

Package ‘packDAMipd’

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Type Package

Title Decision Analysis Modelling Package with Parameters Estimation
Ability from Individual Patient Level Data

Version 0.2.0

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Description

A collection of functions to construct Markov model for model-based cost-effectiveness analysis. This includes creating Markov model (both time homogenous and time dependent models), decision analysis, sensitivity analysis (deterministic and probabilistic). The package allows estimation of parameters for the Markov model from a given individual patient level data, provided the data file follows some standard data entry rules.

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Depends R (>= 3.6.0)

Imports readxl, stringr, data.table, reshape2, rlang, stats, lme4, nlme, flexsurv, survminer, SurvRegCensCov, survival, MASS, systemfit, IPDFileCheck, valueEQ5D, car, ggplot2, grDevices, lmtree, broom, effects, gvlma, methods, relaimpo, tm, tidyverse, tibble, dplyr, tidyr, hash

Suggests ISLR, foreign, knitr, rmarkdown, covr, testthat

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BugReports <https://github.com/sheejamk/packDAMipd/issues>

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adl_scoring	<i>adl_scoring table</i>
-------------	--------------------------

Description

adl_scoring table

Usage

adl_scoring

Format

A 41 by 3 dataframe

Source

created on Jan 15, 2020

assign_parameters	<i>Function to assign the values of nested parameters from the parameter list</i>
-------------------	---

Description

Function to assign the values of nested parameters from the parameter list

Usage

```
assign_parameters(param_list)
```

Arguments

param_list list of parameters, can be nested, or can be used the list returned from define_parameters()

Details

The parameter list should be a list of parameters in the form name value pairs. If the name value pairs is given as a string it throws error as in `assign_parameters(c("cost_A = 100", "a = 10"))` even if you use `assign_parameters(define_parameters(c("cost_A = 100","a = 10")))` but this will be ok if you use the below forms `assign_list2 <- c(a = 10, cost_A = "a + 100", cost_B = 10)` `assign_parameters(assign_list2)` OR `param_list <- define_parameters(a = 10, cost_A = "a + 100", cost_B = 10)` `assign_list <- assign_parameters(param_list)` Also for nested parameters, remember to give the parameters in order so that at run time, the parameters can be evaluated for example, `assign_list = define_parameters(cost_A="a+100", a=10)` `assign_parameters(assign_list)` will throw an error, while `assign_list = define_parameters(a = 10, cost_A = "a + 100")` `assign_parameters(assign_list)` will successfully assign parameters as the parameters 'a' is visible before the calculation of 'cost_A' Another thing to note is that while using `define_parameters`, just enumerate them, no need to create as a list by using `c()` or `list` function

Value

list of assigned parameters

Examples

```
param_list <- define_parameters(
  cost_direct_med_A = 1701, cost_comm_care_A = 1055,
  cost_direct_med_B = 1774, cost_comm_care_B = 1278,
  cost_direct_med_C = 6948,
  cost_comm_care_C = 2059, cost_zido = 2456, cost_health_A =
  "cost_direct_med_A + cost_comm_care_A",
  cost_health_B = "cost_direct_med_B + cost_comm_care_B",
```

```

    cost_health_C = "cost_direct_med_C + cost_comm_care_C",
    cost_drug = "cost_zido"
)
assign_parameters(param_list)

```

blank	<i>Parameter table created</i>
-------	--------------------------------

Description

Parameter table created

Usage

blank

Format

A 2 column 1 observation

Source

created on September 5, 2020

calculate_icer_nmb	<i>Estimation of ICER and NMB</i>
--------------------	-----------------------------------

Description

Estimation of ICER and NMB

Usage

```
calculate_icer_nmb(list_markov, threshold, comparator = NULL)
```

Arguments

list_markov	list of Markov model objects with their Markov trace, cost matrix and utility matrix
threshold	threshold value of WTP
comparator	the strategy to be compared with

Value

ICER and NMB for all the strategies compared to comparator

Examples

```

well <- health_state("well", cost = 0, utility = 1)
disabled <- health_state("disabled", cost = 100, utility = 1)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.6, 0.2, 0.2, 0.6, 0.4, 1),
colnames(tmat))
health_states <- combine_state(well, disabled, dead)
this.strategy <- strategy(tm, health_states, "control")
this_markov <- markov_model(this.strategy, 24, c(1000, 0, 0), c(0,0))
well <- health_state("well", cost = 0, utility = 1)
disabled <- health_state("disabled", cost = 10, utility = 0.5)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.4, 0.4, 0.2, 0.6, 0.4, 1),
colnames(tmat))
health_states <- combine_state(well, disabled, dead)
this.strategy <- strategy(tm, health_states, "intervention")
sec_markov <- markov_model(this.strategy, 24, c(1000, 0, 0), c(0,0))
list_markov <- combine_markov(this_markov, sec_markov)
calculate_icer_nmb(list_markov, 20000, comparator = "control")

```

checks_markov_pick_method

Checks the input to run the Markov cycles and picks correct method

Description

Checks the input to run the Markov cycles and picks correct method

Usage

```

checks_markov_pick_method(
  current_strategy,
  initial_state,
  discount,
  method,
  half_cycle_correction,
  startup_cost,
  startup_util,
  state_cost_only_prevalent,
  state_util_only_prevalent
)

```

Arguments

current_strategy strategy object
 initial_state value of states initially
 discount rate of discount for costs and qalys
 method what type of half cycle correction needed
 half_cycle_correction boolean to indicate half cycle correction
 startup_cost cost of states initially
 startup_util utility of states initially if any
 state_cost_only_prevalent boolean parameter to indicate if the costs for state occupancy is only for those in the state excluding those that transitioned new. This is relevant when the transition cost is provided for eg. in a state with dialysis the cost of previous dialysis is different from the newly dialysis cases. Then the state_cost_only_prevalent should be TRUE
 state_util_only_prevalent boolean parameter to indicate if the utilities for state occupancy is only for those in the state excluding those that transitioned new.

Value

changed method name

Examples

```

tmat <- rbind(c(1, 2), c(3, 4))
colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead")
tm <- populate_transition_matrix(2, tmat, c(0.5, 0.5, 0, 1))
a <- health_state("Healthy", 1, 1, 0, FALSE)
b <- health_state("Dead", 1, 0, 0, TRUE)
health_states <- combine_state(a, b)
this.strategy <- strategy(tm, health_states, "intervention")
checks_markov_pick_method(this.strategy, c(1, 0), c(0, 0),
"half cycle correction", TRUE, NULL, NULL)

```

checks_plot_dsa

Function to do some checks before plotting sensitivity analysis results

Description

Function to do some checks before plotting sensitivity analysis results

Usage

```
checks_plot_dsa(
  result_dsa_control,
  plotfor,
  type,
  result_dsa_treat,
  threshold,
  comparator
)
```

Arguments

result_dsa_control	result from deterministic sensitivity analysis for first or control model
plotfor	the variable to plotfor e.g. cost, utility NMB etc
type	type of analysis, range or difference
result_dsa_treat	result from deterministic sensitivity analysis for the comparative Markov model
threshold	threshold value of WTP
comparator	the strategy to be compared with

Value

the plot variable

check_link_glm	<i>Function to find the keyword for family of distribution in glm</i>
----------------	---

Description

Function to find the keyword for family of distribution in glm

Usage

```
check_link_glm(family, link)
```

Arguments

family	family of distribution
link	function to be used

Details

Check and get the link function for the method glm

Value

the link if they can be accepted else error

Examples

```
check_link_glm("gaussian", "identity")
```

```
check_list_markov_models
```

check the list of Markov models

Description

check the list of Markov models

Usage

```
check_list_markov_models(list_markov)
```

Arguments

`list_markov` list of Markov model objects with their Markov trace, cost matrix and utility matrix

Value

0 if success else error

Examples

```
well <- health_state("well", cost = 0, utility = 1)
disabled <- health_state("disabled", cost = 100, utility = 1)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.6, 0.2, 0.2, 0.6, 0.4, 1),
colnames(tmat))
health_states <- combine_state(well, disabled, dead)
this_strategy <- strategy(tm, health_states, "example")
this_markov <- markov_model(this_strategy, 24, c(1000, 0, 0), c(0,0))
well <- health_state("well", cost = 0, utility = 1)
disabled <- health_state("disabled", cost = 10, utility = 0.5)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.4, 0.4, 0.2, 0.6, 0.4, 1),
colnames(tmat))
health_states <- combine_state(well, disabled, dead)
```

```
this.strategy <- strategy(tm, health_states, "example_two")
sec_markov <- markov_model(this.strategy, 24, c(1000, 0, 0), c(0, 0))
list_markov <- combine_markov(this_markov, sec_markov)
check_list_markov_models(list_markov)
```

check_null_na	<i>Function to check the variable null or NA</i>
---------------	--

Description

Function to check the variable null or NA

Usage

```
check_null_na(variable)
```

Arguments

variable name of variable or list of variable to check

Value

-1 or -2 as error, else return 0 as success

Examples

```
var = c("a")
check_null_na(var)
```

check_trans_prob	<i>Check the transition probabilities for numeric values and unity row sum</i>
------------------	--

Description

Check the transition probabilities for numeric values and unity row sum

Usage

```
check_trans_prob(trans_mat)
```

Arguments

trans_mat transition matrix

Details

checking for rowsum - checks for the class of transition matrix, value of rowsum (to be 1) and numeric values

Value

0 if they add to 1 else error

Examples

```
tmat <- rbind(c(1, 2), c(3, 4))
colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead")
tm <- populate_transition_matrix(2, tmat, list_prob = c(0.5, 0.5, 0, 1))
check_trans_prob(tm)
```

check_treatment_arm *Function to return treatment arm*

Description

Function to return treatment arm

Usage

```
check_treatment_arm(arm)
```

Arguments

arm the arm of the trial

Value

0, if success -1, if failure

Examples

```
check_treatment_arm("control")
```

check_values_states *Check if the values of health states are provided*

Description

Check if the values of health states are provided

Usage

```
check_values_states(health_states)
```

Arguments

health_states list of health_state objects

Details

This is to check if the values are numeric during the run time, else to throw an error

Value

true or false

Examples

```
well <- health_state("well", cost = 0, utility = 1)
disabled <- health_state("disabled", cost = 100, utility = 1)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.6, 0.2, 0.2, 0.6, 0.4, 1))
health_states <- combine_state(well, disabled, dead)
check_values_states(health_states)
```

combine_markov *Join Markov model objects*

Description

Join Markov model objects

Usage

```
combine_markov(markov1, ...)
```

Arguments

markov1 object 1 of class markov_model
 ... any additional objects

Details

Combining Markov models for easiness of comparison

Value

joined objects of type markov_model

Examples

```
well <- health_state("well", cost = 0, utility = 1)
disabled <- health_state("disabled", cost = 100, utility = 1)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.6, 0.2, 0.2, 0.6, 0.4, 1))
health_states <- combine_state(well, disabled, dead)
this.strategy <- strategy(tm, health_states, "example")
this_markov <- markov_model(this.strategy, 24, c(1000, 0, 0))
well <- health_state("well", cost = 0, utility = 1)
disabled <- health_state("disabled", cost = 10, utility = 0.5)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.4, 0.4, 0.2, 0.6, 0.4, 1))
health_states <- combine_state(well, disabled, dead)
this.strategy <- strategy(tm, health_states, "example")
sec_markov <- markov_model(this.strategy, 24, c(1000, 0, 0))
list_markov <- combine_markov(this_markov, sec_markov)
```

combine_state

Join health states

Description

Join health states

Usage

```
combine_state(...)
```

Arguments

... any additional objects

Details

checking each state is a health state and join them

Value

joined health states

Examples

```
a <- health_state("IT", 100, 0.4, 0, FALSE)
b <- health_state("PT", 100, 0.4, 0, FALSE)
combine_state(a, b)
```

convert_freq_diff_basis

Convert frequency medication to given basis

Description

Convert frequency medication to given basis

Usage

```
convert_freq_diff_basis(freq_given, basis = "day")
```

Arguments

freq_given	given frequency
basis	given basis, default is daily

Value

converted frequency

Examples

```
convert_freq_diff_basis("once daily")
convert_freq_diff_basis("bd", "week")
convert_freq_diff_basis("Every 4 days", "day")
```

convert_to_given_timeperiod
Convert period to given basis

Description

Convert period to given basis

Usage

```
convert_to_given_timeperiod(given_time, basis_time = "day")
```

Arguments

given_time	given time
basis_time	given basis, default is "day"

Value

converted unit

Examples

```
convert_to_given_timeperiod("4 weeks")  
convert_to_given_timeperiod("a month")  
convert_to_given_timeperiod("1 week")
```

convert_volume_basis *Convert volume to given basis*

Description

Convert volume to given basis

Usage

```
convert_volume_basis(given_unit, basis = "ml")
```

Arguments

given_unit	given unit
basis	given basis, default is "ml"

Value

converted unit

Examples

```
convert_volume_basis("ml", "liter")
```

```
convert_weight_diff_basis
```

Convert unit strength to given basis

Description

Convert unit strength to given basis

Usage

```
convert_weight_diff_basis(given_unit, basis = "mg")
```

Arguments

given_unit	given unit
basis	given basis, default is "mg"

Value

converted unit

Examples

```
convert_weight_diff_basis("mg")  
convert_weight_diff_basis("kilogram", "micro gram")
```

```
convert_wtpertimediff_basis
```

Convert weight per time to given basis

Description

Convert weight per time to given basis

Usage

```
convert_wtpertimediff_basis(given_unit, basis = "mcg/hour")
```

Arguments

given_unit	given unit
basis	given basis, default is "mg"

Value

converted unit

Examples

```
convert_wtpertimediff_basis("mg/day")
convert_wtpertimediff_basis("mcg/day")
convert_wtpertimediff_basis("mg/hour")
```

costing_AandE_admission

Function to estimate the cost of inpatient admission but taken from GP records where code or description known

Description

Function to estimate the cost of inpatient admission but taken from GP records where code or description known

Usage

```
costing_AandE_admission(
  ind_part_data,
  code_ae,
  descrip_ae,
  number_use_ae,
  type_admit_ae,
  unit_cost_data,
  code_col,
  type_admit_col,
  description_col,
  unit_cost_col,
  cost_calculated_in = "attendance",
  sheet = NULL
)
```

Arguments

ind_part_data	IPD
code_ae	column name of code (for inpatient admission)
descrip_ae	column name of description for inpatient admission
number_use_ae	the number of days spent in each admission if that is a criteria to be included. Otherwise each admission will be costed
type_admit_ae	term indicating admission and type of attendance
unit_cost_data	unit cost data file with code/descriptions and unit costs are listed for inpatient admission

code_col code column name in unit cost data
 type_admit_col colname that describes type of the attendance and
 description_col column name of description of inpatient admission in the unit cost data
 unit_cost_col column name of unit cost in unit_cost_data
 cost_calculated_in name of unit where the cost is calculated assumed to be per admission
 sheet sheet where the unit costs are listed in the unit costs data file

Value

the calculated cost of inpatient admission long with original data

Examples

```
costs_file <- system.file("extdata",
  "National_schedule_of_NHS_costs_2019_AandE.csv", package = "packDAMipd")
datafile <- system.file("extdata", "resource_use_ae_ip.csv",
  package = "packDAMipd")
ind_part_data <- packDAMipd::load_trial_data(datafile)
unit_cost_data <- packDAMipd::load_trial_data(costs_file)
result <- costing_AandE_admission(ind_part_data = ind_part_data,
  code_ae = "code", descrip_ae = NULL, number_use_ae = "number_use",
  type_admit_ae = "type_admit", unit_cost_data = unit_cost_data,
  code_col = "Currency_Code", type_admit_col = "Service_Code",
  description_col = NULL, unit_cost_col = "National_Average_Unit_Cost",
  cost_calculated_in = "attendance")
```

costing_inpatient_daycase_admission

Function to estimate the cost of inpatient admission but taken from GP records where HRG code or description known

Description

Function to estimate the cost of inpatient admission but taken from GP records where HRG code or description known

Usage

```
costing_inpatient_daycase_admission(
  ind_part_data,
  hrg_code_ip_admi,
  descrip_ip_admi,
  number_use_ip_admi,
  elective_col,
  unit_cost_data,
```

```

    hrg_code_col,
    description_col,
    unit_cost_col,
    cost_calculated_in = "admission"
  )

```

Arguments

```

ind_part_data  IPD
hrg_code_ip_admi
                column name of hrg code (for inpatient admission)
descrip_ip_admi
                column name of description for inpatient admission
number_use_ip_admi
                the number of days spent in each admission if that is a criteria to be included.
                Otherwise each admission will be costed
elective_col   colname to say whether it is an elective admission or non elective admission
unit_cost_data unit cost data file with hrg code/descriptions and unit costs are listed for inpatient
                admission
hrg_code_col   hrg code column name in unit cost data
description_col
                column name of description of inpatient admission in the unit cost data
unit_cost_col  column name of unit cost in unit_cost_data
cost_calculated_in
                name of unit where the cost is calculated assumed to be per admission

```

Value

the calculated cost of inpatient admission long with original data

Examples

```

costs_file <- system.file("extdata",
  "National_schedule_of_NHS_costs_2019.csv",
  package = "packDAMipd")
datafile <- system.file("extdata", "resource_use_hc_ip.csv",
  package = "packDAMipd")
ind_part_data <- packDAMipd::load_trial_data(datafile)
unit_cost_data <- packDAMipd::load_trial_data(costs_file)
result <- costing_inpatient_daycase_admission(ind_part_data,
  hrg_code_ip_admi = "HRGcode", descrip_ip_admi = NULL,
  number_use_ip_admi = "number_use", elective_col = "EL",
  unit_cost_data, hrg_code_col = "Currency_Code", description_col = NULL,
  unit_cost_col = "National_Average_Unit_Cost",
  cost_calculated_in = "admission")

```

costing_resource_use *Function to estimate the cost of resource use taken (from IPD)*

Description

Function to estimate the cost of resource use taken (from IPD)

Usage

```
costing_resource_use(
  ind_part_data,
  name_use_col,
  each_length_num_use,
  each_use_provider_indicator = NULL,
  unit_length_use = "day",
  unit_cost_data,
  name_use_unit_cost,
  unit_cost_column,
  cost_calculated_in,
  list_code_use_indicator = NULL,
  list_code_provider_indicator = NULL
)
```

Arguments

`ind_part_data` IPD

`name_use_col` name of the column containing resource use

`each_length_num_use`
list of column names that shows length/number of repeated use eg. hospital admission

`each_use_provider_indicator`
list of column names that shows the bool indicators for the use of resource if this is to be included for the particular provider, say an nhs hospital use

`unit_length_use`
the column name that contains how many or how long used

`unit_cost_data` unit costs data where the assumption is that the unit cost for resources such as hospital use, gp visit are listed in column resource/resource use with unit costs in another column and the units calculated as in another column

`name_use_unit_cost`
name of resource use (the column name in the unit cost data is assumed to be name/resource/type etc) in unit cost data

`unit_cost_column`
column name of unit cost in `unit_cost_data`

`cost_calculated_in`
column name of unit where the cost is calculated

`list_code_use_indicator`
 if the column `name_use_col` shows codes to indicate the resource use provide the list of codes and resource use for eg., `list(c("yes", "no", c(1,2)))`

`list_code_provider_indicator`
 column `each_use_provider_indicator` shows codes to indicate the resource use provide the list of codes and resource use for eg., `list(c("yes", "no", c(1,2)))`

Value

the calculated cost of resource uses along with original data

Examples

```
costs_file <- system.file("extdata", "costs_resource_use.csv",
  package = "packDAMipd")
datafile <- system.file("extdata", "resource_use_hc_2.csv",
  package = "packDAMipd")
ind_part_data <- load_trial_data(datafile)
unit_cost_data <- load_trial_data(costs_file)
res <- costing_resource_use(
  ind_part_data[1, ],
  "hospital_admission_1",
  list("length_1", "length_2"),
  list("nhs_1", "nhs_2"),
  "day",
  unit_cost_data, "Inpatient hospital admissions", "UnitCost",
  "UnitUsed",
  NULL, NULL
)
```

cost_data

cost matrix

Description

cost matrix

Usage

cost_data

Format

A 11 by 2 dataframe

Source

```
created on Nov 26, 2019 from tmat <- rbind(c(1, 2), c(3, 4)) colnames(tmat) <- rownames(tmat) <-
c("Healthy", "Dead") tm <- transition_matrix(2, tmat, c(0.5, 0.5, 0, 1)) a <- health_state("Healthy",
1, 1, FALSE) b <- health_state("Dead", 1, 0, TRUE) health_states <- combine_state(a, b) this.strategy
<- strategy(tm, health_states, "intervention")
```

create_new_dataset	<i>create new dataset while keeping cox regression results and returned coefficients</i>
--------------------	--

Description

create new dataset while keeping cox regression results and returned coefficients

Usage

```
create_new_dataset(var, covar, dataset, categorical)
```

Arguments

var	variable for which the levels have to be identified usually indep variable
covar	the other covariates
dataset	the dataset where these variables contain
categorical	are these variables categorical? True of false

Value

new data frame

Examples

```
dataset <- survival::lung
new = create_new_dataset("status", c("age"), dataset, c(FALSE))
```

define_parameters *Function to return a list of parameters given*

Description

Function to return a list of parameters given

Usage

```
define_parameters(...)
```

Arguments

... any parameters set of name value pairs expected

Details

To return a list of parameters For using with assign_parameters() just list or enumerate the parameters, do not use c() or list() to create a data type list

Value

a list of parameters

Examples

```
define_parameters(rr = 1)
```

define_parameters_psa *Define parameter lists for deterministic sensitivity analysis*

Description

Define parameter lists for deterministic sensitivity analysis

Usage

```
define_parameters_psa(base_param_list, sample_list)
```

Arguments

base_param_list list of parameters that used to define Markov model
sample_list list of parameter values with their sampling distributions

Value

table for probability sensitivity analysis

Examples

```
param_list <- define_parameters(
  cost_zido = 2278, cost_direct_med_A = 1701,
  cost_comm_care_A = 1055, cost_direct_med_B = 1774,
  cost_comm_care_B = 1278,
  cost_direct_med_C = 6948, cost_comm_care_C = 2059,
  tpAtoA = 1251 / (1251 + 483),
  tpAtoB = 350 / (350 + 1384), tpAtoC = 116 / (116 + 1618),
  tpAtoD = 17 / (17 + 1717),
  tpBtoB = 731 / (731 + 527), tpBtoC = 512 / (512 + 746),
  tpBtoD = 15 / (15 + 1243),
  tpCtoC = 1312 / (1312 + 437), tpCtoD = 437 / (437 + 1312), tpDtoD = 1,
  cost_health_A = "cost_direct_med_A+ cost_comm_care_A",
  cost_health_B = "cost_direct_med_B+ cost_comm_care_B",
  cost_health_C = "cost_direct_med_C+ cost_comm_care_C",
  cost_drug = "cost_zido"
)
sample_list <- define_parameters(cost_zido = "gamma(mean = 2756,
sd = sqrt(2756))")
param_table <- define_parameters_psa(param_list, sample_list)
```

define_parameters_sens_anal

Define parameter lists for deterministic sensitivity analysis

Description

Define parameter lists for deterministic sensitivity analysis

Usage

```
define_parameters_sens_anal(param_list, low_values, upp_values)
```

Arguments

param_list	list of parameters that used to define Markov model
low_values	list of lower values of those parameters for whom the sensitivity is to be estimated
upp_values	list of upper values of those parameters for whom the sensitivity is to be estimated

Details

Get the parameter list, min and maximum values of the parameters. The min and max values should have same entries, but they should be contained in param_list too. Copy the exact values of parameters that are in param list but not in min and max values

Value

table for sensitivity analysis

Examples

```
param_list <- define_parameters(
  cost_zido = 2278, cost_direct_med_A = 1701,
  cost_comm_care_A = 1055, cost_direct_med_B = 1774,
  cost_comm_care_B = 1278,
  cost_direct_med_C = 6948, cost_comm_care_C = 2059,
  tpAtoA = 1251 / (1251 + 483),
  tpAtoB = 350 / (350 + 1384), tpAtoC = 116 / (116 + 1618),
  tpAtoD = 17 / (17 + 1717),
  tpBtoB = 731 / (731 + 527), tpBtoC = 512 / (512 + 746),
  tpBtoD = 15 / (15 + 1243),
  tpCtoC = 1312 / (1312 + 437), tpCtoD = 437 / (437 + 1312), tpDtoD = 1,
  cost_health_A = "cost_direct_med_A + cost_comm_care_A",
  cost_health_B = "cost_direct_med_B + cost_comm_care_B",
  cost_health_C = "cost_direct_med_C + cost_comm_care_C",
  cost_drug = "cost_zido"
)
low_values <- define_parameters(cost_direct_med_B = 177.4,
  cost_comm_care_C = 205.9)
upp_values <- define_parameters(cost_direct_med_B = 17740,
  cost_comm_care_C = 20590)
param_table <- define_parameters_sens_anal(param_list, low_values,
  upp_values)
```

define_transition_table

Define the table for transition

Description

Define the table for transition

Usage

```
define_transition_table(tmat)
```

Arguments

tmat transition matrix in the format as in package 'mstate'

Details

Generating a table for transition matrix for efficient understanding and checking The transition matrix in the format as per 'mstate' package is transformed to a table. if tmat is not a square matrix, it gives error else it spells out the transition number, probability name and from state to state

Value

the transition table with the probabilities

Examples

```
tmat <- rbind(c(1, 2), c(3, 4))
colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead")
define_transition_table(tmat)
```

do_psa

*Function to do probabilistic sensitivity analysis***Description**

Function to do probabilistic sensitivity analysis

Usage

```
do_psa(this_markov, psa_table, num_rep)
```

Arguments

this_markov	Markov model object
psa_table	table object from define_parameters_psa
num_rep	number of repetitions

Value

result after sensitivity analysis

Examples

```
param_list <- define_parameters(
  cost_zido = 2278, cost_direct_med_A = 1701,
  cost_comm_care_A = 1055, cost_direct_med_B = 1774,
  cost_comm_care_B = 1278,
  cost_direct_med_C = 6948, cost_comm_care_C = 2059,
  tpAtoA = 1251 / (1251 + 483),
  tpAtoB = 350 / (350 + 1384), tpAtoC = 116 / (116 + 1618),
  tpAtoD = 17 / (17 + 1717),
  tpBtoB = 731 / (731 + 527), tpBtoC = 512 / (512 + 746),
```

```

tpBtoD = 15 / (15 + 1243),
tpCtoC = 1312 / (1312 + 437), tpCtoD = 437 / (437 + 1312), tpDtoD = 1,
cost_health_A = "cost_direct_med_A+ cost_comm_care_A",
cost_health_B = "cost_direct_med_B+ cost_comm_care_B",
cost_health_C = "cost_direct_med_C+ cost_comm_care_C",
cost_drug = "cost_zido"
)
A <- health_state("A", cost = "cost_health_A+ cost_drug ", utility = 1)
B <- health_state("B", cost = "cost_health_B + cost_drug", utility = 1)
C <- health_state("C", cost = "cost_health_C + cost_drug", utility = 1)
D <- health_state("D", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3, 4), c(NA, 5, 6, 7), c(NA, NA, 8, 9),
c(NA, NA, NA, 10))
colnames(tmat) <- rownames(tmat) <- c("A", "B", "C", "D")
tm <- populate_transition_matrix(4, tmat, c(
  "tpAtoA", "tpAtoB", "tpAtoC", "tpAtoD",
  "tpBtoB", "tpBtoC", "tpBtoD", "tpCtoC", "tpCtoD", "tpDtoD"
), colnames(tmat))
health_states <- combine_state(A, B, C, D)
mono_strategy <- strategy(tm, health_states, "mono")
mono_markov <- markov_model(mono_strategy, 20, discount = c(0.06, 0),
initial_state =c(1,0,0,0),param_list)
sample_list <- define_parameters(cost_zido = "gamma(mean = 2756,
sd = sqrt(2756))")
param_table <- define_parameters_psa(param_list, sample_list)
result <- do_psa(mono_markov, param_table, 10)

```

do_sensitivity_analysis

Function to do deterministic sensitivity analysis

Description

Function to do deterministic sensitivity analysis

Usage

```
do_sensitivity_analysis(this_markov, param_table)
```

Arguments

this_markov	Markov model object
param_table	table object from define_parameters_sens_anal() with parameters (base case value, lower and upper)

Value

result after sensitivity analysis

Examples

```

param_list <- define_parameters(
  cost_zido = 2278, cost_direct_med_A = 1701,
  cost_comm_care_A = 1055, cost_direct_med_B = 1774,
  cost_comm_care_B = 1278,
  cost_direct_med_C = 6948, cost_comm_care_C = 2059,
  tpAtoA = 1251 / (1251 + 483),
  tpAtoB = 350 / (350 + 1384), tpAtoC = 116 / (116 + 1618),
  tpAtoD = 17 / (17 + 1717),
  tpBtoB = 731 / (731 + 527), tpBtoC = 512 / (512 + 746),
  tpBtoD = 15 / (15 + 1243),
  tpCtoC = 1312 / (1312 + 437), tpCtoD = 437 / (437 + 1312),
  tpDtoD = 1,
  cost_health_A = "cost_direct_med_A + cost_comm_care_A",
  cost_health_B = "cost_direct_med_B + cost_comm_care_B",
  cost_health_C = "cost_direct_med_C + cost_comm_care_C",
  cost_drug = "cost_zido")
low_values <- define_parameters(cost_direct_med_B = 177.4,
  cost_comm_care_C = 205.9)
upp_values <- define_parameters(cost_direct_med_B = 17740,
  cost_comm_care_C = 20590)
A <- health_state("A", cost = "cost_health_A + cost_drug ", utility = 1)
B <- health_state("B", cost = "cost_health_B + cost_drug", utility = 1)
C <- health_state("C", cost = "cost_health_C + cost_drug", utility = 1)
D <- health_state("D", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3, 4), c(NA, 5, 6, 7), c(NA, NA, 8, 9),
  c(NA, NA, NA, 10))
colnames(tmat) <- rownames(tmat) <- c("A", "B", "C", "D")
tm <- populate_transition_matrix(4, tmat, c("tpAtoA", "tpAtoB", "tpAtoC",
  "tpAtoD", "tpBtoB", "tpBtoC", "tpBtoD", "tpCtoC", "tpCtoD", "tpDtoD"),
  colnames(tmat))
health_states <- combine_state(A, B, C, D)
mono_strategy <- strategy(tm, health_states, "mono")
mono_markov <- markov_model(mono_strategy, 20, c(1, 0, 0, 0),
  discount = c(0.06, 0), param_list)
param_table <- define_parameters_sens_anal(param_list, low_values,
  upp_values)
result <- do_sensitivity_analysis(mono_markov, param_table)

```

encode_codes_data *Function to get the codes and the corresponding entries*

Description

Function to get the codes and the corresponding entries

Usage

```
encode_codes_data(list_code_values, data_column_nos, the_data)
```

Arguments

list_code_values
list of codes and values, given as list of lists

data_column_nos
the column numbers of data to look for the entries

the_data
the data where to look for

Value

weight and vol units

Examples

```
data_file <- system.file("extdata", "medication_liq_codes.xlsx",
  package = "packDAMipd")
ind_part_data <- load_trial_data(data_file)
data_column_nos = c(2,12)
list_of_code_names = list(c(1, 2),c("Morphine", "Oxycodone"))
encode_codes_data(list_of_code_names, data_column_nos, ind_part_data)
```

eval_assign_trans_prob

Attribute parameters to probabilities of transition matrix

Description

Attribute parameters to probabilities of transition matrix

Usage

```
eval_assign_trans_prob(tm, parameter_values)
```

Arguments

tm
A transition matrix in the format from the package 'mstate'

parameter_values
name value pairs of parameter values in the probability matrix

Details

Once the transition matrix is populated, the probabilities in transition matrix gets evaluated and assigned in this function call. If the entry in transition matrix is NA, replaces it with zero. Similarly to evaluate and assign health states, the parameter values is expected to be a list from assign_parameter() and define_parameter(). The exception is that if the parameters are defined directly and no nested calculation is required. For eg. assign_list = c(p1 = 0.2, p2 = 0.3, p3 = 0.4, p4 = 0.5) prob <- eval_assign_trans_prob(tmat, assign_list) will work. For those with nested calculations, this has to be defined as below assign_list<-assign_parameters(define_parameters(p1 = 0.2,

```
p2 = 0.3, p3 = 0.4, p4 = 0.5)) prob <- eval_assign_trans_prob(tmat, assign_list)
The below will give error
assign_list <- c(p1=0.1, p2 = "p1 + 0.2", p3=0, p4=0.3) prob <- eval_assign_trans_prob(tmat,
assign_list)
```

Value

the transition table with the probabilities

Examples

```
tmat <- rbind(c(1, 2), c(3, 4))
colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead")
tmat <- populate_transition_matrix(2, tmat,
list_prob = c("p1", "p2", "p3", "p4"))
tmat_assigned <- eval_assign_trans_prob(tmat,
c(p1 = 0.2, p2 = 0.3, p3 = 0.4, p4 = 0.5))
```

eval_assign_values_states

Attribute values in health states

Description

Attribute values in health states

Usage

```
eval_assign_values_states(health_states, assigned_param)
```

Arguments

health_states list of health_state objects

assigned_param name value pairs of parameter values in the probability matrix expected created using function assign_parameters()

Details

Assigning the param is done for the cost and utility if the param is not numeric, check if it can be evaluated at the run time if yes, assign the evaluated numeric value if not get the parameters between operators, and assign the values to each individual parameters and then evaluate. only works for two levels. For the example shown the cost is sum of cost_A and cost_B which will only get added in the call eval_assign_values_states While initialising the state "well" it will be only saved as expression(cost_A + cost_B) assigned_param (a list) can be expected to be created using assign_parameters() the exception is if parameter is directly assigned with no nested calculation and no missing parameters. For example assigned_param = c(cost_a = 10, cost_b=10) will be ok but not assigned_param = c(a=10, cost_A = "a+100", cost_B =10) as it requires a nested calculation then use define_parameters() with assign_parameters() as in param_list <- define_parameters(a = 10, cost_A = "a + 100", cost_B = 10) assign_list <- assign_parameters(param_list)

Value

health states with assigned values

Examples

```
well <- health_state("well", cost = "cost_A + cost_B", utility = 1)
disabled <- health_state("disabled", cost = 100, utility = 1)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.6, 0.2, 0.2, 0.6, 0.4, 1))
health_states <- combine_state(well, disabled, dead)
eval_assign_values_states(health_states, c(cost_A = 100, cost_B = 11))
```

find_glm_distribution *Function to find the keyword for family of distribution in glm*

Description

Function to find the keyword for family of distribution in glm

Usage

```
find_glm_distribution(text)
```

Arguments

text	distribution
------	--------------

Details

Find the family for glm method

Value

the keyword - the name of distribution

Examples

```
find_glm_distribution("gamma")
```

`find_keyword_rand_generation`

Function to find the keyword for generating random numbers the distribution

Description

Function to find the keyword for generating random numbers the distribution

Usage

```
find_keyword_rand_generation(text)
```

Arguments

`text` name of the probability distribution

Details

This function returns the keyword for generating random number using a keyword provided that is generally used for prob distribution (but R might require a different keyword)

Value

the keyword that should be used in R for generating random numbers

Examples

```
find_keyword_rand_generation("gamma")
```

`find_keyword_regression_method`

Function to find the keyword for regression methods

Description

Function to find the keyword for regression methods

Usage

```
find_keyword_regression_method(text, additional_info = NA)
```

Arguments

`text` regression method
`additional_info` additional information required

Details

This function returns the keyword to use in regression methods. For example linear regression requires lm in R some regression methods require additional info and it has to be provided

Value

the keyword that should be used in R for regression analysis

Examples

```
find_keyword_regression_method("linear")
```

```
find_parameters_btn_operators
```

Function to return parameters with in a expression containing operators

Description

Function to return parameters with in a expression containing operators

Usage

```
find_parameters_btn_operators(expr)
```

Arguments

expr an expression

Details

This function returns the parameters between the operators if the state value or probabilities are defined as expressions, we need to extract the parameters and then assign First the position of all operators are found and then return the parameters separated by those operators This happens only for one level find_parameters_btn_operators("a+b") provides a and b but for find_parameters_btn_operators("mean(a,b)+b") provides mean(a,b) and b

Value

parameters in the expression expr

Examples

```
find_parameters_btn_operators("a+b")
```

`find_required_parameter_combs`

Function to find the parameters that determine the probability distribution

Description

Function to find the parameters that determine the probability distribution

Usage

```
find_required_parameter_combs(name_distri)
```

Arguments

name_distri name of the probability distribution

Details

For each of the probability distribution we require certain parameters and this function provides that required list of parameters.

Value

the parameters that determine the distribution

Examples

```
find_required_parameter_combs("gamma")
```

`find_survreg_distribution`

Function to find the keyword for survreg distribution

Description

Function to find the keyword for survreg distribution

Usage

```
find_survreg_distribution(text)
```

Arguments

text distribution

Details

For survreg method, find the distribution

Value

the keyword - the name of distribution

Examples

```
find_survreg_distribution("weibull")
```

form_expression_glm *Form expression to use with glm()*

Description

Form expression to use with glm()

Usage

```
form_expression_glm(
  param_to_be_estimated,
  indep_var,
  family,
  covariates,
  interaction,
  naaction,
  link
)
```

Arguments

param_to_be_estimated	parameter of interest
indep_var	the independent variable (column name in data file)
family	distribution name eg. for logistic regression -binomial
covariates	list of covariates
interaction	boolean value to indicate interaction in the case of generalised linear models, false by default
naaction	action to be taken with the missing values
link	link function if not the default for each family

Details

Form expression for the method glm

Value

the formula for glm

Examples

```
formula <- form_expression_glm("admit",
  indep_var = "gre", family = "binomial",
  covariates = c("gpa", "rank"), interaction = FALSE, naaction = "na.omit",
  link = NA)
```

form_expression_lm *Form expression to use with lm()*

Description

Form expression to use with lm()

Usage

```
form_expression_lm(param_to_be_estimated, indep_var, covariates, interaction)
```

Arguments

param_to_be_estimated	parameter of interest
indep_var	the independent variable (column name in data file)
covariates	list of covariates
interaction	boolean value to indicate interaction in the case of linear regression, false by default

Details

This function helps to create the expression for liner regression model it takes care of covariates and interaction

Value

the formula for lm

Examples

```
formula <- form_expression_lm("gre", indep_var = "gpa", covariates = NA,
  interaction = FALSE)
```

 form_expression_mixed_model_lme4

Form expression to use with mixed models

Description

Form expression to use with mixed models

Usage

```
form_expression_mixed_model_lme4(
  param_to_be_estimated,
  dataset,
  fix_eff,
  fix_eff_interact_vars,
  random_intercept_vars,
  nested_intercept_vars_pairs,
  cross_intercept_vars_pairs,
  uncorrel_slope_intercept_pairs,
  random_slope_intercept_pairs,
  family,
  link
)
```

Arguments

param_to_be_estimated	column name of dependent variable
dataset	a dataframe
fix_eff	names of variables as fixed effect predictors
fix_eff_interact_vars,	if interaction -true
random_intercept_vars,	names of variables for random intercept
nested_intercept_vars_pairs,	those of the random intercept variables with nested effect
cross_intercept_vars_pairs,	those of the random intercept variables with crossed effect
uncorrel_slope_intercept_pairs,	variables with correlated intercepts
random_slope_intercept_pairs,	random slopes intercept pairs - this is a list of paired variables
family,	family of distribution for non gaussian distribution of predicted variable
link,	link function for the variance

Details

Form the expression for mixed model

Value

result regression result with plot if success and -1, if failure

Examples

```
datafile <- system.file("extdata", "data_linear_mixed_model.csv",
  package = "packDAMipd")
dt = utils::read.csv(datafile, header = TRUE)
formula <- form_expression_mixed_model_lme4("extro",
  dataset = dt,
  fix_eff = c("open", "agree", "social"),
  fix_eff_interact_vars = NULL,
  random_intercept_vars = c("school", "class"),
  nested_intercept_vars_pairs = list(c("school", "class")),
  cross_intercept_vars_pairs = NULL,
  uncorrel_slope_intercept_pairs = NULL,
  random_slope_intercept_pairs = NULL, family = "binomial", link = NA
)
```

generate_wt_time_units

Function to get the weight and time units

Description

Function to get the weight and time units

Usage

```
generate_wt_time_units()
```

Value

weight and time units

Examples

```
ans <- generate_wt_time_units()
```

generate_wt_vol_units *Function to get the weight and volume units*

Description

Function to get the weight and volume units

Usage

```
generate_wt_vol_units()
```

Value

weight and vol units

Examples

```
ans <- generate_wt_vol_units()
```

get_age_details *Function to get the details of the age column*

Description

Function to get the details of the age column

Usage

```
get_age_details(trialdata)
```

Arguments

trialdata, data containing individual level trial data

Details

expecting the data contains the information on age preferably column names "age", "dob" or "yob" or "date of birth". "year of birth", "birth year" If multiple column names match these, then first match will be chosen.

Value

the name of the variable related to age and the unique contents if success, else error

Examples

```
get_age_details(data.frame("Age" = c(21, 15),  
"arm" = c("control", "intervention")))
```

`get_colnames_codedvalues`

Function to keep the column name, coded values and non response code into a dataframe

Description

Function to keep the column name, coded values and non response code into a dataframe

Usage

```
get_colnames_codedvalues(variable, name, code, nrcode = NA)
```

Arguments

variable,	name of the variable in the column
name,	column name
code,	coded values
nrcode,	code for non response

Value

data frame with all the above information

Examples

```
get_colnames_codedvalues("arm", "pat_trial_arm", c("Y", "N"))
```

`get_col_multiple_pattern`

Function to get cols for the pattern given

Description

Function to get cols for the pattern given

Usage

```
get_col_multiple_pattern(pattern, the_data)
```

Arguments

pattern	the pattern to look for
the_data	data where to look at

Value

zero or -1

Examples

```
the_data <- as.data.frame(cbind(c("one", "two"), c("a", "b"), c("aa", "bb")))
colnames(the_data) <- c("name", "brand_one", "two")
get_col_multiple_pattern(c("brand", "trade"), the_data)
```

get_cost_AandE_code *Function to extract the unit hospital inpatient admission by matching code*

Description

Function to extract the unit hospital inpatient admission by matching code

Usage

```
get_cost_AandE_code(
  code,
  type_admit,
  ref_cost_data_file,
  col_name_code,
  unit_cost_col,
  type_admit_col,
  sheet = NULL
)
```

Arguments

code code for AE attendance

type_admit term indicating admission and type of attendance

ref_cost_data_file file that has unit cost

col_name_code name of the column that has the code

unit_cost_col name of the column with the unit cost

type_admit_col colname that describes type of the attendance and that indicates admitted or not

sheet sheet if excel file is given

Value

unit cost the unit cost matching the code

Examples

```
ref_cost_data_file <- system.file("extdata",  
  "National_schedule_of_NHS_costs_2019_AandE.csv", package = "packDAMipd")  
re = get_cost_AandE_code("VB02Z", "T01A", ref_cost_data_file,  
  "Currency_Code", "National_Average_Unit_Cost", "Service_Code")
```

get_cost_AandE_description

Function to extract the unit cost by description of AandE att matching description

Description

Function to extract the unit cost by description of AandE att matching description

Usage

```
get_cost_AandE_description(  
  description,  
  type_admit,  
  ref_cost_data_file,  
  col_name_description,  
  unit_cost_col,  
  type_admit_col,  
  sheet = NULL  
)
```

Arguments

description description of the AE attendance
type_admit term indicating admission and type of attendance
ref_cost_data_file
 file that has unit cost
col_name_description
 name of the column that has the description
unit_cost_col name of the column with the unit cost
type_admit_col colname that describes type of the attendance and
sheet sheet if excel file is given

Value

unit cost the unit cost matching the hrg code

Examples

```
ref_cost_data_file <- system.file("extdata",
  "National_schedule_of_NHS_costs_2019_AandE.csv", package = "packDAMipd")
re = get_cost_AandE_description("Emergency Medicine", "T01A",
  ref_cost_data_file, "Currency_Description", "National_Average_Unit_Cost",
  "Service_Code")
```

```
get_cost_ip_dc_description
```

Function to extract the unit hospital inpatient admission by matching description

Description

Function to extract the unit hospital inpatient admission by matching description

Usage

```
get_cost_ip_dc_description(
  description,
  ref_cost_data_file,
  col_name_description,
  unit_cost_col,
  sheet = NULL
)
```

Arguments

description	description corresponding to the inpatient admission
ref_cost_data_file	file that has unit cost
col_name_description	name of the column that has the description
unit_cost_col	name of the column with the unit cost
sheet	sheet if excel file is given

Value

unit cost the unit cost matching the hrg code

Examples

```
ref_cost_data_file <- system.file("extdata",
  "National_schedule_of_NHS_costs_2019.csv", package = "packDAMipd")
result <- get_cost_ip_dc_description("Cerebrovascular Accident",
  ref_cost_data_file, "Currency_Description",
  "National_Average_Unit_Cost")
```

get_cost_ip_dc_hrg	<i>Function to extract the unit hospital inpatient admission by matching HRG code</i>
--------------------	---

Description

Function to extract the unit hospital inpatient admission by matching HRG code

Usage

```
get_cost_ip_dc_hrg(  
  hrg,  
  ref_cost_data_file,  
  col_name_hrg_code,  
  unit_cost_col,  
  sheet = NULL  
)
```

Arguments

hrg	hrg code corresponding to the inpatient admission
ref_cost_data_file	file that has unit cost
col_name_hrg_code	name of the column that has the hrg code
unit_cost_col	name of the column with the unit cost
sheet	sheet if excel file is given

Value

unit cost the unit cost matching the hrg code

Examples

```
ref_cost_data_file <- system.file("extdata",  
  "National_schedule_of_NHS_costs_2019.csv", package = "packDAMipd")  
get_cost_ip_dc_hrg("AA22C", ref_cost_data_file, "Currency_Code",  
  "National_Average_Unit_Cost")
```

get_eq5d_details *Function to get the details of the EQ5D column*

Description

Function to get the details of the EQ5D column

Usage

```
get_eq5d_details(trialdata)
```

Arguments

trialdata, data containing individual level trial data

Details

Specific to the EQ5D data - the column names are given as certain sets, Tried to give 12 sets as the column names

Value

the name of the variable related to EQ5D and the unique contents if success, else error

Examples

```
get_eq5d_details(data.frame(  
  "MO" = c(1, 2), "SC" = c(1, 2), "UA" = c(1, 2),  
  "PD" = c(1, 2), "AD" = c(1, 2)  
))
```

get_extension_file *Function to get extension of a file name*

Description

Function to get extension of a file name

Usage

```
get_extension_file(filename)
```

Arguments

filename name of a file

Details

if there is no "." character returns error else returns last characters those after string split using "."

Value

the extension

Examples

```
get_extension_file("data.txt")
```

`get_gender_details` *Function to get the details of the gender column*

Description

Function to get the details of the gender column

Usage

```
get_gender_details(trialdata)
```

Arguments

`trialdata`, data containing individual level trial data

Details

expecting the data contains the information on gender preferably column names "gender", "sex" or "male" or "female". If multiple column names match these, then first match will be chosen.

Value

the name of the variable related to gender and the unique contents if success, else error

Examples

```
get_gender_details(data.frame("Age" = c(21, 15), "sex" = c("m", "f")))
```

get_mean_sd_age *Function to return mean age from a data frame*

Description

Function to return mean age from a data frame

Usage

```
get_mean_sd_age(this_data, age_nrcode)
```

Arguments

this_data the data containing column with age
age_nrcode non response code

Details

Age data is complete with the nr code given and get the mean and sd

Value

mean and sd, if success -1, if failure

Examples

```
this_data <- as.data.frame(cbind(num = c(1, 2, 3, 4),  
age = c(14, 25, 26, 30)))  
get_mean_sd_age(this_data, NA)
```

get_mortality_from_file
Get the mortality rate values from reading a file

Description

Get the mortality rate values from reading a file

Usage

```
get_mortality_from_file(paramfile, age, mortality_colname, gender = NULL)
```

Arguments

paramfile	parameter file to get the mortality eg.national life table data
age	age to get the age specific data
mortality_colname	column name with the mortality rates if it is not gender specific
gender	gender details to get the gender specific mortality data

Details

Provides the mortality rates as age and gender dependent Assumes the data contains mortality rate for single year and once it extracted per gender will retrieve single value Age column can consists of range of values, or a particular value also assumes that the mortality rate for each gender is listed under the gender column for gender specific values. if the mortality is not gender specific, the column name should be passed on to the function if gender is not null, mortality_name will be ignored

Value

the paramvalue

Examples

```
paramfile <- system.file("extdata", "LifeTable_USA_Mx_2015.csv",
  package = "packDAMipd"
)
a <- get_mortality_from_file(paramfile, age = 10, mortality_colname =
"total", gender = NULL)
```

get_name_value_probdistrb_def

Function to return the two parameters from a given expression separated by comma,

Description

Function to return the two parameters from a given expression separated by comma,

Usage

```
get_name_value_probdistrb_def(expr)
```

Arguments

expr	an expression
------	---------------

Details

It will return the parameters of the distribution separated by commas and given in usual notation as brackets. It will identify those in between first occurrence of "(" and last occurrence of ")" and from the characters in between search for comma to indicate different parameters then it will extract (from those extracted parameters separated by commas) that on the left side of "equal" sign `get_name_value_probdistrb_def("gamma(mean = sqrt(2), b =17)")` will be ok but `get_name_value_probdistrb_def("gamma(shape, scale)")` and `get_name_value_probdistrb_def("gamma(shape =1 & scale =1)")` will show error

Value

parameters in the expression `expr`

Examples

```
get_name_value_probdistrb_def("gamma(mean = 10, sd =1)")
```

`get_outcome_details` *Function to get the details of the outcome column*

Description

Function to get the details of the outcome column

Usage

```
get_outcome_details(trialdata, name, related_words, multiple = FALSE)
```

Arguments

<code>trialdata</code> ,	data containing individual level trial data
<code>name</code> ,	name of the variable
<code>related_words</code> ,	probable column names
<code>multiple</code> ,	indicates true if there are multiple columns

Details

if the words related to outcome is given, the function will get the columns and the codes used for the outcome, the difference here is that certain outcomes can be distributed in multiple columns

Value

the name of the variable related to health outcome (any) and the unique contents if success, else error

Examples

```
get_outcome_details(  
  data.frame("qo1.M0" = c(1, 2), "qo1.PD" = c(1, 2), "qo1.AD" = c(1, 2)),  
  "eq5d", "qo1", TRUE  
)
```

```
get_parameter_def_distribution
```

Get the definition of given parameter distribution defined in a file

Description

Get the definition of given parameter distribution defined in a file

Usage

```
get_parameter_def_distribution(  
  parameter,  
  paramfile,  
  colnames_paramdistr,  
  strategycol = NA,  
  strategyname = NA  
)
```

Arguments

parameter	parameter of interest
paramfile	data file to be provided
colnames_paramdistr	list of column names for the parameters that define the distribution
strategycol	treatment strategy column name
strategyname	treatment strategy name in the column strategycol

Details

This function reads the parameter distribution from a file and return the parameter obtained This assumes that the file contains parameter, distribution colnames for parameter values for the distribution are passed on to the function assumes the name of each parameter and value are given in the consecutive columns. Once the expression is created using the parameters given in the file, it gets checked for correctness of specifying the distribution in R context using the function `check_estimate_substitute_proper_params` and then evaluated.

Value

the definition of parameter from the given distribution

Examples

```
paramfile <- system.file("extdata", "table_param.csv",  
package = "packDAMipd")  
a <- get_parameter_def_distribution("rr", paramfile, c("Param1_name",  
"Param1_value"))
```

get_parameter_direct *Get the parameter values from reading a file*

Description

Get the parameter values from reading a file

Usage

```
get_parameter_direct(parameter, paramvalue)
```

Arguments

parameter	parameter of interest
paramvalue	parameter value to be assigned

Details

Basic function to assign a parameter directly

Value

the paramvalue

Examples

```
a <- get_parameter_direct("cost_IT", paramvalue = 100)
```

get_parameter_estimated_regression
*Get the parameter values using the provided statistical regression
methods*

Description

Get the parameter values using the provided statistical regression methods

Usage

```

get_parameter_estimated_regression(
  param_to_be_estimated,
  data,
  method,
  indep_var,
  info_get_method = NA,
  info_distribution = NA,
  covariates = NA,
  timevar_survival = NA,
  interaction = FALSE,
  fix_eff = NA,
  fix_eff_interact_vars = NA,
  random_intercept_vars = NA,
  nested_intercept_vars_pairs = NA,
  cross_intercept_vars_pairs = NA,
  uncorrel_slope_intercept_pairs = NA,
  random_slope_intercept_pairs = NA,
  naaction = "stats::na.omit",
  param2_to_be_estimated = NA,
  covariates2 = NA,
  interaction2 = FALSE,
  link = NA,
  cluster_var = NA,
  package_mixed_model = NA
)

```

Arguments

param_to_be_estimated	parameter of interest
data	data to be provided or the data file containing dataset
method	method of estimation (for example, linear, logistic regression etc)
indep_var	the independent variable (column name in data file)
info_get_method	additional information on methods e.g Kaplan-Meier or hazard
info_distribution	distribution name eg. for logistic regression -binomial
covariates	list of covariates-calculations to be done before passing
timevar_survival	time variable for survival analysis
interaction	boolean value to indicate interaction in the case of linear regression
fix_eff	boolean value to indicate interaction in the case of linear regression
fix_eff_interact_vars	boolean value to indicate interaction in the case of linear regression

`random_intercept_vars` boolean value to indicate interaction in the case of linear regression
`nested_intercept_vars_pairs` boolean value to indicate interaction in the case of linear regression
`cross_intercept_vars_pairs` boolean value to indicate interaction in the case of linear regression
`uncorrel_slope_intercept_pairs` boolean value to indicate interaction in the case of linear regression
`random_slope_intercept_pairs` boolean value to indicate interaction in the case of linear regression
`naaction` what action to be taken for the missing values, default is a missing value.
`param2_to_be_estimated` parameter of interest for equation 2 in bivariate regression
`covariates2` list of covariates - for equation 2 in bivariate regression
`interaction2` boolean value to indicate interaction for equation 2 in bivariate regression
`link` link function to be provided if not using the default link for each of the `info_distribution`
`cluster_var` cluster variable if any
`package_mixed_model` package to be used for mixed model ie nlme or lme4

Details

This function is the top in the layer of functions used for regression analysis. Thus it contains many parameters to be passed on. The required ones are parameter to be estimated, data that contains the observation, the method of regression to be used, the independent variable and the information for the distribution and method. If the data is given as a file name, it will load the data in that file. Then it calls the appropriate functions depending on the regression method that is specified. The methods that are considered: Survival analysis, linear regression, logistic regression, generalised linear model, linear multilevel or mixed model, and seemingly unrelated regression.

Value

results of the regression analysis

Examples

```

result <- get_parameter_estimated_regression(
  param_to_be_estimated = "Direction",
  data = ISLR::Smarket, method = "logistic", indep_var = "Lag1",
  info_get_method = NA, info_distribution = "binomial",
  covariates = c("Lag2", "Lag3"), interaction = FALSE,
  naaction = "na.omit", link = NA)

```

get_parameter_read *Get the parameter values from reading a file*

Description

Get the parameter values from reading a file

Usage

```
get_parameter_read(parameter, paramfile, strategycol = NA, strategyname = NA)
```

Arguments

parameter	parameter of interest
paramfile	parameter file to be provided
strategycol	treatment strategy
strategyname	treatment strategy name in the column strategycol

Details

This function read the parameter from a file given that the file has these column names (at least) Parameter and Value Strategy col and name are optional. Check if the data file contains column names parameter and value and then get the results.

Value

the paramvalue

Examples

```
a <- get_parameter_read("cost_IT", paramfile = system.file("extdata",  
"table_param.csv", package = "packDAMipd"))
```

get_slope_intercept *help function to keep slope and intercept portion ready in mixed model expression*

Description

help function to keep slope and intercept portion ready in mixed model expression

Usage

```

get_slope_intercept(
  expression,
  random_intercept_vars,
  random_slope_intercept_pairs,
  uncorrel_slope_intercept_pairs
)

```

Arguments

expression expression created so far

random_intercept_vars,
 names of variables for random intercept

random_slope_intercept_pairs,
 random slopes intercept pairs this is a list of paired variables

uncorrel_slope_intercept_pairs,
 variables with correlated intercepts

Value

expression expression created

get_slope_intercept_cross

*help function to keep slope and intercept portion ready in mixed model
expression*

Description

help function to keep slope and intercept portion ready in mixed model expression

Usage

```

get_slope_intercept_cross(
  expression,
  random_intercept_vars,
  intercept_vars_pairs,
  random_slope_intercept_pairs,
  uncorrel_slope_intercept_pairs
)

```

Arguments

expression expression created so far
 random_intercept_vars,
 names of variables for random intercept
 intercept_vars_pairs,
 those of the random intercept variables with nested effect
 random_slope_intercept_pairs,
 random slopes intercept pairs this is a list of paired variables
 uncorrel_slope_intercept_pairs,
 variables with correlated intercepts

Value

expression expression created

get_slope_intercept_nested

help function to keep slope and intercept portion ready in mixed model expression

Description

help function to keep slope and intercept portion ready in mixed model expression

Usage

```

get_slope_intercept_nested(
  expression,
  random_intercept_vars,
  intercept_vars_pairs,
  random_slope_intercept_pairs,
  uncorrel_slope_intercept_pairs
)

```

Arguments

expression expression created so far
 random_intercept_vars,
 names of variables for random intercept
 intercept_vars_pairs,
 those of the random intercept variables with nested effect
 random_slope_intercept_pairs,
 random slopes intercept pairs this is a list of paired variables
 uncorrel_slope_intercept_pairs,
 variables with correlated intercepts

Value

expression expression created

get_timepoint_details *Function to get the details of the time point column*

Description

Function to get the details of the time point column

Usage

```
get_timepoint_details(trialdata)
```

Arguments

trialdata, data containing individual level trial data

Details

expecting the data contains the information on timepoints preferably column names "time point", "times" or "time" or "timepoint". If multiple column names match these, then first match will be chosen.

Value

the name of the variable related to time point and the unique contents if success, else error

Examples

```
get_timepoint_details(data.frame("time" = c(21, 15),  
"arm" = c("control", "intervention")))
```

get_trial_arm_details *Function to get the details of the trial arm*

Description

Function to get the details of the trial arm

Usage

```
get_trial_arm_details(trialdata)
```

Arguments

trialdata, data containing individual level trial data

Details

expecting the data contains the information on trial arm preferably column names "arm", "trial" or "trial arm". If multiple column names match these, then first match will be chosen.

Value

the name of the variable related to trial arm and the unique contents if success, else error

Examples

```
get_trial_arm_details(data.frame(  
  "Age" = c(21, 15),  
  "arm" = c("control", "intervention")  
))
```

get_var_state	<i>Get the attribute for the health state</i>
---------------	---

Description

Get the attribute for the health state

Usage

```
get_var_state(state, var)
```

Arguments

state	object of class health state
var	attribute of the health state

Details

After checking the given state is a health state and given variable is defined in the health state, the value of the variable is returned

Value

modified health state

Examples

```
get_var_state(health_state("IT", 100, 0.4, 0, FALSE), "cost")
```

health_state	<i>Definition of health state class or health state constructor</i>
--------------	---

Description

Definition of health state class or health state constructor

Usage

```
health_state(name, cost, utility, state_time = 0, absorb = FALSE)
```

Arguments

name	name of the health state
cost	value or expression that represents cost of the health state
utility	value or expression that represents utility of the health state
state_time	time denoting how long in the state
absorb	boolean indicating health state absorbing or not

Details

Initialising the name, cost, utility and time spent for the health state name is the name of the health state cost/utility can be defined as characters e.g. "cost_A" if they are characters, the value is assigned after parsing the text. state_time is integer and absorb is boolean

Value

value of the state

Examples

```
st <- health_state("IT", 100, 0.4, 0, FALSE)
st <- health_state("IT", "cost_A", 0.4, 0, FALSE)
```

init_trace	<i>Define an all zero trace matrix</i>
------------	--

Description

Define an all zero trace matrix

Usage

```
init_trace(health_states, cycles)
```

Arguments

health_states health states
cycles no of cycles

Details

Initialise the trace matrix with all zeros trace matrix will be with no_cycles+1 by no_states matrix

Value

trace matrix -all zero

Examples

```
a <- health_state("Healthy", 1, 1, 0, FALSE)
b <- health_state("Dead", 1, 0.5, 0, FALSE)
health_states <- combine_state(a, b)
init_trace(health_states, 10)
```

keep_results_plot_dsa *Function to do some checks before plotting sensitivity analysis results*

Description

Function to do some checks before plotting sensitivity analysis results

Usage

```
keep_results_plot_dsa(
  result_dsa_control,
  plotfor,
  result_dsa_treat,
  plot_variable,
  threshold,
  comparator
)
```

Arguments

result_dsa_control result from deterministic sensitivity analysis for first or control model
plotfor the variable to plotfor e.g. cost, utility NMB etc
result_dsa_treat result from deterministic sensitivity analysis for the comparative Markov model
plot_variable variable for plotting
threshold threshold value of WTP
comparator the strategy to be compared with

Value

results to plot dsa

list_paramwise_psa_result

Function to list probabilistic sensitivity analysis results parameterwise

Description

Function to list probabilistic sensitivity analysis results parameterwise

Usage

```
list_paramwise_psa_result(
  result_psa_params_control,
  result_psa_params_treat,
  threshold,
  comparator
)
```

Arguments

result_psa_params_control	result from probabilistic sensitivity analysis for first or control model
result_psa_params_treat	result from probabilistic sensitivity analysis for the comparative Markov model
threshold	threshold value of WTP
comparator	the strategy to be compared with

Value

plot of sensitivity analysis

Examples

```
param_list <- define_parameters(
  cost_zido = 2278, cost_direct_med_A = 1701,
  cost_comm_care_A = 1055, cost_direct_med_B = 1774,
  cost_comm_care_B = 1278,
  cost_direct_med_C = 6948, cost_comm_care_C = 2059,
  tpAtoA = 1251 / (1251 + 483),
  tpAtoB = 350 / (350 + 1384), tpAtoC = 116 / (116 + 1618),
  tpAtoD = 17 / (17 + 1717),
  tpBtoB = 731 / (731 + 527), tpBtoC = 512 / (512 + 746),
  tpBtoD = 15 / (15 + 1243),
  tpCtoC = 1312 / (1312 + 437), tpCtoD = 437 / (437 + 1312), tpDtoD = 1,
```

```

cost_health_A = "cost_direct_med_A + cost_comm_care_A",
cost_health_B = "cost_direct_med_B + cost_comm_care_B",
cost_health_C = "cost_direct_med_C + cost_comm_care_C",
cost_drug = "cost_zido"
)
A <- health_state("A", cost = "cost_health_A + cost_drug ", utility = 1)
B <- health_state("B", cost = "cost_health_B + cost_drug", utility = 1)
C <- health_state("C", cost = "cost_health_C + cost_drug", utility = 1)
D <- health_state("D", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3, 4), c(NA, 5, 6, 7), c(NA, NA, 8, 9),
c(NA, NA, NA, 10))
colnames(tmat) <- rownames(tmat) <- c("A", "B", "C", "D")
tm <- populate_transition_matrix(4, tmat, c(
  "tpAtoA", "tpAtoB", "tpAtoC", "tpAtoD",
  "tpBtoB", "tpBtoC", "tpBtoD", "tpCtoC", "tpCtoD", "tpDtoD"
), colnames(tmat))
health_states <- combine_state(A, B, C, D)
mono_strategy <- strategy(tm, health_states, "mono")
mono_markov <- markov_model(mono_strategy, 20, initial_state = c(1,0,0,0),
discount = c(0.06, 0),param_list)
sample_list <- define_parameters(cost_zido = "gamma(mean = 2756,
sd = sqrt(2756))")
param_table <- define_parameters_psa(param_list, sample_list)
result <- do_psa(mono_markov, param_table, 10)
list_paramwise_psa_result(result, NULL, NULL, NULL)

```

load_trial_data

Function to load the file containing trial data and return it

Description

Function to load the file containing trial data and return it

Usage

```
load_trial_data(file = NULL, sheet = NULL)
```

Arguments

file,	name of the file in full
sheet	name of the sheet if excel work book is given

Value

trial data if success, else -1

Examples

```
load_trial_data(system.file("extdata", "trial_data.csv",
  package = "packDAMipd"
))
```

map_eq5d5Lto3L_VanHout

Function to map EQ5D5L scores to EQ5D3L scores and then add to IPD data

Description

Function to map EQ5D5L scores to EQ5D3L scores and then add to IPD data

Usage

```
map_eq5d5Lto3L_VanHout(ind_part_data, eq5d_nrcode)
```

Arguments

ind_part_data a data frame
eq5d_nrcode non response code for EQ5D5L, default is NA

Value

qaly included modified data, if success -1, if failure

Source

http://eprints.whiterose.ac.uk/121473/1/Devlin_et_al-2017-Health_Economics.pdf

Examples

```
library(valueEQ5D)
datafile <- system.file("extdata", "trial_data.csv",
  package = "packDAMipd")
trial_data <- load_trial_data(datafile)
map_eq5d5Lto3L_VanHout(trial_data, NA)
```

markov_model	<i>Definition of Markov model and trace</i>
--------------	---

Description

Definition of Markov model and trace

Usage

```
markov_model(
  current_strategy,
  cycles,
  initial_state,
  discount = c(0, 0),
  parameter_values = NULL,
  half_cycle_correction = TRUE,
  state_cost_only_prevalent = FALSE,
  state_util_only_prevalent = FALSE,
  method = "half cycle correction",
  startup_cost = NULL,
  startup_util = NULL
)
```

Arguments

current_strategy	strategy object
cycles	no of cycles
initial_state	value of states initially
discount	rate of discount for costs and qalys
parameter_values	parameters for assigning health states and probabilities
half_cycle_correction	boolean to indicate half cycle correction
state_cost_only_prevalent	boolean parameter to indicate if the costs for state occupancy is only for those in the state excluding those that transitioned new. This is relevant when the transition cost is provided for eg. in a state with dialysis the cost of previous dialysis is different from the newly dialysis cases. Then the state_cost_only_prevalent should be TRUE
state_util_only_prevalent	boolean parameter to indicate if the utilities for state occupancy is only for those in the state excluding those that transitioned new.
method	what type of half cycle correction needed
startup_cost	cost of states initially
startup_util	utility of states initially if any

Details

Use the strategy, cycles, initial state values creating the markov model and trace. As many probabilities /cost/utility value depend on age/time the evaluation and assignment happens during each cycle. At the heart it does a matrix multiplication using the previous row of the trace matrix and the columns of the transition matrix. Also checks for population loss, calculates cumulative costs and qalys (accounts for discounting and half cycle correction)

Value

Markov trace

Examples

```
tmat <- rbind(c(1, 2), c(3, 4))
colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead")
tm <- populate_transition_matrix(2, tmat, c(0.5, 0.5, 0, 1))
a <- health_state("Healthy", 1, 1, 0, FALSE)
b <- health_state("Dead", 1, 0, 0, TRUE)
health_states <- combine_state(a, b)
this.strategy <- strategy(tm, health_states, "intervention")
markov_model(this.strategy, 10, c(1, 0))
```

microcosting_liquids_long

Function to estimate the cost of liquids when IPD is in long format

Description

Function to estimate the cost of liquids when IPD is in long format

Usage

```
microcosting_liquids_long(
  the_columns,
  ind_part_data_long,
  name_med,
  brand_med = NULL,
  dose_med,
  unit_med = NULL,
  bottle_size,
  bottle_size_unit = NULL,
  bottle_last,
  bottle_last_unit = NULL,
  preparation_dose = NULL,
  preparation_unit = NULL,
  timeperiod,
  unit_cost_data,
```

```

    unit_cost_column,
    cost_calculated_per,
    strength_column,
    list_of_code_names = NULL,
    list_of_code_brand = NULL,
    list_of_code_dose_unit = NULL,
    list_of_code_bottle_size_unit = NULL,
    list_of_code_bottle_last_unit = NULL,
    list_preparation_dose_unit = NULL,
    eqdose_covtab = NULL,
    basis_strength_unit = NULL
)

```

Arguments

the_columns columns that are to be used to convert the data from long to wide
ind_part_data_long
 IPD
name_med name of medication
brand_med brand name of medication if revealed
dose_med dose of medication used
unit_med unit of medication ; use null if its along with the dose
bottle_size size of the bottle used
bottle_size_unit
 unit of bottle volume
bottle_last how long the bottle lasted
bottle_last_unit
 time unit of how long the bottle lasted
preparation_dose
 dose if preparation is given
preparation_unit
 unit of preparatio dose
timeperiod time period for cost calculation
unit_cost_data unit costs data
unit_cost_column
 column name of unit cost in unit_cost_data
cost_calculated_per
 column name of unit where the cost is calculated
strength_column
 column column name that has strength of medication
list_of_code_names
 if names is coded, give the code:name pairs, optional
list_of_code_brand
 if brand names are coded, give the code:brand pairs, optional

list_of_code_dose_unit
if unit is coded, give the code:unit pairs, optional

list_of_code_bottle_size_unit
list of bottle size units and codes

list_of_code_bottle_lastests_unit
list of time of bottle lasts and codes

list_preparation_dose_unit
list of preparation dose units and codes

eqdose_covtab table to get the conversion factor for equivalent doses, optional

basis_strength_unit
strength unit to be taken as basis required for total medication calculations

Value

the calculated cost of tablets along with original data

Examples

```
med_costs_file <- system.file("extdata", "average_unit_costs_med_brand.csv",
package = "packDAMipd")
data_file <- system.file("extdata", "medication_liq.xlsx",
package = "packDAMipd")
ind_part_data <- load_trial_data(data_file)
med_costs <- load_trial_data(med_costs_file)
conv_file <- system.file("extdata", "Med_calc.xlsx",
package = "packDAMipd")
table <- load_trial_data(conv_file)
names <- colnames(ind_part_data)
ending <- length(names)
ind_part_data_long <- tidyr::gather(ind_part_data, measurement, value,
names[2]:names[ending], factor_key = TRUE)
the_columns <- c("measurement", "value")
res <- microcosting_liquids_long(the_columns,
ind_part_data_long = ind_part_data_long,
name_med = "liq_name", brand_med = NULL, dose_med = "liq_strength",
unit_med = NULL, bottle_size = "liq_bottle_size", bottle_size_unit = NULL,
bottle_lastests = "liq_lastests", bottle_lastests_unit = NULL, preparation_dose = NULL,
preparation_unit = NULL, timeperiod = "4 months", unit_cost_data = med_costs,
unit_cost_column = "UnitCost", cost_calculated_per = "Basis",
strength_column = "Strength", list_of_code_names = NULL,
list_of_code_brand = NULL, list_of_code_dose_unit = NULL,
list_of_code_bottle_size_unit = NULL, list_of_code_bottle_lastests_unit = NULL,
list_preparation_dose_unit = NULL, eqdose_covtab = table,
basis_strength_unit = NULL)
```

 microcosting_liquids_wide

Function to estimate the cost of liquids taken (from IPD)

Description

Function to estimate the cost of liquids taken (from IPD)

Usage

```

microcosting_liquids_wide(
  ind_part_data,
  name_med,
  brand_med = NULL,
  dose_med,
  unit_med = NULL,
  bottle_size,
  bottle_size_unit = NULL,
  bottle_last,
  bottle_last_unit = NULL,
  preparation_dose = NULL,
  preparation_unit = NULL,
  timeperiod,
  unit_cost_data,
  unit_cost_column,
  cost_calculated_per,
  strength_column,
  list_of_code_names = NULL,
  list_of_code_brand = NULL,
  list_of_code_dose_unit = NULL,
  list_of_code_bottle_size_unit = NULL,
  list_of_code_bottle_last_unit = NULL,
  list_preparation_dose_unit = NULL,
  eqdose_covtab = NULL,
  basis_strength_unit = NULL
)

```

Arguments

ind_part_data	IPD
name_med	name of medication
brand_med	brand name of medication if revealed
dose_med	dose of medication used
unit_med	unit of medication ; use null if its along with the dose
bottle_size	size of the bottle used

bottle_size_unit unit of bottle volume
bottle_last how long the bottle lasted
bottle_last_unit time unit of how long the bottle lasted
preparation_dose dose if preparation is given
preparation_unit unit of preparatio dose
timeperiod time period for cost calculation
unit_cost_data unit costs data
unit_cost_column column name of unit cost in unit_cost_data
cost_calculated_per column name of unit where the cost is calculated
strength_column column column name that has strength of medication
list_of_code_names if names is coded, give the code:name pairs, optional
list_of_code_brand if brand names are coded, give the code:brand pairs, optional
list_of_code_dose_unit if unit is coded, give the code:unit pairs, optional
list_of_code_bottle_size_unit list of bottle size units and codes
list_of_code_bottle_last_unit list of time of bottle lasts and codes
list_preparation_dose_unit list of preparation dose units and codes
eqdose_covtab table to get the conversion factor for equivalent doses, optional
basis_strength_unit strength unit to be taken as basis required for total medication calculations

Value

the calculated cost of tablets along with original data

Examples

```

med_costs_file <- system.file("extdata", "average_unit_costs_med_brand.csv",
package = "packDAMipd")
data_file <- system.file("extdata", "medication_liq.xlsx",
package = "packDAMipd")
ind_part_data <- load_trial_data(data_file)
med_costs <- load_trial_data(med_costs_file)
conv_file <- system.file("extdata", "Med_calc.xlsx",package = "packDAMipd")
  
```

```

table <- load_trial_data(conv_file)
res <- microcosting_liquids_wide(
  ind_part_data = ind_part_data, name_med = "liq_name", brand_med = NULL,
  dose_med = "liq_strength", unit_med = NULL, bottle_size = "liq_bottle_size",
  bottle_size_unit = NULL, bottle_last = "liq_last",
  bottle_last_unit = NULL, preparation_dose = NULL, preparation_unit = NULL,
  timeperiod = "4 months", unit_cost_data = med_costs,
  unit_cost_column = "UnitCost", cost_calculated_per = "Basis",
  strength_column = "Strength", list_of_code_names = NULL,
  list_of_code_brand = NULL, list_of_code_dose_unit = NULL,
  list_of_code_bottle_size_unit = NULL, list_of_code_bottle_last_unit = NULL,
  list_preparation_dose_unit = NULL, eqdose_covtab = table,
  basis_strength_unit = NULL)

```

```

microcosting_patches_long

```

```

#' #####
#' Function to estimate the cost of patches when IPD is in long format
#' using a IPD data of long format

```

Description

```

#' ##### Function
#' to estimate the cost of patches when IPD is in long format using a IPD data of long format

```

Usage

```

microcosting_patches_long(
  the_columns,
  ind_part_data_long,
  name_med,
  brand_med = NULL,
  dose_med,
  unit_med = NULL,
  no_taken,
  freq_taken,
  timeperiod,
  unit_cost_data,
  unit_cost_column,
  cost_calculated_per,
  strength_column,
  list_of_code_names = NULL,
  list_of_code_freq = NULL,
  list_of_code_dose_unit = NULL,
  list_of_code_brand = NULL,
  eqdose_cov_tab = NULL,
  basis_strength_unit = NULL
)

```

Arguments

the_columns columns that are to be used to convert the data from long to wide
 ind_part_data_long IPD
 name_med name of medication
 brand_med brand name of medication if revealed
 dose_med dose of medication used
 unit_med unit of medication ; use null if its along with the dose
 no_taken how many taken
 freq_taken frequency of medication
 timeperiod time period for cost calculation
 unit_cost_data unit costs data
 unit_cost_column column name of unit cost in unit_cost_data
 cost_calculated_per column name of unit in the cost is calculated
 strength_column column column name that contain strength of medication
 list_of_code_names if names is coded, give the code:name pairs, optional
 list_of_code_freq if frequency is coded, give the code:frequency pairs, optional
 list_of_code_dose_unit if unit is coded, give the code:unit pairs, optional
 list_of_code_brand if brand names are coded, give the code:brand pairs, optional
 eqdose_cov_tab table to get the conversion factor for equivalent doses, optional
 basis_strength_unit strength unit to be taken as basis required for total medication calculations

Value

the calculated cost of tablets along with original data

Examples

```

med_costs_file <- system.file("extdata", "average_unit_costs_med_brand.csv",
package = "packDAMipd")
data_file <- system.file("extdata", "medication.xlsx",
package = "packDAMipd")
ind_part_data <- load_trial_data(data_file)
med_costs <- load_trial_data(med_costs_file)
conv_file <- system.file("extdata", "Med_calc.xlsx", package = "packDAMipd")
table <- load_trial_data(conv_file)
names <- colnames(ind_part_data)

```

```

ending <- length(names)
ind_part_data_long <- tidyr::gather(ind_part_data, measurement, value,
names[2]:names[ending], factor_key = TRUE)
the_columns <- c("measurement", "value")
res <- microcosting_patches_long(the_columns,
ind_part_data_long = ind_part_data_long, name_med = "patch_name",
brand_med = "patch_brand", dose_med = "patch_strength", unit_med = NULL,
no_taken = "patch_no_taken", freq_taken = "patch_frequency",
timeperiod = "4 months", unit_cost_data = med_costs,
unit_cost_column = "UnitCost", cost_calculated_per = "Basis",
strength_column = "Strength", list_of_code_names = NULL,
list_of_code_freq = NULL, list_of_code_dose_unit = NULL,
list_of_code_brand = NULL, eqdose_cov_tab = table,
basis_strength_unit = "mcg/hr")

```

microcosting_patches_wide

Function to estimate the cost of patches taken (from IPD)

Description

Function to estimate the cost of patches taken (from IPD)

Usage

```

microcosting_patches_wide(
  ind_part_data,
  name_med,
  brand_med = NULL,
  dose_med,
  unit_med = NULL,
  no_taken,
  freq_taken,
  timeperiod,
  unit_cost_data,
  unit_cost_column,
  cost_calculated_per,
  strength_column,
  list_of_code_names = NULL,
  list_of_code_freq = NULL,
  list_of_code_dose_unit = NULL,
  list_of_code_brand = NULL,
  eqdose_cov_tab = NULL,
  basis_strength_unit = NULL
)

```

Arguments

ind_part_data	IPD
name_med	name of medication
brand_med	brand name of medication if revealed
dose_med	dose of medication used
unit_med	unit of medication ; use null if its along with the dose
no_taken	how many taken
freq_taken	frequency of medication
timeperiod	time period for cost calculation
unit_cost_data	unit costs data
unit_cost_column	column name of unit cost in unit_cost_data
cost_calculated_per	column name of unit where the cost is calculated
strength_column	column column name that contain strength of medication
list_of_code_names	if names is coded, give the code:name pairs, optional
list_of_code_freq	if frequency is coded, give the code:frequency pairs, optional
list_of_code_dose_unit	if unit is coded, give the code:unit pairs, optional
list_of_code_brand	if brand names are coded, give the code:brand pairs, optional
eqdose_cov_tab	table to get the conversion factor for equivalent doses, optional
basis_strength_unit	strength unit to be taken as basis required for total medication calculations

Details

Assumes individual level data has name of medication, dose, dose unit, number taken, frequency taken, and basis time Assumes unit cost data contains the name of medication, form/type, strength, unit of strength (or the unit in which the cost calculated), preparation, unit cost, size and size unit (in which name, forms, size, size unit, and preparation are not passed on) @importFrom dplyr %>% a patient use 1 mg/hr patches 5 patches once a week that patch comes in a pack of 4 with cost £2.50 we want to estimate the cost for 3 months that means amount of medication 3 months = 21 weeks number of patches taken = 215 = $105 \text{ patches packs} = (105/4) \text{ almost } 27 \text{ packs cost} = 272.50$

Value

the calculated cost of tablets along with original data

Examples

```

med_costs_file <- system.file("extdata", "average_unit_costs_med_brand.csv",
package = "packDAMipd")
data_file <- system.file("extdata", "medication.xlsx",
package = "packDAMipd")
ind_part_data <- load_trial_data(data_file)
med_costs <- load_trial_data(med_costs_file)
conv_file <- system.file("extdata", "Med_calc.xlsx", package = "packDAMipd")
table <- load_trial_data(conv_file)
res <- microcosting_patches_wide(
ind_part_data = ind_part_data, name_med = "patch_name",
brand_med = "patch_brand", dose_med = "patch_strength", unit_med = NULL,
no_taken = "patch_no_taken", freq_taken = "patch_frequency",
timeperiod = "4 months", unit_cost_data = med_costs,
unit_cost_column = "UnitCost", cost_calculated_per = "Basis",
strength_column = "Strength", list_of_code_names = NULL,
list_of_code_freq = NULL, list_of_code_dose_unit = NULL,
list_of_code_brand = NULL, eqdose_cov_tab = table,
basis_strength_unit = "mcg/hr")

```

microcosting_tablets_long

Function to estimate the cost of tablets when IPD is in long format

Description

Function to estimate the cost of tablets when IPD is in long format

Usage

```

microcosting_tablets_long(
  the_columns,
  ind_part_data_long,
  name_med,
  brand_med = NULL,
  dose_med,
  unit_med = NULL,
  no_taken,
  freq_taken,
  timeperiod,
  unit_cost_data,
  unit_cost_column,
  cost_calculated_per,
  strength_column,
  list_of_code_names = NULL,
  list_of_code_freq = NULL,
  list_of_code_dose_unit = NULL,
  list_of_code_brand = NULL,

```

```

    eqdose_cov_tab = NULL,
    basis_strength_unit = NULL
  )

```

Arguments

```

the_columns      columns that are to be used to convert the data from long to wide
ind_part_data_long
                  IPD
name_med         name of medication
brand_med       brand name of medication if revealed
dose_med        dose of medication used
unit_med        unit of medication ; use null if its along with the dose
no_taken        how many taken
freq_taken      frequency of medication
timeperiod      time period for cost calculation
unit_cost_data  unit costs data
unit_cost_column
                column name of unit cost in unit_cost_data
cost_calculated_per
                column name of unit where the cost is calculated
strength_column
                column column name that contain strength of medication
list_of_code_names
                if names is coded, give the code:name pairs, optional
list_of_code_freq
                if frequency is coded, give the code:frequency pairs, optional
list_of_code_dose_unit
                if unit is coded, give the code:unit pairs, optional
list_of_code_brand
                if brand names are coded, give the code:brand pairs, optional
eqdose_cov_tab  table to get the conversion factor for equivalent doses, optional
basis_strength_unit
                strength unit to be taken as basis required for total medication calculations

```

Value

the calculated cost of tablets along with original data

Examples

```

med_costs_file <- system.file("extdata", "average_unit_costs_med_brand.csv",
package = "packDAMipd")
data_file <- system.file("extdata", "medication_all.xlsx",
package = "packDAMipd")

```

```

ind_part_data <- load_trial_data(data_file)
med_costs <- load_trial_data(med_costs_file)
conv_file <- system.file("extdata", "Med_calc.xlsx", package = "packDAMipd")
table <- load_trial_data(conv_file)
names <- colnames(ind_part_data)
ending <- length(names)
ind_part_data_long <- tidyr::gather(ind_part_data, measurement, value,
names[2]:names[ending], factor_key = TRUE)
the_columns <- c("measurement", "value")
res <- microcosting_tablets_long(the_columns,
ind_part_data_long = ind_part_data_long, name_med = "tab_name",
brand_med = "tab_brand", dose_med = "tab_strength",
unit_med = "tab_str_unit",
no_taken = "tab_no_taken", freq_taken = "tab_frequency",
timeperiod = "2 months",unit_cost_data = med_costs,
unit_cost_column = "UnitCost", cost_calculated_per = "Basis",
strength_column = "Strength", list_of_code_names = NULL,
list_of_code_freq = NULL,list_of_code_dose_unit = NULL,
eqdose_cov_tab = table, basis_strength_unit = "mg")

```

microcosting_tablets_wide

Function to estimate the cost of tablets taken (from IPD)

Description

Function to estimate the cost of tablets taken (from IPD)

Usage

```

microcosting_tablets_wide(
  ind_part_data,
  name_med,
  brand_med = NULL,
  dose_med,
  unit_med = NULL,
  no_taken,
  freq_taken,
  timeperiod,
  unit_cost_data,
  unit_cost_column,
  cost_calculated_per,
  strength_column,
  list_of_code_names = NULL,
  list_of_code_freq = NULL,
  list_of_code_dose_unit = NULL,
  list_of_code_brand = NULL,
  eqdose_cov_tab = NULL,
  basis_strength_unit = NULL
)

```

Arguments

ind_part_data IPD
 name_med name of medication
 brand_med brand name of medication if revealed
 dose_med dose of medication used
 unit_med unit of medication ; use null if its along with the dose
 no_taken how many taken
 freq_taken frequency of medication
 timeperiod time period for cost calculation
 unit_cost_data unit costs data
 unit_cost_column
 column name of unit cost in unit_cost_data
 cost_calculated_per
 column name of unit where the cost is calculated
 strength_column
 column column name that contain strength of medication
 list_of_code_names
 if names is coded, give the code:name pairs, optional
 list_of_code_freq
 if frequency is coded, give the code:frequency pairs, optional
 list_of_code_dose_unit
 if unit is coded, give the code:unit pairs, optional
 list_of_code_brand
 if brand names are coded, give the code:brand pairs, optional
 eqdose_cov_tab table to get the conversion factor for equivalent doses, optional
 basis_strength_unit
 strength unit to be taken as basis required for total medication calculations

Details

Assumes individual level data has name of medication, dose, dose unit, number taken, frequency taken, and basis time Assumes unit cost data contains the name of medication, form/type, strength, unit of strength (or the unit in which the cost calculated), preparation, unit cost, size and size unit (in which name, forms, size, size unit, and preparation are not passed on) @importFrom dplyr %>%

Value

the calculated cost of tablets along with original data

Examples

```

med_costs_file <- system.file("extdata", "average_unit_costs_med_brand.csv",
package = "packDAMipd")
data_file <- system.file("extdata", "medication_all.xlsx",
package = "packDAMipd")

```

```

ind_part_data <- load_trial_data(data_file)
med_costs <- load_trial_data(med_costs_file)
conv_file <- system.file("extdata", "Med_calc.xlsx", package = "packDAMipd")
table <- load_trial_data(conv_file)
res <- microcosting_tablets_wide(ind_part_data = ind_part_data,
name_med = "tab_name", brand_med = "tab_brand", dose_med = "tab_strength",
unit_med = "tab_str_unit", no_taken = "tab_no_taken",
freq_taken = "tab_frequency", timeperiod = "2 months",
unit_cost_data = med_costs, unit_cost_column = "UnitCost",
cost_calculated_per = "Basis", strength_column = "Strength",
list_of_code_names = NULL, list_of_code_freq = NULL,
list_of_code_dose_unit = NULL, eqdose_cov_tab = table,
basis_strength_unit = "mg")

```

plot_ceac

*Plot cost effectiveness acceptability curve***Description**

Plot cost effectiveness acceptability curve

Usage

```
plot_ceac(list_markov, threshold_values, comparator, currency = "GBP")
```

Arguments

list_markov	markov_model objects
threshold_values	list of threshold values
comparator	the comparator
currency	currency

Value

plots

Examples

```

well <- health_state("well", cost = 0, utility = 1)
disabled <- health_state("disabled", cost = 100, utility = 1)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.6, 0.2, 0.2, 0.6, 0.4, 1),
colnames(tmat))
health_states <- combine_state(well, disabled, dead)
this.strategy <- strategy(tm, health_states, "control")

```

```

this_markov <- markov_model(this.strategy, 24, c(1000, 0, 0),c(0, 0))
well <- health_state("well", cost = 0, utility = 1)
disabled <- health_state("disabled", cost = 10, utility = 0.5)
dead <- health_state("dead", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead")
tm <- populate_transition_matrix(3, tmat, c(0.4, 0.4, 0.2, 0.6, 0.4, 1),
colnames(tmat))
health_states <- combine_state(well, disabled, dead)
this.strategy <- strategy(tm, health_states, "intervention")
sec_markov <- markov_model(this.strategy, 24, c(1000, 0, 0), c(0, 0))
list_markov <- combine_markov(this_markov, sec_markov)
plot_ceac(list_markov, c(1000, 2000, 3000), comparator = "control")

```

plot_dsa

Function to plot results of sensitivity analysis do_sensitivity_analysis()

Description

Function to plot results of sensitivity analysis do_sensitivity_analysis()

Usage

```

plot_dsa(
  result_dsa_control,
  plotfor,
  type = "range",
  result_dsa_treat = NULL,
  threshold = NULL,
  comparator = NULL
)

```

Arguments

result_dsa_control	result from deterministic sensitivity analysis for first or control model
plotfor	the variable to plotfor e.g. cost, utility NMB etc
type	type of analysis, range or difference
result_dsa_treat	result from deterministic sensitivity analysis for the comparative Markov model
threshold	threshold value of WTP
comparator	the strategy to be compared with

Value

plot of sensitivity analysis

Examples

```

param_list <- define_parameters(
  cost_zido = 2278, cost_direct_med_A = 1701,
  cost_comm_care_A = 1055, cost_direct_med_B = 1774,
  cost_comm_care_B = 1278,
  cost_direct_med_C = 6948, cost_comm_care_C = 2059,
  tpAtoA = 1251 / (1251 + 483),
  tpAtoB = 350 / (350 + 1384), tpAtoC = 116 / (116 + 1618),
  tpAtoD = 17 / (17 + 1717),
  tpBtoB = 731 / (731 + 527), tpBtoC = 512 / (512 + 746),
  tpBtoD = 15 / (15 + 1243),
  tpCtoC = 1312 / (1312 + 437), tpCtoD = 437 / (437 + 1312),
  tpDtoD = 1,
  cost_health_A = "cost_direct_med_A + cost_comm_care_A",
  cost_health_B = "cost_direct_med_B + cost_comm_care_B",
  cost_health_C = "cost_direct_med_C + cost_comm_care_C",
  cost_drug = "cost_zido")
low_values <- define_parameters(cost_direct_med_B = 177.4,
  cost_comm_care_C = 205.9)
upp_values <- define_parameters(cost_direct_med_B = 17740,
  cost_comm_care_C = 20590)
A <- health_state("A", cost = "cost_health_A + cost_drug ",
  utility = 1)
B <- health_state("B", cost = "cost_health_B + cost_drug",
  utility = 1)
C <- health_state("C", cost = "cost_health_C + cost_drug",
  utility = 1)
D <- health_state("D", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3, 4), c(NA, 5, 6, 7), c(NA, NA, 8, 9),
  c(NA, NA, NA, 10))
colnames(tmat) <- rownames(tmat) <- c("A", "B", "C", "D")
tm <- populate_transition_matrix(4, tmat, c("tpAtoA", "tpAtoB", "tpAtoC",
  "tpAtoD", "tpBtoB", "tpBtoC", "tpBtoD", "tpCtoC", "tpCtoD", "tpDtoD"),
  colnames(tmat))
health_states <- combine_state(A, B, C, D)
mono_strategy <- strategy(tm, health_states, "mono")
mono_markov <- markov_model(mono_strategy, 20, c(1, 0, 0, 0),
  discount = c(0.06, 0), param_list)
param_table <- define_parameters_sens_anal(param_list, low_values,
  upp_values)
result <- do_sensitivity_analysis(mono_markov, param_table)
param_list_treat <- define_parameters(
  cost_zido = 3000, cost_direct_med_A = 890,
  cost_comm_care_A = 8976, cost_direct_med_B = 2345,
  cost_comm_care_B = 1278,
  cost_direct_med_C = 6948, cost_comm_care_C = 2059,
  tpAtoA = 1251 / (1251 + 483),
  tpAtoB = 350 / (350 + 1384), tpAtoC = 116 / (116 + 1618),
  tpAtoD = 17 / (17 + 1717),
  tpBtoB = 731 / (731 + 527), tpBtoC = 512 / (512 + 746),
  tpBtoD = 15 / (15 + 1243),

```

```
tpCtoC = 1312 / (1312 + 437), tpCtoD = 437 / (437 + 1312),
tpDtoD = 1,
cost_health_A = "cost_direct_med_A + cost_comm_care_A",
cost_health_B = "cost_direct_med_B + cost_comm_care_B",
cost_health_C = "cost_direct_med_C + cost_comm_care_C",
cost_drug = "cost_zido")
treat_strategy <- strategy(tm, health_states, "treat")
treat_markov <- markov_model(treat_strategy, 20, c(1, 0, 0, 0),
discount = c(0.06, 0), param_list_treat)
treat_low_values <- define_parameters(cost_direct_med_B = 234.5,
cost_comm_care_C = 694.8)
treat_upp_values <- define_parameters(cost_direct_med_B = 23450,
cost_comm_care_C = 69480)
param_table_treat <- define_parameters_sens_anal(param_list_treat,
treat_low_values, treat_upp_values)
result_treat <- do_sensitivity_analysis(treat_markov, param_table)
plot_dsa(result, "NMB", "range", result_treat, 20000, "treat")
```

plot_dsa_difference *Function to do some checks before plotting sensitivity analysis results*

Description

Function to do some checks before plotting sensitivity analysis results

Usage

```
plot_dsa_difference(ob_results, plotfor, plot_var)
```

Arguments

ob_results	results from deterministic sensitivity analysis
plotfor	the quantity plotting
plot_var	the variable

Value

plot

plot_dsa_icer_range *Function to do some checks before plotting sensitivity analysis results*

Description

Function to do some checks before plotting sensitivity analysis results

Usage

```
plot_dsa_icer_range(ob_results, plot_var)
```

Arguments

<code>ob_results</code>	results from deterministic sensitivity analysis
<code>plot_var</code>	the variable

Value

plot

plot_dsa_nmb_range *Function to do some checks before plotting sensitivity analysis results*

Description

Function to do some checks before plotting sensitivity analysis results

Usage

```
plot_dsa_nmb_range(ob_results, plot_var)
```

Arguments

<code>ob_results</code>	results from deterministic sensitivity analysis
<code>plot_var</code>	the variable

Value

plot

plot_dsa_others_range *Function to do some checks before plotting sensitivity analysis results*

Description

Function to do some checks before plotting sensitivity analysis results

Usage

```
plot_dsa_others_range(ob_results, plot_var)
```

Arguments

ob_results	results from deterministic sensitivity analysis
plot_var	the variable

Value

plot

plot_efficiency_frontier
Plot efficiency frontier

Description

Plot efficiency frontier

Usage

```
plot_efficiency_frontier(results_calculate_icer_nmb, threshold)
```

Arguments

results_calculate_icer_nmb	results from cea (from calculate_icer_nmb method)
threshold	threshold value

Value

```
plot well <- health_state("well", cost = 0, utility = 1) disabled <- health_state("disabled", cost =
100, utility = 1) dead <- health_state("dead", cost = 0, utility = 0) tmat <- rbind(c(1, 2, 3), c(NA, 4,
5), c(NA, NA, 6)) colnames(tmat) <- rownames(tmat) <- c("well", "disabled", "dead") tm <- popu-
late_transition_matrix(3, tmat, c(0.6, 0.2, 0.2, 0.6, 0.4, 1), colnames(tmat)) health_states <- com-
bine_state(well, disabled, dead) this.strategy <- strategy(tm, health_states, "control") this_markov
<- markov_model(this.strategy, 24, c(1000, 0, 0), c(0,0)) well <- health_state("well", cost = 0, utility
= 1) disabled <- health_state("disabled", cost = 10, utility = 0.5) dead <- health_state("dead", cost =
0, utility = 0) tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6)) colnames(tmat) <- rownames(tmat)
<- c("well", "disabled", "dead") tm <- populate_transition_matrix(3, tmat, c(0.4, 0.4, 0.2, 0.6,
0.4, 1), colnames(tmat)) health_states <- combine_state(well, disabled, dead) this.strategy <- strat-
egy(tm, health_states, "intervention") sec_markov <- markov_model(this.strategy, 24, c(1000, 0, 0),
c(0,0)) list_markov <- combine_markov(this_markov, sec_markov) results_cea <- calculate_icer_nmb(list_markov,
20000, comparator = "control") plot_efficiency_frontier(results_cea, c(1000, 2000))
```

plot_model

E1. Plot a Markov model

Description

E1. Plot a Markov model

Usage

```
plot_model(markov)
```

Arguments

markov markov_model object

Value

plots

Examples

```
tmat <- rbind(c(1, 2), c(3, 4))
colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead")
tm <- populate_transition_matrix(2, tmat, c(0.5, 0.5, 0, 1))
a <- health_state("Healthy", 1, 1, 0, FALSE)
b <- health_state("Dead", 1, 0, 0, TRUE)
health_states <- combine_state(a, b)
this.strategy <- strategy(tm, health_states, "intervention")
this_markov <- markov_model(this.strategy, 10, c(1, 0), c(0, 0))
p <- plot_model(this_markov)
```

```
plot_prediction_parametric_survival
```

Plot the predicted survival curves for covariates keeping the others fixed

Description

Plot the predicted survival curves for covariates keeping the others fixed

Usage

```
plot_prediction_parametric_survival(  
  param_to_be_estimated,  
  indep_var,  
  covariates,  
  dataset,  
  fit,  
  timevar_survival  
)
```

Arguments

<code>param_to_be_estimated</code>	parameter to be estimated
<code>indep_var</code>	variable for which the levels have to be identified
<code>covariates</code>	the covariates
<code>dataset</code>	the dataset where these variables contain
<code>fit</code>	the fit result survreg
<code>timevar_survival</code>	time variable from the dataset

Value

plot

Examples

```
data_for_survival <- survival::lung  
surv_estimated <- use_parametric_survival("status", data_for_survival,  
  "sex",  
  info_distribution = "weibull", covariates = c("ph.ecog"), "time")  
plot_prediction_parametric_survival("status", "sex",  
  covariates = c("ph.ecog"), data_for_survival, surv_estimated$fit, "time")
```

`plot_return_residual_cox`*Plotting and return the residuals after cox proportional hazard model*

Description

Plotting and return the residuals after cox proportional hazard model

Usage

```
plot_return_residual_cox(  
  param_to_be_estimated,  
  indep_var,  
  covariates,  
  fit,  
  dataset  
)
```

Arguments

<code>param_to_be_estimated</code>	parameter to be estimated
<code>indep_var</code>	independent variable
<code>covariates</code>	covariates
<code>fit</code>	fit object from coxph method
<code>dataset</code>	data used for cox ph model

Value

plot and the residuals

Examples

```
data_for_survival <- survival::lung  
surv_estimated <- use_coxph_survival("status", data_for_survival, "sex",  
  covariates = c("ph.ecog"), "time")  
plot_return_residual_cox("status", "sex", covariates = c("ph.ecog"),  
  surv_estimated$fit, data_for_survival )
```

`plot_return_residual_survival`*Plotting and return the residuals after survival model*

Description

Plotting and return the residuals after survival model

Usage

```
plot_return_residual_survival(  
  param_to_be_estimated,  
  indep_var,  
  covariates,  
  fit  
)
```

Arguments

<code>param_to_be_estimated</code>	parameter to be estimated
<code>indep_var</code>	independent variable
<code>covariates</code>	covariates
<code>fit</code>	fit object from survreg method

Value

plot and the residuals

Examples

```
data_for_survival <- survival::lung  
surv_estimated <- use_parametric_survival("status", data_for_survival,  
  "sex",  
  info_distribution = "weibull", covariates = c("ph.ecog"), "time")  
plot_return_residual_survival("status", "sex",  
  covariates = c("ph.ecog"), surv_estimated$fit)
```

`plot_return_survival_curve`*Plotting survival function for all covariates using survfit*

Description

Plotting survival function for all covariates using survfit

Usage

```
plot_return_survival_curve(  
  param_to_be_estimated,  
  dataset,  
  indep_var,  
  covariates,  
  timevar_survival  
)
```

Arguments

<code>param_to_be_estimated</code>	parameter to be estimated
<code>dataset</code>	param describing the methods
<code>indep_var</code>	independent variable
<code>covariates</code>	covariates
<code>timevar_survival</code>	time variable for survival analysis

Value

plot and the survival function values

Examples

```
data_for_survival <- survival::lung  
plot_return_survival_curve(param_to_be_estimated = "status",  
  dataset = data_for_survival, indep_var = "sex", covariates = c("ph.ecog"),  
  timevar_survival = "time")
```

plot_survival_cox_covariates

Plotting survival function for all covariates calculated from cox regression results and returned coefficients

Description

Plotting survival function for all covariates calculated from cox regression results and returned coefficients

Usage

```
plot_survival_cox_covariates(  
  coxfit,  
  dataset,  
  param_to_be_estimated,  
  covariates,  
  indep_var  
)
```

Arguments

coxfit	cox regression fit result
dataset	param describing the methods
param_to_be_estimated	parameter to be estimated
covariates	covariates
indep_var	independent variable

Value

plot and the survival function values

Examples

```
data_for_survival <- survival::lung  
surv_estimated <- use_coxph_survival("status", data_for_survival, "sex",  
  covariates = c("ph.ecog"), "time")  
plot_survival_cox_covariates(surv_estimated$fit, data_for_survival,  
  "status", covariates = c("ph.ecog"), "sex")
```

populate_transition_matrix
Populate transition matrix

Description

Populate transition matrix

Usage

```
populate_transition_matrix(no_states, tmat, list_prob, name_states = NULL)
```

Arguments

no_states	number of the health states
tmat	A transition matrix in the format from the package 'mstate'
list_prob	list of probabilities as in the order of transitions (row wise)
name_states	names of the health states

Details

If the state names are null, they are replaced with numbers starting from 1 First find those missing probabilities, and fill a list from the given list of probabilities and fill those are not NA in the matrix Note that the probabilities need not be numeric here and no checks are needed for sum

Value

value of the transition matrix

Examples

```
tmat <- rbind(c(1, 2), c(3, 4))  
colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead")  
populate_transition_matrix(2, tmat, list_prob = c(0.2, 0.5, 0, 0.3))
```

predict_coxph *Predict risk/hazard function for cox ph regression*

Description

Predict risk/hazard function for cox ph regression

Usage

```
predict_coxph(
  coxfit,
  dataset,
  param_to_be_estimated,
  covariates,
  indep_var,
  timevar_survival
)
```

Arguments

coxfit	cox regression fit result
dataset	param describing the methods
param_to_be_estimated	parameter to be estimated
covariates	covariates
indep_var	independent variable
timevar_survival	time variable

Details

"risk" option for "type" returns the hazard ratio relative to mean e.g given below For lung data with `data_for_survival <- survival::lung` `fit <- use_coxph_survival("status", data_for_survival, "sex", covariates = c("ph.ecog"), "time")` `coef = fit$coefficients` `r1234 <- exp(coef("sex"))` `lung$sex + coef - fit("ph.ecog")` `lung$ph.ecog` `rMean <- exp(sum(coef(fit) * fit$means, na.rm=TRUE))` `rr <- r1234/rMean`

Value

plot and the survival function values

Examples

```
data_for_survival <- survival::lung
surv_estimated <- use_coxph_survival("status", data_for_survival,
  "sex", covariates = c("ph.ecog"), "time")
predict_coxph(surv_estimated$fit, data_for_survival, "status", "sex",
  covariates = c("ph.ecog"), "time")
```

`report_sensitivity_analysis`*Function to report deterministic sensitivity analysis*

Description

Function to report deterministic sensitivity analysis

Usage

```
report_sensitivity_analysis(  
  result_dsa_control,  
  result_dsa_treat = NULL,  
  threshold = NULL,  
  comparator = NULL  
)
```

Arguments

<code>result_dsa_control</code>	result from deterministic sensitivity analysis for first or control model
<code>result_dsa_treat</code>	result from deterministic sensitivity analysis for the comparative Markov model
<code>threshold</code>	threshold value of WTP
<code>comparator</code>	the strategy to be compared with

Value

report in the form of a table

Examples

```
param_list <- define_parameters(  
  cost_zido = 2278, cost_direct_med_A = 1701,  
  cost_comm_care_A = 1055, cost_direct_med_B = 1774,  
  cost_comm_care_B = 1278,  
  cost_direct_med_C = 6948, cost_comm_care_C = 2059,  
  tpAtoA = 1251 / (1251 + 483),  
  tpAtoB = 350 / (350 + 1384), tpAtoC = 116 / (116 + 1618),  
  tpAtoD = 17 / (17 + 1717),  
  tpBtoB = 731 / (731 + 527), tpBtoC = 512 / (512 + 746),  
  tpBtoD = 15 / (15 + 1243),  
  tpCtoC = 1312 / (1312 + 437), tpCtoD = 437 / (437 + 1312),  
  tpDtoD = 1,  
  cost_health_A = "cost_direct_med_A + cost_comm_care_A",  
  cost_health_B = "cost_direct_med_B + cost_comm_care_B",  
  cost_health_C = "cost_direct_med_C + cost_comm_care_C",
```

```

cost_drug = "cost_zido")
low_values <- define_parameters(cost_direct_med_B = 177.4,
cost_comm_care_C = 205.9)
upp_values <- define_parameters(cost_direct_med_B = 17740,
cost_comm_care_C = 20590)
A <- health_state("A", cost = "cost_health_A + cost_drug ", utility = 1)
B <- health_state("B", cost = "cost_health_B + cost_drug", utility = 1)
C <- health_state("C", cost = "cost_health_C + cost_drug", utility = 1)
D <- health_state("D", cost = 0, utility = 0)
tmat <- rbind(c(1, 2, 3, 4), c(NA, 5, 6, 7), c(NA, NA, 8, 9),
c(NA, NA, NA, 10))
colnames(tmat) <- rownames(tmat) <- c("A", "B", "C", "D")
tm <- populate_transition_matrix(4, tmat, c("tpAtoA", "tpAtoB", "tpAtoC",
"tpAtoD", "tpBtoB", "tpBtoC", "tpBtoD", "tpCtoC", "tpCtoD", "tpDtoD"),
colnames(tmat))
health_states <- combine_state(A, B, C, D)
mono_strategy <- strategy(tm, health_states, "mono")
mono_markov <- markov_model(mono_strategy, 20, c(1, 0, 0, 0),
discount = c(0.06, 0), param_list)
param_table <- define_parameters_sens_anal(param_list, low_values,
upp_values)
result <- do_sensitivity_analysis(mono_markov, param_table)
reporting <- report_sensitivity_analysis(result)

```

```
return0_if_not_null_na
```

Function to return 0 if the param is not null or NA trimming the white spaces

Description

Function to return 0 if the param is not null or NA trimming the white spaces

Usage

```
return0_if_not_null_na(param)
```

Arguments

param the form of medication either tablet or patch

Value

zero or -1

Examples

```
parame = NULL
ans <- return0_if_not_null_na(parame)
parame = 1
ans <- return0_if_not_null_na(parame)
```

return_equal_liststring_col

Function to get the subset of data compared to a string after trimming the white spaces

Description

Function to get the subset of data compared to a string after trimming the white spaces

Usage

```
return_equal_liststring_col(col, the_data, list_str)
```

Arguments

col	the form of medication either tablet or patch
the_data	the data to be get the subset from
list_str	list of strings to be compared

Value

the subset data

Examples

```
the_data <- as.data.frame(cbind(c("one", "two"), c("a", "b")))
colnames(the_data) <- c("name", "brand")
ans <- return_equal_liststring_col(2, the_data, c("a", "cc"))
```

```
return_equal_liststring_listcol
```

Function to get the subset of data compared to a string after trimming the white spaces

Description

Function to get the subset of data compared to a string after trimming the white spaces

Usage

```
return_equal_liststring_listcol(col, the_data, list_str)
```

Arguments

col	the form of medication either tablet or patch
the_data	the data to be get the subset from
list_str	list of strings to be compared

Value

the subset data

Examples

```
the_data <- as.data.frame(cbind(c("one", "two"), c("tablet", "tablets"),
c("aa", "bb")))
colnames(the_data) <- c("name", "brand_a", "xx")
ans <- return_equal_liststring_listcol(2, the_data, c("tablet", "tablets"))
```

```
return_equal_str_col
```

Function to get the subset of data compared to a string after trimming the white spaces

Description

Function to get the subset of data compared to a string after trimming the white spaces

Usage

```
return_equal_str_col(col, the_data, the_str)
```

Arguments

col	the form of medication either tablet or patch
the_data	the data to be get the subset from
the_str	the string to be compared

Value

the subset data

Examples

```
the_data <- as.data.frame(cbind(c("one", "two"), c("a", "b")))
colnames(the_data) <- c("name", "brand")
ans <- return_equal_str_col(2, the_data, "a")
```

set_var_state

Set the attribute for the health state

Description

Set the attribute for the health state

Usage

```
set_var_state(state, var, new_value)
```

Arguments

state	object of class health state
var	attribute of the health state
new_value	new value to be assigned

Details

After checking the given state is a health state the value of the variable is set if the value is not numeric, it is being parsed to form an expression

Value

modified health state

Examples

```
set_var_state(health_state("IT", 100, 0.4, 0, FALSE), "cost", 1)
```

strategy	<i>Definition of strategy - or arm</i>
----------	--

Description

Definition of strategy - or arm

Usage

```
strategy(trans_mat, states, name, trans_cost = NULL, trans_util = NULL)
```

Arguments

trans_mat	transition matrix
states	health states
name	name of the strategy
trans_cost	values of costs if these are attached to transitions
trans_util	values of utility if these are attached to transitions

Details

Defining strategy keeping all transition matrix, states and names together to use in defining Markov model

Value

object strategy

Examples

```
tmat <- rbind(c(1, 2), c(3, 4))
colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead")
tm <- populate_transition_matrix(2, tmat, c(0.5, 0.5, 0, 1))
a <- health_state("Healthy", 1, 1, 0, FALSE)
b <- health_state("Dead", 1, 0.5, 0, FALSE)
states <- combine_state(a, b)
strategy(tm, states, "intervention")
```

summary_plot_psa	<i>Function to summarise and plot probabilistic sensitivity analysis</i>
------------------	--

Description

Function to summarise and plot probabilistic sensitivity analysis

Usage

```
summary_plot_psa(
  result_psa_params_control,
  result_psa_params_treat = NULL,
  threshold = NULL,
  comparator = NULL
)
```

Arguments

result_psa_params_control	result from probabilistic sensitivity analysis for first or control model
result_psa_params_treat	result from probabilistic sensitivity analysis for the comparative Markov model
threshold	threshold value of WTP
comparator	the strategy to be compared with

Value

plot of sensitivity analysis

Examples

```
param_list <- define_parameters(
  cost_direct_med_A = 1701,
  cost_direct_med_B = 1774, tpAtoA = 0.2,
  tpAtoB = 0.5, tpAtoC = 0.3,
  tpBtoB = 0.3, tpBtoC = 0.7,
  tpCtoC = 1, cost_health_A = "cost_direct_med_A",
  cost_health_B = "cost_direct_med_B")
sample_list <- define_parameters(cost_direct_med_A = "gamma(mean = 1701,
sd = sqrt(1701))")
A <- health_state("A", cost = "cost_health_A ", utility = 1)
B <- health_state("B", cost = "cost_health_B", utility = 1)
C <- health_state("C", cost = 0, utility = 0, absorb = "TRUE")
tmat <- rbind(c(1, 2, 3), c(NA, 4, 5), c(NA, NA, 6))
colnames(tmat) <- rownames(tmat) <- c("A", "B", "C")
tm <- populate_transition_matrix(3, tmat, c(
"tpAtoA", "tpAtoB", "tpAtoC", "tpBtoB", "tpBtoC", "tpCtoC"),
```

```

colnames(tmat))
health_states <- combine_state(A, B, C)
mono_strategy <- strategy(tm, health_states, "mono")
mono_markov <- markov_model(mono_strategy, 20, initial_state =c(1,0,0),
discount = c(0.06, 0),param_list)
param_table <- define_parameters_psa(param_list, sample_list)
result <- do_psa(mono_markov, param_table, 3)
result_plot <- summary_plot_psa(result, NULL, NULL, NULL)
param_list_comb <- define_parameters(
cost_direct_med_A = 1800, cost_direct_med_B = 1774, tpAtoA = 0.6,
tpAtoB = 0.1, tpAtoC = 0.3, tpBtoB = 0.3, tpBtoC = 0.7, tpCtoC = 1,
cost_health_A = "cost_direct_med_A", cost_health_B = "cost_direct_med_B")
comb_strategy <- strategy(tm, health_states, "comb")
comb_markov <- markov_model(comb_strategy, 20, c(1, 0, 0),
discount = c(0.06, 0), param_list)
param_table_comb <- define_parameters_psa(param_list_comb, sample_list)
result_comb <- do_psa(comb_markov, param_table_comb, 3)
summary_plot_psa(result, result_comb, 2000, "mono")

```

table_param

Parameter table created

Description

Parameter table created

Usage

```
table_param
```

Format

A 11 by 2 dataframe

Source

created on Jan 15, 2020

trace_data	<i>Trace matrix</i>
------------	---------------------

Description

Trace matrix

Usage

```
trace_data
```

Format

A 11 by 2 dataframe

Source

created on Nov 26, 2019 from `tmat <- rbind(c(1, 2), c(3, 4)) colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead") tm <- transition_matrix(2, tmat, c(0.5, 0.5, 0, 1)) a <- health_state("Healthy", 1, 1, FALSE) b <- health_state("Dead", 1, 0, TRUE) health_states <- combine_state(a, b) this.strategy <- strategy(tm, health_states, "intervention")`

transition_cost_util	<i>Create the the values of cost and utility while transition</i>
----------------------	---

Description

Create the the values of cost and utility while transition

Usage

```
transition_cost_util(
  no_states,
  tmat_cost_util,
  list_values,
  name_states = NULL
)
```

Arguments

<code>no_states</code>	number of the health states
<code>tmat_cost_util</code>	A transition matrix for the cost/utility values in the format from the package 'mstate' use NA to indicate if the value is zero
<code>list_values</code>	list of probabilities as in the order of transitions (row wise)
<code>name_states</code>	names of the health states

Details

Similar to transition matrix but for denoting one time change during transitions

Value

value of the transition matrix

Examples

```
tmat_cost <- rbind(c(NA, 1), c(NA, NA))
colnames(tmat_cost) <- rownames(tmat_cost) <- c("Healthy", "Dead")
transition_cost_util(2, tmat_cost, list_values = c(500))
```

trial_data	<i>Example trial data</i>
------------	---------------------------

Description

Example trial data

Usage

```
trial_data
```

Format

A 31 by 33 dataframe

Source

created on Jan 15, 2020

use_coxph_survival	##### <i>Get the parameter values using the survival analysis using cox proportional hazard</i>
--------------------	--

Description

Get the parameter values using the survival analysis using cox proportional hazard

Usage

```
use_coxph_survival(  
  param_to_be_estimated,  
  dataset,  
  indep_var,  
  covariates,  
  timevar_survival  
)
```

Arguments

param_to_be_estimated	parameter of interest
dataset	data set to be provided
indep_var	the independent variable (column name in data file)
covariates	list of covariates - calculations to be done before passing
timevar_survival	time variable for survival analysis, default is NA false by default

Details

plots baseline cumulative hazard function, survival function for each covariate while keeping the other fixed at the mean value (using `plot_survival_cox_covariates`), survival function for each combination of covariate using `survfit` (using `plot_return_survival_curve`) and test for cox regression results. It also returns risk relative to mean (predicted at mean value of each covariate) along with the fit results coefficients, SE of coefficients, summary, and analysis of deviance.

Value

the results of the regression analysis

Examples

```
data_for_survival <- survival::aml  
surv_estimated <- use_coxph_survival("status", data_for_survival, "x",  
  covariates = NA, "time")  
  
data_for_survival <- survival::lung  
surv_estimated <- use_coxph_survival("status", data_for_survival, "sex",  
  covariates = c("ph.ecog"), "time")
```

```
use_fh2_survival #####
                  Get the parameter values using the survival analysis using FH2
                  method
```

Description

```
##### Get
the parameter values using the survival analysis using FH2 method
```

Usage

```
use_fh2_survival(
  param_to_be_estimated,
  dataset,
  indep_var,
  covariates,
  timevar_survival
)
```

Arguments

```
param_to_be_estimated
                    parameter of interest

dataset            data set to be provided

indep_var          the independent variable (column name in data file)

covariates         list of covariates

timevar_survival   time variable for survival analysis, default is NA false by default
```

Details

This function is for survival analysis using FH2. This plots the cumulative survival function for each combination of covariate. If the covariate is numeric, R takes it as different levels. The plot uses the returned list of `survfit` and extracts the time and the strata from summary of the fit (implemented in `plot_return_survival_curve` function)

Value

the results of the regression analysis

Examples

```
data_for_survival <- survival::aml
surv_estimated <- use_fh2_survival("status", data_for_survival, "x",
  covariates = NA, "time")
```

```
use_generalised_linear_mixed_model
```

Function for generalised linear mixed model

Description

Function for generalised linear mixed model

Usage

```
use_generalised_linear_mixed_model(
  param_to_be_estimated,
  dataset,
  fix_eff,
  fix_eff_interact_vars,
  random_intercept_vars,
  nested_intercept_vars_pairs,
  cross_intercept_vars_pairs,
  uncorrel_slope_intercept_pairs,
  random_slope_intercept_pairs,
  family,
  link,
  package_mixed_model
)
```

Arguments

param_to_be_estimated	column name of dependent variable
dataset	a dataframe
fix_eff	names of variables as fixed effect predictors
fix_eff_interact_vars,	those of the fixed effect predictors that show interaction
random_intercept_vars,	names of variables for random intercept
nested_intercept_vars_pairs,	those of the random intercept variables with nested effect
cross_intercept_vars_pairs,	those of the random intercept variables with crossed effect
uncorrel_slope_intercept_pairs,	variables with no correlated intercepts
random_slope_intercept_pairs,	random slopes intercept pairs - this is a list of paired variables
family,	family of distributions for the response variable
link,	link function for the variances

```
package_mixed_model
      package to be used for mixed model
```

Value

result regression result with plot if success and -1, if failure

Examples

```
datafile <- system.file("extdata", "culcita_data.csv",
  package = "packDAMipd")
dataset <- read.csv(datafile)
results1 = use_generalised_linear_mixed_model("predation",
  dataset = datafile, fix_eff = c("ttt"), family = "binomial",
  fix_eff_interact_vars = NULL, random_intercept_vars = c("block"),
  nested_intercept_vars_pairs = NULL, cross_intercept_vars_pairs = NULL,
  uncorrel_slope_intercept_pairs = NULL, random_slope_intercept_pairs = NULL,
  link = NA, package_mixed_model = NA)
```

```
use_generalised_linear_model
```

```
#####
Get the parameter values using logistic regression
```

Description

```
##### Get
the parameter values using logistic regression
```

Usage

```
use_generalised_linear_model(
  param_to_be_estimated,
  dataset,
  indep_var,
  family,
  covariates,
  interaction,
  naaction,
  link = NA
)
```

Arguments

param_to_be_estimated	parameter of interest
dataset	data set to be provided
indep_var	the independent variable (column name in data file)
family	distribution name eg. for logistic regression -binomial
covariates	list of covariates-calculations to be done before passing
interaction	boolean value to indicate interaction in the case of linear regression
naaction	action to be taken with the missing values
link	link function if not the default for each family

Details

This function returns the results and plots after doing linear regression Requires param to be estimated, dataset, independent variables and information on covariates, and interaction variables if there are Uses form_expression_glm to create the expression as per R standard for e.g glm(y ~ x). Returns the fit result,s summary results as returned by summary(), confidence interval for fit coefficients (ci_coeff), variance covariance matrix, cholesky decomposition matrix, results from correlation test, plot of diagnostic tests and model fit assumptions, plot of model prediction diagnostic include AIC, R2, and BIC. The results of the prediction ie predicted values for fixed other variables will be returned in prediction matrix

Value

the results of the regression analysis

Examples

```
gm_result <- use_generalised_linear_model(
  param_to_be_estimated = "Direction",
  dataset = ISLR::Smarket, indep_var = "Lag1", family = "binomial",
  covariates = c("Lag2", "Lag3"),
  interaction = FALSE, naaction = "na.omit", link = NA)
```

```
use_km_survival #####
                  Get the parameter values using the Kaplan-Meier survival analysis
```

Description

```
##### Get the
parameter values using the Kaplan-Meier survival analysis
```

Usage

```
use_km_survival(  
  param_to_be_estimated,  
  dataset,  
  indep_var,  
  covariates,  
  timevar_survival  
)
```

Arguments

param_to_be_estimated	parameter of interest
dataset	data set to be provided
indep_var	the independent variable (column name in data file)
covariates	list of covariates
timevar_survival	time variable for survival analysis, default is NA

Details

This function is for survival analysis using Kaplan Meier. This plots the cumulative survival function for each combination of covariate. If the covariate is numeric, R takes it as different levels. The plot uses the returned list of `survfit` and extracts the time and the strata from summary of the fit (implemented in `plot_return_survival_curve` function)

Value

the results of the regression analysis, fit results, summary and plot

Examples

```
data_for_survival <- survival::aml  
surv_estimated <- use_km_survival("status", data_for_survival, "x",  
  covariates = NA, "time")  
  
data_for_survival <- survival::lung  
surv_estimated <- use_km_survival("status", data_for_survival, "sex",  
  covariates = c("ph.ecog"), "time")
```

```
use_linear_mixed_model
```

Function for mixed effect regression

Description

Function for mixed effect regression

Usage

```
use_linear_mixed_model(  
  param_to_be_estimated,  
  dataset,  
  fix_eff,  
  fix_eff_interact_vars,  
  random_intercept_vars,  
  nested_intercept_vars_pairs,  
  cross_intercept_vars_pairs,  
  uncorrel_slope_intercept_pairs,  
  random_slope_intercept_pairs,  
  package_mixed_model  
)
```

Arguments

param_to_be_estimated	column name of dependent variable
dataset	a dataframe
fix_eff	names of variables as fixed effect predictors
fix_eff_interact_vars,	those of the fixed effect predictors that show interaction
random_intercept_vars,	names of variables for random intercept
nested_intercept_vars_pairs,	those of the random intercept variables with nested effect
cross_intercept_vars_pairs,	those of the random intercept variables with crossed effect
uncorrel_slope_intercept_pairs,	variables with no correlated intercepts
random_slope_intercept_pairs,	random slopes intercept pairs - this is a list of paired variables
package_mixed_model	package to be used for mixed model

Value

result regression result with plot if success and -1, if failure

Examples

```
datafile <- system.file("extdata", "data_linear_mixed_model.csv",
  package = "packDAMipd")
dataset = utils::read.table(datafile, header = TRUE, sep = ",",
  na.strings = "NA",
  dec = ".", strip.white = TRUE)
result <- use_linear_mixed_model("extro",
  dataset = dataset,
  fix_eff = c("open", "agree", "social"), fix_eff_interact_vars = NULL,
  random_intercept_vars = c("school", "class"),
  nested_intercept_vars_pairs = list(c("school", "class")),
  cross_intercept_vars_pairs = NULL, uncorrel_slope_intercept_pairs = NULL,
  random_slope_intercept_pairs = NULL, package_mixed_model = NA)
```

```
use_linear_regression #####
                        Get the parameter values using the linear regression
```

Description

```
##### Get the
parameter values using the linear regression
```

Usage

```
use_linear_regression(
  param_to_be_estimated,
  dataset,
  indep_var,
  covariates,
  interaction
)
```

Arguments

param_to_be_estimated	parameter of interest
dataset	data set to be provided
indep_var	the independent variable (column name in data file)
covariates	list of covariates-calculations to be done before passing
interaction	boolean value to indicate interaction in the case of linear regression, false by default

Details

This function returns the results and plots after doing linear regression Requires param to be estimated, dataset, independent variables and information on covariates, and interaction variables if there are Uses form_expression_lm to create the expression as per R standard for e.g lm(y ~ x). Returns the fit result,s summary results as returned by summary(), confidence interval for fit coefficients (ci_coeff), variance covariance matrix, cholesky decomposition matrix, Results from correlation test, plot of diagnostic tests and model fit assumptions, plot of model prediction diagnostic include AIC, R2, and BIC. The results of the prediction ie predicted values when each of covariate is fixed will be returned in prediction matrix predicted values will provide the mean value of param_to_to_estimated as calculated by the linear regression formula. ref:<https://www.statmethods.net/stats/regression.html>

Value

the results of the regression analysis

Examples

```
results_lm <- use_linear_regression("dist",
  dataset = cars,
  indep_var = "speed", covariates = NA, interaction = FALSE)
```

```
library(car)
results_lm <- use_linear_regression("mpg",
  dataset = mtcars,
  indep_var = "disp", covariates = c("hp", "wt", "drat"),
  interaction = FALSE)
```

```
use_parametric_survival
```

```
#####
Get the parameter values using the survival analysis parametric survival
```

Description

```
##### Get the
parameter values using the survival analysis parametric survival
```

Usage

```
use_parametric_survival(
  param_to_be_estimated,
  dataset,
  indep_var,
```

```

    info_distribution,
    covariates,
    timevar_survival,
    cluster_var = NA
  )

```

Arguments

```

param_to_be_estimated      parameter of interest
dataset                    data set to be provided
indep_var                  the independent variable (column name in data file)
info_distribution          distribution name eg. for logistic regression -binomial
covariates                 list of covariates
timevar_survival          time variable for survival analysis, default is NA
cluster_var               cluster variable for survival analysis

```

Details

This function is the last in the layer of function for parametric survival analysis. This then returns the parameters of interest, plots the results etc if the distribution is weibull it uses the package `SurvRegCensCov` for easy interpretation of results Returns the fit result, summary of regression, variance-covariance matrix of coeff, cholesky decomposition, the parameters that define the assumed distribution and the plot of model prediction Using `survfit` from survival package to plot the survival curve R's weibull distribution is defined as std weibull in terms of a and b as $(a/b) (x/b)^{(a-1)} \exp(-(x/b)^a)$ where a is the shape and b is the scale In HE the weibull distribution is parameterised as bit different it is like $\text{gamma.lambda. } t^{(\text{gamma}-1)} .\exp(-\text{lambda}*t^{\text{gamma}})$ where gamma is the shape and lambda is the scale. The relationship is as below. $\text{HE_shape} = \text{rweibull_shape}$ $\text{HE_scale} = \text{rweibull_scale}^{(-\text{rweibull_shape})}$ The `survreg` shape and scale are again bit different and they are `rweibull`'s shape and scale as below. $\text{rweibull_shape} = 1/\text{fit}\scale $\text{rweibull_scale} = \exp(\text{fit intercept}) = \exp(\text{fit}\$\text{coefficients})$ remember to use 1st of coefficients This has been utilised in `SurvRegCensCov::ConvertWeibull predict()` for `survreg` object with `type = quantile` will provide the failure times as survival function is 1-CDF of failure time.

Value

the results of the regression analysis

Examples

```

data_for_survival <- survival::lung
surv_estimated <- use_parametric_survival("status",
data_for_survival, "sex", info_distribution = "weibull",
covariates = c("ph.ecog"), "time")

```

```
use_seemingly_unrelated_regression
      Bivariate regression for correlated observations
```

Description

Bivariate regression for correlated observations

Usage

```
use_seemingly_unrelated_regression(
  param1_to_be_estimated,
  param2_to_be_estimated,
  dataset,
  indep_var,
  covariates1,
  covariates2,
  interaction1,
  interaction2
)
```

Arguments

param1_to_be_estimated	parameter of interest
param2_to_be_estimated	parameter of interest
dataset	data set to be provided
indep_var	the independent variable (column name in data file)
covariates1	list of covariates - for equation 1
covariates2	list of covariates - for equation 2
interaction1	boolean value to indicate interaction - for equation 1
interaction2	boolean value to indicate interaction - for equation 2 false by default

Value

the results of the regression analysis

Examples

```
datafile <- system.file("extdata", "sureg_data.csv", package = "packDAMipd")
dataset <- read.csv(datafile, stringsAsFactors = TRUE)
results_sureg <- use_seemingly_unrelated_regression("read", "math",
  dataset = dataset,
  indep_var = "female", covariates1 = c("as.numeric(ses)", "socst"),
```

```

    covariates2 = c("as.numeric(ses)", "science"), interaction1 = FALSE,
    interaction2 = FALSE
)

```

```

use_survival_analysis #####
                        Get the parameter values using the survival analysis

```

Description

```

##### Get
the parameter values using the survival analysis

```

Usage

```

use_survival_analysis(
  param_to_be_estimated,
  dataset,
  indep_var,
  info_get_method,
  info_distribution,
  covariates,
  timevar_survival,
  cluster_var = NA
)

```

Arguments

```

param_to_be_estimated
                        parameter of interest
dataset                 data set to be provided
indep_var               the independent variable (column name in data file)
info_get_method
                        additional information on methods e.g Kaplan-Meier or hazard
info_distribution
                        distribution name eg. for logistic regression -binomial
covariates              list of covariates - calculations to be done before passing
timevar_survival
                        time variable for survival analysis, default is NA
cluster_var            cluster variable for survival analysis

```

Details

This function helps to get the parameter values after the survival analysis Takes into account many different methods like KM.FH, Cox proportional etc. and then calls appropriate functions to do the survival analysis

Value

the results of the regression analysis

Examples

```
data_for_survival <- survival::aml
surv_estimated_aml <- use_survival_analysis("status", data_for_survival,
  "x",
  info_get_method = "parametric", info_distribution = "weibull",
  covariates = NA, "time")
```

utility_data	<i>utility matrix</i>
--------------	-----------------------

Description

utility matrix

Usage

```
utility_data
```

Format

A 11 by 2 dataframe

Source

created on Nov 26, 2019 from `tmat <- rbind(c(1, 2), c(3, 4)) colnames(tmat) <- rownames(tmat) <- c("Healthy", "Dead") tm <- transition_matrix(2, tmat, c(0.5, 0.5, 0, 1)) a <- health_state("Healthy", 1, 1, FALSE) b <- health_state("Dead", 1, 0, TRUE) health_states <- combine_state(a, b) this.strategy <- strategy(tm, health_states, "intervention")`

value_ADL_scores_IPD	<i>Function to convert ADL scores to a T score</i>
----------------------	--

Description

Function to convert ADL scores to a T score

Usage

```
value_ADL_scores_IPD(
  ind_part_data,
  adl_related_words,
  adl_nrcode,
  adl_scoring_table = NULL
)
```

Arguments

`ind_part_data` a data frame containing IPD data

`adl_related_words` related words to find out which columns contain adl data

`adl_nrcode` non response code for ADL

`adl_scoring_table` ADL scoring table, if given as NULL use the default one

Value

ADL scores converted to T score included modified data, if success -1, if failure

Examples

```
datafile <- system.file("extdata", "trial_data.csv", package = "packDAMipd")
trial_data <- load_trial_data(datafile)
value_ADL_scores_IPD(trial_data, c("tpi"), NA, adl_scoring_table = NULL)
```

value_eq5d3L_IPD *Function to add EQ5D3L scores to IPD data*

Description

Function to add EQ5D3L scores to IPD data

Usage

```
value_eq5d3L_IPD(ind_part_data, eq5d_nrcode)
```

Arguments

`ind_part_data` a dataframe

`eq5d_nrcode` non response code for EQ5D3L, default is NA

Value

qaly included modified data, if success -1, if failure

Source

http://eprints.whiterose.ac.uk/121473/1/Devlin_et_al-2017-Health_Economics.pdf

Examples

```
datafile <- system.file("extdata", "trial_data.csv", package = "packDAMipd")
trial_data <- load_trial_data(datafile)
value_eq5d5L_IPD(trial_data, NA)
```

value_eq5d5L_IPD *Function to add EQ5D5L scores to IPD data*

Description

Function to add EQ5D5L scores to IPD data

Usage

```
value_eq5d5L_IPD(ind_part_data, eq5d_nrcode)
```

Arguments

ind_part_data a dataframe
eq5d_nrcode non response code for EQ5D5L, default is NA

Value

qaly included modified data, if success -1, if failure

Source

http://eprints.whiterose.ac.uk/121473/1/Devlin_et_al-2017-Health_Economics.pdf

Examples

```
datafile <- system.file("extdata", "trial_data.csv", package = "packDAMipd")
trial_data <- load_trial_data(datafile)
value_eq5d5L_IPD(trial_data, NA)
```

value_Shows_IPD	<i>Function to estimate the cost of tablets taken (from IPD)</i>
-----------------	--

Description

Function to estimate the cost of tablets taken (from IPD)

Usage

```
value_Shows_IPD(ind_part_data, shows_related_words, shows_nrcode)
```

Arguments

ind_part_data a dataframe containing IPD
shows_related_words a dataframe containing IPD
shows_nrcode non response code for ADL, default is NA

Value

sum of scores, if success -1, if failure

Examples

```
datafile <- system.file("extdata", "trial_data.csv", package = "packDAMipd")  
trial_data <- load_trial_data(datafile)  
value_Shows_IPD(trial_data, "qsy", NA)
```

word2num	<i>Function to check the variable null or NA</i>
----------	--

Description

Function to check the variable null or NA

Usage

```
word2num(word)
```

Arguments

word word for the number

Details

<https://stackoverflow.com/questions/18332463/convert-written-number-to-number-in-r>

Value

return the number

Examples

```
answer <- word2num("one forty one")
answer <- word2num("forty one and five hundred")
answer <- word2num("five thousand two hundred and eight")
```

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