

# Package ‘ImmuneSpaceR’

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**Type** Package

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

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**VignetteBuilder** knitr

**Description** Provides a convenient API for accessing data sets within ImmuneSpace ([www.immunospace.org](http://www.immunospace.org)), the data repository and analysis platform of the Human Immunology Project Consortium (HIPC).

**biocViews** DataImport, DataRepresentation, ThirdPartyClient

**URL** <https://github.com/RGLab/ImmuneSpaceR>

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

**License** GPL-2

**Suggests** knitr, rmarkdown, testthat

**Imports** methods, data.table, RCurl, Rlabkey (>= 2.1.127), Biobase, pheatmap, ggplot2, scales, stats, gtools, gplots, reshape2

**Collate** 'CreateConnection.R' 'ImmuneSpace.R' 'ImmuneSpaceR.R' 'getDataset.R' 'getGEMatrix.R' 'quick\_plot.R' 'utils.R' 'zzz.R'

**RoxygenNote** 5.0.1.9000

**NeedsCompilation** no

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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.

**Author(s)**

Greg Finak

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 CreateConnection    *CreateConnection*


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**Description**

Constructor for ImmuneSpaceConnection class

**Usage**

```
CreateConnection(study = NULL, verbose = FALSE)
```

**Arguments**

study	A "character" vector naming the study.
verbose	A "logical" whether to print the extra details for troubleshooting.

**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.")
}
```

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 ImmuneSpaceConnection-class

*The ImmuneSpaceConnection class*

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**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**

Uses 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. 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"`.

**Value**

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

**Fields**

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

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

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

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

`constants` A list. Used to store information regarding gene-expression data.

## Methods

- `addTrt(x = NULL)` Add treatment information to the `phenoData` of an expression matrix available in the connection object.  
 x: A character. The name of a expression matrix that has been downloaded from the connection.
- `clear_cache()` Clear the `data_cache`. Remove downloaded datasets and expression matrices.
- `EMNames(EM = NULL, colType = "participant_id")` Change the sampleNames of an ExpressionSet fetched by `getGEMatrix` using the information in the `phenoData` slot.  
 x: An ExpressionSet, as returned by `getGEMatrix`.  
 colType: A character. The type of column names. Valid options are 'expsample\_accession' and 'participant\_id'.
- `getDataset(x, original_view = FALSE, reload = FALSE, colFilter = NULL, ...)` Get a dataset form the connection  
 original\_view: A logical. If set tot TRUE, download the ImmPort view. Else, download the default grid view.  
 reload: A logical. Clear the cache. If set to 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`.
- `getGEAnalysis(...)` Downloads data from the gene expression analysis results table.  
 '...': A list of arguments to be passed to `labkey.selectRows`.
- `getGEFiles(files, destdir = ".")` Download gene expression raw data files.  
 files: A character. Filenames as shown on the `gene_expression_files` dataset.  
 destdir: A character. The loacal path to store the downloaded files.
- `getGEMatrix(x = NULL, cohort = NULL, summary = FALSE, reload = FALSE)` Downloads a normalized gene expression matrix from ImmuneSpace.  
 'x': A 'character'. The name of the gene expression matrix to download.  
 'cohort': A 'character'. The name of a cohort that has an associated gene expression matrix. Note that if 'cohort' isn't NULL, then 'x' is ignored. 'summary': A 'logical'. If set to TRUE, Downloads a matrix with expression averaged by gene symbol. 'reload': A 'logical'. If set to TRUE, the matrix will be downloaded again, even if a cached cop exist in the ImmuneSpace-Connection object.
- `listDatasets(which = c("datasets", "expression"))` List the datasets available in the study or studies of the connection.
- `listGEAnalysis()` List available gene expression analysis for the connection.
- `quick_plot(...)` Plots a selected dataset. This is the function used by the DataExplorer module on ImmuneSpace.  
 dataset: A character. The name of the dataset to plot, as displayed by the `listDataset` method.  
 normalize\_to\_baseline: A logical. If set to 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'`.

**'...':** Extra argument to be passed to `ggplot`. e.g: `shape = 'Age'`, `color = 'Race'`.

### See Also

[CreateConnection ImmuneSpaceR-package](#)

### Examples

```
## Not run:
sdy269 <- CreateConnection("SDY269")
sdy269

## End(Not run)
```

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ISpalette

*ImmuneSpace palette*

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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)
```

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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$data_cache)
## Not run:
  saveConnection(new_con, tempfile())

## End(Not run)
```

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theme_IS	<i>theme_IS</i>
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### 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()
```

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