

Package ‘INSPECTumours’

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Title IN-vivo reSPonse Classification of Tumours

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Maintainer Bairu Zhang <bairu.zhang@astrazeneca.com>

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

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Author Bairu Zhang [cre, aut],
Olga Muraeva [aut],
Natasha Karp [aut]

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aggregate_study_info	<i>create a table with aggregated data: each row contains information about control and treatments of a single study</i>
----------------------	--

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	<i>Generate table representing number of animals in classification groups</i>
----------------------------	---

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

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	<i>Calculate probability of categories</i>
------------------	--

Description

Calculate probability of categories

Usage

```
calc_probability(data)
```

Arguments

data data frame with predictions

Value

data frame

calc_survived	<i>Calculate percentage of survived animals</i>
---------------	---

Description

Calculate percentage of survived animals

Usage

```
calc_survived(df)
```

Arguments

df data frame

Value

data frame

change_time_multi	<i>Get an array with change_time for studies from the population-level effects, multiple studies</i>
-------------------	--

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	<i>Get a change time from the population-level effects, single study</i>
--------------------	--

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	<i>Classify individual data points as Responders or Non-responders</i>
---------------------	--

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	<i>Make predictions for subcategories</i>
------------------------	---

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

<code>clean_string</code>	<i>function to remove hyphens, underscores, spaces and transform to lowercase</i>
---------------------------	---

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	<i>Function to plot a control growth profile</i>
---------------------	--

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	<i>Tumour volume data over time for in-vivo studies</i>
--------------	---

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	<i>Plot representing number of animals in classification groups</i>
------------------	---

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	<i>Function to plot classification over growth rate</i>
---------------	---

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	<i>Function to plot classification over tumour volume</i>
---------------	---

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	<i>Make predictions based on non-linear model, single study</i>
--------------------	---

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	<i>Make predictions</i>
--------------------	-------------------------

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	<i>Run the Shiny Application</i>
---------	----------------------------------

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	<i>Fit nonlinear model - continuous hinge function</i>
--------------	--

Description

Fit nonlinear model - continuous hinge function

Usage

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

Arguments

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

Value

object of class brmsfit

`set_waiter`*Set up a waiting screen*

Description

Set up a waiting screen

Usage

```
set_waiter(header)
```

Arguments

header text to display on loading screen

Value

object of a class waiter

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