Package ‘ubiquity’

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Type Package

Title PKPD, PBPK, and Systems Pharmacology Modeling Tools

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Description Complete work flow for the analysis of pharmacokinetic pharmacodynamic (PKPD), physiologically-based pharmacokinetic (PBPK) and systems pharmacology models including: creation of ordinary differential equation-based models, pooled parameter estimation, individual/population based simulations, rule-based simulations for clinical trial design and modeling assays, deployment with a customizable 'Shiny' app, and non-compartmental analysis. System-specific analysis templates can be generated and each element includes integrated reporting with 'PowerPoint' and 'Word'.

URL https://ubiquity.tools/rworkflow

SystemRequirements Perl

BugReports https://github.com/john-harrold/ubiquity/issues

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R topics documented:

build_system .................................................. 3
calculate_halflife .............................................. 4
gg_axis ............................................................ 5
gg_log10_xaxis .................................................... 6
gg_log10_yaxis .................................................... 7
linspace ............................................................. 8
logspace ........................................................... 9
pad_string .......................................................... 10
prepare_figure ...................................................... 10
run_simulation_titrate .......................................... 11
run_simulation_ubiquity ......................................... 12
simulate_subjects .................................................. 13
som_to_df .......................................................... 14
system_check_requirements ....................................... 15
system_check_steady_state ...................................... 15
system_clear_cohorts ............................................ 17
system_define_cohort ............................................ 17
system_define_cohorts_nm ....................................... 20
system_estimate_parameters ..................................... 22
system_fetch_guess ............................................... 23
system_fetch_iiv .................................................. 23
system_fetch_nca ............................................... 24
system_fetch_nca_columns ...................................... 25
system_fetch_parameters ......................................... 26
system_fetch_rpt_officer_object ................................ 26
system_fetch_rpt_onbrand_object ................................ 27
system_fetch_set ................................................ 28
system_fetch_template ........................................... 28
system_fetch_TSSys .............................................. 30
system_glp_init .................................................. 31
system_glp_scenario ............................................ 31
system_load_data ................................................. 34
system_log_debug_save .......................................... 35
system_log_init .................................................. 36
system_nca_parameters_meta ..................................... 36
system_nca_run .................................................. 37
system_nca_summary ............................................. 39
system_new ....................................................... 41
system_new_list .................................................. 43
system_new_tt_rule .............................................. 43
system_od_general ............................................... 44
system_plot_cohorts ............................................. 45
system_rpt_add_doc_content ..................................... 47
system_rpt_add_slide .......................................... 48
system_rpt_estimation .......................................... 48
system_rpt_nca .................................................. 49
build_system

Description

Builds the specified system file creating the targets for R and other languages as well as the templates for performing simulations and estimations.

Usage

```r
build_system(
  system_file = "system.txt",
  distribution = "automatic",
  perlcmd = "perl",
  output_directory = file.path(".", "output"),
  temporary_directory = file.path(".", "transient"),
  verbose = TRUE,
  ubiquity_app = FALSE,
  debug = TRUE
)
```
Arguments

system_file  name of the file defining the system in the ubiquity format (default = 'system.txt'), if the file does not exist a template will be created and compiled.
distribution  indicates weather you are using a 'package' or a 'stand alone' distribution of ubiquity. If set to 'automatic' the build script will first look to see if the ubiquity R package is installed. If it is installed it will use the package. Otherwise, it will assume a "sand alone" distribution.
perlcmd  system command to run perl ("perl")
output_directory  location to store analysis outputs (file.path(".", "output"))
temporary_directory  location to templates and otehr files after building the system (file.path(".", "transient"))
verbose  enable verbose messaging (TRUE)
ubiquity_app  set to TRUE when building the system to be used with the ubiquty App (FALSE)
debug  Boolean variable indicating if debugging information should be displayed (TRUE)

Value

initialized ubiquity system object

Examples

fr = system_new(file_name = "system.txt",
system_file = "mab_pk",
overwrite = TRUE,
output_directory = tempdir())
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
output_directory = file.path(tempdir(), "output"),
temporary_directory = tempdir())

calculate_halflife  Calculate the halflife of data

Description

Determines the terminal halflife of a sequence of corresponding times and values with optional minimum and maximum times to censor data.

Usage

calculate_halflife(times = NULL, values = NULL, tmin = NULL, tmax = NULL)
**Arguments**

- **times**: sequence of times
- **values**: corresponding sequence of values
- **tmin**: minimum time to include (NULL)
- **tmax**: maximum time to include (NULL)

**Value**

List with the following names

- **thalf**: Halflife in units of times above
- **mod**: Result of lm used to fit the log transformed data
- **df**: Dataframe with the data and predicted values at the time within tmin and tmax

**Examples**

```r
x = c(0:100)
y = exp(-.1*x)
th = calculate_halflife(times=x, values=y)
thal = th$thalf
```

---

**Description**

used to convert the x and y-axis of a ggplot to a log 10 scale that is more visually satisfying than the ggplot default.

**Usage**

```r
gg_axis(
  fo,
  yaxis_scale = TRUE,
  xaxis_scale = TRUE,
  ylim_min = NULL,
  ylim_max = NULL,
  xlim_min = NULL,
  xlim_max = NULL,
  x_tick_label = TRUE,
  y_tick_label = TRUE
)
```
Arguments

- **fo**: ggplot figure object
- **yaxis_scale**: TRUE indicates that the y-axis should be log10 scaled
- **xaxis_scale**: TRUE indicates that the x-axis should be log10 scaled
- **ylim_min**: set to a number to define the lower bound of the y-axis
- **ylim_max**: set to a number to define the upper bound of the y-axis
- **xlim_min**: set to a number to define the lower bound of the x-axis
- **xlim_max**: set to a number to define the upper bound of the x-axis
- **x_tick_label**: TRUE to show x tick labels, FALSE to hide the x tick labels
- **y_tick_label**: TRUE to show y tick labels, FALSE to hide the y tick labels

Value

- ggplot object with formatted axis

See Also

- [gg_log10_xaxis](#) and [gg_log10_yaxis](#)

Examples

```r
library("ggplot2")
df = data.frame(x = seq(0.01,10,.01),
                y = seq(0.01,10,.01)^2)
p = ggplot(df, aes(x=x, y=y)) + geom_line()
# pretty up the axes
p = prepare_figure(fo=p, purpose="print")
# pretty log10 y-axis
p_logy = gg_log10_yaxis(fo=p)
# pretty log10 x-axis
p_logx = gg_log10_xaxis(fo=p)
# pretty log10 yx-axis
p_logxy = gg_axis(fo=p)
```

---

**gg_log10_xaxis**  
*Make Pretty ggplot x-Axis Log 10 Scale*

Description

- Wrapper for [gg_axis](#) to create a log 10 x-axis
Usage

```
gg_log10_yaxis(
  fo,
  xlim_min = NULL,
  xlim_max = NULL,
  y_tick_label = TRUE,
  x_tick_label = TRUE
)
```

Arguments

- **fo**: ggplot figure object
- **xlim_min**: set to a number to define the lower bound of the x-axis
- **xlim_max**: set to a number to define the upper bound of the x-axis
- **y_tick_label**: TRUE to show y tick labels, FALSE to hide the y tick labels
- **x_tick_label**: TRUE to show x tick labels, FALSE to hide the x tick labels

Value

ggplot object with formatted axis

See Also

- `gg_axis`
- `gg_log10_xaxis`

Examples

```r
library("ggplot2")
df = data.frame(x = seq(0.01,10,.01),
  y = seq(0.01,10,.01)^2)
p = ggplot(df, aes(x=x, y=y)) + geom_line()
# pretty up the axes
p = prepare_figure(fo=p, purpose="print")
# pretty log10 y-axis
p_logy = gg_log10_yaxis(fo=p)
# pretty log10 x-axis
p_logx = gg_log10_xaxis(fo=p)
# pretty log10 yx-axis
p_logxy = gg_axis(fo=p)
```

Description

Wrapper for `gg_axis` to create a log 10 y-axis
Usage

```r
gg_log10_yaxis(
  fo,
  ylim_min = NULL,
  ylim_max = NULL,
  y_tick_label = TRUE,
  x_tick_label = TRUE
)
```

Arguments

- **fo**: ggplot figure object
- **ylim_min**: set to a number to define the lower bound of the y-axis
- **ylim_max**: set to a number to define the upper bound of the y-axis
- **y_tick_label**: TRUE to show y tick labels, FALSE to hide the y tick labels
- **x_tick_label**: TRUE to show x tick labels, FALSE to hide the x tick labels

Value

ggplot object with formatted axis

See Also

- `gg_axis`
- `gg_log10_xaxis`

Examples

```r
library("ggplot2")
df = data.frame(x = seq(0.01, 10, 0.01),
  y = seq(0.01, 10, 0.01)^2)
p = ggplot(df, aes(x=x, y=y)) + geom_line()
  # pretty up the axes
p = prepare_figure(fo=p, purpose="print")
  # pretty log10 y-axis
p_logy = gg_log10_yaxis(fo=p)
  # pretty log10 x-axis
p_logx = gg_log10_xaxis(fo=p)
  # pretty log10 yx-axis
p_logxy = gg_axis(fo=p)
```

---

**linspace**

Implementation of the `linspace` Function from Matlab

Description

Creates a vector of n elements equally spaced apart.
logspace

Usage

\[ \text{linspace}(a, b, n = 100) \]

Arguments

- \( a \)  
  initial number
- \( b \)  
  final number
- \( n \)  
  number of elements (integer \( \geq 2 \))

Value

vector of numbers from \( a \) to \( b \) with \( n \) linearly spaced apart

Examples

\[ \text{linspace}(0, 100, 20) \]

logspace

Implementation of the logspace Function from Matlab

Description

Creates a vector of \( n \) elements logarithmically spaced apart.

Usage

\[ \text{logspace}(a, b, n = 100) \]

Arguments

- \( a \)  
  initial number
- \( b \)  
  final number
- \( n \)  
  number of elements (integer \( \geq 2 \))

Value

vector of numbers from \( a \) to \( b \) with \( n \) logarithmically (base 10) spaced apart

Examples

\[ \text{logspace}(-2, 3, 20) \]
### pad_string  
*Pad String with Spaces*

**Description**
Adds spaces to the beginning or end of strings until it reaches the `maxlength`. Used for aligning text.

**Usage**
```r
pad_string(str, maxlength = 1, location = "beginning")
```

**Arguments**
- `str`: string
- `maxlength`: length to pad to
- `location`: either "beginning" to pad the left or "end" to pad the right

**Value**
Padded string

**Examples**
```r
pad_string("bob", maxlength=10)
pad_string("bob", maxlength=10, location="end")
```

### prepare_figure  
*Make ggplot Figure Pretty*

**Description**
Takes a ggplot object and alters the line thicknesses and makes other cosmetic changes to make it more appropriate for exporting.

**Usage**
```r
prepare_figure(
    purpose = "present",
    fo,
    y_tick_minor = FALSE,
    y_tick_major = FALSE,
    x_tick_minor = FALSE,
    x_tick_major = FALSE
)
```
**run_simulation_titrate**

**Simulate With Titration or Rule-Based Inputs**

**Description**

Provides an interface to `run_simulation_ubiquity` to start and stop simulations and apply rules to control dosing and state-resets.

**Usage**

`run_simulation_titrate(SIMINT_p, SIMINT_cfg, SIMINT_dropfirst = TRUE)`

**Arguments**

- **SIMINT_p** list of system parameters
- **SIMINT_cfg** ubiquity system object
- **SIMINT_dropfirst** when TRUE it will drop the first sample point (prevents bolus doses from starting at 0)

**Example**

```r
cf = data.frame(x = seq(0.01,10,.01),
        y = seq(0.01,10,.01)^2)
p = ggplot(cf, aes(x=x, y=y)) + geom_line()
# pretty up the axes
p = prepare_figure(fo=p, purpose="print")
# pretty log10 y-axis
p_logy = gg_log10_yaxis(fo=p)
# pretty log10 x-axis
p_logx = gg_log10_xaxis(fo=p)
# pretty log10 yx-axis
p_logxy = gg_axis(fo=p)
```
run_simulation_ubiquity

Value

som

See Also

system_new_tt_rule, system_set_tt_cond and the titration vignette (vignette("Titration", package = "ubiquity"))

---

run_simulation_ubiquity

Simulate Individual Response

Description

Controls the execution of individual simulations with deSolve using either R scripts or loadable C libraries.

Usage

run_simulation_ubiquity(SIMINT_parameters, SIMINT_cfg, SIMINT_dropfirst = TRUE)

Arguments

SIMINT_parameters vector of parameters
SIMINT_cfg ubiquity system object
SIMINT_dropfirst when TRUE it will drop the first sample point (prevents bolus doses from starting at 0)

Value

The simulation output is mapped (som) is a list. time-course is stored in the simout element.

- The first column (time) contains the simulation time in the units of the simulation.
- Next there is a column for each: State, output and system parameter
- Models with covariate will contain the initial value (prefix: SIMINT_CVIC_) as well as the values at each time point
- Each static and dynamic system parameter is also passed through
- A column for each timescale is returned with a "ts." prefix.

See Also

Simulation vignette (vignette("Simulation", package = "ubiquity"))
simulate_subjects  Run Population Simulations

Description

Used to run Population/Monte Carlo simulations with subjects generated from either provided variance/covariance information or a dataset.

Usage

simulate_subjects(
  parameters,
  cfg,  
  show_progress = TRUE,  
  progress_message = "Simulating Subjects:"
)

Arguments

parameters  list containing the typical value of parameters
cfg  ubiquity system object
show_progress  Boolean value controlling the display of a progress indicator (TRUE)
progress_message  text string to prepend when called from the ShinyApp

Details

Failures due to numerical instability or other integration errors will be captured within the function. Data for those subjects will be removed from the output. Their IDs will be displayed as messages and stored in the output.

For more information on setting options for population simulation see the stochastic section of the system_set_option help file.

Value

Mapped simulation output with individual predictions, individual parameters, and summary statistics of the parameters. The Vignettes below details on the format of the output.

See Also

Vignette on simulation (vignette("Simulation", package = "ubiquity")) titration (vignette("Titration", package = "ubiquity")) as well as som_to_df
**som_to_df**

Converts the Wide/Verbose Output Simulation Functions into Data Frames

---

**Description**

The functions `run_simulation_ubiquity`, `simulate_subjects`, or `run_simulation_titrate` provide outputs in a more structured format, but it may be useful to convert this "wide" format to a tall/skinny format.

**Usage**

```r
som_to_df(cg, som)
```

**Arguments**

- `cfg` ubiquty system object
- `som` simulation output from `run_simulation_ubiquity`, `simulate_subjects`, or `run_simulation_titrate`

**Value**

Data frame of the format:

When applied to the output of `run_simulation_ubiquity` or `run_simulation_titrate`

- `ts.time` - timescale of the system
- `ts.ts1`, ... `ts.tsn` - timescales defined in the system (<TS>)
- `pred` - predicted/simulated response
- `tt.ti1.x` - titration event information (*)
- `name` - state or output (<O>) name corresponding to the prediction

When applied to the output of `simulate_subjects`

- `ID` - subject ID
- `ts.time` - timescale of the system
- `ts.ts1`, ... `ts.tsn` - timescales defined in the system (<TS>)
- `pred` - predicted/simulated response
- `tt.ti1.x` - titration event information (*)
- `P1`, `P2`, ... `Pn` - system parameters for the subject (<P>)
- `name` - state or output (<O>) name corresponding to the prediction

(* - field present when titration is enabled)

**See Also**

`run_simulation_titrate` internally when running simulations.
system_check_requirements

*Check For Perl and C Tools*

**Description**

Check the local installation for perl and verify C compiler is installed and working.

**Usage**

```r
system_check_requirements(
    checklist = list(perl = list(check = TRUE, perlcmd = "perl"),
                     C = list(check = TRUE)),
    verbose = TRUE
)
```

**Arguments**

- **checklist** list with names corresponding to elements of the system to check.
- **verbose** enable verbose messaging

**Value**

List fn result of all packages

**Examples**

```r
invisible(system_check_requirements())
```

---

system_check_steady_state

*Verify System Steady State*

**Description**

Takes the ubiquity system object and other optional inputs to verify the system is running at steady state. This also provides information that can be helpful in debugging systems not running at steady state.
system_check_steady_state

Usage

```r
system_check_steady_state(
  cfg,
  parameters = NULL,
  zero_rates = TRUE,
  zero_bolus = TRUE,
  output_times = seq(0, 100, 1),
  offset_tol = .Machine$double.eps * 100,
  derivative_tol = .Machine$double.eps * 100,
  derivative_time = 0
)
```

Arguments

- `cfg` :: ubiquity system object
- `parameters` :: optional set of parameters (NULL) to check at steady state (if set to NULL then the parameters for the currently selected parameter set will be used)
- `zero_rates` :: Boolean value to control removing all rate inputs (TRUE)
- `zero_bolus` :: Boolean value to control removing all bolus inputs (TRUE)
- `output_times` :: sequence of output times to simulate for offset determination (seq(0, 100, 1))
- `offset_tol` :: maximum percent offset to be considered zero (.Machine$double.eps*100)
- `derivative_tol` :: maximum derivative value to be considered zero (.Machine$double.eps*100)
- `derivative_time` :: time to evaluate derivatives to identify deviations (0), set to NULL to skip derivative evaluation

Value

List with the following names

- `steady_state` :: Boolean indicating whether the system was at steady state
- `states_derivative` :: Derivatives that had values greater than the derivative_tol
- `states_simulation` :: States that had values greater than the offset_tol
- `som` :: Simulated output
- `derivatives` :: Derivatives
- `states_derivative_NA_NaN` :: States that had derivatives that evaluated as either NA or NaN
- `states_simulation_NA_NaN` :: States with simulation values that had either NA or NaN
- `derivative_tc` :: Data frame with the timecourse of states where the derivative was found to be greater than tolerance (states_derivative)
**system_clear_cohorts**  
*Clear all Cohorts*

**Description**

Clear previously defined cohorts

**Usage**

```
system_clear_cohorts(cfg)
```

**Arguments**

- `cfg` : ubiquity system object

**Value**

ubiquity system object with no cohorts defined

---

**system_define_cohort**  
*Define Estimation Cohort*

**Description**

Define a cohort to include in a parameter estimation

**Usage**

```
system_define_cohort(cfg, cohort)
```

**Arguments**

- `cfg` : ubiquity system object
- `cohort` : list with cohort information

**Details**

Each cohort has a name (eg d5mpk), and the dataset containing the information for this cohort is identified (the name defined in `system_load_data`)

```r
cohort = list(
    name = "d5mpk",
    dataset = "pm_data",
    inputs = NULL,
    outputs = NULL)
```
Next if only a portion of the dataset applies to the current cohort, you can define a filter (cf field). This will be applied to the dataset to only return values relevant to this cohort. For example, if we only want records where the column DOSE is 5 (for the 5 mpk cohort). We can use the following:

```r
cohort["cf"] = list(DOSE = c(5))
```

If the dataset has the headings ID, DOSE and SEX and cohort filter had the following format:

```r
cohort["cf"] = list(ID = c(1:4),
                    DOSE = c(5,10),
                    SEX = c(1))
```

It would be translated into the boolean filter:

```
(ID==1) | (ID==2) | (ID==3) | (ID==4)) & ((DOSE == 5) | (DOSE==10)) & (SEX == 1)
```

Optionally you may want to fix a system parameter to a different value for a given cohort. This can be done using the cohort parameter (cp) field. For example if you had the body weight defined as a system parameter (BW), and you wanted to fix the body weight to 70 for the current cohort you would do the following:

```r
cohort["cp"] = list(BW = c(70))
```

Note that you can only fix parameters that are not being estimated.

By default the underlying simulation output times will be taken from the general output_times option (see `system_set_option`). However it may also be necessary to specify simulation output times for a specific cohort. The output_times field can be used for this. Simply provide a vector of output times:

```r
cohort["output_times"] = seq(0,100,2)
```

Next we define the dosing for this cohort. It is only necessary to define those inputs that are non-zero. So if the data here were generated from animals given a single 5 mpk IV at time 0. Bolus dosing is defined using `<B:times>` and `<B:events>`. If Cp is the central compartment, you would pass this information to the cohort in the following manner:

```r
cohort["inputs"][["bolus"]][["Cp"]][["TIME"]]] = c( 0)
cohort["inputs"][["bolus"]][["Cp"]][["AMT"]]] = c( 5)
```

Inputs can also include any infusion rates (infusion_rates) or covariates (covariates). Covariates will have the default value specified in the system file unless overwritten here. The units here are the same as those in the system file

Next we need to map the outputs in the model to the observation data in the dataset. Under the outputs field there is a field for each output. Here the field ONAME can be replaced with something more useful (like PK).
cohort["outputs"]["ONAME"] = list()

If you want to further filter the dataset. Say for example you have two outputs and the \texttt{cf} applied above reduces your dataset down to both outputs. Here you can use the "of" field to apply an "output filter" to further filter the records down to those that apply to the current output \texttt{ONAME}.

cohort["outputs"]["ONAME"]["of"] = list(
  COLNAME = c(),
  COLNAME = c())

If you do not need further filtering of data, you can you can just omit the field.

Next you need to identify the columns in the dataset that contain your times and observations. This is found in the \texttt{obs} field for the current observation:

cohort["outputs"]["ONAME"]["obs"] = list(
  time = "TIMECOL",
  value = "OBSCOL",
  missing = -1)

The times and observations in the dataset are found in the 'TIMECOL' column and the 'OBSCOL' column (optional missing data option specified by -1).

These observations in the dataset need to be mapped to the appropriate elements of your model defined in the system file. This is done with the \texttt{model} field:

cohort["outputs"]["ONAME"]["model"] = list(
  time = "TS",
  value = "MODOUTPUT",
  variance = "PRED^2")

First the system time scale indicated by the \texttt{TS} placeholder above must be specified. The time scale must correspond to the data found in \texttt{TIMECOL} above. Next the model output indicated by the \texttt{MODOUTPUT} placeholder needs to be specified. This is defined in the system file using \texttt{<O>} and should correspond to \texttt{OBSCOL} from the dataset. Lastly the variance field specifies the variance model. You can use the keyword \texttt{PRED} (the model predicted output) and any variance parameters. Some examples include:

- \texttt{variance = "1"} - Least squares
- \texttt{variance = "PRED^2"} - Weighted least squares proportional to the prediction squared
- \texttt{variance = "(SLOPE*PRED)^2"} Maximum likelihood estimation where \texttt{SLOPE} is defined as a variance parameter \texttt{(<VP>)}

The following controls the plotting aspects associated with this output. The color, shape and line values are the values used by ggplot functions.

cohort["outputs"]["ONAME"]["options"] = list(
  marker_color = "black",
  marker_shape = 16,
  marker_line = 1 )
If the cohort has multiple outputs, simply repeat the process above for the additional cohorts. The estimation vignettes contain examples of this.

**Note:** Output names should be consistent between cohorts so they will be grouped together when plotting results.

**Value**

ubiquity system object with cohort defined

**See Also**

Estimation vignette (vignette("Estimation", package = "ubiquity"))

**system_define_cohorts_nm**

*Define Cohorts from NONMEM Input File*

**Description**

This function allows the user to define cohorts automatically from a NONMEM dataset

**Usage**

```r
system_define_cohorts_nm(
  cfg,
  DS = "DSNAME",
  col_ID = "ID",
  col_CMT = "CMT",
  col_DV = "DV",
  col_TIME = "TIME",
  col_AMT = "AMT",
  col_RATE = "RATE",
  col_EVID = "EVID",
  col_GROUP = NULL,
  filter = NULL,
  INPUTS = NULL,
  OBS = NULL
)
```

**Arguments**

- `cfg` ubiquity system object
- `DS` Name of the dataset loaded using `system_load_data`
- `col_ID` Column of unique subject identifier
- `col_CMT` Compartment column
- `col_DV` Column with observations or "." for input
col.TIME  Column with system time of each record
col.AMT  Infusion/dose amounts (these need to be in the same units specified in the system.txt file)
col.RATE  Rate of infusion or ‘.’ for bolus
col.EVID  EVID (0 - observation, 1 dose)
col.GROUP  Column name to use for defining similar cohorts when generating figures.
filter  List used to filter the dataset or NULL if the whole dataset is to be used (see filter rules or nm_select_records or a description of how to use this option)
INPUTS  List mapping input information in the dataset to names used in the system.txt file
OBS  List mapping obseravation information in the dataset to names used in the system.txt file

Details

NOTE: to use this function it is necessary that a timescale be define for the system time scale. For example, if the system time scale was days, something like the following is needed:

<TS:days> 1

Include all records in the dataset

filter = NULL

Include only records matching the following filter

filter = list()
fILTER$COLNAME = c()

Mapping information:
The inputs mapping information (INPUTMAP) is a list with a field for each type of input: input:

• bolus List with a name for each bolus state in the dataset (<B:?>): each bolus name should have a CMT_NUM field indicating the compartment number for that state
• infusion_rates List with a name for each rate in the dataset (<R:?>): each rate name should have a CMT_NUM field indicating the compartment number for that state
• covariates List with for each covariate in the dataset (<CV:?>): each covariate name should have a col_COV indicating the column in the database that contains that covariate

From a coding perspective it looks like this:

INPUTMAP = list()
INPUTMAP$bolus$SPECIES$CMT_NUM = 1
INPUTMAP$infusion_rates$RATE$CMT_NUM = 1
INPUTMAP$covariates$CVNAME$col_COV = 'CNAME'
The observation mapping information (OBSMAP) is a list with elements for each output as described in for system_define_cohort. Each output is a list with the following names:

- variance Variance model for this output
- CMT Compartment number mapping observations for this output
- output Name of the output (<O>) corresponding with the observations
- missing Value indicating a missing observation or NULL

From a coding perspective it looks like this:

```
OBSMAP = list()
OBSMAP$ONAME=list(variance = 'PRED^2',
                   CMT = 1,
                   output = '<O>',
                   missing = NULL )
```

Value

ubiquity system object with cohorts defined.

See Also

Estimation vignette (vignette("Estimation", package = "ubiquity"))

system_estimate_parameters

Control Estimation Process

Description

Manages the flow of parameter estimation using data specified with system_define_cohort.

Usage

```
system_estimate_parameters(
  cfg,
  flowctl = "plot guess",
  analysis_name = "my_analysis",
  archive_results = TRUE
)
```

Arguments

- `cfg` ubiquity system object
- `flowctl` string to control what the flow of the function
- `analysis_name` string containing the name of the analysis
- `archive_results` boolean variable to control whether results will be archived
system_fetch_guess

Details

The flowctl argument can have the following values

- "plot guess" return the initial guess
- "estimate" perform estimation
- "previous estimate as guess" load previous estimate for analysis_name and use that as the initial guess
- "plot previous estimate" return the previous estimate for analysis_name

Value

parameter estimates

---

system_fetch_guess    Fetch Current Parameter Guesses

Description

Fetch a list of the guesses for the current parameter set and parameters selected for estimation

Usage

system_fetch_guess(cfg)

Arguments

cfg                     ubiquity system object

Value

list of current parameter guesses

---

system_fetch_iiv     Fetch Variability Terms

Description

Extract elements of the current variance/covariance matrix specified in the system file with <IIV:? :?>?, <IIVCOR:? :?>?, <IIVSET:? :?> ?, <IIVCORSET:? :?>?

Usage

system_fetch_iiv(cfg, IIV1, IIV2)
system_fetch_iiv

Arguments

cfg ubiquity system object
IIV1 row name of the variance/covariance matrix
IIV2 column name of the variance/covariance matrix

Value

Value from the variance/covariance matrix

See Also

system_set_iiv

Examples

# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
    system_file = "mab_pk",
    overwrite = TRUE,
    output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
    output_directory = file.path(tempdir(), "output"),
    temporary_directory = tempdir())

# Covariance term for ETACL and ETAVc
val = system_fetch_iiv(cfg, IIV1="ETACL", IIV2="ETAVc")

system_fetch_nca

Fetch NCA Results

Description

Fetches the NCA summary from the ubiquity system object.

Usage

system_fetch_nca(cfg, analysis_name = "analysis")

Arguments

cfg ubiquity system object
analysis_name string containing the name of the NCA analysis (default 'analysis')
Value

List with a data frame of the NCA results (NCA_summary), the raw output from PKNCA (PKNCA_results), and also a list element indicating the overall success of the function call (isgood)

See Also

Vignette on NCA (vignette("NCA", package = "ubiquity"))

Description

Show the columns available in a given NCA analysis

Usage

system_fetch_nca_columns(cfg, analysis_name = "analysis")

Arguments

cfg      ubiquity system object

analysis_name string containing the name of the NCA analysis (default 'analysis')

Value

List with the following elements:

- isgood Boolean variable to identify if the function executed properly (TRUE) or if there were any errors (FALSE)
- NCA_col_summary dataframe with the columns from the analysis in analysis_name (col_name - NCA short name, from - where the parameter was derived from, label - verbose text label for the column, and description, verbose text description of the parameter.
- len_NCA_col maximum length of the col_name column
- len_from maximum length of the from column
- len_label maximum length of the label column
- len_description maximum length of the description column

See Also

Vignette on NCA (system_nca_parameters_meta)
system_fetch_parameters

Fetch System Parameters

Description

Fetch the parameters of the currently selected parameter set. To switch between parameter sets use system_select_set

Usage

system_fetch_parameters(cfg)

Arguments

cfg: ubiquity system object

Value

List of parameters for the selected parameter set

Examples

# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
system_file = "mab_pk",
overwrite = TRUE,
output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
output_directory = file.path(tempdir(), "output"),
temporary_directory = tempdir())

# Fetching the default parameter set
parameters = system_fetch_parameters(cfg)

system_fetch_rpt_officer_object

Extracts the officer Object From the Specified ubiquity Report

Description

This will extract an officer object from the ubiquity system object for the specified report name.
Usage

    system_fetch_rpt_officer_object(cfg, rptname = "default")

Arguments

    cfg                 ubiquity system object
    rptname             ubiquity report name

Value

    officer report object

See Also

    system_set_rpt_officer_object

---

**system_fetch_rpt_onbrand_object**

*Extracts the onbrand Object From the Specified ubiquity Report*

Description

This will extract an onbrand object from the ubiquity system object for the specified report name.

Usage

    system_fetch_rpt_onbrand_object(cfg, rptname = "default")

Arguments

    cfg                 ubiquity system object
    rptname             ubiquity report name

Value

    onbrand report object

See Also

    system_set_rpt_onbrand_object
system_fetch_set  

**Fetch Mathematical Set**

**Description**

Fetch the elements of the specified mathematical set that was defined in the system file.

**Usage**

```r
system_fetch_set(cfg, set_name = NULL)
```

**Arguments**

- `cfg`: ubiquity system object
- `set_name`: name of mathematical set

**Value**

A sequence containing the elements of the parameter set or NULL if if there was a problem.

**Examples**

```r
# Creating a system file from the pbpk example
fr = system_new(file_name = "system.txt",
                 system_file = "pbpk",
                 overwrite = TRUE,
                 output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
                   output_directory = file.path(tempdir(), "output"),
                   temporary_directory = tempdir())

# Fetching the contents of the ORG mathematical set
ORG_elements = system_fetch_set(cfg, "ORG")
```

---

system_fetch_template  

**Create New Analysis Template**

**Description**

Building a system file will produce templates for R and other languages. This function provides a method to make local copies of these templates.
Usage

```
system_fetch_template(
  cfg,
  template = "Simulation",
  overwrite = FALSE,
  output_directory = getwd()
)
```

Arguments

- **cfg**: ubiquity system object
- **template**: template type
- **overwrite**: if TRUE the new system file will overwrite any existing files present
- **output_directory**: directory where workshop files will be placed (getwd())

Details

The template argument can have the following values for the R workflow:

- "Simulation" produces `analysis_simulate.R`: R-Script named with placeholders used to run simulations
- "Estimation" produces `analysis_estimate.R`: R-Script named with placeholders used to perform naive-pooled parameter estimation
- "NCA" produces `analysis_nca.R`: R-Script to perform non-compartmental analysis (NCA) and report out the results
- "ShinyApp" produces `ubiquity_app.R`, `server.R` and `ui.R`: files needed to run the model through a Shiny App either locally or on a Shiny Server
- "Model Diagram" produces `system.svg`: SVG template for producing a model diagram (Go to [https://inkscape.org](https://inkscape.org) for a free SVG editor)
- "Shiny Rmd Report" produces `system_report.Rmd` and `test_system_report.R`: R-Markdown file used to generate report tabs for the Shiny App and a script to test it
- "myOrg" produces `myOrg.R`: R-Script for defining functions used within your organization

And this will create files to use in other software:

- "Adapt" produces `system_adapt.for` and `system_adapt.prm`: Fortran and parameter files for the currently selected parameter set in Adapt format.
- "Berkeley Madonna" produces `system_berkeley_madonna.txt`: text file with the model and the currently selected parameter set in Berkeley Madonna format
- "nlmixr" produces `system_nlmixr.R`: For the currently selected parameter set to define the system in the 'nlmixr' format.
- "NONMEM" produces `system_nonmem.R`: For the currently selected parameter set as a NONMEM control stream.
• "Monolix" produces `system_monolix.txt` for the currently selected parameter set as a NON-MEM control stream.
• "mrgsolve" produces `system_mrgsolve.cpp`: text file with the model and the currently selected parameter set in mrgsolve format

**Value**

List with vectors of template sources, destinations and corresponding write success (`write_file`), also a list element indicating the overall success of the function call (`isgood`)

**Examples**

```r
# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
                system_file = "mab_pk",
                overwrite = TRUE,
                output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
                    output_directory = file.path(tempdir(), "output"),
                    temporary_directory = tempdir())

# Creating a simulation template
fr = system_fetch_template(cfg,
                           template = "Simulation",
                           output_directory = tempdir())
```

---

**system_fetch_TSsys**  
*Fetch System Timescale*

**Description**

Reads through the system information and tries to determine the system time scale (the timescale that has a value of 1)

**Usage**

`system_fetch_TSsys(cfg)`

**Arguments**

`cfg`  
ubiquity system object

**Value**

Name of the system timescale or NULL if it was not found
system_glp_init

Initialize GLP study design

Description

Creates a new GLP study design

Usage

system_glp_init(cfg, study_title = "Study Title", study_name = "default")

Arguments

cfg ubiquity system object

study_title String containing descriptive information about the study

study_name short name used to identify the study in other functions ("default")

Value

cfg ubiquity system object with the study initialized

system_glp_scenario

Design GLP Study For a Scenario

Description

Identifies the top dose required in a GLP tox study in order to match human metrics (Cmax and AUCs) within a specified multiplier.

For a given set of human parameters the human doses required to hit the target Cmin and AUC (both or one) will be identified. The Cmax and AUC associated with the largest of those doses will be determined and the corresponding doses for a tox species (and provided parameters) will be determined for specific tox multipliers.

Optionally, simulations can be be run by specifying doses for either/or the human or tox species. Sample times can also be specified to generate annotated figures and tables to be given to analysts to facilitate assay design.

The system file requires the following components:

- Output for the drug concentration
- Output for the cumulative AUC
- Bolus dosing defined in a specific compartment
- Timescale specified for the system timescale (e.g. if the timescale is hours then you need <T>S> hours = 1.0)
Usage

```r
system_glp_scenario(
  cfg,
  output_Conc = NULL,
  output_AUC = NULL,
  timescale = NULL,
  units_Conc = "",
  units_AUC = "",
  study_scenario = "Tox Study",
  human_sim_times = NULL,
  study_name = "default",
  human_parameters = NULL,
  human_bolus = NULL,
  human_ndose = 1,
  human_dose_interval = 1,
  human_Cmin = NULL,
  human_AUC = NULL,
  human_sample_interval = NULL,
  human_sim_doses = NULL,
  human_sim_samples = NULL,
  tox_species = "Tox",
  tox_sim_times = NULL,
  tox_parameters = NULL,
  tox_bolus = NULL,
  tox_ndose = 1,
  tox_dose_interval = 1,
  tox_Cmax_multiple = 10,
  tox_AUC_multiple = 10,
  tox_sample_interval = NULL,
  tox_sim_doses = NULL,
  tox_sim_samples = NULL,
  annotate_plots = TRUE
)
```

Arguments

- `cfg` ubiquity system object
- `output_Conc` model output specified with `<O>` containing the concentration associated with drug exposure.
- `output_AUC` model output specified with `<O>` containing the cumulative exposure
- `timescale` system timescale specified with `<TS>` used for AUC comparisons and plotting
- `units_Conc` units of concentration ("")
- `units_AUC` units of AUC ("")
- `study_scenario` string containing a descriptive name for the tox study
- `human_sim_times` user-specified simulation output times for humans (same timescale as the system)
study_name: name of the study to append the scenario to set with 'system_glp_init()' ('default'): When a report is initialized using system_rpt_read_template the report name is 'default' unless otherwise specified. To disable reporting set this to NULL, and to use a different report specify the name here.

human_parameters: list containing the human parameters
human_bolus: string containing the dosing state for human doses (specified with <B:?>)
human_ndose: number of human doses to simulate
human_dose_interval: dosing interval in humans (time units specified with <B:?>)
human_Cmin: target Cmin in humans (corresponding to output_Conc above)
human_AUC: target AUC in humans (corresponding to output_AUC above)
human_sample_interval: time interval in units specified by timescale above to evaluate the trough concentration and AUC (e.g. c(1.99, 4.001) would consider the interval between 2 and 4)
human_sim_doses: optional list of doses into human_bolus to simulate (see Details below)
human_sim_samples: optional list of sample times in units specified by timescale above to label on plots of simulated doses (the default NULL will disable labels)
tox_species: optional name of the tox species ("Tox")
tox_sim_times: user-specified simulation output times for the tox species (same timescale as the system)
tox_parameters: list containing the parameters for the tox species
tox_bolus: string containing the dosing state for tox species doses (specified with <B:?>)
tox_ndose: number of tox doses to simulate
tox_dose_interval: dosing interval in the tox species (time units specified with <B:?>)
tox_Cmax_multiple: for each target (Cmin and AUC) the dose in the tox species will be found to cover this multiple over the projected Cmax in humans (10)
tox_AUC_multiple: for each target (Cmin and AUC) the dose in the tox species will be found to cover this multiple over the projected AUC in humans (10)
tox_sample_interval: interval to consider the AUC and Cmax for comparing the human prediction to the tox multiple
tox_sim_doses: optional list of doses into tox_bolus to simulate (see Details below)
tox_sim_samples: optional list of sample times in units specified by timescale above to label on plots of simulated doses (the default NULL will disable labels)
analyze_plots: Boolean switch to indicate if human_sim_samples and tox_sim_samples should be labeled on their respective plots (TRUE)
Details

Both human_sim_doses and tox_sim_doses are lists with names corresponding to the label of the dose. Each element has an AMT and TIME element which corresponds to the dosing times and amounts in the units specified with $\text{<B:?>}$ in the system file.

For example if you wanted to simulate four weekly doses of 20 mg to a 70 kg person and the units of bolus doses were days and mg/kg for the times and amounts you would do the following:

```r
human_sim_doses = list()
human_sim_doses[["20 mg QW"]]
$\text{TIME} = c(0, 7, 14, 21)
human_sim_doses[["20 mg QW"]]
$\text{AMT} = c(0.2857, 0.2857, 0.2857, 0.2857)
```

Value

cfg ubiquity system object with the scenario added if successful

Description

Loads datasets at the scripting level from a variable if data_file is a data.frame or from the following formats (based on the file extension)

- csv - comma delimited
- tab - tab delimited
- xls or xlsx - excel spread sheet

Multiple datasets can be loaded as long as they are given different names. Datasets should be in a NONMEM-ish format with the first row containing the column header names.

Usage

```r
system_load_data(cfg, dsname, data_file, data_sheet)
```

Arguments

- cfg: ubiquity system object
- dsname: short name of the dataset to be used to link this dataset to different operations
- data_file: the file name of the dataset or a data frame containing the data
- data_sheet: argument identifying the name of the sheet in an excel file

Value

Ubiquity system object with the dataset loaded
system_log_debug_save  Save variables to files

Description
Triggered when debugging is enabled, this function will save the contents of values to the specified file name in the ubiquity temporary directory.

Usage
system_log_debug_save(cfg, file_name = "my_file", values = NULL)

Arguments
cfg           ubiquity system object
file_name      name of the save file without the ".RData" extension
values         named list of variables to save

Value
Boolean variable indicating success

Examples

# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
                system_file = "mab_pk",
                overwrite = TRUE,
                output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
                   output_directory = file.path(tempdir(), "output"),
                   temporary_directory = tempdir())

# enable debugging:
cfg=system_set_option(cfg, group = "logging",
                       option = "debug",
                       value = TRUE)

# Saving the cfg variable
system_log_debug_save(cfg,
                       file_name = 'my_file',
                       values = list(cfg=cfg))
system_log_init

Initialize System Log File

Description

Initializes the currently specified system log file.

Usage

system_log_init(cfg)

Arguments

cfg                 ubiquity system object

Value

ubiquity system object with logging enabled

Examples

# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
                system_file = "mab_pk",
                overwrite = TRUE,
                output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
                    output_directory = file.path(tempdir(), "output"),
                    temporary_directory = tempdir())

# Initializing the log file
cfg = system_log_init(cfg)

system_nca_parameters_meta

List NCA parameters, text names and descriptions

Description

Provides a verbose information about NCA parameters

Usage

system_nca_parameters_meta(cfg)
system_nca_run

Arguments

cfg     ubiquity system object

Value

List with the following elements:

- isgood Boolean value indicating the success of the function call.
- parameters List with element names for each standard column header for NCA output. Each element name is a list with the following elements:
  - label Textual descriptor of the parameter.
  - description Verbose description of the parameter.
  - from Text indicating the source of the parameter (either PKNCA or ubiquity).

See Also

Vignette on NCA (vignette("NCA", package = "ubiquity"))

system_nca_run  Automatic NCA

Description

Performs NCA in an automated fashion

Usage

system_nca_run(
  cfg,
  dsname = "PKDS",
  dscale = 1,
  NCA_options = NULL,
  NCA_min = 4,
  analysis_name = "analysis",
  dsfilter = NULL,
  extrapol_C0 = TRUE,
  extrapol_N = 2,
  sparse = FALSE,
  dsmap = list(TIME = "TIME", NTIME = "NTIME", CONC = "CONC", DOSE = "DOSE", ID = "ID",
               ROUTE = "ROUTE", DOSENUM = NULL, BACKEXTRAP = NULL, SPARSEGROUP = NULL),
  dsinc = NULL
)

system_nca_run

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cfg</td>
<td>ubiquity system object</td>
</tr>
<tr>
<td>dsname</td>
<td>name of dataset loaded with (<a href="#">system_load_data</a>)</td>
</tr>
<tr>
<td>dscale</td>
<td>factor to multiply the dose to get it into the same units as concentration (default 1): if you are dosing in mg/kg and your concentrations is in ng/ml, then dscale = 1e6</td>
</tr>
<tr>
<td>NCA_options</td>
<td>specify a list of options for PKNCA to overwrite the defaults (default NULL will use defaults). For example if you want to set the maximum extrapolation of AUCinf to 10 half-life half-life of 0.8 you would use: list(max.aucinf.pext=10, min.hl.r.squared=.9)</td>
</tr>
<tr>
<td>NCA_min</td>
<td>minimum number of points required to perform NCA for a given subset (default 4)</td>
</tr>
<tr>
<td>analysis_name</td>
<td>string containing the name of the analysis (default ‘analysis’) to archive to files and reference results later</td>
</tr>
<tr>
<td>dsfilter</td>
<td>list of names corresponding to the column names in the dataset and values are a sequence indicating values to keep (default NULL). Multiple names are and-ed together. For example the following would keep all of the records where dose is 1, 2, or 5 and the dose_number is 1</td>
</tr>
<tr>
<td>extrap_C0</td>
<td>Boolean variable to enable automatic determination of initial drug concentration if no value is specified; the rules used by WinNonlin will be used:</td>
</tr>
<tr>
<td>extrap_N</td>
<td>number of points to use for back extrapolation (default 2); this number can be overwritten for each subject using the BACKEXTRAP column in the dataset</td>
</tr>
<tr>
<td>sparse</td>
<td>Boolean variable used to indicate data used sparse sampling and the analysis should use the average at each time point (the SPARSEGROUP column must be specified in the dsmap below)</td>
</tr>
<tr>
<td>dsmap</td>
<td>list with names specifying the columns in the dataset (* required):</td>
</tr>
</tbody>
</table>

- **TIME**: Time since the first dose; "TIME" (default)
- **NTIME**: Nominal time since last dose; "NTIME" (default)
- **CONC**: Concentration data; "CONC" (default)
- **DOSE**: Dose given; "DOSE" (default)
- **ID**: Subject ID; "ID" (default)
- **ROUTE**: Route of administration; "ROUTE" (default), can be either "iv bolus", "ivinfusion" or "extra-vascular". Variants such as "IV_bolus" and "extravascular" should work as well.
- **DOSENUM**: Numeric dose (starting at 1) used for grouping multiple dose data; optional, NULL (default) for single dose data
• **BACKEXTRAP** Specifying the number of points to use to extrapolate the initial concentration for "iv bolus" dosing; optional if NULL (default) will use the value defined in extrap\_N (note this value must be <= NCA\_min)

• **SPARSEGROUP** Column containing a unique value grouping cohorts for pooling data. Needed when sparse is set to TRUE; optional, NULL (default)

**dsinc** (NOT CURRENTLY IMPLEMENTED) optional character vector of columns from the dataset to include in the output summary (default NULL)

**Value**

cfg ubiquity system object with the NCA results and if the analysis name is specified:

• output/analysis\_name-nca\_summary-pknca.csv NCA summary

• output/analysis\_name-pknca\_summary.csv Raw output from PKNCA with subject and dose number columns appended

• output/analysis\_name-nca\_data.RData objects containing the NCA summary and a list with the ggplot grobs

**See Also**

Vignette on NCA (vignette("NCA", package = "ubiquity"))

---

**system\_nca\_summary**  
**Summarize NCA Results in Tabular Format**

**Description**

Creates tabular summaries of NCA results

**Usage**

```r
system\_nca\_summary(
  cfg,
  analysis\_name = "analysis",
  treat\_as\_factor = c("ID", "Dose\_Number", "Dose"),
  params\_include = c("ID", "cmax", "tmax", "auclast"),
  params\_header = NULL,
  rptname = "default",
  label\_format = NULL,
  summary\_stats = NULL,
  summary\_labels = list(MEAN = "Mean", STD = "Std Dev", MEDIAN = "Median", N = "N obs", SE = "Std Err."),
  summary\_location = NULL,
  ds\_wrangle = NULL,
  digits = 3,
  table\_theme = "theme\_zebra"
)
```
Arguments

cfg            ubiquity system object
analysis_name  string containing the name of the analysis (default 'analysis') that was previously run

treat_as_factor sequence of column names to be treated as factors (default c("ID", "Dose_Number", "Dose")). Use this to report values without added decimals.

params_include vector with names of parameters to include (default c("ID", "cmax", "tmax", "auclast")

params_header list with names of parameters followed by a vector of headers. You can use the placeholder "<label>" to include the standard label (e.g. list(cmax=c("<label>", "(ng/ml)")), with a default of NULL.

rptname        report name (either PowerPoint or Word) that this table will be used in ("default")

label_format   string containing the format in which headers and labels are being specified, either "text", or "md" (default NULL assumes "text" format)

summary_stats  list with strings as names containing placeholders for summary statistics and the values indicate the parameters to apply those statistics to. for example, if you want to calculate mean and standard deviation of AUClast you could use list("<MEAN> (<STD>)"=c("auclast")). This would create a row at the bottom of the table with this information for just the listed parameters. To split this up across two rows just do the following: list("<MEAN>"=c("auclast"), "<STD>"=c("auclast")). Any NA values will be ignored when calculating statistics. The allowed summary statistics are the mean (<MEAN>), median (<MEDIAN>), standard deviation (<STD>), standard error (<SE>), and the number of observations used to calculate statistics. (<N>). The default value of NULL prevents any summary statistics from being included.

summary_labels list containing the mapping of summary statistics defined by summary_stats with their text labels in the output tables:

    list(MEAN = "Mean",
         STD  = "Std Dev",
         MEDIAN = "Median",
         N    = "N obs",
         SE   = "Std Err.")

summary_location column where to put the labels (e.g. Mean (Std)) for summary statistic. The default (NULL) will leave these labels off. If you set this to the "ID" column it will put them under the subject IDs.

ds_wrangle     ds_wrangle = list(Dose=c(30), Dose_Number = c(1))

digits         number of significant digits to report (3) or NULL to prevent rounding

table_theme     flextable theme see the flextable package for available themes, and set to NULL to prevent themes from being applied. (default="theme_zebra")
Value

list with the following elements

- isgood Boolean variable indicating success (TRUE) or failure (FALSE) if the call is successful
- nca_summary dataframe containing the summary table with headers and any summary statistics appended to the bottom
- nca_summary_ft same information in the nca_summary output as a flextable object
- components list with the elements of the summary table each as dataframes (header, data, and summary)

See Also

Vignette on NCA (vignette("NCA", package = "ubiquity"))
Usage

```r
system_new(  
  file_name = "system.txt",
  system_file = "template",
  overwrite = FALSE,
  output_directory = getwd()
)
```

Arguments

- `file_name`: name of the new file to create
- `system_file`: name of the system file to copy
- `overwrite`: if TRUE the new system file will overwrite any existing files present
- `output_directory`: getwd() directory where system file will be placed

Details

References


Value

TRUE if the new file was created and FALSE otherwise

Examples

```r
# To create an example system file named example_system.txt:
system_new(system_file = "mab_pk",
           file_name = "system_example.txt",
           overwrite = TRUE,
           output_directory = tempdir())
```
**system_new_list**  
*Fetch List of Available System Templates*

**Description**

Returns a list of internal templates with descriptions of their contents and file locations.

**Usage**

```python
system_new_list()
```

**Value**

list with the template names as the keys

- `file_path` Full path to the system file
- `description` Description of what this system file provides

**Examples**

```python
# To get a list of systems
systems = system_new_list()
```

---

**system_new_tt_rule**  
*Titration Rules*

**Description**

Defines a new titration rule and the times when that rule is evaluated.

**Usage**

```python
system_new_tt_rule(cfg, name, times, timescale)
```

**Arguments**

- `cfg` ubiquity system object
- `name` name for the titration rule
- `times` list of times when the rule will be evaluated
- `timescale` time scale associated with the titration times (as defined by `<TS:?>`)
A titration rule identifies a set of times (\texttt{times}) and an associated time scale (\texttt{timescale}) in which titration events can potentially occur. Any times scale, as defined in the system file with \texttt{<TS:?>}, can be used in place of "weeks" above. The name, "rname" above, is used to link the titration rule to different conditions discussed below. The name should be a string beginning with a letter, and it can contain any combination of numbers, letters, and underscores. With the rule created we can then add conditions to that rule.

\section*{Value}

Ubiquity system object with the titration rule created

\section*{See Also}

\texttt{system_set_tt_cond, run_simulation_titrate}

\section*{system_od_general \hspace{1cm} General Observation Details Function}

\subsection*{Description}

Used to calculate observation details based on cohorts created with \texttt{system_define_cohort}

\subsection*{Usage}

\texttt{system_od_general(pest, cfg, estimation = TRUE, details = FALSE)}

\subsection*{Arguments}

\begin{description}
\item[pest] vector of parameters to be estimated
\item[cfg] ubiquity system object
\item[estimation] \texttt{TRUE} when called during an estimation and \texttt{FALSE} when called to test objective function or generate observation information for plotting
\item[details] \texttt{TRUE} to display information about cohorts as they are simulated (useful for debugging when passed through \texttt{system_simulate_estimation_results})
\end{description}
Value

If estimation is TRUE then the output is a matrix of observation details of the format:

\[ \text{od$pred} = [\text{TIME, OBS, PRED, VAR, OUTPUT, COHORT}] \]

The values are the observed (OBS) data, predicted values (PRED) and variance (VAR) at the given TIME. The columns OUTPUT and COHORT can be used for sorting. These should be unique numbers.

When estimation is FALSE we output od$pred is a data frame with the following headings:

\[ \text{od$pred} = [\text{TIME, OBS, PRED, VAR, SMOOTH, OUTPUT, COHORT}] \]

The TIME, OBS, PRED and VAR are the same as those listed above. The SMOOTH variable is FALSE for rows that correspond to records in the dataset and TRUE when the PRED represents the smooth predictions. The OUTPUT and COHORT columns here are text values used when defining the cohorts.

Also the od$all list item is created with all of the simulation information stored for each cohort:

\[ \text{od$all} = [\text{ts.time, ts.ts1, ... ts.tsn, pred, name, cohort}] \]

- \( \text{ttime} \) - timescale of the system
- \( \text{ts.ts1, ... ts.tsn} \) - timescales defined in the system
- \( \text{pred} \) - smooth prediction
- \( \text{name} \) - state or output name corresponding to the prediction
- \( \text{cohort} \) - name of the cohort for these predictions

Lastly the field isgood will be set to FALSE if any problems are encountered, and TRUE if everything worked.

\[ \text{od$isgood} = \text{TRUE} \]

See Also

system_define_cohort and system_simulate_estimation_results

---

**system_plot_cohorts**  
*Plot Estimation Results*

**Description**

Generates figures for each cohort/output for a given set of parameter estimates.
Usage

```r
system_plot_cohorts(
  erp,
  plot_opts = c(),
  cfg,
  analysis_name = "analysis",
  archive_results = TRUE,
  prefix = NULL
)
```

Arguments

- **erp**: output from `system_simulate_estimation_results`
- **plot_opts**: list controlling how predictions and data are overlaid
- **cfg**: ubiquity system object
- **analysis_name**: string containing the name of the analysis
- **archive_results**: boolean variable to control whether results will be archived
- **prefix**: depreciated input mapped to `analysis_name`

Details

The general format for a plot option for a given output (OUTPUT) is:

```r
plot_opts$outputs$OUTPUTt$option = value
```

The following options are:

- `yscale` and `xscale` = "linear" or "log"
- `ylabel` and `xlabel` = "text"
- `xlim` and `ylim` = c(min, max)

It is also possible to control the height and width of the time course tc and observed vs predicted op file by specifying the following in the default units of `ggsave`.

```r
  plot_opts$tc$width = 10
  plot_opts$tc$height = 5.5
  plot_opts$op$width = 10
  plot_opts$op$height = 8.0
```

To control the figures that are generated you can set the purpose to either "print", "present" (default) or "shiny".

```r
plot_opts$purpose = "present"
```
Value

List of plot outputs containing two elements `timecourse` and `obs_pred`, for the time course of and observed vs predicted, respectively. Both of these fields contain three elements for a given output. For example, say there is an output named `PK` the both the `timecourse` and `obs_pred` elements will have a field named `PK` containing a ggplot object and two fields `PK_png` and `PK_pdf` containing the paths to the files containing that figure in the respective formats.

See Also

The estimation vignette (`vignette("Estimation", package = "ubiquity")`)
**system_rpt_add_slide**  
*Add Slide to a Powerpoint Report*

**Description**

Add a slide to a ubiquity report.

**Usage**

```r
system_rpt_add_slide(
  cfg,
  template = NULL,
  elements = NULL,
  rptname = "default"
)
```

**Arguments**

- `cfg`: ubiquity system object
- `template`: Name of slide template to use
- `elements`: List with content to populate placeholders in the slide. See the onbrand functions `report_add_slide` and `add_pptx_ph_content` for details on the expected format of this list.
- `rptname`: Report name

**Value**

ubiquity system object with the slide added to the specified report

**See Also**

- `report_add_slide`, `add_pptx_ph_content`, and Reporting vignette (`vignette("Reporting", package = "ubiquity")`)

---

**system_rpt_estimation**  
*Generate a Report from Parameter Estimation*

**Description**

This will take the output generated during a parameter estimation and append those results to a specified report.

**Usage**

```r
system_rpt_estimation(cfg, rptname = "default", analysis_name = NULL)
```
system_rpt_nca

Arguments

cfg ubiquity system object
rptname report name ("default")
analysis_name string containing the name of the estimation analysis and used as a prefix to store the results

Value

ubiquity system object with estimation report appended

See Also

system_rpt_read_template, the reporting vignette (vignette("Reporting", package = "ubiquity")) and the estimation vignette (vignette("Estimation", package = "ubiquity"))

---

**system_rpt_nca**  
*Report NCA*

Description

Appends the results of NCA to a report

Usage

```r
system_rpt_nca(
  cfg,
  rptname = "default",
  analysis_name = "analysis",
  rows_max = 10,
  table_headers = TRUE
)
```

Arguments

- **cfg**: ubiquity system object
- **rptname**: report name (either PowerPoint or Word)
- **analysis_name**: string containing the name of the NCA analysis (default 'analysis')
- **rows_max**: maximum number of rows per slide when generating tabular data
- **table_headers**: Boolean variable to add descriptive headers to output tables (default TRUE)

Value

cfg ubiquity system object with the NCA results appended to the specified report and if the analysis name is specified:
system_rpt_read_template

Initialize a New Report

Description

Creates a new officer report based either on the ubiquity template or one specified by the user. Once created, content can then be added.

Usage

```r
system_rpt_read_template(
  cfg,
  template = "PowerPoint",
  mapping = NULL,
  rptname = "default"
)
```

Arguments

- **cfg**: ubiquity system object
- **template**: Type of internal template to use ("PowerPoint" or "Word") or path to template file.
- **mapping**: Path to an onbrand yaml mapping file: If an internal ubiquity template has been supplied, this argument will be ignored and the yaml file from ubiquity will be used.
- **rptname**: report name

Details

The `template` and `mapping` inputs can specify either the internal ubiquity templates or user-defined templates. If you specify `template` values of 'PowerPoint' or 'Word' then the internal ubiquity templates for PowerPoint or Word will be used and the mapping information will be ignored.

If templates other than the values above are specified you will need also supply a yaml mapping file for an 'onbrand' reporting template. The vignette below highlights how to go about creating these files.

Value

ubiquity system object with an empty report initialized
See Also

Reporting vignette (vignette("Reporting", package = "ubiquity"))
Custom Office Template vignette (vignette("Custom_Office_Templates", package="onbrand"))

system_rpt_save_report

Save Report to a File

Description

Saves a ubiquity report to the specified file.

Usage

system_rpt_save_report(cfg, output_file = NULL, rptname = "default")

Arguments

- **cfg**: ubiquity system object
- **output_file**: File to save the report to (must be either .pptx or .docx depending on the type of report)
- **rptname**: ubiquity report name

Value

list with the following elements

- isgood Boolean variable indicating success or failure
- msgs Verbose description of the save results

See Also

Reporting vignette (vignette("Reporting", package = "ubiquity"))
system_rpt_template_details

Generate Details about Report Template

Description

Wrapper for the onbrand::template_details function, see the help for that function for more information.

Usage

system_rpt_template_details(cfg, rptname = "default")

Arguments

cfg       ubiquity system object
rptname   Report name

Value

list with template information, see template_details for information on the structure of this list.

See Also

template_details and Reporting vignette (vignette("Reporting", package = "ubiquity"))

system_select_set

Selecting Parameter Sets

Description

The system file can contain multiple parameterizations using the <PSET:?:?>? notation. This function provides the means for switching between these parameterizations, and (optionally) specifying a subset of parameters estimated when performing parameter estimation.

Usage

system_select_set(cfg, set_name = "default", parameter_names = NULL)

Arguments

cfg       ubiquity system object
set_name   string containing the name of the parameter set
parameter_names
          list of parameter names to be estimated
system_set_bolus

**Value**

Ubiquity system object with the specified parameter set active

**Examples**

```r
# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
                system_file = "mab_pk",
                overwrite = TRUE,
                output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
                    output_directory = file.path(tempdir(), "output"),
                    temporary_directory = tempdir())

# Selecting the default parameter set
cfg = system_select_set(cfg, "default")
```

---

**system_set_bolus**  
*Set Bolus Inputs*

**Description**

Defines infusion rates specified in the system file using `<B:times>` and `<B:events>`

**Usage**

```r
system_set_bolus(cfg, state, times, values)
```

**Arguments**

- **cfg**: ubiquity system object
- **state**: name of the state to apply the bolus
- **times**: list of injection times
- **values**: corresponding list injection values

**Value**

Ubiquity system object with the bolus information set

**See Also**

`system_zero_inputs`
Examples

# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
    system_file = "mab_pk",
    overwrite = TRUE,
    output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
    output_directory = file.path(tempdir(), "output"),
    temporary_directory = tempdir())

# Clearing all inputs
cfg = system_zero_inputs(cfg)

# SC dose of 200 mg
cfg = system_set_bolus(cfg, state = "At",
    times = c(0.0), # day
    values = c(200.0)) # mg

system_set_covariate  Set Covariate Values

Description

Covariates specified in the system file using <CV:?> and <CVSET:?:?> will have their default values for a given parameter set. This function is a means to overwrite those values.

Usage

system_set_covariate(cfg, covariate, times, values)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cfg</td>
<td>ubiquity system object</td>
</tr>
<tr>
<td>covariate</td>
<td>name of the covariate</td>
</tr>
<tr>
<td>times</td>
<td>list of times (system time units)</td>
</tr>
<tr>
<td>values</td>
<td>corresponding list of values</td>
</tr>
</tbody>
</table>

Value

Ubiquity system object with the covariate set
system_set_guess

Examples

# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
    system_file = "mab_pk",
    overwrite = TRUE,
    output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
    output_directory = file.path(tempdir(), "output"),
    temporary_directory = tempdir())

# Setting the covariate WT to 50
cfg = system_set_covariate(cfg,
    covariate = "WT",
    times = c(0),
    values = c(50))

system_set_guess

Alter Initial Guess and Parameter Bounds

Description

Default values for parameters are taken from the system.txt file either when the parameter was defined (\texttt{<P>}) or when it was reassigned for a parameter set (\texttt{<PSET:?:?>}). These can be altered at the scripting level using this function.

Usage

\texttt{system_set_guess(cfg, pname, value, lb = NULL, ub = NULL)}

Arguments

- \texttt{cfg} ubiquity system object
- \texttt{pname} name of parameter to set
- \texttt{value} value to assign
- \texttt{lb} optionally change the lower bound (NULL)
- \texttt{ub} optionally change the upper bound (NULL)

Details

When performing a parameter estimation, the initial guess will be the value specified in the system.txt file for the currently selected parameter set. The following command can be used after the parameter set has been selected to specify the value (VALUE) of the parameter \texttt{PNAME} and optionally the lower (\texttt{lb}) and upper (\texttt{ub}) bounds:
.cfg = system_set_guess(cfg, pname="PNAME", value=VALUE, lb=NULL, ub=NULL)

To set the initial guess for the parameter Vc to a value of 3, the following would be used:

.cfg = system_set_guess(cfg, "Vc", value=3)

To specify the guess and overwrite the upper bound on Vc and set it to 5

.cfg = system_set_guess(cfg, "Vc", value=3, ub=5)

Value

cfg ubiquity system object with guess and bounds assigned

---

**system_set_iiv**  
Set Variability Terms

**Description**

Set elements of the current variance covariance matrix specified in the system file with <IIV:?:?>, <IIVCOR:?:?>, <IIVSET:?:?>, <IIVCORSET:?:?>

**Usage**

`system_set_iiv(cfg, IIV1, IIV2, value)`

**Arguments**

- **cfg** ubiquity system object
- **IIV1** row name of the variance/covariance matrix
- **IIV2** column name of the variance/covariance matrix element
- **value** value to assign to the variance/covariance matrix element

**Value**

Ubiquity system object with IIV information set

**See Also**

`system_fetch_iiv`
system_set_option

Examples

# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
               system_file = "mab_pk",
               overwrite = TRUE,
               output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
                   output_directory = file.path(tempdir(), "output"),
                   temporary_directory = tempdir())

# Clearing all inputs
cfg = system_zero_inputs(cfg)

# Setting the covariance element for CL and Vc to 0.03
cfg = system_set_iiv(cfg,
                     IIV1 = "ETACL",
                     IIV2 = "ETAVc",
                     value=0.03)

system_set_option Setting Analysis Options

Description

Different options associated performing analyses (e.g running simulations, performing parameter estimation, logging, etc.) can be set with this function

Usage

system_set_option(cfg, group, option, value)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cfg</td>
<td>ubiquity system object</td>
</tr>
<tr>
<td>group</td>
<td>options are grouped together by the underlying activity being performed: &quot;estimation&quot;, &quot;general&quot;, &quot;logging&quot;, &quot;simulation&quot;, &quot;solver&quot;, &quot;stochastic&quot;, or &quot;titration&quot;</td>
</tr>
<tr>
<td>option</td>
<td>for each group there are a set of options</td>
</tr>
<tr>
<td>value</td>
<td>corresponding value for the option</td>
</tr>
</tbody>
</table>
Details

group="estimation"

The default estimation in R is performed using either the optim or optimx libraries. This is selected by setting the optimizer option:

```
cfg = system_set_option(cfg,
    group = "estimation",
    option = "optimizer",
    value = "optim")
```

The optimization routine then specified using the method. By default this option is set to Nelder-Mead.

```
cfg = system_set_option(cfg,
    group = "estimation",
    option = "method",
    value = "Nelder-Mead")
```

And different attributes are then selected using the control.

```
cfg = system_set_option(cfg,
    group = "estimation",
    option = "control",
    value = list(trace = TRUE,
                 maxit = 500,
                 REPORT = 10))
```

For the different methods and control options, see the documentation for the optim and optimx libraries.

To perform a global optimization you can install either the particle swarm (pso) genetic algorithm (GA) libraries. To use the particle swarm set the optimizer and method:

```
cfg = system_set_option(cfg,
    group = "estimation",
    option = "optimizer",
    value = "pso")
```

```
cfg = system_set_option(cfg,
    group = "estimation",
    option = "method",
    value = "psoptim")
```

The control option is a list described pso documentation.

To use the genetic algorithm set the optimizer and method:
```r
cfg = system_set_option(cfg, 
  group = "estimation", 
  option = "optimizer", 
  value = "ga")

cfg = system_set_option(cfg, 
  group = "estimation", 
  option = "method", 
  value = "ga")
```

The control option is a list and the list elements are the named options in the GA documentation. Use the following as an example:

```r
cfg = system_set_option(cfg, 
  group = "estimation", 
  option = "control", 
  value = list(maxiter = 10000, 
               optimArgs = list(
                 method = "Nelder-Mead", 
                 maxiter = 1000)))
```

To alter initial guesses see: `system_set_guess`

When performing parameter estimation, the internal function `system_od_general` is used. This is the function that simulates your system at the conditions defined for the different cohorts. This is pretty flexible but if you want to go beyond this you can set the `observation_function` option:

```r
cfg = system_set_option(cfg, 
  group = "estimation", 
  option = "observation_function", 
  value = "my_od")
```

That will instruct the optimization routines to use the user defined function `my_od`. You will need to construct that function to have the same input/output format as `system_od_general`.

**group=general**

- "output_directory" = String where analysis outputs will be placed. Generally you wont want to change this, but it can be useful in Shiny apps where you need to have each shiny user generate output in that users directory: `file.path(".", "output")`

**group=logging**

By default ubiquity prints different information to the console and logs this information to a log file. The following options can be used to control this behavior:

- "enabled" = Boolean variable to control logging: TRUE
- "file" = String containing the name of the log file: `file.path("transient", "ubiquity_log.txt")`
- "timestamp" = Boolean switch to control appending a time stamp to log entries: TRUE
- "ts_str" = String format of timestamp: "}
• "debug" = Boolean switch to control debugging (see below): FALSE
• "verbose" = Boolean switch to control printing to the console FALSE

To enable debugging of different functions (like when performing estimation), set the debug option to TRUE. Important function calls will be trapped and information will be logged and reported to the console.

```
cfg = system_set_option(cfg,
    group = "estimation",
    option = "debug",
    value = FALSE)
```

```

group="simulation"

• "include_important_output_times" - Automatically add bolus, infusion rate switching times, etc: "yes" (default), "no".
• "integrate_with" - Specify if the ODE solver should use the Rscript ("r-file") or compiled C ("c-file"), if the build process can compile and load the C version it will be the default otherwise it will switch over to the R script.
• "output_times" - Vector of times to evaluate the simulation (default seq(0,100,1)).
• "solver" - Selects the ODE solver: "lsoda" (default), "lsode", "vode", etc.; see the documentation for deSolve for an exhaustive list.
• "sample_bolus_delta" - Spacing used when sampling around bolus events (default 1e-6).
• "sample_forcing_delta" - Spacing used when sampling around forcing functions (infusion rates, covariates, etc) (default 1e-3).

```

group=solver

Depending on the solver, different options can be set. The documentation for deSolve lists the different solvers. For a full list of options, see the documentation for the specific solver (e.g. ?lsoda). Some common options to consider are:

• "atol" - Relative error tolerance
• "rtol" - Absolute error tolerance
• "hmin" - Minimum integration step size
• "hmax" - Maximum integration step size

To select the vode solver and set the maximum step size to 0.01, the following would be used:

```
cfg=system_set_option(cfg,
    group = "simulation",
    option = "solver",
    value = "vode")
```

```

cfg=system_set_option(cfg,
    group = "solver",
    option = "hmax",
    value = 0.01)
```
When running stochastic simulations (inter-individual variability applied to system parameters) it can be useful to specify the following:

- **"ci"** - Confidence interval (default 95)
- **"nsub"** - Number of subjects (default 100)
- **"seed"** - Seed for the random number generator (default 8675309)
- **"ponly"** - Only generate the subject parameters but do not run the simulations (default FALSE)
- **"ssp"** - A list of the calculated static secondary parameters to include (default all parameters defined by <As>)
- **"outputs"** - A list of the predicted outputs to include (default all outputs defined by <O>)
- **"states"** - A list of the predicted states to include (default all states)
- **"sub_file"** - Name of data set loaded with (system_load_data) containing subject level parameters and covariates
- **"sub_file_sample"** - Controls how subjects are sampled from the dataset

If you wanted to generate 1000 subjects but only wanted the parameters, you would use the following:

```r
cfg = system_set_option(cfg,
    group = "stochastic",
    option = "nsub",
    value = 1000)

cfg = system_set_option(cfg,
    group = "stochastic",
    option = "ponly",
    value = TRUE)
```

If you wanted to exclude both states and secondary parameters, while only including the output \(\text{Cp}_\text{nM}\), you would do the following:

```r
cfg = system_set_option(cfg,
    group = "stochastic",
    option = "ssp",
    value = list())

cfg = system_set_option(cfg,
    group = "stochastic",
    option = "states",
    value = list())

cfg = system_set_option(cfg,
    group = "stochastic",
    option = "outputs",
    value = c("Cp\_nM"))
```
To pull subject information from a data file instead of generating the subject parameters from IIV information the `sub_file` option can be used. The value here `SUBFILE_NAME` is the name given to a dataset loaded with (`system_load_data`):

```
cfg=system_set_option(cfg,
    group = "stochastic",
    option = "sub_file",
    value = "SUBFILE_NAME")
```

Sampling from the dataset can be controlled using the `sub_file_sample` option:

```
cfg=system_set_option(cfg,
    group = "stochastic",
    option = "sub_file_sample",
    value = "with replacement")
```

Sampling can be done sequentially ("sequential"), with replacement ("with replacement"), or without replacement ("without replacement")

```
group="titration"
"titrate" - By default titration is disable (set to FALSE). If you are going to use titration, enable it here by setting this option to TRUE. This will force `simulate_subjects` to use `run_simulation_titrate` internally when running simulations.
```

**Value**

Ubiquity system object with the option set

---

**system_set_parameter**  
*Set Value for Parameter*

**Description**

Assigns a value for a named parameter in a parameter list.

**Usage**

```
System_set_parameter(cfg, parameters, pname, value)
```

**Arguments**

- `cfg` ubiquity system object
- `parameters` vector of parameters
- `pname` parameter name
- `value` value
Details

To set the parameter Vc to a value of 3, the following would be used:

```r
parameters = system_fetch_parameters(cfg)
parameters = system_set_parameter(cfg, parameters, pname = 'Vc', value = 3)
```

Value

parameters vector with pname set to value

---

**system_set_rate**  
*Set Infusion Rate Inputs*

**Description**

Defines infusion rates specified in the system file using `<R:?>`

**Usage**

`system_set_rate(cfg, rate, times, levels)`

**Arguments**

- `cfg`: ubiquity system object
- `rate`: name of infusion rate
- `times`: list of time values
- `levels`: corresponding list of infusion values

**Value**

Ubiquity system object with the infusion rate set

**See Also**

`system_zero_inputs`

**Examples**

```r
# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
                system_file = "mab_pk",
                overwrite = TRUE,
                output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
```

```
system_set_rpt_officer_object

Sets the officer Object for the Specified ubiquity Report

Description

This will replace the officer object in the ubiquity system object for the specified report name with the value supplied.

Usage

system_set_rpt_officer_object(cfg, rpt = NULL, rptname = "default")

Arguments

cfg         ubiquity system object
rpt         officer report object
rptname     ubiquity report name

Value

ubiquity system object with the replaced officer object

See Also

system_fetch_rpt_officer_object
**system_set_rpt_onbrand_object**

*Sets the onbrand Object for the Specified ubiquity Report*

**Description**

This will reset the onbrand object in the ubiquity system object for the specified report name.

**Usage**

```r
system_set_rpt_onbrand_object(cfg, obnd = NULL, rptname = "default")
```

**Arguments**

- **cfg**: ubiquity system object
- **obnd**: onbrand report object
- **rptname**: ubiquity report name

**Value**

ubiquity system object with onbrand report set

**See Also**

`system_fetch_rpt_onbrand_object`

---

**system_set_tt_cond**  
*Define Titration Triggers and Actions*

**Description**

Once a rule has been defined using `system_new_tt_rule`, it can then be used by specifying checks at each of the titration time points that, when true, will perform some actions.

**Usage**

```r
system_set_tt_cond(cfg, name, cond, action, value = "-1")
```
Arguments

- **cfg**: ubiquity system object
- **name**: string containing the name for the titration rule to which this condition applies
- **cond**: string that evaluates a boolean value that is TRUE when the action should be triggered
- **action**: stringing that evaluates to what should be done when the condition is met (e.g. changing the dose, state change, etc)
- **value**: code to be stored in the titration history to track when this condition has been triggered

Details

The general syntax for setting a new condition is:

```python
cfg = system_new_tt_cond(cfg,
    name = "rname",
    cond = "BOOLEAN EXPRESSION",
    action = "EXPRESSION",
    value = "VALUE")
```

The `name` input will associate this condition with a previously defined rule. For each time defined when the rule was created, the condition (cond) will be evaluated. If that condition evaluates as TRUE then the action will be evaluated. Lastly, when a condition action is evaluated, the value is stored in the titration history.

Multiple conditions can be associated with a rule. The internal titration history will track each one where a condition has been evaluated as true, but the simulation output will only show the last condition to be evaluated as true.

The `cond` field is a string that, when evaluated, will produce a boolean value (TRUE or FALSE). If you simply want to force an action at each of the times for a given rule you can use: `cond = "TRUE"`. Alternatively you can provide mathematical expressions or even complicated user defined functions.

The `action` field is evaluated when `cond` is true. To modify how a simulation is going to be performed, you will want to modify the SIMINT_cfgtt variable using the different system commands. Certain common tasks have prototype functions created to make it easier for the user:

- **SI_TT_BOLUS**: Set bolus dosing
- **SI_TT_RATE**: Set infusion inputs
- **SI_TT_STATE**: Reset system states

**Note**: Prototype functions are strings but sometimes it is necessary to specify strings within this string. For the main string use double quotes (""), and for the internal strings use single quotes (’). SI_TT_BOLUS

The simplest way to apply a bolus when the condition is true is to use the following:
action = "SI_TT_BOLUS[state='At',
        values=c(10, 10, 10),
        times=c(0, 1, 2)]"

The values and times are vectors of numbers of equal length. The dosing and time units are those specified in the system.txt file for the `<B:?>` delimiter. The times are relative to the titration time. So 0 above means at the titration time.

It’s possible to specify an interval and a number of times to repeat the last dose using the following:

action = "SI_TT_BOLUS[state = 'At',
                      values = c(5, 5, 10),
                      times = c(0, 2, 4),
                      repdose = 'last',
                      number = 7,
                      interval = 4]"

This will give a dose of 5 at the titration point and 2 time units later. The dose of 10 at time 4 will be repeated 7 times every 4 time units. So a total of 8 (7 + 1) doses at 10 will be administered. Remember the time units were those defined in `<B:?>`. The input repdose can be either 'last' or 'none'.

**Note:** The main string is in double quotes " " but the strings in the prototype argument (e.g. 'last') are in single quotes ' '.

**SI_TT_RATE**

If you created an infusion named Dinf using `<R:?>` and the infusion units are min (times) and mg/min (rates). To have a 60 minute infusion of 20 mg/min then we would do the following:

action = "SI_TT_RATE[rate='Dinf', times=c(0, 60), levels=c(20.0, 0)]"

If we wanted to do this every day for 9 more days (a total of 10 days) we can repeat the sequence:

action = "SI_TT_RATE[rate = 'Dinf',
                      times = c(0, 60),
                      levels = c(20, 0),
                      repdose = 'sequence',
                      number = 9,
                      interval = 24*60]"

The input repdose can be either 'sequence' or 'none'.

**Note:** The time units and dosing rate are those specified using `<R:?>`.

**SI_TT_STATE**

To provide fine control over states at titration points the state reset prototype is provided. For example, if you are modeling an assay where there is a wash step and you want to drop a concentration to zero. If you have a state named Cc defined in your system.txt and you want to set it to 0.0 in a condition the following action would work.

action = "SI_TT_STATE[Cc][0.0]"
The value here is a number but you can use any mathematical combination of variables available in the titration environment. Also you can create your own user function and place the function call within the brackets above.

**Titration Environment**

The cond, action, and value statements can use any variables available in the titration environment. If you want to perform complicated actions, you can simply create a user defined functions and pass it the variables from the titration environment that you need. These include named variables from the model as well as internal variables used to control the titration.

**States and Parameters**

System parameters ($\langle P \rangle$), static secondary parameters ($\langle As \rangle$) and the initial value of covariates are available. Also the state values (at the current titration time) can be used. These are all available as the names specified in the `system.txt` file. Since system resets (SI_TT_STATE) are processed first, any changes made to states are the values that are active for other actions.

**Internal Simulation Variables**

Internal variables are used to control titration activities. These variables can also be used in the conditions and actions.

- SIMINT_p - list of system parameters
- SIMINT_cfg - system configuration sent into the titration routine
- SIMINT_cfgtt - system configuration at the current titration event time
- SIMINT_ttimes - vector of titration times (in simulation units)
- SIMINT_ttime - current titration time (in simulation units)
- SIMINT_tt_ts - list of time scales for the current titration
- SIMINT_history - data frame tracking the history of conditions that evaluated true with the following structure:
  - tname - name of titration rule
  - value - value indicating condition that was satisfied
  - simtime - simulation time when that rule/value were triggered
  - timescale - time at the rule timescale when that rule/value were triggered

**Individual Simulations**

To run an individual titration simulation use the following:

```r
som = run_simulation_titrate(parameters, cfg)
```

This provides the same output as `run_simulation_ubiquity` with two extra fields. The first, `som$titation`, contains three columns for each titration rule. The columns will have a length equal and corresponding to the simulation times. If the rule name is rname, then the column headers will have the following names and meanings:

- tt.rname.value - Value of the rule for the active condition or -1 if not triggered
- tt.rname.simtime - Simulation time where the last condition became active
- tt.rname.timescale - Simulation time in the time scale the rule was specified in
The second field is `som$titration_history` which contains a summary list of all of the titration events that were triggered.

- `tname` - Titration rule name
- `value` - Value of the rule for the active condition or -1 if not triggered
- `sitime` - Simulation time where the last condition became active
- `timescale` - Simulation time in the time scale the rule was specified in

To convert this structured list into a data frame the `som_to_df` command can be used:

```r
sdf = som_to_df(cfg, som)
```

To run stochastic titration simulations, the same function is used:

```r
som = simulate_subjects(parameters, cfg)
```

This will add a data a list element called `som$titration` with three fields for each titration rule:

- `tt.rname.value` - Value of the rule for the active condition or -1 if not triggered
- `tt.rname.sitime` - Simulation time where the last condition became active
- `tt.rname.timescale` - Simulation time in the time scale the rule was specified in

Each of these fields is a matrix with an entry for each simulation time (column) and each subject (row). This data structure can also be converted to a data frame using `som_to_df`.

**Value**

Ubiquity system object with the titration condition defined

**See Also**

`system_new_tt_rule`, `run_simulation_titrate`, `som_to_df`, `simulate_subjects`

---

**Description**

The prototype function `SI_TT_RATE` provides an abstract interface to this function. Based on the input from `SI_TT_RATE` infusion rate inputs will be updated for the current titration time.
Usage

```r
system_set_tt_rate(
  cfg,
  rate,
  times,
  levels,
  tt_ts,
  tsinfo,
  repdose = "none",
  interval = 1,
  number = 0
)
```

Arguments

- **cfg**: ubiquity system object
- **rate**: name of the infusion rate to update (Defined in `<R:`)
- **times**: vector of switching times relative to the current titration time (in time units defined by `<R:`)
- **levels**: vector of infusion rates (in dosing units defined by `<R:`)
- **tt_ts**: list of timescale values for the current titration time
- **tsinfo**: list with timescale information for inputs (bolus, rates, etc)
- **repdose**: "none" or "sequence"
- **interval**: interval to repeat in the units defined in `<R:`
- **number**: number of times to repeat

Value

ubiquity system object with the infusion rates updated.

---

**system_simulate_estimation_results**

*Simulate Results at Estimates*

Description

Simulates the system at the parameter estimates `pest` for creating diagnostic plots

Usage

```r
system_simulate_estimation_results(pest, cfg, details = FALSE)
```
system_view

Arguments

pest vector of parameters
cfg ubiquity system object
details set TRUE to display information about cohorts as they are simulated (useful for debugging)

Value

observations in a list, see system_od_general when estimation=FALSE

See Also

system_define_cohort, system_plot_cohorts and the vignette on parameter estimation (vignette("Estimation", package = "ubiquity"))

Description

Displays information (dosing, simulation options, covariates, etc) about the system.

Usage

system_view(cfg, field = "all", verbose = FALSE)

Arguments

cfg ubiquity system object
field string indicating the aspect of the system to display
verbose Boolean variable that when set to true will echo the information to the screen

Value

sequence of strings with system in formation (one line per element)
The field

- "all" will show all information about the system
- "parameters" summary of parameter information
- "bolus" currently set bolus dosing
- "rate" infusion rate dosing
- "covariate" covariates
- "iiv" variance/covariance information
- "datasets" loaded datasets
- "simulation" simulation options
- "estimation" estimation options
- "nca" non-compartmental analyses that have been performed
Examples

# To log and display the current system information:

# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
                system_file = "mab_pk",
                overwrite = TRUE,
                output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
                    output_directory = file.path(tempdir(), "output"),
                    temporary_directory = tempdir())

msgs = system_view(cfg, verbose=TRUE)

---

system_zero_inputs  Zero All Model Inputs

Description

Multiple default inputs can be specified in the system file. At the scripting level this function can be used to set all inputs to zero. Then only the subsequently specified inputs will be applied.

Usage

system_zero_inputs(cfg, bolus = TRUE, rates = TRUE)

Arguments

cfg  ubiquity system object
bolus Boolean value indicating weather bolus inputs should be set to zero
rates Boolean value indicating weather infusion rate inputs should be set to zero

Value

Ubiquity system object with the specified inputs set to zero

See Also

system_set_rate, system_set_bolus
Examples

# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
                system_file = "mab_pk",
                overwrite = TRUE,
                output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
                    output_directory = file.path(tempdir(), "output"),
                    temporary_directory = tempdir())

# Clear only infusion rates
cfg = system_zero_inputs(cfg, bolus=TRUE, rates=FALSE)

# Clear all inputs:
cfg = system_zero_inputs(cfg)

tic

Implementation of Matlab tic() command

Description

Used in conjunction with toc() to find the elapsed time when code is executed.

Usage

tic(type = c("elapsed", "user.self", "sys.self"))

Arguments

  type can be either "elapsed" "user.self" or "sys.self"

Value

time tic was called

See Also

toc

Examples

tic()
Sys.sleep(3)
toc()
toc

**Implementation of Matlab toc() command**

**Description**

Used in conjunction with tic() to find the elapsed time when code is executed.

**Usage**

toc()

**Value**

time in seconds since tic() was called

**See Also**

tic

**Examples**

tic()
Sys.sleep(3)
toc()

var2string

**Converts Numeric Variables into Padded Strings**

**Description**

Mechanism for converting numeric variables into strings for reporting.

**Usage**

var2string(vars, maxlength = 0, nsig_e = 3, nsig_f = 4)

**Arguments**

- **vars**
  - numeric variable or a vector of numeric variables
- **maxlength**
  - if this value is greater than zero spaces will be added to the beginning of the string until the total length is equal to maxlength
- **nsig_e**
  - number of significant figures for scientific notation
- **nsig_f**
  - number of significant figures for numbers (2.123)
Value

Number as a string padded

Examples

```r
var2string(pi, nsig_f=20)
var2string(.0001121, nsig_e=2, maxlength=10)
```

---

**Print and Log Messages**

**Description**

Used to print messages to the screen and the log file.

**Usage**

```r
vp(cfg, str, fmt = "alert")
```

**Arguments**

- `cfg`: ubiquity system object
- `str`: sequence of strings to print
- `fmt`: string format should be one of the following: "h1", "h2", "h3", "verbatim", "alert" (default), "warning", "danger".

**Value**

Boolean variable indicating success (TRUE) or failure (FALSE)

**Examples**

```r
# Creating a system file from the mab_pk example
fr = system_new(file_name = "system.txt",
                system_file = "mab_pk",
                overwrite = TRUE,
                output_directory = tempdir())

# Building the system
cfg = build_system(system_file = file.path(tempdir(), "system.txt"),
                   output_directory = file.path(tempdir(), "output"),
                   temporary_directory = tempdir())

# Initializing the log file
vp(cfg, "Message that will be logged")
```
workshop_fetch  

*Fetch Ubiquity Workshop Sections*

**Description**

With the ubiquity package this function can be used to fetch example files for different sections of the workshop.

**Usage**

```r
workshop_fetch(
  section = "Simulation",
  overwrite = FALSE,
  copy_files = TRUE,
  output_directory = getwd()
)
```

**Arguments**

- `section`: Name of the section of workshop to retrieve ("Simulation")
- `overwrite`: if TRUE the new workshop files will overwrite any existing files present (FALSE)
- `copy_files`: if TRUE the files will be written to the output_directory, if FALSE only the names and locations of the files will be returned (TRUE)
- `output_directory`: directory where workshop files will be placed (getwd())

**Details**

Valid sections are "Simulation", "Estimation", "Titration" "Reporting", and "NCA"

**Value**

list

**Examples**

```r
workshop_fetch("Estimation", output_directory=tempdir(), overwrite=TRUE)
```
Index

add_pptx_ph_content, 48
build_system, 3
calculate_halflife, 4
desolve, 60
gg_axis, 5, 6–8
gg_log10_xaxis, 6, 6, 7, 8
gg_log10_yaxis, 6
linspace, 8
logspace, 9
nm_select_records, 21
pad_string, 10
prepare_figure, 10
report_add_doc_content, 47
report_add-slide, 48
run_simulation_titrate, 11, 14, 44, 62, 69
run_simulation_ubiquity, 11, 12, 14, 68
simulate_subjects, 13, 14, 62, 69
som_to_df, 13, 14, 69
system_check_requirements, 15
system_check_steady_state, 15
system_clear_cohorts, 17
system_define_cohort, 17, 45, 71
system_define_cohorts_nm, 20
system_estimate_parameters, 22
system_fetch_guess, 23
system_fetch_iiv, 23, 56
system_fetch_nca, 24
system_fetch_nca_columns, 25
system_fetch_parameters, 26
system_fetch_rpt_officer_object, 26, 64
system_fetch_rpt_onbrand_object, 27, 65
system_fetch_set, 28
system_fetch_template, 28
system_fetch_TSSys, 30
system_glp_init, 31
system_glp_scenario, 31
system_load_data, 17, 34, 38, 61, 62
system_log_debug_save, 35
system_log_init, 36
system_nca_parameters_save, 25, 36
system_nca_run, 37
system_nca_summary, 39
system_new, 41
system_new_list, 43
system_new_tt_rule, 12, 43, 65, 69
system_od_general, 44, 59, 71
system_plot_cohorts, 45, 71
system_rpt_add_doc_content, 47
system_rpt_add-slide, 48
system_rpt_estimation, 48
system_rpt_nca, 49
system_rpt_read_template, 33, 49, 50
system_rpt_save_report, 51
system_rpt_template_details, 52
system_select_set, 26, 52
system_set_bolus, 53, 72
system_set_covariate, 54
system_set_guess, 55, 59
system_set_iiv, 24, 56
system_set_option, 13, 18, 57
system_set_parameter, 62
system_set_rate, 63, 72
system_set_rpt_officer_object, 27, 64
system_set_rpt_onbrand_object, 27, 65
system_set_tt_cond, 12, 44, 65
system_set_tt_rate, 69
system_simulate_estimation_results, 44, 45, 70
system_view, 71
system_zero inputs, 53, 63, 72
template_details, 52
tic. 73, 74

toc. 73, 74

var2string. 74

vp. 75

workshop_fetch. 76