Package ‘epivizrStandalone’

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Title Run Epiviz Interactive Genomic Data Visualization App within R

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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 5.0.1

VignetteBuilder knitr

biocViews Visualization, Infrastructure, GUI

NeedsCompilation no

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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 intializes 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

`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

```
# 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., chromsome 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

`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

```
# 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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