

# Package ‘epivizrStandalone’

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

**Version** 1.34.0

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**Description** This package imports the epivizr 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\_20

**git\_last\_commit** 94beb58

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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**

<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()
```

---

startStandaloneApp     *Start a standalone epivizr session.*

---

### Description

Uses the local installation of the epivizr desktop app to start a standalone epivizr session through the [startEpivizr](#) function. The epivizr 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 epivizr 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_epivizr_things,
  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 epivizr app. Used for testing and development.
<code>host</code>	(character) host address for application (127.0.0.1 by default)
<code>...</code>	additional arguments passed to <a href="#">startEpivizr</a> .

### Value

An object of class [EpivizrApp](#)

**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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