Package ‘epivizrStandalone’

March 22, 2024

Title  Run Epiviz Interactive Genomic Data Visualization App within R
Version  1.30.0
Maintainer  Hector Corrada Bravo <hcorrada@gmail.com>
Author  Hector Corrada Bravo, Jayaram Kancherla
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
License  MIT + file LICENSE
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
biocView  Visualization, Infrastructure, GUI
NeedsCompilation  no
git_url  https://git.bioconductor.org/packages/epivizrStandalone
git_branch  RELEASE_3_18
git_last_commit  85a3638
git_last_commit_date  2023-10-24
Repository  Bioconductor 3.18
Date/Publication  2024-03-22
R topics documented:

- setStandalone
- startStandalone
- startStandaloneApp

---

**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
def 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`.
**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()
```

---

**startStandaloneApp**  
*Start a standalone epiviz session.*

**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.
**startStandaloneApp**

- `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()
```
Index

EpivizApp, 4, 5
OrganismDb, 3, 4
Seqinfo, 3, 4
setStandalone, 2
startEpiviz, 3–5
startStandalone, 2, 3
startStandaloneApp, 4

TxDb, 3, 4