

Header titles should be labeled as illustrated in our examples below (ie chrom1, not chromosome1). Additional headers will be ignored by DNA Rchitect.

File format	Required headers
bed	chrom, start, stop
bedpe	chrom1, start1, end1, chrom2, start2, end2, score, samplenum
bedgraph	chrom, start, stop, value

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

chrom1	start1	end1	chrom2	start2	end2	name	score	FDR	strand1	strand2	samplenum
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

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

Suggestions for visualization of HiC and other chromatin conformation data using DNA Rchitect:

- Pre-filtering of highly reproducible or significant interactions may be required for proper visualization using DNA Rchitect.

- Large anchors or overlapping anchors may need to be adjusted or merged (can use GenomicRanges R package for this) prior to loading in DNA Rchitect to ensure proper network visualization and interpretation.

DNA Rchitect

Upload File Plots

Step 1: Select the types of data you want to analyze
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

Genomes supported by web version. Select human Hg19 for tutorial.

Genome
mouse_mm9
mouse_mm10
human_Hg19
human_Hg38
drosophila_melanogaster_6

Genome
mouse_mm9

Interactive Tutorial Reload App

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

Load Sample Data
Type file name
K562_NHEK_GM12878-loops
GSM1704495_GMPPro_Cap_rep1_filt5
GSM1704494_JKProCap_Rep1_Filt5

Separator
☐ Comma
☐ Semicolon
☒ Tab

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.

Publically available sample HiC and Promoter Capture HiC data

Select **K562-NHEK-GM12878** HiC data and select **Process Data** button for tutorial

HIC

Process Data

Go to Plots

HIC

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

Load Sample Data
K562_NHEK_GM12878-loops

chrom1	start1	end1	chrom2	start2	end2	score	samplenumber
chr10	100180000	100190000	chr10	100410000	100420000	39	1
chr10	101600000	101610000	chr10	101800000	101810000	93	1
chr10	102100000	102105000	chr10	102190000	102195000	59	1
chr10	102100000	102105000	chr10	102265000	102270000	40	1
chr10	102190000	102200000	chr10	102260000	102270000	90	1
chr10	102800000	102810000	chr10	102890000	102900000	78	1

Selecting **Go to Plots** allows you to visualize generate plots tab

Upload File Plots

Number of Samples in HiC Dataset
1

Search By:
☒ Coordinates
☐ Genes

HIC Sample 1
Sample ID

Select colors for bezier curves

Chr Number
chr1

Start Coordinate
60853778

End Coordinate
60948071

Submit Parameters

Select number of samples (3 for tutorial)

Select colors for 3 samples

Network Hubs Degree Distribution Groups Node Degree

Upload File

Plots

Number of Samples in HiC Dataset

3

Search By:

☐ Coordinates
 ☒ Genes

Number of samples

Sample Labeling

HiC Sample 2

NHEK

HiC Sample 3

GM12878

Select colors for bezier curves

Blue Red Gray

Type gene name: (backspace to clear)

MYC

MYCL chr1:40361098-40367928

MYCN chr2:16080686-16087129

MYCBP chr1:39328636-39347289

MYC chr8:128747680-128753674

MYCNUN chr2:16060521-16076139

Submit Parameters

Type gene name: (backspace to clear)

MYC chr8:128747680-128753674

Genomic interval to left of gene (bases)

1000000

Genomic interval to right of gene (bases)

1000000

Select the gene MYC. Set Genomic intervals left and right of gene to 1Mb (1000000) for tutorial

Network

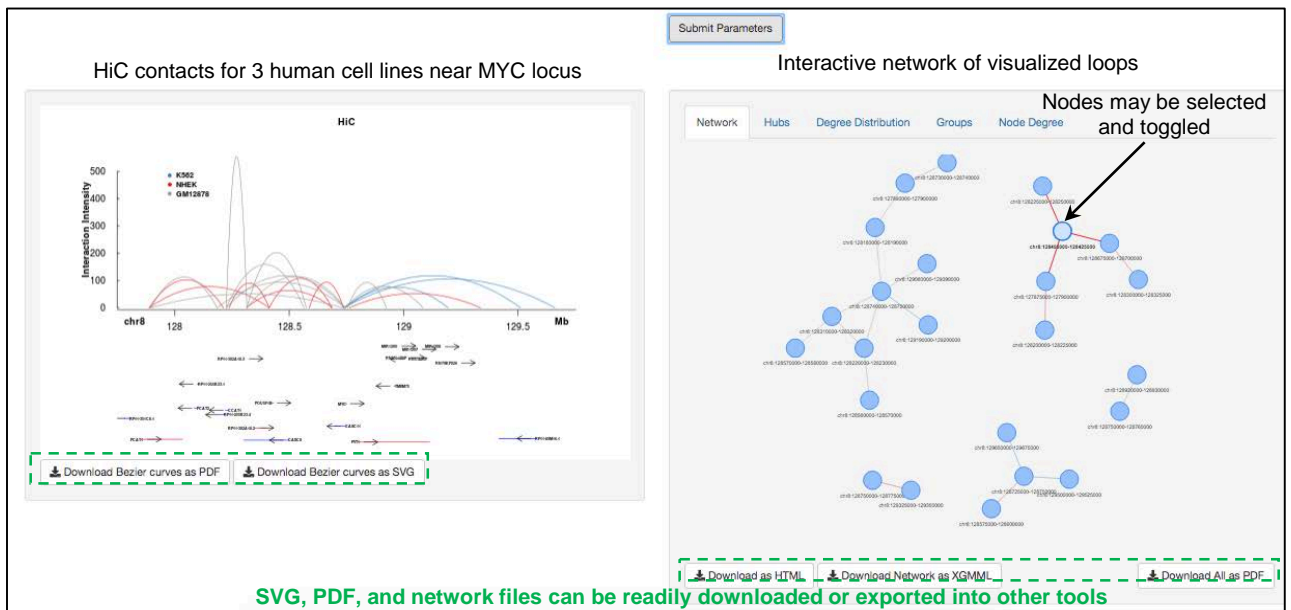
Hubs

Degree Distribution

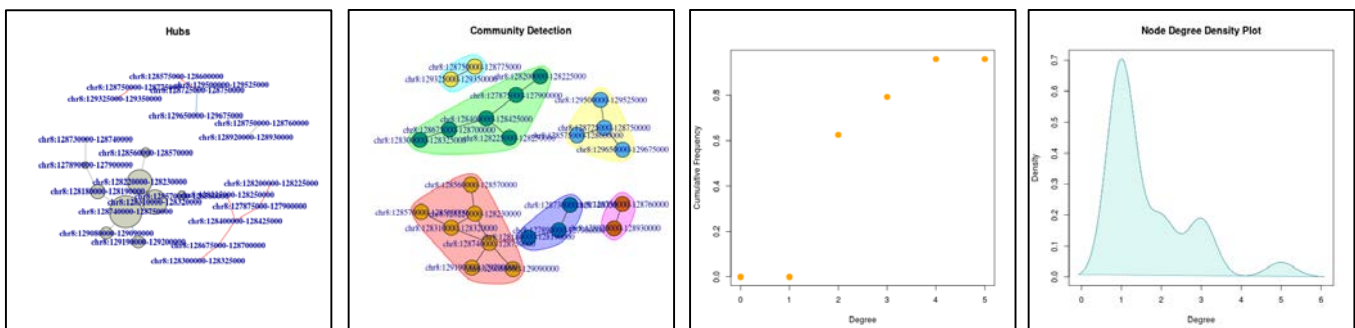
Groups

Node Degree

Selecting **Submit Parameters** allows you to visualize your data



Various **network analysis** can be readily viewed and downloaded for this genomic locus



Upload File

Plots

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

Select Data Types

ATAC

Select ATAC data format

Bed

Bed

Bedgraph

Choose a TXT, CSV, or BG File

Browse...

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

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

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

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

Select Data Types

ATAC

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

Process Data

Select ATAC data format

Bedgraph

ATAC

Choose a TXT, CSV, or BG File

Browse...

ATAC.bg

Upload complete

☒ Header

Separator

☐ Comma

☐ Semicolon

☒ Tab

Quote

☐ None

☒ Double Quote

☐ Single Quote

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

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

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

Download Plot

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.

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

ChIP

Choose a TXT, CSV, or BG File

Browse... No file selected

Data type selected is ChIP-seq in Bed format

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

ChIP

Choose a TXT, CSV, or BG File

Browse... Peaks.txt Upload complete

☒ Header

Separator

☐ Comma

☐ Semicolon

☒ Tab

chrom	start	stop
chr2	98666982	98667306
chr17	39847589	39847913
chr3	5860289	5860613
chr12	3108799	3110123
chr9	123461860	123462184
chr9	3000396	3000720

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

Upload File

Plots

Number of Samples in HiC Dataset

1

HiC Sample 1

A

Type gene name:

Let1 chr3:131110470-131224356

Genomic interval to left of gene (bases)

50000

Genomic interval to right of gene (bases)

50000

Search by Coordinates

Submit Parameters

Download Plot

Plot can be downloaded as a PNG

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.

Troubleshooting and error handling

1. Error will appear if Bedpe file format is incorrect.

Bedpe Input File Header Incorrect

The uploaded Bedpe file does not have the correct header. The required header contains: 'chrom1','start1','end1','chrom2','start2','end2','score','samplenumber'. Please see our [github](#) for details on file formats and header requirements.

The header must be exactly as specified in the documentation

Dismiss

2. Error shown of HiC plotting. This is due to the anchor plotting boundary. This can be resolved by adjusting the genomic window coordinates.

Upload File Plots

Number of Samples in HiC Dataset: 2

Search by Coordinates: ☐

HiC Sample 1: A

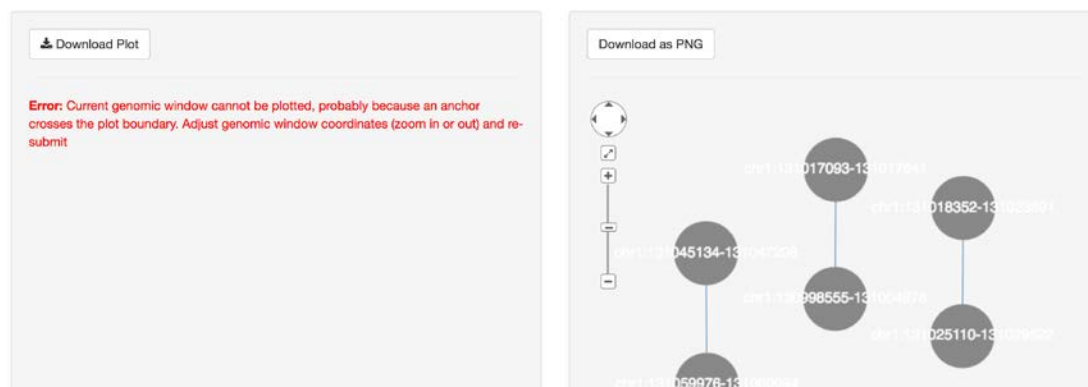
HiC Sample 2: B

Type gene name: II10 chr1:131019844-131024974

Submit Parameters

Genomic interval to left of gene (bases): 50000

Genomic interval to right of gene (bases): 50000



3. Error in cytoscape network graph. No graph is shown as this genomic window does not contain any data.

Upload File Plots

Number of Samples in HiC Dataset: 2

Search by Coordinates: ☐

HiC Sample 1: A

HiC Sample 2: B

Type gene name: II2 chr3:37120522-37125959

Submit Parameters

Genomic interval to left of gene (bases): 50000

Genomic interval to right of gene (bases): 50000

