

# Package ‘ImmuneSpaceR’

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**Type** Package

**Title** A Thin Wrapper around the ImmuneSpace Database

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**Description** Provides a convenient API for accessing data sets within ImmuneSpace ([www.immunespace.org](http://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>

**License** GPL-2

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ImmuneSpaceR-package    *A Thin Wrapper Around ImmuneSpace*

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### 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            *Check netrc file*

---

### 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

*CreateConnection*

---

**Description**

Constructor for ImmuneSpaceConnection class.

**Usage**

```
CreateConnection(study = NULL, login = NULL, password = NULL,
  use.data.frame = FALSE, verbose = FALSE, onTest = FALSE)
```

**Arguments**

<code>study</code>	A "character" vector naming the study.
<code>login</code>	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.
<code>password</code>	A "character". Optional. The password for the selected login.
<code>use.data.frame</code>	A "logical". If set to TRUE, the functions will return <code>data.frame</code> objects instead of <code>data.table</code> .
<code>verbose</code>	A "logical" whether to print the extra details for troubleshooting.
<code>onTest</code>	A "logical" whether to connect to the test server ( <a href="https://test.immunespace.org/">https://test.immunespace.org/</a> ) instead of the production server ( <a href="https://www.immunespace.org/">https://www.immunespace.org/</a> ).

**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")) {
  print("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.

**Usage**

```
ISCon
```

**Format**

An object of class R6ClassGenerator of length 24.

**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(..., config = NULL)` 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)` 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.

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

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

`getDataset(x, original_view = FALSE, reload = FALSE, colFilter = NULL, ...)` Get a dataset form 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", ...)` Downloads a probe-level or gene-symbol summarized expression matrix from ImmuneSpace. 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`: one of 'raw', 'normalized' or 'summary'. If 'raw' then 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`: one of 'default', 'latest', or 'ImmSig'. Determines which feature annotation set 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 exist 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.

getGEFiles(files, destdir = ".", quiet = FALSE) 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.

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

getParticipantData(group, dataType, original\_view = FALSE, ...) Returns a dataframe with ImmuneSpace data subset by groupId.

group: Use con\$listParticipantGroups() to find Participant groupId or groupName.

dataType: Use con\$listDatasets('datasets') to see possible dataType inputs.

addTreatment(matrixName = NULL) Adds treatment information to the phenoData of an expression matrix available in the connection object.

matrixName: A character. The name of a expression matrix 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 phenodData slot.

EM: An ExpressionSet, as returned by getGEMatrix.

colType: A character. The type of column names. Valid options are 'exsample\_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.

## 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)
```

---

interactive_netrc	<i>Interactively write a netrc file</i>
-------------------	---

---

**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

---

ISpalette	<i>ImmuneSpace palette</i>
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**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>
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---

**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)
```

---

theme_IS	<i>theme_IS</i>
----------	-----------------

---

### 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**

`login`            A character. The email address used for logging in on ImmuneSpace.

`password`        A character. The password associated with the login.

`machine`         A character. The server to connect.

`file`            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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