

# Package ‘iSEEindex’

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**Title** iSEE extension for a landing page to a custom collection of data sets

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**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 selected from and directly load objects into an iSEE web-application.

**License** Artistic-2.0

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## R topics documented:

iSEEindex . . . . .	2
iSEEindex-pkg . . . . .	5
iSEEindexHttpsResource-class . . . . .	6
iSEEindexLocalhostResource-class . . . . .	7
iSEEindexRcallResource-class . . . . .	8
iSEEindexResource-class . . . . .	9
iSEEindexResource-generics . . . . .	10
iSEEindexS3Resource-class . . . . .	11

<b>Index</b>	<b>14</b>
--------------	-----------

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iSEEindex	<i>iSEEindex App</i>
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### 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"),
  body.header = NULL,
  body.footer = NULL
)
```

### Arguments

bfc	An <a href="#">BiocFileCache()</a> 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 <a href="#">selectizeInput()</a> . See <a href="#">iSEEindex()</a> .

<code>default.position</code>	Character scalar indicating whether the default initial configuration should be added as the "first" or "last" option in the Shiny <code>selectizeInput()</code> .
<code>body.header</code>	UI element to display <i>above</i> the main landing page body.
<code>body.footer</code>	UI element to display <i>below</i> 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:

```
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:

```
list(
  list(
    id = "config01",
    datasets = c("dataset01")
    title = "Configuration 01",
    uri = "https://example.com/1.R",
    description = "My first configuration."
  ),
  list(
    id = "config02",
    title = "Configuration 02",
    uri = "https://example.com/2.R",
    description = "My second configuration."
  )
)
```

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

```
##
# BiocFileCache ----
##

library(BiocFileCache)
bfc <- BiocFileCache(cache = tempdir())

##
# iSEEindex ----
##

dataset_fun <- function() {
  x <- yaml::read_yaml(system.file(package = "iSEEindex", "example.yaml"))
  x$datasets
}

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)
}
```

---

iSEEindex-pkg

*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 selected from and directly load objects into an iSEE web-application.

## See Also

Useful links:

- <https://github.com/iSEE/iSEEindex>
- Report bugs at <https://support.bioconductor.org/t/iSEEindex>

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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 of 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

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

---

`iSEEindexLocalhostResource-class`*The iSEEindexLocalhostResource class*

---

## Description

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

## Usage

```
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 **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**

```
iSEEindexLocalhostResource(list(uri = "localhost:///example/absolute/path"))
iSEEindexLocalhostResource(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**

```
iSEEindexRcallResource(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**

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

---

iSEEindexResource-class

*The iSEEindexResource class*

---

**Description**

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

**Usage**

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

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

**Arguments**

<code>object</code>	An <code>iSEEindexResource</code> object.
<code>x</code>	An <code>iSEEindexResource</code> object.
<code>bfc</code>	A <code>BiocFileCache()</code> object.
<code>id</code>	A data set identifier as a character scalar.
<code>...</code>	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**

<code>x</code>	An <code>iSEEindexResource</code> object.
<code>bfc</code>	A <code>BiocFileCache()</code> object.
<code>id</code>	A data set identifier as a character scalar.
<code>...</code>	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')")
))
precache(x, bfc, "ID0")
```

---

iSEEindexS3Resource-class

*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**

```
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)
```

# Index

## \* **internal**

- iSEEindex-pkg, [5](#)
- BiocFileCache(), [2](#), [3](#), [9](#), [10](#)
- iSEE::iSEE(), [3](#)
- iSEEindex, [2](#)
- iSEEindex(), [2](#)
- iSEEindex-pkg, [5](#)
- iSEEindexHttpsResource, [6](#)
- iSEEindexHttpsResource
  - (iSEEindexHttpsResource-class), [6](#)
- iSEEindexHttpsResource-class, [6](#)
- iSEEindexLocalhostResource, [7](#)
- iSEEindexLocalhostResource
  - (iSEEindexLocalhostResource-class), [7](#)
- iSEEindexLocalhostResource-class, [7](#)
- iSEEindexRcallResource, [9](#)
- iSEEindexRcallResource
  - (iSEEindexRcallResource-class), [8](#)
- iSEEindexRcallResource-class, [8](#)
- iSEEindexResource, [3](#), [4](#), [6–11](#)
- iSEEindexResource-class, [9](#)
- iSEEindexResource-generics, [10](#)
- iSEEindexS3Resource, [12](#)
- iSEEindexS3Resource
  - (iSEEindexS3Resource-class), [11](#)
- iSEEindexS3Resource-class, [11](#)
- precache, [6](#), [7](#), [9](#), [10](#), [12](#)
- precache (iSEEindexResource-generics), [10](#)
- precache, iSEEindexHttpsResource-method
  - (iSEEindexHttpsResource-class), [6](#)
- precache, iSEEindexLocalhostResource-method
  - (iSEEindexLocalhostResource-class), [7](#)
- precache, iSEEindexRcallResource-method
  - (iSEEindexRcallResource-class), [8](#)
- precache, iSEEindexResource-method
  - (iSEEindexResource-class), [9](#)
- precache, iSEEindexS3Resource-method
  - (iSEEindexS3Resource-class), [11](#)
- show, iSEEindexResource-method
  - (iSEEindexResource-class), [9](#)