Package ‘iSEEmindex’

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Author Kevin Rue-Albrecht [aut, cre] (<https://orcid.org/0000-0003-3899-3872>), Thomas Sandmann [ctb] (<https://orcid.org/0000-0002-6601-8890>), Federico Marini [aut] (<https://orcid.org/0000-0003-3252-7758>), Denali Therapeutics [fnd]

Maintainer Kevin Rue-Albrecht <kevinrue67@gmail.com>

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iSEEindex-package  iSEEindex: iSEE extension for a landing page to a custom collection of data sets

Description

This package provides an interface to any collection of data sets within a single iSEE web-application. The main functionality of this package is to define a custom landing page allowing app maintainers to list a custom collection of data sets that users can select from and directly load objects into an iSEE web-application.

Author(s)

Maintainer: Kevin Rue-Albrecht <kevinrue67@gmail.com> (ORCID)
Authors:
  • Federico Marini <marinif@uni-mainz.de> (ORCID)

Other contributors:
  • Thomas Sandmann <tomsing1@gmail.com> (ORCID) [contributor]
  • Denali Therapeutics [funder]

See Also

Useful links:
  • https://github.com/iSEE/iSEEindex
  • Report bugs at https://support.bioconductor.org/t/iSEEindex
iSEEindex App

Description

Generate an iSEE app that includes a landing page enabling users to choose from a custom set of data sets and initial configuration states prepared by the app maintainer.

Usage

iSEEindex(
  bfc,
  FUN.datasets,
  FUN.initial = NULL,
  default.add = TRUE,
  default.position = c("first", "last"),
  app.title = NULL,
  body.header = NULL,
  body.footer = NULL
)

Arguments

bfc An BiocFileCache() object.
FUN.datasets A function that returns a list of metadata for available data sets.
FUN.initial A function that returns a list of metadata for available initial configuration states.
default.add Logical scalar indicating whether a default initial configuration should be added as a choice in the Shiny selectizeInput(). See iSEEindex().
default.position Character scalar indicating whether the default initial configuration should be added as the "first" or "last" option in the Shiny selectizeInput().
app.title Character string to specify the desired title to be displayed in the main window of the dashboard.Defaults to NULL, which displays some info on the versions of the iSEEindex and iSEE packages.
body.header UI element to display above the main landing page body.
body.footer UI element to display below the main landing page body.

Value

An iSEE::iSEE() app with a custom landing page using a BiocFileCache() to cache a selection of data sets.
Data Sets

The function passed to the argument FUN.datasets must return a list that contains metadata about the available data sets.

For each data set, required metadata are:

id  A unique identifier for the data set.
title  A short human-readable title for the data set, displayed in the 'Info' panel when the data set is selected.
uri  A Uniform Resource Identifier (URI) that indicates the location of the data file that contains the data set.
description  A more detailed description of the data set, displayed in the 'Info' panel when the data set is selected.

Example:

```r
list(
  list(
    id = "dataset01",
    title = "Dataset 01",
    uri = "https://example.com/1.rds",
    description = "My first data set."
  ),
  list(
    id = "dataset02",
    title = "Dataset 02",
    uri = "https://example.com/1.rds",
    description = "My second data set."
  )
)
```

The individual sub-lists may also contain optional named metadata specific to individual iSEEindexResource classes (refer to the help page of those classes for details).

Important: The id value is used to identify the data set file in the BiocFileCache. Thus, we recommend using a dedicated BiocFileCache() for the app, using the BiocFileCache(cache) argument to specify an on-disk location (directory path) for the dedicated cache.

Initial Configurations

The function passed to the argument FUN.initial must return a list that contains metadata about the available initial configurations, or NULL in the absence of any custom initial configuration (default settings will be applied to all data sets.).

For each initial configuration, required metadata are:

id  A unique identifier for the initial configuration.
title  A short human-readable title for the initial configuration, representing the initial configuration in the 'Initial settings' dropdown menu.
uri A Uniform Resource Identifier (URI) that indicates the location of the R script that contains the
initial configuration.

description A more detailed description of the initial configuration, displayed in the 'Configure
and launch' panel when the initial configuration is selected.

For each initial configuration, optional metadata are:

datasets A series of data set identifiers for which the configuration should be made available. If
missing, the configuration will be available for all data sets.

Example:

```r
dataset_fun <- function() {
  x <- yaml::read_yaml(system.file(package = "iSEEIndex", "example.yaml"))
}
```

The individual sub-lists may also contain additional optional named metadata specific to individual
*iSEEIndexResource* classes (refer to the help page of those classes for details).

**Author(s)**

Kevin Rue-Albrecht

**Examples**

```r
library(BiocFileCache)
bfc <- BiocFileCache(cache = tempdir())
```
initial_fun <- function() {
  x <- yaml::read_yaml(system.file(package = "iSEEindex", "example.yaml"))
  x$initial
}

app <- iSEEindex(bfc, dataset_fun, initial_fun)

if (interactive()) {
  shiny::runApp(app, port = 1234)
}

---

**iSEEindexHttpsResource-class**

*The iSEEindexHttpsResource class*

**Description**

The `iSEEindexHttpsResource` class represents a resource accessible through an HTTPS link. A URI for this type of resource uses the prefix “https://”.

**Usage**

```
iSEEindexHttpsResource(x)
```

**Arguments**

- `x` List of metadata. See Details.

**Details**

Required metadata:

- `uri` Character scalar. URI of the resource.

**Value**

The constructor function `iSEEindexHttpsResource()` returns an object of object class `iSEEindexHttpsResource`.

**Slot overview**

This class inherits all slots from its parent class `iSEEIndexResource`. 
Supported methods

In the following code snippets, `x` is an instance of a `iSEEindexHttpsResource` class. Refer to the documentation for each method for more details on the remaining arguments.

- `precache(x, bfc, id, ...)` caches the resource located at the given URI using BioCFileCache and returns the file path to the cached file.

Author(s)

Kevin Rue-Albrecht

Examples

```r
iSEEindexHttpsResource(list(uri = "https://example.com"))
```

---

The `iSEEindexLocalhostResource` class

The `iSEEindexLocalhostResource` class represents a resource accessible through a local filepath. A URI for this type of resource uses the prefix “localhost://”.

Usage

```r
iSEEindexLocalhostResource(x)
```

Arguments

- `x` List of metadata. See Details.

Details

Required metadata:

- `uri` Character scalar. URI of the resource.

Value

The constructor function `iSEEindexLocalhostResource()` returns an object of object of class `iSEEindexLocalhostResource`.

Slot overview

This class inherits all slots from its parent class `iSEEindexResource`. 
Supported methods

In the following code snippets, x is an instance of a iSEEindexLocalhostResource class. Refer to the documentation for each method for more details on the remaining arguments.

- `precache(x, ...)` trims the localhost:// prefix, and caches a copy of the resource located at the resulting file path using Bioconductor's `BiocFileCache`, before returning the file path to the cached file.

Absolute and relative paths

Absolute and relative paths are both supported.

Absolute paths require an additional / (forward slash) following the double forward slash // separating the scheme component of the URI.

For instance:

- `localhost://path/to/file` refers to the relative path `path/to/file` (relative to the working directory when the Shiny application is launched).
- `localhost:///path/to/file` refers to the absolute path `/path/to/file`.

Author(s)

Kevin Rue-Albrecht

Examples

```r
callLocalhostResource(list(uri = "localhost:///example/absolute/path"))
callLocalhostResource(list(uri = "localhost://example/relative/path"))
```

---

iSEEindexRcallResource-class

*The iSEEindexRcallResource class*

Description

The iSEEindexRcallResource class represents a resource accessible through the result of an R call. A URI for this type of resource uses the prefix “rcall://”.

Usage

```r
callRcallResource(x)
```

Arguments

- `x` List of metadata. See Details.
Details

Required metadata:

uri  Character scalar. R call which, once evaluated, produces a character scalar that is the URI of the resource.

Value

The constructor function `iSEEindexRcallResource()` returns an object of object of class `iSEEindexRcallResource`.

URI format

The URI must contain valid R code, once the prefix `rcall://` is removed. The code must return the path to an existing file on the local filesystem.

For instance:

```
rcall://system.file(package='iSEEindex', 'ReprocessedAllenData_config_01.R')
```

Slot overview

This class inherits all slots from its parent class `iSEEindexResource`.

Supported methods

In the following code snippets, `x` is an instance of a `iSEEindexRcallResource` class. Refer to the documentation for each method for more details on the remaining arguments.

- `precache(x, ...)` trims the `rcall://` prefix, evaluates the remainder of the URI as R code, and caches a copy of the resource located at the resulting file path using `BiocFileCache`, before returning the file path to the cached file.

Author(s)

Kevin Rue-Albrecht

Examples

```r
iSEEindexRcallResource(list(
  uri = "rcall://system.file(package='iSEEindex', 'ReprocessedAllenData_config_01.R")"
))
```
The iSEEindexResource class

Description

The iSEEindexResource class is a virtual class from which classes of supported resource must be derived.

Usage

```r
## S4 method for signature 'iSEEindexResource'
show(object)
```

```r
## S4 method for signature 'iSEEindexResource'
precache(x, bfc, id, ...)
```

Arguments

- `object`: An iSEEindexResource object.
- `x`: An iSEEindexResource object.
- `bfc`: A BiocFileCache() object.
- `id`: A data set identifier as a character scalar.
- `...`: additional arguments passed to and from other methods.

Value

- `show()`: returns NULL after displaying a summary of the object.
- `precache()` throws an error if no method is found for the derived class.

Slot overview

- `uri`, a character scalar specifying the URI of a resource.

Supported methods

In the following code snippets, `x` is an instance of a iSEEindexResource class. Refer to the documentation for each method for more details on the remaining arguments.

- `precache(x, bfc, id, ...)`: throws an error, encouraging users to develop a method for derived classes that are not supported yet.

Author(s)

Kevin Rue-Albrecht
Examples

showClass("iSEEindexResource")

iSEEindexResource-generics

Generics for iSEEindexResources Objects

Description

An overview of the generics for iSEEindexResources objects.

Usage

precache(x, bfc, id, ...)

Arguments

x  
An iSEEindexResource object.

bfc  
A BiocFileCache() object.

id  
A data set identifier as a character scalar.

...  
additional arguments passed to and from other methods.

Value

precache() returns the file path to the cached copy of a resource fetched from a given URI.

Preparing and caching resources

precache(x, bfc, id, ...) retrieves and caches a resource from an URI, caches it, and returns the path to the cached file.

Author(s)

Kevin Rue-Albrecht

Examples

library(BiocFileCache)
bfc <- BiocFileCache(cache = tempdir())
x <- iSEEindexRcallResource(list(
    uri = "rcall://system.file(package='iSEEindex',""
      "ReprocessedAllenData_config_01.R")"
))
pPrecache(x, bfc, "ID0")
The `iSEEindexS3Resource` class

Description

The `iSEEindexS3Resource` class represents a cloud storage resource accessible via the `paws.storage` R package. A URI for this type of resource uses the prefix “s3://”.

Usage

```r
iSEEindexS3Resource(x)
```

Arguments

- `x` List of metadata. See Details.

Details

Required metadata:

- `uri` Character scalar. URI of the resource.

Value

The constructor function `iSEEindexS3Resource()` returns an object of object of class `iSEEindexS3Resource`.

Slot overview

This class inherits all slots from its parent class `iSEEindexResource`.

Furthermore, this class defines the additional slot(s) below:

- `region` AWS region.

Supported methods

In the following code snippets, `x` is an instance of a `iSEEindexS3Resource` class. Refer to the documentation for each method for more details on the remaining arguments.

- `precache(x, ..., temp_dir = tempdir())` trims the `s3://` prefix, parses information encoded in the remainder of the URI, downloads the resource from AWS S3 using that information, and caches a copy of the resource located at the resulting file path using `BiocFileCache`, before returning the file path to the cached file.
**URI format**

The URI must correspond to an existing file in an AWS S3 compatible cloud storage system. For instance:

```
s3://bucket/prefix/index.rds
```

For details about authentication, see section “AWS Credentials” below.

**Pre-caching**

Additional arguments to the `precache(x, ..., temp_dir = tempdir())`:

```
temp_dir  Scalar character, the directory to store the downloaded file in before it is handed over to 
           BiocFileCache. This directory will be created recursively if it doesn’t already exist.
```

**AWS Credentials and region settings**

For detailed information, please consult the paws R package documentation.

Currently, you must have the AWS Command Line Interface installed to use AWS SSO with `paws.storage`.

A default AWS region can be set in the file `~/.aws/config`. For instance:

```
[default]
region=eu-west-2
```

Optionally, a field named `region` can be added in the list of resource metadata to set the AWS S3 region for each individual resource, e.g.

```
- id: ID1
  title: ReprocessedAllenData
  uri: s3://example/ReprocessedAllenData.rds
  description: |
    Reprocessed Allen Data.
  region: eu-west-2
```

Regions set in individual resource metadata override the default AWS region set in `~/.aws/config` (if any). The region metadata does not need to be set for resources that should use the default region, and resource classes that do not require region information.

If a default region is NOT set in `~/.aws/config`, then the region MUST be set in the metadata.

Credentials for all services can be set in the AWS shared credentials file `~/.aws/credentials`. For instance:

```
[default]
aws_access_key_id=your AWS access key
aws_secret_access_key=your AWS secret key
```
Author(s)

Thomas Sandmann, Kevin Rue-Albrecht

Examples

# Without region metadata
metadata <- list(uri = "s3://example/path/to/bucket")
x <- iSEEindexS3Resource(metadata)
str(x)

# With region metadata
# NOTE: The @region slot is set to NA pending bugfix (see above).
metadata <- list(uri = "s3://example/path/to/bucket", region = "eu-west-2")
x <- iSEEindexS3Resource(metadata)
str(x)
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