	0.00	.	.	1
chr9	32707989	32712792	chr9	32714366	32728804	NA	126	0.00	.	.	1
chr2	127310094	127315729	chr2	127316794	127324916	NA	121	0.00	.	.	1

Required columns and heading titles

2. Bedgraph format for visualizing bp resolution signal from ATAC-seq, ChIP-seq, RNA-seq, or other sequencing data types. Values must be non-negative values.

chrom	start	stop	value
chr1	3010964	3010966	4
chr1	3012331	3012337	4
chr1	3015732	3015736	4
chr1	3015736	3015738	5
chr1	3015738	3015739	6
chr1	3015739	3015745	5

Required columns and heading titles

3. Bed format for visualizing genomic segments from ATAC-seq, ChIP-seq, or other sequencing data types.

chrom	start	stop
chr2	98666982	98667306
chr17	39847589	39847913
chr3	5860289	5860613
chr12	3109799	3110123
chr9	123461860	123462184
chr9	3000396	3000720

Required columns and heading titles

Genomic Data Browser

Upload File Plots

Step 1: Select the types of data you want to analyze, then browse for your files

Select Data Types

HiC

Step 2: After browsing for your files, click the button to process the data for plotting

Process Data

Step 3: Make sure your data looks correctly formatted in the tabs below. Then, click on the Plots tab to visualize your data

Go to Plots

HiC

Choose a TXT, CSV, or BG File

Browse... No file selected

Header

Separator

- Comma
- Semicolon
- Tab

Quote

- None
- Double Quote
- Single Quote

Display

- Head
- Tail

1

Upload File Plots

Step 1: Select the types of data you want to analyze, then browse for your files

Select Data Types

HiC

ATAC

ChIP

mRNA

HIC

Data upload selection options available for visualization. Accommodates bed, bedpe, and bedgraph formats for data types like HiC, ChIP-seq, ATAC-seq and RNA-seq. Upload data types from local directory.

2

Step 1: Select the types of data you want to analyze, then browse for your files

Select Data Types

HiC

HiC

Choose a TXT, CSV, or BG File

Browse... HIC_test.txt

Upload complete

Header

Separator

- Comma
- Semicolon
- Tab

Successful uploading of HiC (bedpe format) data.

3

Step 1: Select the types of data you want to analyze, then browse for your files

Select Data Types

HiC

HiC

Choose a TXT, CSV, or BG File

Browse... HIC_test.txt

Upload complete

Header

Separator

- Comma
- Semicolon
- Tab

Step 2: After browsing for your files, click the button to process the data for plotting

Process Data

After browsing for your files, click to process the data for plotting

Step 3: Make sure your data looks correctly formatted in the tabs below. Then, click on the Plots tab to visualize your data

Go to Plots

chrom1	start1	end1	chrom2	start2	end2	name	score	FDR	strand1	strand2	samplenumber
chr6	129208442	129220492	chr6	129231288	129240143	NA	210	0.00	.	.	1
chr2	58151949	58157732	chr2	58158964	58165186	NA	150	0.00	.	.	1
chr7	28371327	28377361	chr7	28377868	28386880	NA	135	0.00	.	.	1
chr7	83649993	83657438	chr7	83658517	83662316	NA	132	0.00	.	.	1
chr9	32707989	32712792	chr9	32714366	32728804	NA	126	0.00	.	.	1
chr2	127310094	127315729	chr2	127316794	127324916	NA	121	0.00	.	.	1

Pressing the **Process Data** button allows for visualization of data uploaded. Please ensure that headings follow our bedpe required formatting in order to proceed with plotting.

4

Step 1: Select the types of data you want to analyze, then browse for your files

Select Data Types: HIC

Step 2: After browsing for your files, click the button to process the data for plotting

Process Data

Step 3: Make sure your data looks correctly formatted in the tabs below. Then, click on the Plots tab to visualize your data

Go to Plots Click to visualize your data

Select Go to Plots tab to view data

chrom1	start1	end1	chrom2	start2	end2	name	score	FDR	strand1	strand2	samplenumber
chr6	129208442	1292020492	chr6	129231286	129240143	NA	210	0.00	.	.	1
chr2	58151949	58157732	chr2	58158964	58165186	NA	150	0.00	.	.	1
chr7	28371327	28377361	chr7	28377668	28386860	NA	135	0.00	.	.	1
chr7	8349993	83657438	chr7	83658517	83662316	NA	132	0.00	.	.	1
chr9	32707989	32712792	chr9	32714366	32728804	NA	126	0.00	.	.	1
chr2	127310094	127315729	chr2	127316794	127324916	NA	121	0.00	.	.	1

5 Navigating the Plot tab

Number of samples to view.

This is indicated by
samplenumber column in
bedpe file. Supports up to 10.

Labeling samples

HIC

Choose a TXT, CSV, or BG File

Browse... HIC-test.txt Upload complete

Header
Separator
Comma
Semicolon

Navigate loci by gene selection.

Type gene name:

V1
4933401J01Rik chr1:3073252-3074322
Gm26206 chr1:3102015-3102125
Xkr4 chr1:3214461-3671498
Gm37180 chr1:3365730-3368549
Gm37363 chr1:3375555-3377788

Search by genomic coordinate

Genomic interval to left of gene (bases): 50000
Genomic interval to right of gene (bases): 50000

Expand genomic window (bp)

a Upload File Plots

Number of Samples in HIC Dataset: 1

b HIC Sample 1: Sample ID: A

c Type gene name: V1

d Genomic interval to left of gene (bases): 50000
Genomic interval to right of gene (bases): 50000

e

f Download Plot
g Download as PNG

Select sample number, and either gene or gene coordinates and press Submit Parameters

6

Upload File Plots

Number of Samples in HIC Dataset: 2

HIC Sample 1: A

HIC Sample 2: B

Type gene name: Lef1 chr3:13110470-131224356

Genomic interval to left of gene (bases): 50000

Genomic interval to right of gene (bases): 50000

Download PNG of plots

Download as PNG

Gene models

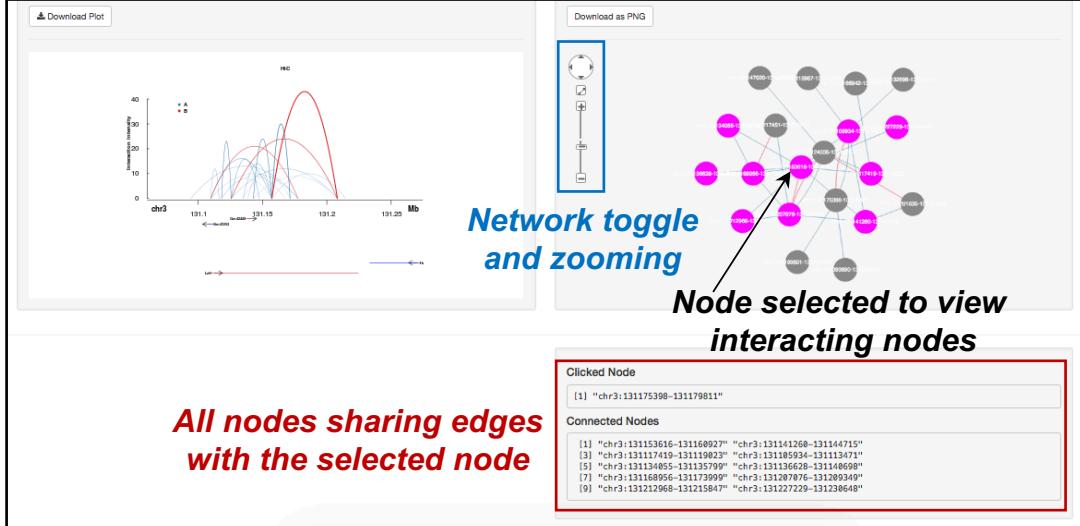
Arcs/Loops

Cytoscape network from Arc data

For this example two samples are plotted A (Blue) and B in (Red). The gene *Lef1* was selected for this example.

7

DNA Rchitect



1 Genomic Data Browser

Upload File

Step 1: Select the types of data you want to analyze, then browse for your files
Select Data Types

Select ATAC data format

Choose a TXT, CSV, or BG File
 No file selected

Header
Separator
 Comma
 Semicolon
 Tab
Quote
 None
 Double Quote
 Single Quote

Step 2: After browsing for your files, click the button to process the data for plotting

Step 3: Make sure your data looks correctly formatted in the tabs below. Then, click on the Plots tab to visualize your data

Data type is ATAC-seq with options for Bed or Bedgraph format.

2

Step 1: Select the types of data you want to analyze, then browse for your files
Select Data Types

Select ATAC data format

ATAC

Choose a TXT, CSV, or BG File
 ATAC.bg

Header
Separator
 Comma
 Semicolon
 Tab
Quote
 None
 Double Quote
 Single Quote

Step 2: After browsing for your files, click the button to process the data for plotting

ATAC-seq bedgraph upload successful.
Process Data allows one to view data processed and ready for plotting.

3

Upload File

Number of Samples in HiC Dataset

HIC Sample 1

Type gene name:

Genomic interval to left of gene (bases)

Genomic interval to right of gene (bases)

Plot can be downloaded as a PNG

Select **sample number**, and either **gene** or **gene coordinates** and press **Submit Parameters**
For this example ATAC-seq bedgraph file is shown for the *Lef1* gene.

1

Genomic Data Browser

Upload File Plots

Step 1: Select the types of data you want to analyze, then browse for your files

Select Data Types

ChIP

Step 2: After browsing for your files, click the button to process the data for plotting

Process Data

Step 3: Make sure your data looks correctly formatted in the tabs below. Then, click on the Plots tab to visualize your data

Go to Plots

Select ChIP data format

Bed

Choose a TXT, CSV, or BG File

Browse... No file selected

Data type selected is ChIP-seq in Bed format

2

Step 1: Select the types of data you want to analyze, then browse for your files

Select Data Types

ChIP

Step 2: After browsing for your files, click the button to process the data for plotting

Process Data

Step 3: Make sure your data looks correctly formatted in the tabs below. Then, click on the Plots tab to visualize your data

Go to Plots

Select ChIP data format

Bed

Choose a TXT, CSV, or BG File

Browse... Peaks.txt Upload complete

Header
Separator
Comma
Semicolon
Tab

ChIP

chrom	start	stop
chr2	98666982	98667306
chr17	39847589	39847913
chr3	5860289	5860613
chr12	3109799	3110123
chr9	123461860	123462184
chr9	3000396	3000720

ChIP-seq bed upload successful.

Process Data allows one to view data processed and ready for plotting.

3

Upload File Plots

Number of Samples in HIC Dataset

1

HIC Sample 1

A

Type gene name:

Lef1 chr3:131110470-131224356

Genomic interval to left of gene (bases)

50000

Genomic interval to right of gene (bases)

50000

Search by Coordinates

Submit Parameters

Plot can be downloaded as a PNG

Download Plot

ChIP-seq Data

Pressing the **Process Data** button allows for visualization of data uploaded. Please ensure that headings follow our **bed** required formatting in order to proceed with plotting.

1 Genomic Data Browser

Upload File Plots

Step 1: Select the types of data you want to analyze, then browse for your files
Select Data Types
HIC ATAC ChIP

Step 2: After browsing for your files, click the button to process the data for plotting
Process Data

Step 3: Make sure your data looks correctly formatted in the tabs below. Then, click on the Plots tab to visualize your data
Go to Plots

Select ATAC data format: Bedgraph
Select ChIP data format: Bed

Uploading all data types

HIC ATAC ChIP

Choose a TXT, CSV, or BG File
Browse... No file selected

chrom1	start1	end1	chrom2	start2	end2	name	score	FDR	strand1	strand2	samplenumber
chr6	129208442	1292020492	chr6	129231288	129240143	NA	210	0.00	.	.	1
chr2	58151949	58157732	chr2	58158964	58165186	NA	150	0.00	.	.	1
chr7	28371327	28377361	chr7	28377668	28386880	NA	135	0.00	.	.	1
chr7	83649993	83657438	chr7	8365817	83662316	NA	132	0.00	.	.	1
chr9	32707989	32712792	chr9	32714366	32728804	NA	126	0.00	.	.	1
chr2	127310094	127315729	chr2	127316794	127324916	NA	121	0.00	.	.	1

2

Upload File Plots

Number of Samples in HiC Dataset: 2
HiC Sample 1: A
HiC Sample 2: B

Type gene name: Left chr3:131110470-131224356
Genomic Interval to left of gene (bases): 50000
Genomic Interval to right of gene (bases): 50000

Plotting all data types for same gene locus

Download Plot

Download as PNG

Download Plot

Download Plot