

Package ‘epiRomics’

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Type Package

Title epigenomic analysis package built for R (epiRomics)

Version 0.1.2

Maintainer Alex M. Mawla <ammawla@ucdavis.edu>

Description A package designed to integrate various levels of epigenomic information, including, but not limited to ChIP and Histone next-generation sequencing. Regulatory network analysis can be done by using combinatorial approaches to infer regions of significance, such as enhancers. Downstream analysis can identify co-occurrence of epigenomic data located at regions of interest. Finally, this package allows for various results to be visualized. This package is currently in development. Please contact <ammawla@ucdavis.edu> for suggestions, feedback, or bug reporting.

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Encoding UTF-8

LazyData true

Imports data.table (>= 1.12-8),
GenomicRanges (>= 1.41-5),
BiocGenerics (>= 0.35-4),
ChIPseeker (>= 1.5-1),
GenomeInfoDb (>= 1.25-0),
Gviz (>= 1.33-2),
IRanges (>= 2.23-10),
annotatr (>= 1.15-2),
party (>= 1.3-3),
methods (>= 4.0-2),
AnnotationDbi (>= 1.50-3),
GenomicFeatures (>= 1.40-1),
rtracklayer (>= 1.48-0),
plyr (>= 1.8.6),
org.Hs.eg.db (>= 3.13.0),
TxDb.Hsapiens.UCSC.hg38.knownGene (>= 3.13.0)

RoxygenNote 7.1.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

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epiRomicsS4-class	<i>An S4 class to manage epiRomics databases and downstream results</i>
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Description

An S4 class to manage epiRomics databases and downstream results

Slots

- annotations GRanges
- meta data.frame
- txdb txdb string name
- organism org.db string name
- genome genome name, e.g. 'mm10' or 'hg38'

epiRomics_build_dB	<i>Build epiRomics database</i>
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Description

Build epiRomics database

Usage

```
epiRomics_build_dB(  
  epiRomics_db_file,  
  txdb_organism,  
  epiRomics_genome,  
  epiRomics_organism  
)
```

Arguments

`epiRomics_db_file`
 character string of path to properly formatted csv file containing epigenetic data.
 [See vignette for more details]

`txdb_organism` a character string containing the TxDB associated with your data.

`epiRomics_genome`
 a character string containing the genome associated with your data. e.g. "mm10"
 or "hg19".

`epiRomics_organism`
 a character string containing the org.db associated with your data.

Value

Variable of class `epiRomics` for further downstream analysis

`epiRomics_build_dB_2` *Build epiRomics database*

Description

Build epiRomics database

Usage

```
epiRomics_build_dB_2(  
  epiRomics_db_file,  
  txdb_organism,  
  epiRomics_genome,  
  epiRomics_organism  
)
```

Arguments

`epiRomics_db_file`
 character string of path to properly formatted csv file containing epigenetic data.
 [See vignette for more details]

`txdb_organism` a character string containing the TxDB associated with your data.

`epiRomics_genome`
 a character string containing the genome associated with your data. e.g. "mm10"
 or "hg38".

`epiRomics_organism`
 a character string containing the org.db associated with your data.

Value

Variable of class `epiRomics` for further downstream analysis

```
epiRomics_chromatin_tracks
```

Visualizes chromatin availability

Description

Visualizes chromatin availability

Usage

```
epiRomics_chromatin_tracks(
  epiRomics_gene_name,
  epiRomics_dB,
  epiRomics_track_connection
)
```

Arguments

```
epiRomics_gene_name      character of name of gene to visualize
epiRomics_dB             epiRomics class database containing all data initially loaded
epiRomics_track_connection data frame containing bigwig track locations and their names
```

Value

GViz plot

```
epiRomics_enhanceosome
```

Identifies putative enhanceosome regions by cross-referencing candidate enhancer regions against co-TF enrichment

Description

Identifies putative enhanceosome regions by cross-referencing candidate enhancer regions against co-TF enrichment

Usage

```
epiRomics_enhanceosome(epiRomics_putative_enhancers, epiRomics_dB)
```

Arguments

```
epiRomics_putative_enhancers epiRomics class database containing putative enhancer calls
epiRomics_dB                 epiRomics class database containing all data initially loaded
```

Value

Variable of class epiRomics further exploring candidate enhanceosome regions using co-ChIP hits

epiRomics_enhancers *Identifies putative enhancer regions utilizing select histone marks*

Description

Identifies putative enhancer regions utilizing select histone marks

Usage

```
epiRomics_enhancers(  
  epiRomics_dB,  
  epiRomics_histone_mark_1 = "h3k4me1",  
  epiRomics_histone_mark_2 = "h3k27ac"  
)
```

Arguments

epiRomics_dB epiRomics class database containing all data initially loaded

epiRomics_histone_mark_1
 name of first histone mark, must match name in epiROMics_dB@meta, default set to h3k4me1

epiRomics_histone_mark_2
 name of second histone mark, must match name in epiROMics_dB@meta default set to h3k27ac

Value

Variable of class epiRomics further exploring candidate enhancer regions identified after histone integration

epiRomics_enhancers_filter
 Filters putative enhancers called by epiRomics_enhancers by crossing against curated FANTOM data

Description

Filters putative enhancers called by epiRomics_enhancers by crossing against curated FANTOM data

Usage

```
epiRomics_enhancers_filter(  
  epiRomics_putative_enhancers,  
  epiRomics_dB,  
  epiRomics_type = "mm10_custom_fantom"  
)
```

Arguments

epiRomics_putative_enhancers
 epiRomics class database containing putative enhancer calls

epiRomics_dB epiRomics class database containing all data initially loaded

epiRomics_type epiRomics reference containing database to validate putative enhancers against

Value

Variable of class epiRomics with filtered candidate enhancer regions

epiRomics_enhancer_predictor_test

Interrogates various histone marks against a curated database to determine which are most informative

Description

Interrogates various histone marks against a curated database to determine which are most informative

Usage

```
epiRomics_enhancer_predictor_test(
  epiRomics_dB,
  epiRomics_histone = "h3k4me1",
  epiRomics_curated_database = "fantom"
)
```

Arguments

epiRomics_dB epiRomics class database containing all data initially loaded

epiRomics_histone
 name or vector of histone mark(s), must match name in epiROmics_dB@meta,
 default set to h3k4me1

epiRomics_curated_database
 database to test histone marks against, must match name in epiROmics_dB@meta
 default set to fantom

Value

Variable of class dataframe further exploring top histone marks that may determine enhancer regions

epiRomics_predictors	<i>Predicts TF behavior in association with enhanceosome presence in accordance with functional annotation</i>
----------------------	--

Description

Predicts TF behavior in association with enhanceosome presence in accordance with functional annotation

Usage

```
epiRomics_predictors(epiRomics_putative_enhanceosome)
```

Arguments

epiRomics_putative_enhanceosome
epiRomics class database containing putative enhanceosome calls

Value

Returned decision tree available for plotting

epiRomics_regions_of_interest	<i>Evaluates whether regions of interest derived from external experiments, such as ATAC-Seq, correspond with enhanceosome regions</i>
-------------------------------	--

Description

Evaluates whether regions of interest derived from external experiments, such as ATAC-Seq, correspond with enhanceosome regions

Usage

```
epiRomics_regions_of_interest(  
  epiRomics_putative_enhanceosome,  
  epiRomics_test_regions  
)
```

Arguments

epiRomics_putative_enhanceosome
epiRomics class database containing putative enhanceosome calls
epiRomics_test_regions
GRanges containing regions of interest

Value

Variable of class epiRomics with enhanceosome regions overlapping with regions of interest

```
epiRomics_region_tracks
```

Visualizes chromatin availability at custom regions

Description

Visualizes chromatin availability at custom regions

Usage

```
epiRomics_region_tracks(  
  epiRomics_region,  
  epiRomics_dB,  
  epiRomics_track_connection  
)
```

Arguments

```
epiRomics_region      GRanges of region to visualize  
  
epiRomics_dB          epiRomics class database containing all data initially loaded  
epiRomics_track_connection  data frame containing bigwig track locations and their names
```

Value

GViz plot

```
epiRomics_track_layer  Visualizes data from epiRomics results
```

Description

Visualizes data from epiRomics results

Usage

```
epiRomics_track_layer(  
  epiRomics_putative_enhanceosome,  
  epiRomics_index,  
  epiRomics_dB,  
  epiRomics_track_connection,  
  epiRomics_keep_epitracks = TRUE  
)
```


Arguments

epiRomics_putative_enhanceosome
epiRomics class database containing putative enhanceosome calls

epiRomics_index
numeric of row value from epiRomics_putative_enhanceosome to visualize

epiRomics_dB
epiRomics class database containing all data initially loaded

epiRomics_track_connection
data frame containing bigwig track locations and their names

epiRomics_keep_epitracks
logical indicating whether to show enhancer and chip tracks, default is TRUE

Value

GViz plot

epiRomics_track_layer_human
Visualizes data from epiRomics results

Description

Visualizes data from epiRomics results

Usage

```
epiRomics_track_layer_human(  
  epiRomics_putative_enhanceosome,  
  epiRomics_index,  
  epiRomics_dB,  
  epiRomics_track_connection,  
  epiRomics_keep_epitracks = TRUE  
)
```

Arguments

epiRomics_putative_enhanceosome
epiRomics class database containing putative enhanceosome calls

epiRomics_index
numeric of row value from epiRomics_putative_enhanceosome to visualize

epiRomics_dB
epiRomics class database containing all data initially loaded

epiRomics_track_connection
data frame containing bigwig track locations and their names

epiRomics_keep_epitracks
logical indicating whether to show enhancer and chip tracks, default is TRUE

Value

GViz plot

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