

Package ‘epivizrStandalone’

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Title Run Epiviz Interactive Genomic Data Visualization App within R

Version 1.35.0

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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 devel

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Contents

| | |
|------------------------------|---|
| setStandalone | 2 |
| startStandalone | 3 |
| startStandaloneApp | 4 |

| | |
|--------------|----------|
| Index | 6 |
|--------------|----------|

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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 (<code>"https://github.com/epiviz/epiviz.git"</code>). |
| <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)
```

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

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

startStandaloneApp *Start a standalone epivizr session.*

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

| | |
|----------------|--|
| 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

```
# 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()
```

Index

EpivizApp, [4](#), [5](#)

OrganismDb, [3](#), [4](#)

Seqinfo, [3](#), [4](#)

setStandalone, [2](#)

startEpiviz, [3–5](#)

startStandalone, [2](#), [3](#)

startStandaloneApp, [4](#)

TxDB, [3](#), [4](#)