

# Package: DoOR.functions (via r-universe)

November 27, 2024

**Type** Package

**Title** Integrating Heterogeneous Odorant Response Data into a Common Response Model: A DoOR to the Complete Olfactome

**Version** 2.0.2

**URL** <https://docs.ropensci.org/DoOR.functions>,  
<http://neuro.uni.kn/DoOR>, <http://dx.doi.org/10.1038/srep21841>,  
<http://dx.doi.org/10.1093/chemse/bjq042>,  
<https://github.com/ropensci/DoOR.functions>

**BugReports** <https://github.com/ropensci/DoOR.functions/issues>

**Description** This is a function package providing functions to perform data manipulations and visualizations for DoOR.data. See the URLs for the original and the DoOR 2.0 publication.

**License** GPL-3

**Encoding** UTF-8

**Imports** utils

**Depends** DoOR.data (>= 2.0.1), R (>= 3.4.1)

**Remotes** Dahaniel/DoOR.data@v2.0.1

**Suggests** ggplot2, grid, gridExtra (>= 2.0.0), knitr, class, rmarkdown, testthat

**VignetteBuilder** knitr

**RoxygenNote** 6.0.1

**Repository** <https://ropensci.r-universe.dev>

**RemoteUrl** <https://github.com/ropensci/DoOR.functions>

**RemoteRef** master

**RemoteSha** 14728b933e5829a558687ae04b3f33c366ccede7

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---

back\_project

*back\_project*

---

## Description

project the model response values back into your scale of interest (spike, deltaF/F..)

**Usage**

```
back_project(template.data, responding.unit,  
            response_matrix = door_default_values("door_response_matrix"))
```

**Arguments**

`template.data` data frame, the data that provides the scale to transform to, containing InChIKeys in a column called "odorants" and responses in a column called "responses"

`responding.unit` character, the name of the receptor/OSN/glomerulus which responses should be transformed

`response_matrix` DoOR response matrix, the source data is picked from here

**Details**

The process of back projection is the following:

1. rescale both data sets to [0,1],
2. find the best fitting model between "bp.data" and "cons.data" (lowest MD value),
3. project the consensus data onto the fitted curv, these are now our normalized, back projected responses
4. rescale all responses to the scale of the original data via a linear fit.

**Value**

Output of `back_project` is a list containing a data frame with the back\_projected data, the original data, the data used as a template and the data that resulted from fitting source and template (before rescaling to the template scale). additionally the parameters of the linear fit between the source and template response scale is returned.

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>  
Shouwen Ma <<shouwen.ma@uni-konstanz.de>>

**Examples**

```
# load some data sets  
data(Or22a)  
data(door_response_matrix)  
  
# create example data we are going to back project  
template.data <- data.frame(odorants = Or22a$InChIKey,  
                           responses = Or22a$Hallem.2004.EN)  
  
# run back_project and plot the results  
bp <- back_project(template.data, "Or22a")
```

```
plot(bp$back_projected$original.data,
     bp$back_projected$back_projected.data,
     xlab = "DoOR consensus response",
     ylab = "back_projected data [spikes, Hallem.2004.EN]")
)
```

---

```
calculate_model      'select the best model function'
```

---

### Description

calculate\_model is used to return the best model function that represent the relationship between responses from study x and y.

### Usage

```
calculate_model(x, y, select.MD = door_default_values("select.MD"))
```

### Arguments

x, y                    data vectors from study x and y (can contain NA)  
select.MD                logical, if TRUE, only the best model function (in terms of MD) will be returned.

### Details

calculate\_model chooses the best model function from following: linear, exponential function, sigmoid, asymptotic model with x intercept, asymptotic model with y intercept and their inverse versions. (If your are interested in these functions please check the sources at <https://github.com/Dahaniel/DoOR.functions>)

### Author(s)

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>  
Daniel Münch <<daniel.muench@uni-konstanz.de>>

### Examples

```
# load a data set
library(DoOR.data)
data(Or35a)

# pick 2 data sets for Or35a and rescale the data [0,1]
x <- door_norm(Or35a[,6])
y <- door_norm(Or35a[,9])
# run calculate_model
calM_xy <- calculate_model(x,y, select.MD = door_default_values("select.MD"))
```

---

count_studies	<i>count_studies</i>
---------------	----------------------

---

## Description

returns a matrix indicating how many studies have recorded individual receptor-odorant combinations

## Usage

```
count_studies(ors = door_default_values("ORs"),
              odor_data = door_default_values("odor"),
              char.columns = door_default_values("num.charColumns"),
              ident = door_default_values("ident"))
```

## Arguments

ors	data.frame containing all receptors existing in DoOR.
odor_data	data.frame containing information about the odorants in DoOR.
char.columns	number of character columns in each receptor data.frame.
ident	odorant identifier to be used as rownames.

## Value

matrix

## Examples

```
# load some data
library(DoOR.data)
load_door_data(nointeraction = TRUE)

#run count studies and plot the result
count <- count_studies()
image(count)
head(count)
```

---

create\_door\_database    *Compose a Response Matrix of All Odor Receptors*

---

### Description

computes the complete response model for all receptors in the database (calls [model\\_response](#) for all receptors). Overwrites `response_matrix`, `door_response_matrix_non_normalized` and `door_excluded_data`.

### Usage

```
create_door_database(tag = door_default_values("tag"),
  select.MDValue = door_default_values("select.MDValue"),
  overlapValues = door_default_values("overlapValues"), ...)
```

### Arguments

tag	character string, format for rownames, possibilities: "InChIKey", "CAS", "CID", "Name"
select.MDValue	a numeric, threshold on the MD, this is used to reject studies that do not align sufficiently well to the response model
overlapValues	numeric, a criterion using to refuse a data set that has not enough overlap value.
...	pass more parameters to <a href="#">model_response</a>

### Author(s)

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>  
Daniel Münch <<daniel.muench@uni-konstanz.de>>

### See Also

[model\\_response](#)

### Examples

```
## Not run:
# load DoOR data
library(DoOR.data)
load_door_data()

# create a new consensus matrix
create_door_database()

## End(Not run)
```

---

DoOR.functions.package

*DoOR Functions*

---

## Description

Functions package providing manipulation and application of the DoOR.

## Details

Package: DoOR.functions  
Type: Package  
Version: 2.0.0  
Date: 2016-01-25  
License: GPL-3  
LazyLoad: yes

**Type** `help(package = DoOR.functions)` **to see a complete list of datasets and functions. Below is what you need for a quick start.**

First, load the DoOR packages, data and function package:

```
library(DoOR.functions):  
library(DoOR.data):
```

then, load all datasets including the precomputed response matrix:

`load_door_data:` Load all data into current active environment (function comes with DoOR.data) .

or, load all odorant response data into a list:

`load2list:` Load odorant response data only and compose them as a list.

Try some visualizations (e.g. producing the plots from the paper):

`dplot_al_map:` response to a chemical mapped onto an image of the antennal lobe.  
`dplot_compare_profiles:` compare the results of two studies.  
`dplot_response_matrix:` Dot Plot of Odorant Responses Across Receptors.  
`dplot_response_profile:` bar plot: one receptor, all chemicals.  
`dplot_tuningCurve:` pyramid diagram depicting a receptor's tuning breadth.

Try some queries:

`get_responses`: given a chemical, get original responses from all studies in the database.  
`get_normalized_responses`: given a chemical, get normalised responses from all studies in the database.

In case you wish to create your own response model (e.g. because you want to include your own datasets):

`create_door_database`: compute the complete response model for all receptors in the database (calls `model_response` for  
`model_response`: run the DoOR algorithm, that merges all measurements for one receptor.

Estimate odorant responses:

`estimate_missing_value`: estimate NA entries in a consensus response data.

Project the model response values back to tested values:

`back_project`: project the model response values back to tested values.

Introduce new data into DoOR and update the supported data sets:

`import_new_data`: import new data into DoOR, and update the weight, response range and receptor names.  
`update_door_database`: update response matrix by calculating new consensus response data for a given receptor.

See the Vignettes and the help pages for more documentation.

### Author(s)

C. Giovanni Galizia  
Daniel Muench  
Martin Strauch  
Anja Nissler  
Shouwen Ma

Maintainer: Daniel Münch <daniel.muench@uni-konstanz.de>

### References

<http://neuro.uni-konstanz.de/DoOR>

### See Also

DoOR.data



---

door\_default\_values     *default values for DoOR functions*

---

**Description**

door\_default\_values is used to return default values for DoOR functions.

**Usage**

```
door_default_values(DoOR_default)
```

**Arguments**

DoOR\_default     a character string, indicating which argument is to be returned for DoOR functions.

**Details**

There are six categories for default value. real number, integer, logical, NULL, character string and character vector.

**Author(s)**

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>

**Examples**

```
# extract DoOR default values
door_default_values(DoOR_default = "select.MD")
```

---

door\_norm             *rescale the data values from 0 to 1*

---

**Description**

door\_norm is used to normalize the data in values from 0 to 1.

**Usage**

```
door_norm(x)
```

**Arguments**

x                    a numeric vector

**Author(s)**

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>  
 Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
# create example data
x <- rnorm(10)

# run door_norm on it
door_norm(x)
```

---

dplot\_across\_osns      *dplot\_across\_osns*

---

**Description**

plot the activation patterns of one or several odorants across OSNs

**Usage**

```
dplot_across_osns(odorants,
  response_matrix = door_default_values("door_response_matrix"),
  odor_data = door_default_values("odor"),
  door_mappings = door_default_values("door_mappings"),
  zero = door_default_values("zero"), tag = "Name", sub, plot.type = 1,
  base_size = 12)
```

**Arguments**

odorants	character vector, one or several InChIKeys
response_matrix	DOOR response matrix, contains the data to plot
odor_data	data frame, contains the odorant information.
door_mappings	data frame, containing the mappings of response profiles to morphological structures.
zero	character, InChIKey of the odorant that should be set to 0 (e.g. SFR)
tag	character, the chemical identifier to use in the plot, one of colnames(odor)
sub	character vector, specify one or several classes of sensilla the plot should be restricted to. One or several of: "ab" "ac", "at", "ai", "pb", "sacI", "sacII"
plot.type	integer, 1 or 2, defining the type of plot (1: facet_grid of odorants * sensillae, 2: facet_wrap across OSNs)
base_size	numeric, the base font size for the ggplot2 plot

## Details

DoOR response profiles will be selected and ordered according to the OSNs they are related to. Several DoOR response profiles might exist for a given OSN (e.g. one for the OSN itself and one for the OSNs misexpressed receptor protein) but only one will be shown. Which DoOR profile is mapped to which OSN is controlled via the "code.OSN" column in DoORmappings.

## Value

a ggplot2 object

## Author(s)

Daniel Münch <<daniel.muench@uni-konstanz.de>>

## Examples

```
# load DoOR data & functions
library(DoOR.data)
library(DoOR.functions)

# pick example odorants by name and transform their ID to InChIKey
odorants <- trans_id(c("1-butanol", "isopentyl acetate", "carbon dioxide", "water"),
  from = "Name", to = "InChIKey")

# plot
dplot_across_osns(odorants)
# plot only across ac and at sensillae
dplot_across_osns(odorants, sub = c("ac", "at"))
# plot across sensory neurons
dplot_across_osns(odorants, plot.type = 2)
```

---

dplot\_across\_ru

*dplot\_across\_ru*

---

## Description

barplot of DoOR responses of a set of odorant across all responding units in DoOR

## Usage

```
dplot_across_ru(odorant,
  response_matrix = door_default_values("door_response_matrix"),
  odor_data = door_default_values("odor"),
  zero = door_default_values("zero"), tag = "Name", limits,
  base_size = 12)
```

**Arguments**

odorant	character vecto, one or several InChIKeys
response_matrix	DoOR response matrix, a DoOR response matrix as data source
odor_data	data frame, contains the odorant information.
zero	character, an InChIKey of the odorant that should be set to 0
tag	character, the chemical identifier to plot as odorant name (one of colnames(odor))
limits	numeric of length 2, if provided the ylim will range accordingly
base_size	numeric, the base font size for the ggplot2 plot

**Value**

a ggplot object

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
# load data
library(DoOR.data)
library(DoOR.functions)
data(odor)

# plot activation pattern of one or several odorants
dplot_across_ru(trans_id("123-92-2"), tag = "CAS")
dplot_across_ru(odor$InChIKey[4:10])
```

---

dplot\_al\_map

*dplot\_al\_map*


---

**Description**

Plot an antennal lobe map with color coded odorant responses.

**Usage**

```
dplot_al_map(InChIKey,
  response_matrix = door_default_values("door_response_matrix"),
  odor_data = door_default_values("odor"),
  door_mappings = door_default_values("door_mappings"),
  zero = door_default_values("zero"),
  tag = door_default_values("tag.ALmap"), main = "Name",
  scalebar = door_default_values("scalebar"),
```

```
door_AL_map = door_default_values("door_AL_map"),
colors = door_default_values("colors"), legend = TRUE, limits,
base_size = 12)
```

### Arguments

InChIKey	InChIKey specifying the odorant to plot
response_matrix	the input data (e.g. door_response_matrix or door_response_matrix_non_normalized)
odor_data	data frame, contains the odorant information.
door_mappings	the data frame containing the mapping information
zero	the odorant to set to zero (defaults to "SFR")
tag	the labels to plot on top of the glomeruli (one of the following door_mappings columns: "receptor", "sensillum", "ORN", "glomerulus" or "co.receptor")
main	the title, one column of odor, defaults to "Name"
scalebar	whether or not to add a scalebar
door_AL_map	a list containing the AL model
colors	a vector containing 6 color values (2 for values below 0, 1 0 value and 3 steps between 0 and 1)
legend	logical, plot a legend?
limits	the limits for the color scale, if empty the range of the response matrix is taken (after setting "zero" to 0)
base_size	numeric, the base font size for the ggplot plot

### Details

Normalized, color coded odor responses across receptors are mapped onto a map of the *Drosophila* antennal lobe. The antennal lobe map was a kind gift from Veit Grabe.

### Value

a ggplot2 object

### Author(s)

Daniel Münch <daniel.muench@uni-konstanz.de>

Daniel Münch <<daniel.muench@uni-konstanz.de>>

### References

Grabe, V., Strutz, A., Baschwitz, A., Hansson, B.S., Sachse, S., 2014. A digital in vivo 3D atlas of the antennal lobe of *Drosophila melanogaster*. *J. Comp. Neurol.* n/a–n/a. doi:10.1002/cne.23697

### See Also

[get\\_normalized\\_responses](#), [ggplot2](#), [grid](#)

**Examples**

```

# load data
library(DoOR.data)
library(DoOR.functions)

# map responses on antennal lobe scheme
dplot_al_map("MLFHJEHSLIIPHL-UHFFFAOYSA-N", scalebar = FALSE)

# change colors
dplot_al_map("MLFHJEHSLIIPHL-UHFFFAOYSA-N", tag = "Ors",
  color = c("magenta", "pink", "white", "yellow", "orange", "red"))

# pass some ggplot2 theming parameters
dplot_al_map(trans_id("123-92-2"), scalebar = FALSE) +
  ggplot2::theme(legend.position = "bottom",
    panel.background = ggplot2::element_rect(fill = "grey90", color = NA)) +
  ggplot2::ggtitle("responses elicited by isopentyl acetate")

# export as pdf
## Not run:
p <- dplot_al_map(trans_id("123-92-2"))
ggplot2::ggsave("AL.response.pdf", p, width = 6, height = 2, scale = 2)

## End(Not run)

```

---

dplot\_compare\_profiles

*Compare two response profiles*

---

**Description**

Orderdered bar plots for two studies, allowing for an easy comparison of the two studies / response profiles'.

**Usage**

```
dplot_compare_profiles(x, y, by.x, by.y, tag = "Name", base_size = 12)
```

**Arguments**

x	the input data frame the first response profile will be taken from
y	the input data frame the second response profile will be taken from (x will be taken if y is missing)
by.x	character string, specifying a column in x
by.y	character string, specifying a column in y
tag	character, the chemical identifier that will be used as odorant label.
base_size	numeric, the base font size for the ggplot2 plot

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
# load data
library(DoOR.data)
library(DoOR.functions)
data(Or22a)
data(door_response_range)
data(door_response_matrix)

# compare the Hallem and the Pelz data set for Or22a
dplot_compare_profiles(x = Or22a, y = Or22a,
                      by.x = "Hallem.2006.EN",
                      by.y = "Pelz.2006.AntEC50")

# comparedata from two different sensory neurons and add odorant labels
dplot_compare_profiles(x = cbind(door_response_matrix, InChIKey =
rownames(door_response_matrix)), y = cbind(door_response_matrix, InChIKey =
rownames(door_response_matrix)), by.x = "Or22a", by.y = "Or10a")
```

---

dplot\_response\_matrix *dplot\_response\_matrix*

---

**Description**

plot DoOR responses as a point matrix

**Usage**

```
dplot_response_matrix(data, odor_data = door_default_values("odor"),
                      tag = door_default_values("tag"), colors = door_default_values("colors"),
                      flip = FALSE, fix = TRUE, bw = FALSE, point = FALSE, limits,
                      base_size = 12)
```

**Arguments**

<code>data</code>	a subset of e.g. <code>door_response_matrix</code>
<code>odor_data</code>	data frame, contains the odorant information.
<code>tag</code>	the chemical identifier to plot (one of <code>colnames(odor)</code> )
<code>colors</code>	the colors to use if negative values are supplied (range of 5 colors, 2 for negative values, 1 for 0 and 3 for positive values)
<code>flip</code>	logical, if TRUE the x and y axes will be flipped
<code>fix</code>	logical, whether to fix the ratio of the tiles when plotting as a heatmap

bw	logical, whether to plot b&w or colored
point	logical, if TRUE a point matrix instead of a heatmap will be returned (the default if you supply only positive values)
limits	the limits of the scale, will be calculated if not set
base_size	numeric, the base font size for the ggplot2 plot

**Value**

a dotplot if `limits[1] >= 0` or a heatmap if `limits[1] < 0`

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
# load data
library(DoOR.data)
data(door_response_matrix)

# reset the spontaneous firing rate to 0
tmp <- reset_sfr(door_response_matrix, "SFR")

# plot heatmap / coloured tiles
dplot_response_matrix(tmp[10:50,], tag = "Name",
  limits = range(tmp, na.rm = TRUE))

# plot dotplot
dplot_response_matrix(door_response_matrix[10:50,], tag = "Name",
  limits = range(door_response_matrix, na.rm = TRUE))
```

---

dplot\_response\_profile

*dplot\_response\_profile*

---

**Description**

create a barplot of a DoOR response profile

**Usage**

```
dplot_response_profile(receptor,
  response_matrix = door_default_values("door_response_matrix"),
  odor_data = door_default_values("odor"), tag = door_default_values("tag"),
  colored = TRUE, colors = door_default_values("colors"), limits,
  zero = door_default_values("zero"),
  scalebar = door_default_values("scalebar"), base_size = 12)
```



**Arguments**

receptor	character, receptor name, any of colnames(door_response_matrix)
response_matrix	a DoOR door_response_matrix
odor_data	data frame, contains the odorant information.
tag	character, chemical identifier for annotation
colored	logical, color code the bars according to the response value?
colors	character vector, a vector of 5 colors (2 for values < 0, 1 value for 0 and 3 values > 0)
limits	numeric of length 2, the limits for the colorscale and the x axis, global range of data will be used if empty
zero	character, the odorant response that is set to 0, defaults to "SFR"
scalebar	logical, add or suppress scalebars
base_size	numeric, the base font size for the ggplot2 plot

**Value**

ggplot2 plot

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
# load data
library(DoOR.data)
data(door_response_matrix)

# plot with default parameters
dplot_response_profile("Or22a", door_response_matrix)

# plot wit odorant names
dplot_response_profile("Or22a", door_response_matrix, tag = "Name")
```

---

dplot\_tuningCurve      *dplot\_tuningCurve*

---

**Description**

plot a receptor or odorant tuning curve

**Usage**

```
dplot_tuningCurve(receptor, odorant, response.vector,
  response_matrix = door_default_values("door_response_matrix"),
  odor_data = door_default_values("odor"),
  zero = door_default_values("zero"),
  fill.receptor = door_default_values("color.receptor"),
  fill.odorant = door_default_values("color.odorant"), odor.main = "Name",
  limits, base_size = 12)
```

**Arguments**

receptor	character, a receptor name (one of ORS\$OR)
odorant	character, an odorant name (InChIKey)
response.vector	numerical vector, a vector with responses, if empty this is taken from door_response_matrix
response_matrix	DoOR response matrix, response vector will be taken from here, not needed if response.vector is given
odor_data	data frame, contains the odorant information.
zero	InChIKey, will be set to zero, default is SFR, ignored when data is provided via response.vector, set to "" if you don't want to subtract anything
fill.receptor	color code, bar color for receptor tuning curve
fill.odorant	color code, bar color for odorant tuning curve
odor.main	the odor identifier to plot, one of colnamed(odor)
limits	the numerical vector of length 2, y limits for the tuning curve
base_size	numeric, the base font size for the ggplot2 plot

**Value**

a ggplot object

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
# load data
library(DoOR.data)
data(door_response_matrix)
data(odor)

# plot a tuning curve for an odorant
dplot_tuningCurve(odorant = odor$InChIKey[2])
# or for a receptor
dplot_tuningCurve(receptor = "Or22a")
```

```
# adjust the plotting range
range <- range(reset_sfr(door_response_matrix, "SFR"), na.rm = TRUE)
dplot_tuningCurve(receptor = "Or10a", limits = range,
                  fill.receptor = "magenta")

# plot with manual input data as receptor tuning curve
dplot_tuningCurve(receptor = "receptor X", response.vector = c(1:100))
# or as odor tuning curve
dplot_tuningCurve(odorant = "odor X", response.vector = rnorm(200))
```

---

estimate\_missing\_value

*Estimate the missing entries in a response data*

---

## Description

Estimate the missing entries in a response data

## Usage

```
estimate_missing_value(data, nodor, method = "PC")
```

## Arguments

data	a data frame or matrix, containing the consensus response values
nodor	a numeric value, specifying the number of the selected odors
method	character string, specifying the method ("PC" (Pearson's coefficient) and "Knn" (k nearest neighbors)) for estimation, the default is "PC".

## Details

A wrapper program for using Pearson Correlation or k-nearest neighbors to estimate the missing entries in a response matrix.

## Author(s)

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>

## References

Kim, H., Golub, G. H. & Park, H., Missing value estimation for DNA microarray gene expression data: local least squares imputation., 2005, Bioinformatics, 21, 187-198

**Examples**

```
## Not run:
# load data
library(DoOR.data)
data(door_response_matrix)

# pick an example subset
subset <- door_response_matrix[1:100, 11:30]

# estimate missing values
est.data <- estimate_missing_value(data = subset, nodor = 6)

## End(Not run)
```

---

export_door_data	<i>export data</i>
------------------	--------------------

---

**Description**

export odor response data and supported data

**Usage**

```
export_door_data(file.format, directory,
  odorantReceptors = door_default_values("ORs"),
  response_matrix = door_default_values("door_response_matrix"),
  responseRange = door_default_values("door_response_range"),
  unglobalNorm_RM = door_default_values("door_response_matrix_non_normalized"),
  weightGlobNorm = door_default_values("door_global_normalization_weights"),
  all.data = TRUE)
```

**Arguments**

file.format	character string, the format of given file, either ".txt" or ".csv"
directory	character string, naming a directory for writing. If missing, the exported data are saved in current working directory.
odorantReceptors	data frame, receptor names and expressions
response_matrix	data matrix, an global unnormalized responses matrix
responseRange	data frame, response ranges for each study
unglobalNorm_RM	data matrix, an unnormalized responses matrix
weightGlobNorm	data frame, weight matrix for global normalizazion
all.data	logical, if TRUE, export odorant response data and supported data "door_response_matrix", "door_response_range", "door_response_matrix_non_normalized", "door_response_matrix", "door_global_normalization_weights" and "ORs".

**Details**

Please load ORs from data package DoOR.data by typing (data(ORs)) before use.

**Author(s)**

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>

**Examples**

```
## Not run:  
# load data  
library(DoOR.data)  
library(DoOR.functions)  
load_door_data()  
  
# export odorant response data only  
export_door_data(".txt", all.data = FALSE)  
  
## End(Not run)
```

---

get\_dataset

*getDataset*

---

**Description**

aggregates original data from a given study

**Usage**

```
get_dataset(study, na.rm = FALSE)
```

**Arguments**

study	character, the name of the study you want to aggregate the data from
na.rm	logical, whether or not to exclude odorants that were not measured in the study

**Value**

returns a data frame containing all the odorant responses measured in study

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>

## Examples

```
# load data
library(DoOR.data)
load_door_data(nointeraction = TRUE)

# get all recordings from the Hallem.2004.EN data set
get_dataset("Hallem.2004.EN", na.rm = TRUE)
```

---

get\_normalized\_responses

*Find normalised receptor responses*

---

## Description

given a chemical, get normalised receptor responses from all studies in the database.

## Usage

```
get_normalized_responses(odors, zero = door_default_values("zero"),
  response_matrix = door_default_values("door_response_matrix"), round = 3,
  na.rm = FALSE)
```

## Arguments

odors	character vector, one or more odors provided as InChIKey.
zero	InChIKey of background that should be set to zero. The default is "SFR", i.e. the spontaneous firing rate.
response_matrix	a data frame, as e.g. "door_response_matrix" that is loaded by <a href="#">model_response</a> . It is also possible to create this frame manually using <a href="#">model_response</a> .
round	numeric, round to this amount of digits, set to NA if you do not want to round
na.rm	logical, remove NAs?

## Author(s)

Daniel Münch <daniel.muench@uni-konstanz.de>

## See Also

[model\\_response](#), [create\\_door\\_database](#)

## Examples

```
# load data
library(DoOR.data)
data(door_response_matrix)

# define a list of odorants
odors <- c("MLFHJEHSLIIPHL-UHFFFAOYSA-N",
           "OBNCCKNCVKJNDBV-UHFFFAOYSA-N",
           "IKHGUXGNUITLKF-UHFFFAOYSA-N")

# get the normalized responses for these odorants
result <- get_normalized_responses(odors,
                                  response_matrix = door_response_matrix)
```

---

get_responses	<i>Find receptor responses</i>
---------------	--------------------------------

---

## Description

given a chemical, get original receptor responses from all studies in the database.

## Usage

```
get_responses(odorant,
              responseRange = door_default_values("door_response_range"),
              Or.list = load2list())
```

## Arguments

odorant	a single odor provided as InChIKey
responseRange	data frame, response ranges of studies
Or.list	a list contains reponse data of all available receptors. It can be loaded using <a href="#">load2list</a> .

## Details

output is a data frame containing response values of given odor across receptors from all available studies.

## Author(s)

Daniel Münch <daniel.muench@uni-konstanz.de>

**Examples**

```
# load data
library(DoOR.data)
load_door_data(nointeraction = TRUE)

# get raw responses for odorant MLFHJEHSLIIPHL-UHFFFAOYSA-N
responses <- get_responses(odorant = 'MLFHJEHSLIIPHL-UHFFFAOYSA-N')
```

---

```
identify_sensillum    identify_sensillum
```

---

**Description**

correlates the result from a SSR recording of several odorants against all DoOR response profiles

**Usage**

```
identify_sensillum(recording,
  response_matrix = door_default_values("door_response_matrix"),
  odor_data = door_default_values("odor"),
  door_mappings = door_default_values("door_mappings"), tag = "Name",
  min.cor = 0.9, nshow = 10, method = "cor", sub, base_size = 12,
  plot = TRUE, use = "everything")
```

**Arguments**

recording	data frame, a data frame with the following columns "odorants" containing InChIKeys of the tested odorant, and one column called "unit1" etc. for each unit, containing responses (or estimates) scaled between 0 and 1 (see examples)
response_matrix	DoOR response matrix, the data to compare against
odor_data	data frame, contains the odorant information.
door_mappings	the data frame containing the mapping information
tag	character, the chemical identifier to use in plots, one of colnames(odor)
min.cor	numeric, a minimum correlation value, the function will check whether there is a higher correlation for all units within a single sensillum
nshow	numeric, the number of plots to show, plot e.g. only the top 10 matches
method	character, the method for similarity calculations: correlation ("cor") or Euclidean distances ("dist")
sub	character, if you know the class of sensillum you were recording from you can restrict the search to this subset here ("ab", "ac", "at", "pb", "sac")
base_size	numeric, the base font size of the ggplot plots
plot	logical, if TRUE returns the plot, else returns the data frame with the correlations/distances



use character, the "use" option from the cor function, "all" returns NA when pairs are incomplete, "na.or.complete" only uses complete observations to calculate correlations; see [cor](#) for details

### Value

either a plot (gtable) with responses sorted by highest correlations or lowest distances, or a data frame containing all calculated correlations or Euclidean distances

### Author(s)

Daniel Münch <<daniel.muench@uni-konstanz.de>>

### Examples

```
# load data
library(DoOR.data)

# create an example recording
recording <- data.frame(
  odorants = c(trans_id(c("BEDN", "ETAS"), "Code"),
    trans_id("carbon dioxide", "Name")),
  unit1 = c(.9, .1, .1),
  unit2 = c(0, .1, 1)
)

# run the identification
identify_sensillum(recording)
identify_sensillum(recording, method = "dist", nshow = 5)
```

---

import_new_data	<i>Import new data into DoOR</i>
-----------------	----------------------------------

---

### Description

Import or update new data and update door\_global\_normalization\_weights, door\_response\_range, odor, ORs and receptor data frames.

### Usage

```
import_new_data(file.name,
  dataFormat = door_default_values("door_data_format"),
  odor_data = door_default_values("odor"),
  weightGlobNorm = door_default_values("door_global_normalization_weights"),
  responseRange = door_default_values("door_response_range"),
  receptors = door_default_values("ORs"),
  ident = door_default_values("ident"), round = 3)
```

**Arguments**

file.name	character string, the name of given file that contains response values of one or more odorant receptors, either a .csv or .txt file.
dataFormat	data frame, a data frame does not contain any response value but odorant information.
odor_data	data frame, contains the odorant information.
weightGlobNorm	data matrix, indicates whether given receptor has been measured by given study.
responseRange	data frame, contains the information about response range of each study and how many odors have been measured in each study.
receptors	data frame, contains the receptor and OSN names and their expression.
ident	the identifier used for matching, usually the InChIKey is used.
round	the number of digits the imported values are rounded to.

**Details**

`import_new_data` is used to import new data into database. If the data contains a new receptor or ORN, then build a new data frame for this receptor or ORN. If the data contains a receptor that is already present in database, then merge the imported data into old data frame. The information (e.g. response range, how many receptors and odors were measured from given study) will be integrated into data `door_response_range`, `odor`, `ORs` and `door_global_normalization_weights`. If an existing study is imported, `remove_study` will be run first in order to perform an update.

**Author(s)**

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>

Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
## Not run:
import new data named "odorantResponses_Orx.txt" into database and update the
support data.
library(DoOR.data)
import_new_data(file.name = "odorantResponses_Orx.csv")

## End(Not run)
```

---

load2list

*load2list*

---

**Description**

returns all original DoOR response data as a list

**Usage**

```
load2list()
```

**Value**

a list

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
# load DoOR.data
library(DoOR.data)
load_door_data(nointeraction = TRUE)

# write the data into a list
lst <- load2list()
```

---

map\_receptor

*map\_receptor*

---

**Description**

Identifying the source of unknown response data by correlating it against all DoOR responding units.

**Usage**

```
map_receptor(data,
  response_matrix = door_default_values("door_response_matrix"), sub,
  threshold.p, threshold.cor, nshow)
```

**Arguments**

data	data frame, containing two columns, one called "odorants" and one "responses" providing InChIKeys and odorant responses respectively.
response_matrix	output is a numeric vector that contains the Pearson Correlation Coefficient between given data and selected consensus data in
sub	character, a subset of responding units returned response matrix
threshold.p	numeric, a p-value threshold, only correlations below will be returned
threshold.cor	numeric, a correlation-coefficient threshold, only correlations above will be returned
nshow	numeric, if defined, only this number of results will be

**Author(s)**

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>  
 Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
# load data
load_door_data(nointeraction = TRUE)

# pick example data
data <- data.frame(odorants = Or22a$InChIKey,
                  responses = Or22a$Hallem.2004.EN)
data <- na.omit(data)

# find the corresponding receptor / responding unit
map_receptor(data = data)
```

---

model_response	<i>Generates a model response</i>
----------------	-----------------------------------

---

**Description**

Runs the DoOR algorithm, that merges all measurements for one receptor into a common response model.

**Usage**

```
model_response(da, select.MDValue = door_default_values("select.MDValue"),
              overlapValues = door_default_values("overlapValues"),
              responseRange = door_default_values("door_response_range"),
              weightGlobNorm = door_default_values("door_global_normalization_weights"),
              glob.normalization = door_default_values("glob.normalization"),
              plot = door_default_values("plot"))
```

**Arguments**

da	data frame, a selected receptor containing measured responses from studies.
select.MDValue	numeric, threshold on the MD for rejecting a fit.
overlapValues	numeric, a criterion using to refuse a data set that has not enough overlap value.
responseRange	data frame, contains response ranges for all studies.
weightGlobNorm	data frame, a binary data matrix, 1 indicates given odor has been measured in given study, NA indicates NOT.
glob.normalization	logical, default is TRUE, performs a global normalization for the model response. Otherwise (FALSE) response values will be given in value from 0 to 1.
plot	logical, If FALSE, plotting is suppressed. Default is FALSE.

## Details

Merging a data is processed by following:

1. Normalize all response data in value [0,1].
2. Compute the correlation between studies and selected the best pair using [select\\_model](#).
3. Merge the first pair using function [project\\_points](#).
4. Add other datasets if the correlation between the growing model response and the new dataset is below the correlation threshold (select.MDValue). Datasets excluded based on this criterion will be appended in a separate list.

## Author(s)

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>

## Examples

```
# load data
library(DoOR.data)
data(Or35a)
data(door_global_normalization_weights)
data(door_response_range)

# merge all existing data sets for Or35a into a consensus model response
model_response_Or35a <- model_response(Or35a, plot = TRUE)
```

---

model\_response\_seq     *model\_response\_seq*

---

## Description

generates a model response and merge data in given sequence

## Usage

```
model_response_seq(data, SEQ,
  overlapValues = door_default_values("overlapValues"),
  select.MDValue = door_default_values("select.MDValue"), strict = TRUE,
  plot = FALSE)
```

## Arguments

data	data frame, odorant response data, e.g. Or22a.
SEQ	character vector, containing the names of studies indicating given sequence for merging data.
overlapValues	minimum overlap between studies to perform a merge

`select.MDValue` the minimum mean distance between studies to perform a merge  
`strict` logical, if TRUE merging a permutation will be stopped once a single merge has a mean distance above `select.MDValue`  
`plot` logical

### Details

```

# model_response_seq.R: #####
# merges studies in a given sequence (determined by the user or by exhaustive enumeration and
choosing the optimal sequence)
# input parameters: #####
# data : data frame, odorant response data for a given receptor, e.g. Or22a # SEQ : character vector,
contains the names of studies that measured this receptor in a specific order (the merging sequence)
# output is a numeric vector: response values
  
```

### Author(s)

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>

### Examples

```

# load data
library(DoOR.data)
data(Or35a)
data(door_response_range)

# specify a sequence of merging
SEQ <- c("Hallem.2006.EN", "Kreher.2008.EN", "Hallem.2006.EN")

# perform the merging
selected_merg <- model_response_seq(Or35a, SEQ = SEQ, plot = TRUE)
  
```

---

private\_odorant      *private\_odorant*

---

### Description

return an odorant that activates the receptor of interest exclusively

### Usage

```

private_odorant(receptor, sensillum = FALSE,
  response_matrix = door_default_values("door_response_matrix"),
  door_mappings = door_default_values("door_mappings"),
  zero = door_default_values("zero"), nshow = 5, tag)
  
```

**Arguments**

receptor	character, name of a DoOR responding unit (one of ORs\$Or)
sensillum	logical, restrict the search to the sensillum the receptor is expressed in?
response_matrix	DoOR response matrix, the input data to perform the search on
door_mappings	the data frame containing the mapping information
zero	character, an odorant that should be set to 0
nshow	numeric, the number of private odorants to return
tag	character, the chemical identifier to give the odorant names in (on of colnames(odor))

**Value**

a data.frame containing odorants and the response in the receptor of interest as well as the maximum response of the remaining receptors and their difference

**Examples**

```
# load data
library(DoOR.data)

# find a private odorant for Gr21a.Gr63a (the carbon dioxide receptor)
# private_odorant("Gr21a.Gr63a", tag = "Name")

# now find an odorant that within the ab3 sensillum specifically activates
# Or22a
private_odorant("Or22a", tag = "Name", sensillum = TRUE)
```

---

project\_points      *project\_points*

---

**Description**

projects data points onto the curve defined by the model function

**Usage**

```
project_points(x, y, xlim, best.model, plot = door_default_values("plot"),
  points_cex = door_default_values("points.cex"),
  title = door_default_values("title"), ...)
```

**Arguments**

<code>x, y</code>	numeric vectors of data values, coordinate vectors of points to plot, the coordinates can contain NA values.
<code>xylim</code>	numeric vectors, x, y limits of the plot.
<code>best.model</code>	a list, containing the parameters, function, inverse function, Leibniz's notation for distance calculation and MD value. if missing, the best model will be generated automatically.
<code>plot</code>	logical, If FALSE, plotting is suppressed. Default is FALSE.
<code>points_cex</code>	a numerical value, giving the magnification level of symbols relative to the default size.
<code>title</code>	logical, If TRUE, title is shown. Default is FALSE.
<code>...</code>	further graphical parameters

**Details**

For internal use in the merging process (see also [model\\_response](#)). The model function is chosen by [calculate\\_model](#). [project\\_points](#) then projects the data points from the datasets to be merged onto the curve defined by the model function. It computes the closest distance from a data point to a point on the curve by numerical optimisation.

A list with two data frames "double.observations" and "single.observations" is returned, which give the coordinates of double observations (defined as (x,y)) and coordinates of single observation (defined as (x,NA) or (NA,y)). Both data frames contain seven columns: "ID" indicating the original position of data x and y, "x", "y" indicating the coordinate of observation, "X", "Y" indicating the coordinate of projected point on the function, "distance" indicating the distances between (xmin, f(xmin)) and all points on the functional line, "NDR" indicating the normalized distances across all the distance values.

**Author(s)**

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>

**See Also**

[calculate\\_model](#), [optimize](#), [integrate](#)

**Examples**

```
# load data
library(DoOR.data)
data(Or23a)

# normalize two example data sets
x <- door_norm(Or23a[, 'Hallem.2004.EN'])
y <- door_norm(Or23a[, 'Hallem.2006.EN'])

# find the best fitting function and project the remaining points (measured
# only in one of the data sets) onto the fit.
project_points(x = x, y = y, plot = TRUE)
```



---

remove_study	<i>Remove a study from DoOR</i>
--------------	---------------------------------

---

### Description

Use this function to remove a study from the DoOR database. `import_new_data.R` uses this function when it detects an existing study during the import process (e.g. because you imported updated data).

### Usage

```
remove_study(study, receptors = door_default_values("ORs"),
             responseRange = door_default_values("door_response_range"),
             weightGlobNorm = door_default_values("door_global_normalization_weights"))
```

### Arguments

<code>study</code>	a string containing the name of the study you want to remove (e.g. 'Bruyne.2001.WT')
<code>receptors</code>	a vector of all the receptors to be checked. Defaults to all receptors existing in DoOR.
<code>responseRange</code>	the dataframe containing the info about the response ranges of all studies ( <code>door_response_range</code> )
<code>weightGlobNorm</code>	the dataframe containing the info about the relative weights between receptors ( <code>door_global_normalization_weights</code> )

### Author(s)

Daniel Münch <<daniel.muench@uni-konstanz.de>>

### See Also

[import\\_new\\_data](#)

### Examples

```
# load data
library(DoOR.data)
load_door_data(nointeraction = TRUE)

# remove Bruyne.2001.WT from DoOR
remove_study('Bruyne.2001.WT')
```

---

reset_sfr	<i>reset SFR</i>
-----------	------------------

---

**Description**

A function for resetting SFR to zero

**Usage**

```
reset_sfr(x, sfr)
```

**Arguments**

x	numeric or DoOR response matrix, input values
sfr	numeric or character, either a value to subtract if x is a vector or an InChIKey if x is a DoOR response matrix

**Details**

Performs a simple subtraction of the SFR value.

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>

**Examples**

```
# load data
library(DoOR.data)
data(door_response_matrix)

# create a response matrix with the SFR reset to 0
door_response_matrix_SFRreset <- reset_sfr(door_response_matrix, "SFR")
```

---

select_model	<i>compute the data pairwise and and selects a pair with the lowest "MD" value.</i>
--------------	---

---

**Description**

compute the data pairwise using function [calculate\\_model](#) and selects a pair with the lowest "MD" value.

**Usage**

```
select_model(candidate, data_candidate, merged_data,  
             overlapValues = door_default_values("overlapValues"),  
             merged = door_default_values("merged"))
```

**Arguments**

candidate        a character vector, contains the names of studies.  
data\_candidate   a data frame, odorant response data that only contains value columns.  
merged\_data      numeric vector, merged data  
overlapValues    numeric, a criterion using to refuse a data set that has not enough overlap value.  
merged           logical, if merged is TRUE, calculate models between merged\_data and candidate data. If FALSE, calculate models between candidates.

**Details**

This function is used in [model\\_response](#) to select the first pair or next data set for merging. The output is a list containing "selected.x" and "selected.y" that specify which data plots against another, and "best.model" that is used in function [project\\_points](#).

**Author(s)**

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>

**See Also**

[project\\_points](#), [model\\_response](#)

**Examples**

```
# load data  
library(DoOR.data)  
data(ac3B)  
  
# split into data and header  
studies <- names(ac3B)[c(7:8)]  
data_candidate <- ac3B[,c(7:8)]  
  
# rescale data  
norm_data_candidate <- apply(data_candidate, 2, door_norm)  
  
# find the best fitting model  
select_model(candidate = studies, data_candidate = norm_data_candidate,  
             merged = FALSE)
```

---

sparse	<i>Calculate the sparseness of a vector.</i>
--------	--

---

**Description**

Sparseness can be calculated as lifetime kurtosis (LTK, Willmore and Tolhurst, 2001) or as lifetime sparseness (LTS, Bhandawat et al., 2007).

**Usage**

```
sparse(x, method = "ltk")
```

**Arguments**

x	numerical input vector
method	type of sparseness measure, either 'ltk' for lifetime kurtosis or 'lts' for lifetime sparseness (see references).

**Details**

LTS scales between  $[0,1]$  while LTK is not restricted. LTS only takes positive values.

**Author(s)**

Daniel Münch <<daniel.muench@uni-konstanz.de>>

**References**

Bhandawat, V., Olsen, S.R., Gouwens, N.W., Schlief, M.L., Wilson, R.I., 2007. Sensory processing in the Drosophila antennal lobe increases reliability and separability of ensemble odor representations. *Nature neuroscience* 10, 1474–82. doi:10.1038/nn1976

Willmore, B., Tolhurst, D.J., 2001. Characterizing the sparseness of neural codes. *Network* 12, 255–270. doi:10.1080/net.12.3.255.270

---

trans_id	<i>trans_id</i>
----------	-----------------

---

**Description**

Translate chemical identifiers from one to the other.

**Usage**

```
trans_id(x, from = "CAS", to = "InChIKey",
        odor_data = door_default_values("odor"))
```

**Arguments**

x	character vector, one or many chemical identifiers
from	character, the type of identifier to translate from (one of the column names of “odor“)
to	character, the type of identifier to translate from (one of the column names of “odor“)
odor_data	the data frame containing the odor information (defaults to “odor“).

**Value**

character vector of translated chemical identifiers

**Examples**

```
# load data
library(DoOR.data)

# transform CAS to InChIKey
trans_id("123-92-2")

# transform Name to InChIKey
trans_id("isopentyl acetate", "Name")

# transform SMILE to InChIKey
trans_id("C(C(C)C)COC(=O)C", "SMILES", "Name")
```

---

update\_door\_database    *update response matrix*

---

**Description**

update the globally response matrix and the unglobally normalized response matrix `door_response_matrix_non_normal` by introducing new consensus response data of given receptor.

**Usage**

```
update_door_database(receptor, permutation = TRUE, perm,
  response_matrix_nn = door_default_values("door_response_matrix_non_normalized"),
  response_matrix = door_default_values("door_response_matrix"),
  responseRange = door_default_values("door_response_range"),
  weightGlobNorm = door_default_values("door_global_normalization_weights"),
  select.MDValue = door_default_values("select.MDValue"), strict = TRUE,
  overlapValues = door_default_values("overlapValues"),
  door_excluded_data = door_default_values("door_excluded_data"),
  plot = FALSE)
```

**Arguments**

receptor	character string, name of given odorant receptor.
permutation	logical, if TRUE, the sequence is chosen from permutation, if FALSE, sequence is chosen by the routine process.
perm	a matrix with one sequence of study names per row, if empty, all possible permutations of study names will be provided.
response_matrix_nn	data frame, response data that has not been globally normalized.
response_matrix	data frame, globally normalized response data.
responseRange	data frame, response range of studies.
weightGlobNorm	data frame, weight matrix for global normalization.
select.MDValue	the minimum mean distance between studies to perform a merge (used if permutation == FALSE or if permutation == TRUE AND strict == TRUE)
strict	logical, if TRUE merging a permutation will be stopped once a single merge has a mean distance above select.MDValue (only valid if permutation == TRUE)
overlapValues	minimum overlap between studies to perform a merge
door_excluded_data	the data frame that contains the list of excluded data sets.
plot	logical

**Details**

The merging sequence could be arranged by the routine process (using [model\\_response](#) or taking the optimized sequence that is chosen from permutations. The mean correlation between merged responses and each original recording will be computed for each permutation, the optimized sequence is with the highest correlation.

**Author(s)**

Shouwen Ma <<shouwen.ma@uni-konstanz.de>>  
 Shouwen Ma <<daniel.muench@uni-konstanz.de>>

**See Also**

[model\\_response](#), [model\\_response\\_seq](#)

**Examples**

```
## Not run:
# load data
library(DoOR.data)
load_door_data()
# update the entry "Or67b" of data "door_response_matrix" and
# "door_response_matrix_non_normalized" with permutations.
update_door_database(receptor="Or67b", permutation = TRUE)

## End(Not run)
```

---

update\_door\_odorinfo    *update\_door\_odorinfo*

---

**Description**

Update the DoOR odor data with info from odor. For the function to work, all DoOR data has to be loaded to the current environment.

**Usage**

```
update_door_odorinfo()
```

**Author(s)**

Daniel Münch, <daniel@muench.bio>

**Examples**

```
# load data
load_door_data(nointeraction = TRUE)
# modify odor
odor[1,1] <- "acid"

# run
update_door_odorinfo()

# check that data sets have been updated
head(Or22a)
```

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