

Package ‘epivizrStandalone’

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Title Run Epiviz Interactive Genomic Data Visualization App within R

Version 1.36.0

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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 7.1.1

VignetteBuilder knitr

biocViews Visualization, Infrastructure, GUI

NeedsCompilation no

git_url <https://git.bioconductor.org/packages/epivizrStandalone>

git_branch RELEASE_3_21

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setStandalone	<i>Set settings for epiviz standalone repository.</i>
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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

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

Arguments

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

Value

path to the epiviz app git repository

Examples

```
# 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)
```

startStandalone	<i>Start a standalone epivizr session.</i>
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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

```
startStandalone(
  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,
  use_viewer_option = FALSE,
  host = "127.0.0.1",
  ...
)
```

Arguments

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

Value

An object of class `EpivizApp`

Examples

```
# 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()
```

startStandaloneApp	<i>Start a standalone epivizr session.</i>
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Description

Uses the local installation of the epiviz desktop 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

```
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

<code>gene_track</code>	(OrganismDb) an object of type <code>OrganismDb</code> or <code>TxDb</code>
<code>seqinfo</code>	(Seqinfo) an object of type <code>Seqinfo</code> from which sequence names and lengths are obtained
<code>keep_seqlevels</code>	(character) vector of sequence names to include in the standalone app
<code>chr</code>	(character) chromosome to browse to on app startup.
<code>start</code>	(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

```
# 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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