

Package: INSPECTumours (via r-universe)

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Title IN-vivo reSPonse Classification of Tumours

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Description This is a shiny app used for the statistical classifying and analysing pre-clinical tumour responses.

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Depends R (>= 3.5.0)

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aggregate_study_info *create a table with aggregated data: each row contains information about control and treatments of a single study*

Description

create a table with aggregated data: each row contains information about control and treatments of a single study

Usage

```
aggregate_study_info(df)
```

Arguments

```
df          data.frame
```

Value

```
data.frame
```

```
animal_info_classification
```

Generate table representing number of animals in classification groups

Description

Generate table representing number of animals in classification groups

Usage

```
animal_info_classification(data)
```

Arguments

```
data          final classification data
```

Value

```
data frame
```

```
assess_efficacy
```

Credible interval (or say “Bayesian confidence interval”) of the mean difference between two groups (treatment and reference) is used to assess the efficacy. If 0 falls outside the interval, the drug was considered significantly effective

Description

Credible interval (or say “Bayesian confidence interval”) of the mean difference between two groups (treatment and reference) is used to assess the efficacy. If 0 falls outside the interval, the drug was considered significantly effective

Usage

```
assess_efficacy(data, reference = "Control")
```

Arguments

data	prediction results
reference	name of the reference treatment

Value

dataframe with information about drug efficacy

below_min_points	<i>makes df with data to be excluded</i>
------------------	--

Description

makes df with data to be excluded

Usage

```
below_min_points(df, min_points)
```

Arguments

df	initial data frame
min_points	minimum number of data points for one animal_id per study

Value

df

calc_gr	<i>Function to return rate of growth (e.g. the slope after a log transformation of the tumour data against time)</i>
---------	--

Description

Function to return rate of growth (e.g. the slope after a log transformation of the tumour data against time)

Usage

```
calc_gr(df, log_tv = "log_tv", day = "day")
```

Arguments

df subset, one animal_id
log_tv name of the column, tumour volume
day name of the column, days

Value

tibble with GR and GR_SE

calc_probability *Calculate probability of categories*

Description

Calculate probability of categories

Usage

calc_probability(data)

Arguments

data data frame with predictions

Value

data frame

calc_survived *Calculate percentage of survived animals*

Description

Calculate percentage of survived animals

Usage

calc_survived(df)

Arguments

df data frame

Value

data frame

change_time_multi *Get an array with change_time for studies from the population-level effects, multiple studies*

Description

Get an array with change_time for studies from the population-level effects, multiple studies

Usage

```
change_time_multi(model)
```

Arguments

model an object of class brmsfit

Value

data frame

change_time_single *Get a change time from the population-level effects, single study*

Description

Get a change time from the population-level effects, single study

Usage

```
change_time_single(model)
```

Arguments

model an object of class brmsfit

Value

a numeric vector of length one

`classify_data_point` *Classify individual data points as Responders or Non-responders*

Description

Classify individual data points as Responders or Non-responders

Usage

```
classify_data_point(df_newstudy, pred_newstudy)
```

Arguments

`df_newstudy` data from new study
`pred_newstudy` data frame with predictions

Value

data frame with "Responder"/"Non-responder" for individual data points

`classify_subcategories`
Make predictions for subcategories

Description

Make predictions for subcategories

Usage

```
classify_subcategories(data, model)
```

Arguments

`data` data frame with classification results
`model` object of class `brmsfit`

Value

data frame

classify_type_responder

Classify tumour based on the growth rate and the p_value for a two-sided T test Tumour will be considered as "Non-responder", "Modest responder", "Stable responder" or "Regressing responder"

Description

Classify tumour based on the growth rate and the p_value for a two-sided T test Tumour will be considered as "Non-responder", "Modest responder", "Stable responder" or "Regressing responder"

Usage

```
classify_type_responder(df)
```

Arguments

df data frame

Value

data frame with a new column classify_tumour

clean_string *function to remove hyphens, underscores, spaces and transform to lowercase*

Description

function to remove hyphens, underscores, spaces and transform to lowercase

Usage

```
clean_string(string)
```

Arguments

string to modify

Value

modified string

control_growth_plot *Function to plot a control growth profile*

Description

Function to plot a control growth profile

Usage

```
control_growth_plot(df, model_type, col_palette)
```

Arguments

df	data frame
model_type	string
col_palette	character palette

Value

ggplot object

example_data *Tumour volume data over time for in-vivo studies*

Description

A dataset containing the repeatedly measurements of tumour volume data over time for individual animals.

Usage

```
example_data
```

Format

A data frame with 1462 rows and 6 variables:

study study identifier

group group identifier

treatment treatment type

animal_id animal identifier

day day after implant

tumour_volume volume in mm³

exclude_data	<i>Filter rows to exclude from the analysis</i>
--------------	---

Description

Filter rows to exclude from the analysis

Usage

```
exclude_data(df, study_id_ex, animal_id_ex, day_ex, reason)
```

Arguments

df	initial df
study_id_ex	string: study id
animal_id_ex	string: animal id
day_ex	string: day
reason	string: why it should be excluded

Value

dataframe with rows that meets exclusion criteria

expand_palette	<i>Function to expand a vector of colors if needed</i>
----------------	--

Description

Function to expand a vector of colors if needed

Usage

```
expand_palette(col_palette, n)
```

Arguments

col_palette	character palette to color the treatments
n	how many colors are needed

Value

a character vector of colors

f_start	<i>Calculate coefficients for a nonlinear model</i>
---------	---

Description

Calculate coefficients for a nonlinear model

Usage

```
f_start(df, x, y, r_change)
```

Arguments

df	data frame with x as a predictor and y is an outcome
x	predictor string
y	outcome string
r_change	numeric

Value

list of coefficients

get_responder	<i>Classify tumour based on response status of individuals</i>
---------------	--

Description

Classify tumour based on response status of individuals

Usage

```
get_responder(x, n)
```

Arguments

x	character vector with response statuses of one animal
n	consecutive measurements for classification

Value

"Responder" or "Non-responder"

guess_match	<i>function to search for the possible critical columns in a data.frame</i>
-------------	---

Description

function to search for the possible critical columns in a data.frame

Usage

```
guess_match(colnames_df, crit_cols)
```

Arguments

colnames_df	a character vector with names
crit_cols	a character vector

Value

list: possible match to each critical column

hide_outliers	<i>Function to hide outliers in boxplots with jitterdodge as suggested</i>
---------------	--

Description

Function to hide outliers in boxplots with jitterdodge as suggested

Usage

```
hide_outliers(x)
```

Arguments

x	plotly object
---	---------------

Value

plotly object without boxplot outliers

load_data	<i>function to read data from users (.csv or .xlsx files)</i>
-----------	---

Description

function to read data from users (.csv or .xlsx files)

Usage

```
load_data(path, name)
```

Arguments

path	path to a temp file
name	filename provided by the web browser

Value

data frame

make_terms	<i>Create a character vector with the names of terms from model, for which predictions should be displayed Specific values are specified in square brackets</i>
------------	---

Description

Create a character vector with the names of terms from model, for which predictions should be displayed Specific values are specified in square brackets

Usage

```
make_terms(days, studies = NULL)
```

Arguments

days	vector with days with which to predict
studies	vector with studies with which to predict

Value

vector with values for predictions

model_control	<i>Build model and make predictions</i>
---------------	---

Description

Build model and make predictions

Usage

```
model_control(df_control, df_newstudy, method, end_day)
```

Arguments

df_control	data frame with control data (including historical control, if provided)
df_newstudy	data frame, data from new study
method	"Two-stage non-linear model" or "Linear model"
end_day	period of time used for the statistical modelling of the control data

Value

list: two data frames with prediction results (for new study and for control data)

notify_error_and_reset_input	<i>Display a popup message and reset fileInput</i>
------------------------------	--

Description

Display a popup message and reset fileInput

Usage

```
notify_error_and_reset_input(message_text)
```

Arguments

message_text	the modal's text
--------------	------------------

ordered_regression	<i>Fit model (Bayesian ordered logistic regression)</i>
--------------------	---

Description

Fit model (Bayesian ordered logistic regression)

Usage

```
ordered_regression(df, formula, n_cores)
```

Arguments

df	data frame with classification results. Tumour classification is converted into ordinal data
formula	string
n_cores	number of cores to use

Value

object of class brmsfit

plotly_volume	<i>Create volume plot for one-batch data</i>
---------------	--

Description

Create volume plot for one-batch data

Usage

```
plotly_volume(  
  df,  
  col_palette = NULL,  
  faceting_var,  
  y_name,  
  y_var,  
  p_title,  
  ...  
)
```

Arguments

df	data.frame, single-batch long format
col_palette	character palette to color the treatments
faceting_var	string
y_name	string
y_var	string: column name for y axis
p_title	plot title
...	arguments passed to plot_ly

Value

plotly object

plot_animal_info *Plot representing number of animals in classification groups*

Description

Plot representing number of animals in classification groups

Usage

```
plot_animal_info(data, col_palette)
```

Arguments

data	final classification data
col_palette	character palette

Value

ggplot object

plot_class_gr *Function to plot classification over growth rate*

Description

Function to plot classification over growth rate

Usage

```
plot_class_gr(df, col_palette)
```

Arguments

df	data frame
col_palette	character palette

Value

ggplot object

plot_class_tv *Function to plot classification over tumour volume*

Description

Function to plot classification over tumour volume

Usage

```
plot_class_tv(df, col_palette, title_name)
```

Arguments

df	data frame
col_palette	named vector
title_name	character

Value

ggplot object

plot_proportions	<i>Plot estimated proportions</i>
------------------	-----------------------------------

Description

Plot estimated proportions

Usage

```
plot_proportions(data, col_palette)
```

Arguments

data	table of the category prediction
col_palette	character palette

plot_waterfall	<i>Function to plot waterfall</i>
----------------	-----------------------------------

Description

Function to plot waterfall

Usage

```
plot_waterfall(df, col_palette, study_name)
```

Arguments

df	data frame
col_palette	character palette
study_name	string: to show on title

Value

ggplot object

predict_lm	<i>Make predictions, linear model</i>
------------	---------------------------------------

Description

Make predictions, linear model

Usage

```
predict_lm(model, newdata, single)
```

Arguments

model	a model object
newdata	data frame in which to look for variables with which to predict
single	logical: TRUE if single study experiment

Value

data frame with predictions

predict_nlm_multi	<i>Make predictions based on non-linear model, multiple studies</i>
-------------------	---

Description

Make predictions based on non-linear model, multiple studies

Usage

```
predict_nlm_multi(model, newdata, change_time)
```

Arguments

model	an object of class brmsfit
newdata	data frame in which to look for variables with which to predict
change_time	data frame

Value

data frame with predictions

predict_nlm_single *Make predictions based on non-linear model, single study*

Description

Make predictions based on non-linear model, single study

Usage

```
predict_nlm_single(model, newdata, change_time)
```

Arguments

model	an object of class brmsfit
newdata	data frame in which to look for variables with which to predict
change_time	numeric

Value

data frame with predictions

predict_regr_model *Make predictions*

Description

Make predictions

Usage

```
predict_regr_model(model, df)
```

Arguments

model	object of class brmsfit
df	data frame with classification results

Value

data frame

`run_app`*Run the Shiny Application*

Description

Run the Shiny Application

Usage

```
run_app(...)
```

Arguments

... additional options passed to shinyApp()

Value

No return value, called for the shiny app interface

`run_nl_model`*Fit nonlinear model - continuous hinge function*

Description

Fit nonlinear model - continuous hinge function

Usage

```
run_nl_model(start, df_mod, formula, n_cores)
```

Arguments

<code>start</code>	df with coefficients
<code>df_mod</code>	data of all variables used in the model
<code>formula</code>	an object of class brmsformula
<code>n_cores</code>	number of cores to use

Value

object of class brmsfit

set_waiter	<i>Set up a waiting screen</i>
------------	--------------------------------

Description

Set up a waiting screen

Usage

```
set_waiter(header)
```

Arguments

header	text to display on loading screen
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Value

object of a class waiter

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