Package 'epiRomics'

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Type Package

Title Epigenomic Analysis Package Built for R (epiRomics)

Version 0.1.3

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 combinatory approaches to infer regions of significance, such as
enhancers. Downstream analysis can identify co-occurance 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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Depends R (>= 4.0.0)

biocViews

Imports AnnotationDbi (>= 1.54.1),
annotatr (>= 1.18.1),
BiocGenerics (>= 0.38.0),
BiocManager (>= 1.30.16),
ChIPseeker (>= 1.28.3),
data.table (>= 1.12.8),
GenomeInfoDb (>= 1.28.1),
GenomicFeatures (>= 1.44.1),
GenomicRanges (>= 1.44.0),
Gviz (>= 1.36.2),
igraph (>= 1.2.6),
IRanges (>= 2.26.0),
methods (>= 4.0.2),
party (>= 1.3.3),
plyr (>= 1.8.6),
rtracklayer (>= 1.52.1),
utils

Suggests covr,
org.Hs.eg.db (>= 3.13.0),
TxDb.Hsapiens.UCSC.hg38.knownGene (>= 3.13.0),
knitr,

> testthat (>= 3.0.0),
> rmarkdown,
> enrichplot,
> pkgdown

VignetteBuilder knitr

Remotes GuangchuangYu/enrichplot,
GuangchuangYu/ChipSeeker

Config/testthat/edition 3

ByteCompile true

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

R topics documented:

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epiRomicsS4-class *An S4 class to manage epiRomics databases and downstream results*

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   *Build epiRomics database*

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

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

---

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

Index