

# Package ‘epivizrStandalone’

March 30, 2021

**Title** Run Epiviz Interactive Genomic Data Visualization App within R

**Version** 1.18.0

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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** 6.0.1

**VignetteBuilder** knitr

**biocViews** Visualization, Infrastructure, GUI

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/epivizrStandalone>

**git\_branch** RELEASE\_3\_12

**git\_last\_commit** 3178098

**git\_last\_commit\_date** 2020-10-27

**Date/Publication** 2021-03-29

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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

```
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., 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**

`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()
```

---

`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 <a href="#">OrganismDb</a> or <a href="#">TxDb</a>                      |
| seqinfo           | (Seqinfo) an object of type <a href="#">Seqinfo</a> 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 <a href="#">startEpiviz</a> .   |

**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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