

# Package ‘epivizrStandalone’

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

**Version** 1.32.0

**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

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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

**git\_last\_commit** d278f10

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

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## Contents

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

|              |          |
|--------------|----------|
| <b>Index</b> | <b>6</b> |
|--------------|----------|

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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> |
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### 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 <a href="#">OrganismDb</a> or <a href="#">TxDb</a>  |
| <code>seqinfo</code>           | (Seqinfo) an object of type <a href="#">Seqinfo</a> 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 <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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startStandaloneApp      *Start a standalone epivizr session.*

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**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 [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](#)