

Package ‘ImmuneSpaceR’

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Description Provides a convenient API for accessing data sets within ImmuneSpace (www.immunespace.org), the data repository and analysis platform of the Human Immunology Project Consortium (HIPC).

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BugReports <https://github.com/RGLab/ImmuneSpaceR/issues>

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ImmuneSpaceR-package *A Thin Wrapper Around ImmuneSpace*

Description

ImmuneSpaceR provides a convenient API for accessing data sets within the ImmuneSpace database.

Details

Uses the Rlabkey package to connect to ImmuneSpace. Implements caching, and convenient methods for accessing data sets.

See Also

[CreateConnection](#)

check_netrc	<i>Check netrc file</i>
-------------	-------------------------

Description

Check that there is a netrc file with a valid entry for ImmuneSpace.

Usage

```
check_netrc()
```

Details

In order to connect to ImmuneSpace, you will need a '.netrc' file in your contains a 'machine' name (hostname of ImmuneSpace), and 'login' and 'password'. See [here](<https://www.labkey.org/wiki/home/Documentation/>) for more information. By default Rcurl will look for the file in your home directoty.

If no netrc is available or it is not formatted properly, write_netrc can be used to write one. Otherwise, when specifying login and password in CreateConnection, a temporary file will be created for that connection.

Value

The name of the netrc file

See Also

CreateConnection write_netrc

Examples

```
try(check_netrc())
```

CreateConnection	<i>CreateConnection</i>
------------------	-------------------------

Description

Constructor for ImmuneSpaceConnection class.

Usage

```
CreateConnection(  
  study = NULL,  
  login = NULL,  
  password = NULL,  
  verbose = FALSE,  
  onTest = FALSE  
)
```

Arguments

study	A "character" vector naming the study.
login	A "character". Optional argument. If there is no netrc file a temporary one can be written by passing login and password of an active ImmuneSpace account.
password	A "character". Optional. The password for the selected login.
verbose	A "logical" whether to print the extra details for troubleshooting.
onTest	A "logical" whether to connect to the test server (https://test.immunespace.org/) instead of the production server (https://www.immunespace.org/).

Details

Instantiates an ImmuneSpaceConnection for study. The constructor will try to take the values of the various 'labkey.*' parameters from the global environment. If they don't exist, it will use default values. These are assigned to 'options', which are then used by the ImmuneSpaceConnection class.

Value

an instance of an ImmuneSpaceConnection

See Also

[ImmuneSpaceConnection](#)

Examples

```
## Not run:
# Single study
con <- CreateConnection("SDY269")
# Cross study
con <- CreateConnection("")

## End(Not run)

sdy <- try(CreateConnection("SDY269"))
if (inherits(sdy, "try-error")) {
  warning("Read the Introduction vignette for more information on how to set
up a .netrc file.")
}
```

ImmuneSpaceConnection *The ImmuneSpaceConnection class*

Description

A connection represents a study or a set of studies available on ImmuneSpace. It provides function to download and display the data within these studies.

Details

The ImmuneSpaceConnection will initialize itself, and look for a `.netrc` file in `"~/`" the user's home directory. The `.netrc` file should contain a machine, login, and password entry to allow access to ImmuneSpace, where machine is the host name like `"www.immunespace.org"`.

It can also use global variables `labkey.url.base`, and `labkey.url.path`, to access a study. `labkey.url.base` should be `https://www.immunespace.org/`. `labkey.url.path` should be `/Studies/studyname`, where 'studyname' is the accession number of the study.

Value

An instance of an ImmuneSpaceConnection for a study in `labkey.url.path`.

Constructor

[CreateConnection](#)

Fields

`study` A character. The study accession number. Use an empty string (`""`) to create a connection at the project level.

`availableDatasets` A data.table. The table of datasets available in the connection object.

`cache` A list. Stores the data to avoid downloading the same tables multiple times.

`config` A list. Stores configuration of the connection object such as URL, path and username.

Methods

`initialize()` Initialize ImmuneSpaceConnection class. See [CreateConnection](#).

`print()` Print ImmuneSpaceConnection class.

`listDatasets(output = c("datasets", "expression"))` Lists the datasets available in the study or studies of the connection.

`listGEMatrices(verbose = FALSE, reload = FALSE, participantIds = NULL)` Lists available gene expression matrices for the connection.

`verbose`: A logical. If TRUE, whether to print the extra details for troubleshooting.

`reload`: A logical. If TRUE, retrieve the table of available gene expression matrices whether a cached version exist or not.

`participantIds`: A character vector of participant ids to filter by. Only matrices with data from `participantIds` will be returned. If NULL, all matrices are returned.

`listGEAnalysis()` Lists available gene expression analysis for the connection.

`listParticipantGroups()` Lists available participant groups on the ImmuneSpace portal.

`listParticipantGEMatrices(group, verbose = FALSE)` Lists available gene expression matrices for participants in group.

`group`: A character or integer. Call `con$listParticipantGroups()` to see available participants groups. Use `group_id` or `group_name` as input.

`verbose`: A logical. If TRUE, whether to print the extra details for troubleshooting.

`listWorkspaces(reload = FALSE)` Lists available workspaces for the connection.

`reload`: A logical. If TRUE, download the table whether a cached version exist or not.

`listGatingSets(reload = FALSE)` Lists available gating sets for the connection.

`reload`: A logical. If TRUE, download the table whether a cached version exist or not.

`summarizeCyto()` Prints a summary of cytometry data for the connection.

`summarizeGatingSet(gatingSet)` Prints a summary of a gating set. Note that this method currently works only in the ImmuneSpace RStudio session.

`gatingSet`: A character. The name of the gating set to summarize.

`loadGatingSet(gatingSet)` Loads a gating set via `flowWorkspace::load_gs` to the current environment. Note that this method currently works only in the ImmuneSpace RStudio Docker session.

`gatingSet`: A character. The name of the gating set to load.

`getDataset(x, original_view = FALSE, reload = FALSE, colFilter = NULL, ...)` Get a dataset from the connection.

`x`: A character. The name of the dataset to download.

`original_view`: A logical. If TRUE, download the original ImmPort view; else, download the default grid view.

`reload`: A logical. If TRUE, download the dataset whether a cached version exist or not.

`colFilter`: A character. A filter as returned by Rlabkey's `makeFilter` function.

`...`: Extra arguments to be passed to `labkey.selectRows`.

`getGEMatrix(matrixName = NULL, cohortType = NULL, outputType = "summary", annotation = "latest", reload = FALSE)` Downloads a probe-level or gene-symbol summarized expression matrix from ImmuneSpace and constructs an ExpressionSet. Use `experimentData()` on the resulting ExpressionSet object to see version info for annotation.

`matrixName`: A character. The name of the gene expression matrix to download.

`cohortType`: A character. The name of a cohortType that has an associated gene expression matrix. Note that if this argument is not NULL, then `matrixName` is ignored. CohortType is a concatenation of "cohort" and "cell type" that allows the user to specify a matrix for the cell type subset of a cohort.

`outputType`: A character. one of 'raw', 'normalized' or 'summary'. If 'raw', returns an expression matrix of non-normalized values by probe. 'normalized' returns normalized values by probe. 'summary' returns normalized values averaged by gene symbol.

`annotation`: A character. one of 'default', 'latest', or 'ImmSig'. Determines which feature annotation set (FAS) is used. 'default' uses the FAS from when the matrix was generated. 'latest' uses a recently updated FAS based on the original. 'ImmSig' is specific to studies involved in the ImmuneSignatures project and uses the annotation from when the meta-study's manuscript was created.

`reload`: A logical. If set to TRUE, the matrix will be downloaded again, even if a cached copy exists in the ImmuneSpaceConnection object.

`verbose`: A logical. If set to TRUE, notes on how the expressionSet object was created will be printed, including normalization, summarization, `feature_annotation_set`, and `alias2symbol` mapping version of `org.Hs.eg.db`.

`getGEAnalysis(...)` Downloads data from the gene expression analysis results table.

`...`: A list of arguments to be passed to `labkey.selectRows`.

`getGEInputs()` Downloads data from the gene expression input samples table.

`getParticipantData(group, dataType, original_view = FALSE, ...)` Returns a data.table with data subset by participant group.

`group`: A character or integer. Call `con$listParticipantGroups()` to see available participants groups. Use `group_id` or `group_name` as input.

`dataType`: A character. Use `con$availableDatasets` to see available dataset names.

`getParticipantGEMatrix(group, outputType = "summary", annotation = "latest", reload = FALSE)`
 Downloads probe-level or gene-symbol summarized expression matrices for all participants within group from ImmuneSpace and constructs an ExpressionSet containing observations for each participant in group where gene expression data is available.
 group: A character or integer. Call `con$listParticipantGroups()` to see available participants groups. Use `group_id` or `group_name` as input.
 outputType: A character. one of 'raw', 'normalized' or 'summary'. If 'raw', returns an expression matrix of non-normalized values by probe. 'normalized' returns normalized values by probe. 'summary' returns normalized values averaged by gene symbol.
 annotation: A character. one of 'default', 'latest', or 'ImmSig'. Determines which feature annotation set (FAS) is used. 'default' uses the FAS from when the matrix was generated. 'latest' uses a recently updated FAS based on the original. 'ImmSig' is specific to studies involved in the ImmuneSignatures project and uses the annotation from when the meta-study's manuscript was created.
 reload: A logical. If set to TRUE, matrices will be downloaded again, even if a cached copy exists in the ImmuneSpaceConnection object.

`downloadGEFiles(files, destdir = ".")` Downloads gene expression raw data files.
 files: A character. Filenames as shown on the `gene_expression_files` dataset.
 destdir: A character. The local path to store the downloaded files.

`addTreatment(expressionSet)` Adds treatment information to the `phenoData` of an ExpressionSet.
 expressionSet: An ExpressionSet. The ExpressionSet object that has been downloaded from the connection.

`mapSampleNames(EM = NULL, colType = "participant_id")` Changes the sampleNames of an ExpressionSet fetched by `getGEMatrix` using the information in the `phenoData` slot.
 EM: An ExpressionSet, as returned by `getGEMatrix`.
 colType: A character. The type of column names. Valid options are 'expsample_accession' and 'participant_id'.

`plot(...)` Visualizes a selected dataset. This method is used by the DataExplorer module on the ImmuneSpace portal.
 dataset: A character. The name of the dataset to plot, as displayed by the `listDataset` method.
 normalize_to_baseline: A logical. If TRUE, the values are plotted as log2 fold-change from baseline.
 type: A character. The type of plot. Valid choices are 'auto', 'heatmap', 'boxplot', 'lineplot', 'violinplot'. If set to 'auto', the function will select an appropriate plot type for the selected data.
 filter: A filter as created by the `makeFilter` function from Rlabkey.
 facet: The faceting for ggplot2 based plots. Valid choices are 'grid' and 'wrap'.
 text_size: The size of all text elements in the plot.
 legend: A character. Columns of the dataset or demographics to be added as legend on the heatmap. This argument is ignored if the plot type isn't heatmap.
 show_virus_strain: A logical. Should all the virus strains be shown or should the values be averaged. Only used when `dataset = 'hai'`.
 interactive: A logical. If TRUE, an interactive plot will be created. The default is FALSE.
 ...: Extra argument to be passed to ggplot. e.g: `shape = 'Age'`, `color = 'Race'`.

`clearCache()` Clears the cache. Removes downloaded datasets and expression matrices.

Methods

Public methods:

- `ISCon$listWorkspaces()`
- `ISCon$listGatingSets()`
- `ISCon$summarizeCyto()`
- `ISCon$summarizeGatingSet()`
- `ISCon$loadGatingSet()`
- `ISCon$listDatasets()`
- `ISCon$getDataset()`
- `ISCon$listGEMatrices()`
- `ISCon$listGEAnalysis()`
- `ISCon$getGEMatrix()`
- `ISCon$getGEAnalysis()`
- `ISCon$getGEInputs()`
- `ISCon$getGEFiles()`
- `ISCon$downloadGEFiles()`
- `ISCon$addTreatment()`
- `ISCon$mapSampleNames()`
- `ISCon$listParticipantGroups()`
- `ISCon$getParticipantData()`
- `ISCon$listParticipantGEMatrices()`
- `ISCon$getParticipantGEMatrix()`
- `ISCon$plot()`
- `ISCon$print()`
- `ISCon$clearCache()`
- `ISCon$new()`
- `ISCon$clone()`

Method `listWorkspaces()`:

Usage:

```
ISCon$listWorkspaces(reload = FALSE)
```

Method `listGatingSets()`:

Usage:

```
ISCon$listGatingSets(reload = FALSE)
```

Method `summarizeCyto()`:

Usage:

```
ISCon$summarizeCyto()
```

Method `summarizeGatingSet()`:

Usage:

```
ISCon$summarizeGatingSet(gatingSet)
```

Method `loadGatingSet()`:

Usage:

```
ISCon$loadGatingSet(gatingSet)
```


Method listDatasets():*Usage:*

```
ISCon$listDatasets(output = c("datasets", "expression"))
```

Method getDataset():*Usage:*

```
ISCon$getDataset(  
  x,  
  original_view = FALSE,  
  reload = FALSE,  
  colFilter = NULL,  
  transformMethod = "none",  
  ...  
)
```

Method listGEMatrices():*Usage:*

```
ISCon$listGEMatrices(verbose = FALSE, reload = FALSE, participantIds = NULL)
```

Method listGEAnalysis():*Usage:*

```
ISCon$listGEAnalysis()
```

Method getGEMatrix():*Usage:*

```
ISCon$getGEMatrix(  
  matrixName = NULL,  
  cohortType = NULL,  
  outputType = "summary",  
  annotation = "latest",  
  reload = FALSE,  
  verbose = FALSE  
)
```

Method getGEAnalysis():*Usage:*

```
ISCon$getGEAnalysis(...)
```

Method getGEInputs():*Usage:*

```
ISCon$getGEInputs()
```

Method getGEFiles():*Usage:*

```
ISCon$getGEFiles(files, destdir = ".", quiet = FALSE)
```

Method downloadGEFiles():*Usage:*

```
ISCon$downloadGEFiles(files, destdir = ".")
```

Method addTreatment():*Usage:*

ISCon\$addTreatment(expressionSet)

Method mapSampleNames():*Usage:*

ISCon\$mapSampleNames(EM = NULL, colType = "participant_id")

Method listParticipantGroups():*Usage:*

ISCon\$listParticipantGroups()

Method getParticipantData():*Usage:*

```
ISCon$getParticipantData(  
  group,  
  dataType,  
  original_view = FALSE,  
  reload = FALSE,  
  colFilter = NULL,  
  transformMethod = "none",  
  ...  
)
```

Method listParticipantGEMatrices():*Usage:*

ISCon\$listParticipantGEMatrices(group, verbose = FALSE)

Method getParticipantGEMatrix():*Usage:*

```
ISCon$getParticipantGEMatrix(  
  group,  
  outputType = "summary",  
  annotation = "latest",  
  reload = FALSE  
)
```

Method plot():*Usage:*

ISCon\$plot(...)

Method print():*Usage:*

ISCon\$print()

Method clearCache():*Usage:*

ISCon\$clearCache()

Method new():

Usage:

```
ISCon$new(
  study = NULL,
  login = NULL,
  password = NULL,
  verbose = FALSE,
  onTest = FALSE
)
```

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
ISCon$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

[CreateConnection ImmuneSpaceR-package](#)

Examples

```
## Not run:
# Create a connection (Initiate a ImmuneSpaceConnection object)
sdy269 <- CreateConnection("SDY269")

# Print the connection object
sdy269

# Retrieve the HAI dataset
HAI <- sdy269$getDataset("hai")

# Fetch a summarized gene expression matrix with latest annotation
LAIV <- sdy269$getGEMatrix("LAIV_2008")

# Visualize the ELISA dataset
sdy269$plot("elisa")

## End(Not run)

sdy <- try(CreateConnection("SDY269"))
if (inherits(sdy, "try-error")) {
  warning("Read the Introduction vignette for more information on how to set
up a .netrc file.")
}
```

interactive_netrc

Interactively write a netrc file

Description

Write a netrc file that is valid for accessing ImmuneSpace

Usage

```
interactive_netrc()
```

Value

A netrc file that is verified to connect to ImmuneSpace

Examples

```
## Not run:  
interactive_netrc()  
  
## End(Not run)
```

ISpalette

ImmuneSpace palette

Description

Create a color gradient of the selected length that matches the ImmuneSpace theme.

Usage

```
ISpalette(n)
```

Arguments

n A numeric. The length of the desired palette.

Value

A character vector colors in hexadecimal code of length n.

Examples

```
plot(1:10, col = ISpalette(10), cex = 10, pch = 16)
```

loadConnection	<i>Save/Load an ImmuneSpaceConnection object from disk</i>
----------------	--

Description

Connection can hold a lot of data in cache. If a lot of work has been done (e.g: lots of downloaded datasets and gene-expression matrices), it can be useful to save the connection for later work or even offline use.

Usage

```
loadConnection(file)

saveConnection(con, file)
```

Arguments

file	The file name to be saved to or loaded from
con	An ImmuneSpaceConnection. The connection to save to file. To be loaded later using loadConnection.

Value

An ImmuneSpaceConnection object

Examples

```
# Sample saved connection with pre-downloaded expression matrices and datasets
saved <- system.file("extdata/saved_con.rds", package = "ImmuneSpaceR")
new_con <- loadConnection(saved)
new_con
names(new_con$cache)
## Not run:
saveConnection(new_con, tempfile())

## End(Not run)
```

template_IS	<i>template_IS</i>
-------------	--------------------

Description

A HTML template for knitted reports that matches ImmuneSpace's graphic style. It is based on [html_document](#) from the **rmarkdown** package with css, theme, and template parameters disabled.

Usage

```
template_IS(...)
```

Arguments

... See [html_document](#)

Details

See the documentation for [html_document](#) or the [online documentation](#) for additional details on using the `html_document` format. Compared to `html_document`, it:

- uses a custom css stylesheet
- does not use bootstrap themes

Value

R Markdown output format to pass to [render](#)

Examples

```
## Not run:
library(ImmuneSpaceR)
rmarkdown::render("input.Rmd", template_IS())
rmarkdown::render("input.Rmd", template_IS(toc = TRUE))

## End(Not run)
template_IS()
```

theme_IS

theme_IS

Description

Theme that matches ImmuneSpace's graphic style. The theme modifies the background, the grid lines, the axis, and the colors used by continuous and gradient scales.

Usage

```
theme_IS(base_size = 12)
```

Arguments

`base_size` A numeric. Base font size.

Details

List of modified ggplot2 elements: `panel.background`, `panel.grid.major`, `panel.grid.minor`, `axis.ticks`, `axis.line.x`, `axis.line.y`, `plot.title`, and `strip.background`.

The default `scale_fill_gradient`, `scale_fill_continuous`, `scale_colour_gradient` and `scale_colour_continuous` are also replaced by a custom scale.

Value

A theme object

Examples

```
library(ggplot2)
p <- ggplot(data = mtcars) + geom_point(aes(x = mpg, y = cyl, color = hp)) + facet_grid(vs ~ am)
p + theme_IS()
```

`write_netrc`*Write a netrc file*

Description

Write a netrc file that is valid for accessing ImmuneSpace

Usage

```
write_netrc(login, password, machine = "www.immunespace.org", file = NULL)
```

Arguments

<code>login</code>	A character. The email address used for logging in on ImmuneSpace.
<code>password</code>	A character. The password associated with the login.
<code>machine</code>	A character. The server to connect.
<code>file</code>	A character. The credentials will be written into that file. If left NULL, the netrc will be written into a temporary file.

Value

A character vector containing the file paths for netrc

Examples

```
write_netrc("immunespaceuser@gmail.com", "mypassword")
```

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