Package ‘epivizrStandalone’

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Title  Run Epiviz Interactive Genomic Data Visualization App within R

Version  1.4.0

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Description  This package imports the epiviz visualization JavaScript app for genomic data interactive visualization. The ‘epivizrServer’ package is used to provide a web server running completely within R. This standalone version allows to browse arbitrary genomes through genome annotations provided by Bioconductor packages.

Depends  R (>= 3.2.3), epivizr (>= 2.3.6), methods

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LazyData  true

Imports  git2r, epivizrServer, GenomeInfoDb, BiocGenerics, GenomicFeatures, S4Vectors

Suggests  testthat, knitr, rmarkdown, OrganismDbi (>= 1.13.9), Mus.musculus, Biobase, BiocStyle

RoxygenNote  6.0.1

VignetteBuilder  knitr

biocViews  Visualization, Infrastructure, GUI

NeedsCompilation  no

R topics documented:

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Description

The epiviz app run by function `startStandalone` in this package is cloned as a git repository. This function initializes the settings specifying which git repository is used. It can be either a github repository (the usual case), or local repository containing the epiviz JS app (used for testing and development).

Usage

```r
setStandalone(url = "https://github.com/epiviz/epiviz.git", branch = "min", local_path = NULL, non_interactive = FALSE)
```

Arguments

- `url` (character) github url to use. defaults to ("https://github.com/epiviz/epiviz.git").
- `branch` (character) branch on the github repository. defaults to (master).
- `local_path` (character) if you already have a local instance of epiviz and would like to run standalone use this.
- `non_interactive` (logical) don’t download repo, used for testing purposes.

Value

path to the epiviz app git repository

Examples

```r
# argument non_interactive here to avoid downloading when testing
# package. Remove non_interactive argument when you try it out.
setStandalone(url="https://github.com/epiviz/epiviz.git", branch="master", non_interactive=TRUE)
```

Description

Uses the local repository of epiviz JS app to start a standalone epivizr session through the `startEpiviz` function. The epiviz app requires a list of sequence names and lengths (e.g., chromosome names and lengths) to setup genome browsing. These can be passed in the seqinfo argument or derived from the gene_track argument. The gene_track argument can be used to pass a genome annotation and add a gene track to the epiviz browser. See package vignette for further detail.
Usage

```r
startStandalone(gene_track = NULL, seqinfo = NULL, keep_seqlevels = NULL,
    chr = NULL, start = NULL, end = NULL, non_interactive = FALSE,
    register_function = epiviz:::.register_all_the_epiviz_things,
    use_viewer_option = FALSE, host = "127.0.0.1", ...)
```

Arguments

- `gene_track` (OrganismDb): An object of type `OrganismDb` or `TxDb`
- `seqinfo` (Seqinfo): An object of type `Seqinfo` from which sequence names and lengths are obtained
- `keep_seqlevels` (character): Vector of sequence names to include in the standalone app
- `chr` (character): Chromosome to browse to on app startup.
- `start` (integer): Start location to browse to on app startup.
- `end` (integer): End location to browse to on app startup.
- `non_interactive` (logical): Run server in non-interactive mode. Used for testing and development.
- `register_function` (function): Function used to initialize actions in epiviz app. Used for testing and development.
- `use_viewer_option` (logical): Run application in viewer defined by `getOption("viewer")`. This allows standalone app to run in RStudio's viewer (FALSE by default)
- `host` (character): Host address for application (127.0.0.1 by default)
- `...` Additional arguments passed to `startEpiviz`.

Value

An object of class `EpivizApp`

Examples

```r
# see package vignette for example usage
seqinfo <- GenomeInfoDb::Seqinfo(c("chr1","chr2"), c(10,20))
app <- startStandalone(seqinfo=seqinfo, non_interactive=TRUE)
app$stop_app()
```

Description

Uses the local installation of the epiviz desktop app to start a standalone epiviz session through the `startEpiviz` function. The epiviz app requires a list of sequence names and lengths (e.g., chromosome names and lengths) to setup genome browsing. These can be passed in the `seqinfo` argument or derived from the `gene_track` argument. The `gene_track` argument can be used to pass a genome annotation and add a gene track to the epiviz browser. See package vignette for further detail.
Usage

```r
startStandaloneApp(gene_track = NULL, seqinfo = NULL,
                 keep_seqlevels = NULL, chr = NULL, start = NULL, end = NULL,
                 non_interactive = FALSE,
                 register_function = epivizr:::.register_all_the_epiviz_things,
                 host = "127.0.0.1", ...)
```

Arguments

- `gene_track` (OrganismDb) an object of type `OrganismDb` or `TxDb`
- `seqinfo` (Seqinfo) an object of type `Seqinfo` from which sequence names and lengths are obtained
- `keep_seqlevels` (character) vector of sequence names to include in the standalone app
- `chr` (character) chromosome to browse to on app startup.
- `start` (integer) start location to browse to on app startup.
- `end` (integer) end location to browse to on app startup.
- `non_interactive` (logical) run server in non-interactive mode. Used for testing and development.
- `register_function` (function) function used to initialize actions in epiviz app. Used for testing and development.
- `host` (character) host address for application (127.0.0.1 by default)
- `...` additional arguments passed to `startEpiviz`.

Value

An object of class `EpivizApp`

Examples

```r
# see package vignete for example usage
seqinfo <- GenomeInfoDb::Seqinfo(c("chr1","chr2"), c(10,20))
app <- startStandalone(seqinfo=seqinfo, non_interactive=TRUE)
app$stop_app()
```
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