Package ‘epivizrStandalone’

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Title Run Epiviz Interactive Genomic Data Visualization App within R

Version 1.32.0

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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_19
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setStandalone Set settings for epiviz standalone repository.

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 = "master",
    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)
```
## startStandalone

Start a standalone epivizr session.

### 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 = epivizr:::.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`. 
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()
```

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.
\texttt{startStandaloneApp}

\begin{verbatim}
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)
\ldots additional arguments passed to \texttt{startEpiviz}.
\end{verbatim}

\textbf{Value}

An object of class \texttt{EpivizApp}

\textbf{Examples}

\begin{verbatim}
# 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()
\end{verbatim}
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