Package 'clinPK'

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Author Ron Keizer

Maintainer Ron Keizer <ronkeizer@gmail.com>

Description Calculates equations commonly used in clinical pharmacokinetics and clinical pharmacology, such as equations for dose individualization, compartmental pharmacokinetics, drug exposure, anthropomorphic calculations, clinical chemistry, and conversion of common clinical parameters. Where possible and relevant, it provides multiple published and peer-reviewed equations within the respective R function.

Imports testit, curl

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`clinPK-package` *clinPK*

Description

Equations and tool for clinical pharmacokinetics

Author(s)

Ron Keizer <ronkeizer@gmail.com>

`add_ruv` *Add residual variability to data*

Description

Add residual variability to data

Usage

```
add_ruv(x, ruv = list())
```

Arguments

x	data
ruv	list with arguments prop, add, exp

Examples

```
y <- pk_1cmt_inf()$y
y + add_ruv(y, list(prop = 0.1, add = 0.05))
```

as.num — *factors or characters to numeric*

Description

factors or characters to numeric

Usage

```
as.num(x)
```

Arguments

x	value

auc2dose — *Convert AUCtau or AUCt to dose (for 1-compartment linear PK model)*

Description

Convert AUCtau or AUCt to dose (for 1-compartment linear PK model)

Usage

```
auc2dose(auc, CL, V, t_auc = NA)
```

Arguments

auc	AUCtau
CL	Clearance
V	Volume of distribution
t_auc	if AUCtau is not known but only AUCt, ‘t_auc‘ specifies time until which AUC_t is calculated to be able to calculate dose

Examples

```
auc2dose(450, CL = 5, V = 50)
```

calc_abw *Calculate adjusted body weight (ABW)*

Description

Often used for chemotherapy calculations when actual weight > 120

Usage

```
calc_abw(weight = NULL, ibw = NULL, factor = 0.4, verbose = TRUE, ...)
```

Arguments

weight	actual body weight in kg
ibw	ideal body weight in kg
factor	weighting factor, commonly 0.4 or 0.3
verbose	show output?
...	parameters passed to ibw function (if 'ibw' not specified)

Examples

```
calc_abw(weight = 80, ibw = 60)
calc_abw(weight = 80, height = 160, sex = "male", age = 60)
```

calc_amts_for_conc *Calculate the amounts in all compartments in a compartmental PK system based on a given concentration in the central compartment, and assuming steady state.*

Description

Calculate the amounts in all compartments in a compartmental PK system based on a given concentration in the central compartment, and assuming steady state.

Usage

```
calc_amts_for_conc(conc = 10, parameters = NULL, n_cmt = 1)
```

Arguments

conc	concentration in central compartment
parameters	for PK model
n_cmt	number of compartments

Examples

```
calc_amts_for_conc(conc = 10, parameters = list(CL = 5, V = 50), n_cmt = 1)
calc_amts_for_conc(
  conc = 10,
  parameters = list(CL = 5, V = 50, Q = 20, V2 = 100),
  n_cmt = 2)
calc_amts_for_conc(
  conc = 10,
  parameters = list(CL = 5, V = 50, Q = 20, V2 = 100, Q2 = 30, V3 = 200),
  n_cmt = 3)
```

---

calc_bmi *Calculate BMI*

Description

Calculate BMI

Usage

```
calc_bmi(weight, height)
```

Arguments

weight	weight in kg
height	height in cm

Examples

```
calc_bmi(weight = 70, height = 160)
```

---

calc_bsa *Calculate body surface area*

Description

Get an estimate of body-surface area based on weight and height

Usage

```
calc_bsa(weight = NULL, height = NULL, method = "dubois")
```

Arguments

weight	weight
height	height
method	estimation method, choose from ‘dubois‘, ‘mosteller‘, ‘haycock‘, ‘gehan_george‘, ‘boyd‘

Examples

```
calc_bsa(weight = 70, height = 170)
calc_bsa(weight = 70, height = 170, method = "gehan_george")
```

---

calc_creat *Estimate serum creatinine*

Description

Calculate an estimated serum creatinine. Function takes vectorized input as well.

Usage

```
calc_creat(sex = NULL, age = NULL, digits = 1)
```

Arguments

sex	sex, either ‘male‘ or ‘female‘
age	age in years
digits	number of digits to round to

Details

Uses equations described in Ceriotti et al. Clin Chem. 2008, and Junge W et al. Clin Chim Acta. 2004. For age 15-18, a linear interpolation is used between equations for <15 and >18 years as described in Johanssen A et al. Ther Drug Monit 2011.

Examples

```
calc_creat(sex = "male", age = 40)
calc_creat(sex = "male", age = c(10, 17, 60))
```

calc_creat_neo *Estimate serum creatinine in neonates*

Description

Calculate an estimated serum creatinine. Function takes vectorized input as well.

Usage

```
calc_creat_neo(pma = NULL, digits = 1)
```

Arguments

pma	post-natal age in weeks
digits	number of digits to round to

Details

Uses equations described in Germovsek E et al. (http://www.ncbi.nlm.nih.gov/pubmed/27270281) based on data from Cuzzolin et al. (http://www.ncbi.nlm.nih.gov/pubmed/16773403) and Rudd et al. (http://www.ncbi.nlm.nih.gov/pubmed/6838252)

Examples

```
calc_creat_neo(pma = 36)
convert_creat_unit(calc_creat_neo(pma = 36))
```

calc_egfr *Calculate eGFR*

Description

Calculate the estimated glomerulal filtration rate (an estimate of renal function) based on measured serum creatinine using one of the following approaches: - Cockcroft-Gault (using weight, ideal body weight, or adjusted body weight) - Revised Lund-Malmo - Modification of Diet in Renal Disease study (MDRD) - Schwartz - Schwartz revised - Jelliffe - Jelliffe (for unstable renal function) - Wright

Usage

```
calc_egfr(method = "cockcroft_gault", sex = NULL, age = NULL,
  scr = NULL, scr_unit = NULL, scr_assay = NULL, race = "other",
  weight = NULL, height = NULL, bsa = NULL, preterm = FALSE,
  ckd = FALSE, times = NULL, bsa_method = "dubois", relative = NULL,
  unit_out = "mL/min", ...)
```

Arguments

method	eGFR estimation method, choose from ‘cockcroft_gault‘, ‘cockcroft_gault_ideal‘, ‘mdrd‘, ‘ckd_epi‘, malmo_lund_revised‘, ‘schwartz‘, ‘jelliffe‘, ‘jellife_unstable‘, ‘wright‘
sex	sex
age	age
scr	serum creatinine (mg/dL)
scr_unit,	‘mg/dL‘ or ‘micromol/L‘ (==‘umol/L‘)
scr_assay,	‘jaffe‘ or ‘enzymatic‘ or ‘idms‘
race	‘black‘ or ‘other‘
weight	weight
height	height, only relevant when converting to/from BSA-relative unit
bsa	body surface area
preterm	is patient preterm?
ckd	chronic kidney disease? (Schwartz equations only)
times	vector of sampling times for creatinine (only used in Jelliffe equation for unstable patients)
bsa_method	BSA estimation method, see ‘bsa()‘ for details
relative	‘TRUE‘/‘FALSE‘. Report eGFR as per 1.73 m2? Requires BSA if re-calculation required. If ‘NULL‘ (=default), will choose value typical for ‘method‘.
unit_out	‘ml/min‘ (default), ‘L/hr‘, or ‘mL/hr‘
...	arguments passed on

Details

Equations for estimation of eGFR from Cystatin C concentrations are available from the ‘calc_egfr_cystatin()‘ function.

Examples

```
calc_egfr(sex = "male", age = 50, scr = 1.1, weight = 70)
calc_egfr(sex = "male", age = 50, scr = 1.1, weight = 70, unit_out = "L/hr")
calc_egfr(sex = "male", age = 50, scr = 1.1, weight = 70, bsa = 1.8, method = "ckd_epi")
calc_egfr(sex = "male", age = 50, scr = c(1.1, 0.8),
  weight = 70, height = 170, method = "jelliffe")
calc_egfr(sex = "male", age = 50, scr = c(1.1, 0.8),
  weight = 70, height = 170, method = "jelliffe_unstable")
calc_egfr(sex = "male", age = 50, scr = 1.1,
  weight = 70, bsa = 1.6, method = "malmo_lund_rev", relative = FALSE)
```

calc_egfr_cystatin *Calculate eGFR based on Cystatin C measurements*

Description

Calculate eGFR based on Cystatin C measurements

Usage

```
calc_egfr_cystatin(cystatin = NULL, cystatin_unit = "mg/L",
  method = "grubb", unit_out = "mL/min")
```

Arguments

cystatin	serum cystatin concentration (mg/L)
cystatin_unit,	only ‘mg/L‘ available
method	eGFR estimation method, choose from ‘grubb‘, ‘larsson‘
unit_out	eGFR output unit, choose from ‘ml/min‘, ‘ml/hr‘, ‘l/min‘, ‘l/hr‘

Examples

```
calc_egfr_cystatin(1.0)
calc_egfr_cystatin(1.0, method = "larsson")
calc_egfr_cystatin(1.0, unit_out = "l/hr")
```

calc_ffm *Calculate fat-free mass*

Description

Get an estimate of body-surface area based on weight, height, and sex (and age for Storset equation).

Usage

```
calc_ffm(weight = NULL, bmi = NULL, sex = NULL, height = NULL,
  age = NULL, method = "green", digits = 1)
```

Arguments

weight	total body weight in kg
bmi	BMI, only used in ‘green‘ method. If ‘weight‘ and ‘height‘ are both specified, ‘bmi‘ will be calculated on-the-fly.
sex	sex, either ‘male‘ of ‘female‘
height	height in cm, only required for ‘holford‘ method, can be used instead of ‘bmi‘ for ‘green‘ method
age	age, only used for Storset equation
method	estimation method, either ‘green‘ (default), ‘holford‘, or ‘storset‘
digits	round to number of digits

Details

References: ‘green‘: Janmahasatian et al. Clin Pharmacokinet. 2005;44(10):1051-65) ‘al-sallami‘: Al-Sallami et al. Clin Pharmacokinet 2015 ‘storset‘: Storset E et al. TDM 2016

Examples

```
calc_ffm(weight = 70, bmi = 25, sex = "male")
calc_ffm(weight = 70, height = 180, age = 40, sex = "female", method = "storset")
```

---

calc_ibw *Calculate ideal body weight for children and adults*

Description

Get an estimate of ideal body weight. This function allows several commonly used equations

Usage

```
calc_ibw(weight = NULL, height = NULL, age = NULL, sex = "male",
  method_children = "standard", method_adults = "devine", digits = NULL)
```

Arguments

weight	weight in kg, can be vector
height	height in cm, can be vector
age	age in years, can be vector
sex	either ‘male‘ or ‘female‘, can be vector
method_children	method to use for children >1 and <18 years. Choose from ‘standard‘, ‘mclaren‘ (McLaren DS, Read WWC. Lancet. 1972;2:146-148.), ‘moore‘ (Moore DJ et al. Nutr Res. 1985;5:797-799), ‘bmi‘ (), ‘ada‘ (American Dietary Association)
method_adults	method to use for >=18 years. Choose from ‘devine‘ (default, Devine BJ. Drug Intell Clin Pharm. 1974;8:650-655).
digits	number of decimals (can be NULL to for no rounding)

Details

Equations:

<1yo Use actual body weight

1-17 years old ('standard'): if height < 5ft: IBW= (height in cm2 x 1.65)/1000 if height > 5ft: IBW (male) = 39 + (2.27 x height in inches over 5 feet) IBW (female) = 42.2 + (2.27 x height in inches over 5 feet)

Methods not implemented yet: McLaren: IBW = - step1: x = 50th percentile height for given age - step2: IBW = 50th percentile weight for x on weight-for-height scale Moore: IBW = weight at percentile x for given age, where x is percentile of height for given age BMI: IBW = 50th percentile of BMI for given age x (height in m)^2 ADA: IBW = 50th percentile of WT for given age

>= 18 years old (Devine equation) IBW (male) = 50 + (2.3 x height in inches over 5 feet) IBW (female) = 45.5 + (2.3 x height in inches over 5 feet)

Examples

```
calc_ibw(weight = 70, height = 170, age = 40, sex = "female")
calc_ibw(weight = 30, height = 140, age = 10, sex = "female")
```

---

calc_kel_single_tdm *Calculate elimination rate when given a single TDM sample*

Description

Using iterative k_el calculation, and based on given Volume

Usage

```
calc_kel_single_tdm(dose = 1000, V = 50, t = 10, dv = 10, tau = 12,
  t_inf = 1, kel_init = 0.1, n_iter = 25)
```

Arguments

dose	dose amount
V	volume of distribution
t	time or time after dose
dv	observed value
tau	dosing interval
t_inf	infusion time
kel_init	estimate of elimination rate
n_iter	number of iterations to improve estimate of elimination rate

Examples

```
calc_kel_single_tdm(dose = 1000, t = 18)
```

calc_lbw *Calculate lean body weight*

Description

Get an estimate of lean body weight (LBW) based on weight, height, and sex.

Usage

```
calc_lbw(weight = NULL, bmi = NULL, sex = NULL, height = NULL,
  method = "green", digits = 1)
```

Arguments

weight	total body weight in kg
bmi	bmi
sex	sex, either 'male' of 'female'
height	height in cm
method	estimation method, either 'green' (default), 'boer', 'james', 'hume'
digits	round to number of digits

Details

Note: technically not the same as fat-free mass, although difference is small.

References: 'green': Green and Duffull. Clin Pharmacol Ther 2002; 'james': Absalom AR et al. Br J Anaesth 2009; 103:26-37. James W. Research on obesity. London: Her Majesty's Stationary Office, 1976. 'hume' : Hume R et al. J Clin Pathol. 1966 Jul; 19(4):389-91. 'boer' : Boer P et al. Am J Physiol 1984; 247: F632-5

Examples

```
calc_lbw(weight = 80, height = 170, sex = "male")
calc_lbw(weight = 80, height = 170, sex = "male", method = "james")
```

calc_t12 *Calculate half-life based on two points*

Description

based on two sampling points (in same interval)

Usage

```
calc_t12(t1, t2, y1, y2)
```

Arguments

t1	first sampling timepoint
t2	second sampling timepoint
y1	first sample value
y2	second sample value

Examples

```
calc_t12(3, 24, 30, 10)
```

---

cm2inch *Convert cm to inch*

Description

Convert cm to inch

Usage

```
cm2inch(cm)
```

Arguments

cm	vector

Examples

```
cm2inch(2.54)
```

---

conc2mol *Convert concentration to molar*

Description

Convert concentration to molar

Usage

```
conc2mol(conc = NULL, unit_conc = NULL, mol_weight = NULL,
  unit_mol = NULL)
```

Arguments

conc	concentration in e.g. g/L
unit_conc,	one of ‘g/l‘, ‘mg/l‘, ‘microg/l‘, ‘mcg/l", ‘ng/l‘, ‘mg/ml‘, ‘microg/ml‘, ‘mcg/ml‘, ‘ng/ml‘
mol_weight	concentration in g/mol
unit_mol	one of ‘mol/L‘, ‘mmol/mL‘, ‘mmol/L‘

Examples

```
conc2mol(100, unit_conc = "g/l", mol_weight = 180.15588)
```

---

convert_creat_assay *Convert serum creatinine from various assays to Jaffe*

Description

Based on equations as reported in Srivastava et al. 2009 (Pediatr Res. 2009 Jan;65(1):113-6. doi: 10.1203/PDR.0b013e318189a6e8)

Usage

```
convert_creat_assay(scr, from = "idms", to = "jaffe")
```

Arguments

scr	vector of serum creatinine values
from	assay type, either ‘jaffe‘, ‘enzymatic‘ or ‘idms‘
to	assay type, either ‘jaffe‘, ‘enzymatic‘ or ‘idms‘

Examples

```
convert_creat_assay(scr = c(1.1, 0.8, 0.7), from = "enzymatic", to = "jaffe")
```

convert_creat_unit *Convert creatinine to different unit*

Description

Convert creatinine to different unit

Usage

```
convert_creat_unit(value = NULL, unit_in = "mg/dL")
```

Arguments

value	serum creatinine in either mg/dL or micromol/L
unit_in	unit, either ‘mg/dL‘ or ‘micromol/L‘

Examples

```
convert_creat_unit(1)
convert_creat_unit(88.42, unit_in = "micromol/l")
```

dose2auc *Convert dose to expected AUCinf or AUCt for 1 compartment linear PK model*

Description

Convert dose to expected AUCinf or AUCt for 1 compartment linear PK model

Usage

```
dose2auc(dose, CL, V, t_auc = NULL)
```

Arguments

dose	dose amount
CL	Clearance
V	Volume of distribution
t_auc	if AUC_t is desired, ‘t_auc‘ specifies time until which AUC_t is calculated

Examples

```
dose2auc(dose = 1000, CL = 5, V = 50)
dose2auc(dose = 1000, CL = 5, V = 50, t_auc = c(12, 24, 48, 72))
```

find_nearest_dose *Generic function to calculate the dose nearest to a specific dose unit increment*

Description

Generic function to calculate the dose nearest to a specific dose unit increment

Usage

```
find_nearest_dose(dose = NULL, increment = 250, type = "round")
```

Arguments

dose	dose value
increment	available increments of dose
type	how to round, one of 'round', 'floor', or 'ceiling'

Examples

```
find_nearest_dose(573)
find_nearest_dose(573, increment = 50)
```

find_nearest_interval *Generic function to calculate the interval nearest to a possible dosing interval*

Description

Generic function to calculate the interval nearest to a possible dosing interval

Usage

```
find_nearest_interval(interval = NULL, possible = c(4, 6, 8, 12, 24, 36,
  48), type = "absolute")
```

Arguments

interval	dose value
possible	available increments of dose
type	pick either 'nearest' absolute interval, or nearest 'lower', or nearest 'higher' interval.

Examples

```
find_nearest_interval(19.7)
find_nearest_interval(19.7, c(6, 8, 12))
```

inch2cm *Convert inch to cm*

Description

Convert inch to cm

Usage

```
inch2cm(inch)
```

Arguments

inch	vector

Examples

```
inch2cm(1)
```

is.nil *Check if values in vector are empty*

Description

Check if values in vector are empty

Usage

```
is.nil(x)
```

Arguments

x	vector

kg2lbs *Convert kg to lbs*

Description

Convert kg to lbs

Usage

```
kg2lbs(kg)
```

Arguments

kg	vector

Examples

```
kg2lbs(1)
```

lbs2kg *Convert lbs to kg*

Description

Convert lbs to kg

Usage

```
lbs2kg(lbs)
```

Arguments

lbs	vector

Examples

```
lbs2kg(2.20462)
```

mol2conc *Convert molar to concentration*

Description

Convert molar to concentration

Usage

```
mol2conc(mol = NULL, unit_mol = NULL, unit_conc = NULL,
  mol_weight = NULL)
```

Arguments

mol	concentration in molars
unit_mol	unit of input concentration (molar), one of 'mol/L', 'mmol/mL', 'mmol/L'
unit_conc,	output unit, one of 'g/l', 'mg/l', 'microg/l', 'mcg/l", 'ng/l', 'mg/ml', 'microg/ml', 'mcg/ml', 'ng/ml'
mol_weight	concentration in g/mol

Examples

```
mol2conc(1, unit_mol = "mmol/l", mol_weight = 180)
```

nca *Perform an NCA based on a NONMEM-style dataset*

Description

Perform an NCA based on a NONMEM-style dataset

Usage

```
nca(data = NULL, dose = 100, tau = 6, method = "log_linear",
  scale = list(auc = 1, conc = 1), dv_min = 0.001)
```

Arguments

data	data.frame with time and dv columns
dose	dose amount
tau	dosing frequency
method	'log_linear' or 'linear'
scale	list with scaling for auc and concentration ('conc')
dv_min	minimum concentrations, lower observations will be set to this value

Examples

```
data <- data.frame(time = c(0, 2, 4, 6, 8, 12, 16),
                   dv   = c(0, 10, 14, 11, 9, 5, 1.5))
nca(data)
```

`pct_bmi_for_age` *Percentile BMI for age for children*

Description

Based on tables from WHO: http://www.who.int/growthref/who2007_bmi_for_age/en/

Usage

```
pct_bmi_for_age(age = NULL, bmi = NULL, sex = NULL, height = NULL, ...)
```

Arguments

`age`	age in years
`bmi`	bmi Optional, if specified, will calculate closest percentile and return in list as 'percentile'
`sex`	either 'male' or 'female'
`height`	height
`...`	parameters passed to 'read_who_table()'

Examples

```
pct_bmi_for_age(age = 8, sex = "male")
pct_bmi_for_age(age = 8, bmi = 15, sex = "male")
```

`pct_for_age_generic` *Percentile height or weight for age for children*

Description

This is the underlying function, the exposed functions are pct_weight_for_age() and pct_height_for_age()
Based on tables from WHO: http://www.who.int/childgrowth/standards/height_for_age/en/

Usage

```
pct_for_age_generic(age = NULL, value = NULL, sex = NULL,
  variable = "weight", ...)
```

Arguments

age	age in years
value	height in kg. Optional, if specified, will calculate closest percentile and return in list as ‘percentile‘
sex	either ‘male‘ or ‘female‘
variable	weight or height?
...	parameters passed to ‘read_who_table()‘

---

pct_height_for_age *Percentile height for age for children*

Description

Based on tables from WHO: http://www.who.int/childgrowth/standards/height_for_age/en/

Usage

```
pct_height_for_age(age = NULL, height = NULL, sex = NULL, ...)
```

Arguments

age	age in years
height	height in kg. Optional, if specified, will calculate closest percentile and return in list as ‘percentile‘
sex	either ‘male‘ or ‘female‘
...	parameters passed to ‘read_who_table()‘

Examples

```
pct_height_for_age(age = 5, sex = "female")
pct_height_for_age(age = 5, height = 112, sex = "female")
```

pct_weight_for_age *Percentile weight for age for children*

Description

Based on tables from WHO: http://www.who.int/childgrowth/standards/weight_for_age/en/

Usage

```
pct_weight_for_age(age = NULL, weight = NULL, sex = NULL, ...)
```

Arguments

age	age in years
weight	weight in kg. Optional, if specified, will calculate closest percentile and return in list as ‘percentile‘
sex	either ‘male‘ or ‘female‘
...	parameters passed to ‘read_who_table()‘

Examples

```
pct_weight_for_age(age = 5, sex = "female")
pct_weight_for_age(age = 5, weight = 20, sex = "female")
```

pk_1cmt_bolus *Concentration predictions for 1-compartmental PK model after single or multiple bolus doses*

Description

Concentration predictions for 1-compartmental PK model after single or multiple bolus doses

Usage

```
pk_1cmt_bolus(t = c(0:24), dose = 100, tau = 12, CL = 3, V = 30,
  ruv = NULL)
```

Arguments

t	vector of time
dose	dose
tau	dosing interval
CL	clearance
V	volume of distribution
ruv	residual error (list)

Examples

```
pk_1cmt_bolus(dose = 500, tau = 12, CL = 5, V = 50)
pk_1cmt_bolus(dose = 500, tau = 12, CL = 5, V = 50, t = 24)
pk_1cmt_bolus(
  dose = 500, tau = 12, CL = 5, V = 50,
  ruv = list(prop = 0.1, add = 0.1))
```

---

pk_1cmt_bolus_cmax_ss *Cmax for linear 1-compartment PK model at steady state, bolus dosing*

Description

Takes single values for dose or model parameters, or vector of either dose or parameters (but not both).

Usage

```
pk_1cmt_bolus_cmax_ss(dose = 100, tau = 12, CL = 3, V = 30,
  ruv = NULL)
```

Arguments

dose	dose
tau	dosing interval
CL	clearance
V	volume of distrubition
ruv	residual variability, specified as list with optional arguments for proportional, additive, or exponential components, e.g. 'list(prop=0.1, add=1, exp=0)'

Examples

```
pk_1cmt_bolus_cmax_ss(
  dose = 500, tau = 12, CL = 5, V = 50)
```

pk_1cmt_bolus_cmin_ss *Cmin (trough) for linear 1-compartment PK model at steady state, bolus dosing*

Description

Takes single values for dose or model parameters, or vector of either dose or parameters (but not both).

Usage

```
pk_1cmt_bolus_cmin_ss(dose = 100, tau = 12, CL = 3, V = 30,
  ruv = NULL)
```

Arguments

dose	dose
tau	dosing interval
CL	clearance
V	volume of distrubition
ruv	residual variability, specified as list with optional arguments for proportional, additive, or exponential components, e.g. 'list(prop=0.1, add=1, exp=0)'

Examples

```
pk_1cmt_bolus_cmin_ss(
  dose = 500, tau = 12, CL = 5, V = 50)
```

pk_1cmt_bolus_dose_from_cmax *Calculate dose to achieve steady state Cmax for 1-compartmental PK model bolus dosing at steady state*

Description

Calculate dose to achieve steady state Cmax for 1-compartmental PK model bolus dosing at steady state

Usage

```
pk_1cmt_bolus_dose_from_cmax(cmax = 1, tau = 12, CL = 3, V = 30)
```

Arguments

cmax	desired trough concentration
tau	dosing interval
CL	clearance
V	volume of distribution

Examples

```
dos <- pk_1cmt_bolus_dose_from_cmax(
  cmax = 10, tau = 12, CL = 5, V = 50)
find_nearest_dose(dos, 100)
```

---

pk_1cmt_bolus_dose_from_cmin

Calculate dose to achieve steady state trough for 1-compartmental PK model bolus dosing at steady state

---

Description

Calculate dose to achieve steady state trough for 1-compartmental PK model bolus dosing at steady state

Usage

```
pk_1cmt_bolus_dose_from_cmin(cmin = 1, tau = 12, CL = 3, V = 30)
```

Arguments

cmin	desired trough concentration
tau	dosing interval
CL	clearance
V	volume of distribution

Examples

```
dos <- pk_1cmt_bolus_dose_from_cmin(
  cmin = 5, tau = 12, CL = 5, V = 50)
find_nearest_dose(dos, 100)
```

pk_1cmt_bolus_ss — *Concentration predictions for 1-compartmental PK model with bolus dosing at steady state*

Description

Concentration predictions for 1-compartmental PK model with bolus dosing at steady state

Usage

```
pk_1cmt_bolus_ss(t = c(0:24), dose = 100, tau = 12, CL = 3, V = 30,
  ruv = NULL)
```

Arguments

t	vector of time
dose	dose
tau	dosing interval
CL	clearance
V	volume of distribution
ruv	residual variability, specified as list with optional arguments for proportional, additive, or exponential components, e.g. 'list(prop=0.1, add=1, exp=0)'

Examples

```
pk_1cmt_bolus_ss(dose = 500, tau = 12, CL = 5, V = 50)
pk_1cmt_bolus_ss(
  dose = 500, tau = 12, CL = 5, V = 50,
  ruv = list(prop = 0.1, add = 0.1))
```

pk_1cmt_inf — *Concentration predictions for 1-compartmental PK model after single or multiple bolus doses*

Description

Concentration predictions for 1-compartmental PK model after single or multiple bolus doses

Usage

```
pk_1cmt_inf(t = c(0:24), dose = 100, tau = 12, t_inf = 2, CL = 3,
  V = 30, ruv = NULL)
```

Arguments

t	vector of time
dose	dose
tau	dosing interval
t_inf	infusion time
CL	clearance
V	volume of distribution
ruv	residual error (list)

Examples

```
pk_1cmt_inf(dose = 500, tau = 12, t_inf = 2, CL = 5, V = 50)
pk_1cmt_inf(
  dose = 500, tau = 12, t_inf = 2, CL = 5, V = 50,
  ruv = list(prop = 0.1, add = 0.1))
```

---

pk_1cmt_inf_cmax_ss *Cmax for linear 1-compartment PK model at steady state*

Description

Takes single values for dose or model parameters, or vector of either dose or parameters (but not both).

Usage

```
pk_1cmt_inf_cmax_ss(dose, tau, CL, V, t_inf, ruv = NULL)
```

Arguments

dose	dose
tau	dosing interval
CL	clearance
V	volume of distrubition
t_inf	infusion time
ruv	residual variability, specified as list with optional arguments for proportional, additive, or exponential components, e.g. ‘list(prop=0.1, add=1, exp=0)‘

Examples

```
pk_1cmt_inf_cmax_ss(dose = 500, tau = 12, t_inf = 2, CL = 5, V = 50)
```

pk_1cmt_inf_cmin_ss *Cmin (trough) for linear 1-compartment PK model at steady state*

Description

Takes single values for dose or model parameters, or vector of either dose or parameters (but not both).

Usage

```
pk_1cmt_inf_cmin_ss(dose = 100, tau = 12, CL = 3, V = 30, t_inf = 2,
  ruv = NULL)
```

Arguments

dose	dose
tau	dosing interval
CL	clearance
V	volume of distrubition
t_inf	infusion time
ruv	residual variability, specified as list with optional arguments for proportional, additive, or exponential components, e.g. 'list(prop=0.1, add=1, exp=0)'

Examples

```
pk_1cmt_inf_cmin_ss(dose = 500, tau = 12, t_inf = 2, CL = 5, V = 50)
```

pk_1cmt_inf_dose_from_cmax *Calculate dose to achieve steady state Cmax for 1-compartmental PK model with infusion dosing at steady state*

Description

Calculate dose to achieve steady state Cmax for 1-compartmental PK model with infusion dosing at steady state

Usage

```
pk_1cmt_inf_dose_from_cmax(cmax = 1, tau = 12, t_inf = 1, CL = 3,
  V = 30)
```

Arguments

cmax	desired trough concentration
tau	dosing interval
t_inf	infusion time
CL	clearance
V	volume of distribution

Examples

```
pk_1cmt_inf_dose_from_cmax(cmax = 20, tau = 12, t_inf = 2, CL = 5, V = 50)
```

---

pk_1cmt_inf_dose_from_cmin

Calculate dose to achieve steady state trough for 1-compartmental PK model with infusion dosing at steady state

---

Description

Calculate dose to achieve steady state trough for 1-compartmental PK model with infusion dosing at steady state

Usage

```
pk_1cmt_inf_dose_from_cmin(cmin = 1, tau = 12, t_inf = 1, CL = 3,
  V = 30)
```

Arguments

cmin	desired trough concentration
tau	dosing interval
t_inf	infusion time
CL	clearance
V	volume of distribution

Examples

```
dos <- pk_1cmt_inf_dose_from_cmin(
  cmin = 20, tau = 12, t_inf = 2,
  CL = 5, V = 50)
find_nearest_dose(dos, 100)
```

pk_1cmt_inf_ss — *Concentration predictions for 2-compartmental PK model with infusion dosing at steady state*

Description

Concentration predictions for 2-compartmental PK model with infusion dosing at steady state

Usage

```
pk_1cmt_inf_ss(t = c(0:24), dose = 100, t_inf = 1, tau = 12, CL = 3,
  V = 30, ruv = NULL)
```

Arguments

t	vector of time
dose	dose
t_inf	infusion time
tau	dosing interval
CL	clearance
V	volume of distribution
ruv	residual variability, specified as list with optional arguments for proportional, additive, or exponential components, e.g. 'list(prop=0.1, add=1, exp=0)'

Examples

```
pk_1cmt_inf_ss(dose = 500, tau = 12, t_inf = 2, CL = 5, V = 50)
pk_1cmt_inf_ss(
  dose = 500, tau = 12, t_inf = 2, CL = 5, V = 50,
  ruv = list(prop = 0.1, add = 0.1))
```

pk_1cmt_oral — *Concentration predictions for 1-compartmental oral PK model after single or multiple bolus doses*

Description

Concentration predictions for 1-compartmental oral PK model after single or multiple bolus doses

Usage

```
pk_1cmt_oral(t = c(0:24), dose = 100, tau = 12, KA = 1, CL = 3,
  V = 30, F = 1, ruv = NULL)
```

Arguments

t	vector of time
dose	dose
tau	dosing interval
KA	absorption rate
CL	clearance
V	volume of distribution
F	bioavailability, commonly between 0 an 1.
ruv	residual error (list)

References

Garrett ER. The Bateman function revisited: a critical reevaluation of the quantitative expressions to characterize concentrations in the one compartment body model as a function of time with first-order invasion and first-order elimination. J Pharmacokinet Biopharm (1994) 22(2):103-128.

Bialer M. A simple method for determining whether absorption and elimination rate constants are equal in the one-compartment open model with first-order processes. J Pharmacokinet Biopharm (1980) 8(1):111-113

Nielsen JC, Hutmacher MM et al. J Pharmacokinet Pharmacodyn. 2012 Dec;39(6):619-34. doi: 10.1007/s10928-012-9274-0. Epub 2012 Sep 23.

https://static-content.springer.com/esm/art

Examples

```
pk_1cmt_oral(dose = 500, tau = 12, CL = 5, V = 50, KA = 1)
```

---

pk_1cmt_t12 *Calculate terminal half-life for 1-compartment model*

Description

Calculate terminal half-life for 1-compartment model

Usage

```
pk_1cmt_t12(CL = 3, V = 30)
```

Arguments

CL	clearance
V	volume of central compartment

Examples

```
pk_1cmt_t12(CL = 5, V = 50)
```

pk_2cmt_bolus *Concentration predictions for 1-compartmental PK model, single or multiple bolus doses*

Description

Concentration predictions for 1-compartmental PK model, single or multiple bolus doses

Usage

```
pk_2cmt_bolus(t = c(0:24), dose = 100, tau = 12, CL = 3, V = 30,
  Q = 2, V2 = 20, ruv = NULL)
```

Arguments

t	vector of time
dose	dose
tau	dosing interval
CL	clearance
V	volume of central compartment
Q	inter-compartimental clearance
V2	volume of peripheral compartment
ruv	residual error (list)

Examples

```
pk_2cmt_bolus(dose = 1000, tau = 24, CL = 5, V = 50, Q = 15, V2 = 200)
```

pk_2cmt_bolus_cmax_ss *Cmax for 2-compartmental PK model, bolus dosing at steady state*

Description

Cmax for 2-compartmental PK model, bolus dosing at steady state

Usage

```
pk_2cmt_bolus_cmax_ss(dose = 100, tau = 12, CL = 3, V = 30, Q = 2,
  V2 = 20, ruv = NULL)
```

Arguments

dose	dose
tau	dosing interval
CL	clearance
V	volume of central compartment
Q	inter-compartimental clearance
V2	volume of peripheral compartment
ruv	residual error (list)

Examples

```
pk_2cmt_bolus_cmax_ss(dose = 1000, tau = 12, CL = 5, V = 50, Q = 20, V2 = 200)
```

---

pk_2cmt_bolus_cmin_ss *Cmin (trough) for 2-compartmental PK model, bolus dosing at steady state*

Description

Cmin (trough) for 2-compartmental PK model, bolus dosing at steady state

Usage

```
pk_2cmt_bolus_cmin_ss(dose = 100, tau = 12, CL = 3, V = 30, Q = 2,
  V2 = 20, ruv = NULL)
```

Arguments

dose	dose
tau	dosing interval
CL	clearance
V	volume of central compartment
Q	inter-compartimental clearance
V2	volume of peripheral compartment
ruv	residual error (list)

Examples

```
pk_2cmt_bolus_cmin_ss(dose = 1000, tau = 12, CL = 5, V = 50, Q = 20, V2 = 200)
```

pk_2cmt_bolus_dose_from_cmax

Calculate dose to achieve steady state Cmax for 2-compartmental PK model bolus dosing at steady state

Description

Calculate dose to achieve steady state Cmax for 2-compartmental PK model bolus dosing at steady state

Usage

```
pk_2cmt_bolus_dose_from_cmax(cmax = 1, tau = 12, CL = 3, V = 30,
  Q = 2, V2 = 20)
```

Arguments

cmax	desired trough concentration
tau	dosing interval
CL	clearance
V	volume of distribution
Q	inter-compartimental clearance
V2	volume of peripheral compartment

Examples

```
dos <- pk_2cmt_bolus_dose_from_cmax(
  cmax = 10, tau = 12,
  CL = 5, V = 50, Q = 20, V2 = 200)
find_nearest_dose(dos, 100)
```

pk_2cmt_bolus_dose_from_cmin

Calculate dose to achieve steady state trough for 2-compartmental PK model bolus dosing at steady state

Description

Calculate dose to achieve steady state trough for 2-compartmental PK model bolus dosing at steady state

Usage

```
pk_2cmt_bolus_dose_from_cmin(cmin = 1, tau = 12, CL = 3, V = 30,
  Q = 2, V2 = 20)
```

Arguments

cmin	desired trough concentration
tau	dosing interval
CL	clearance
V	volume of distribution
Q	inter-compartimental clearance
V2	volume of peripheral compartment

Examples

```
dos <- pk_2cmt_bolus_dose_from_cmin(
  cmin = 5, tau = 12,
  CL = 5, V = 50, Q = 20, V2 = 200)
find_nearest_dose(dos, 100)
```

---

pk_2cmt_bolus_ss *Concentration predictions for 2-compartmental PK model, bolus dosing at steady state*

Description

Concentration predictions for 2-compartmental PK model, bolus dosing at steady state

Usage

```
pk_2cmt_bolus_ss(t = c(0:24), dose = 100, tau = 12, CL = 3, V = 30,
  Q = 2, V2 = 20, ruv = NULL)
```

Arguments

t	vector of time
dose	dose
tau	dosing interval
CL	clearance
V	volume of central compartment
Q	inter-compartimental clearance
V2	volume of peripheral compartment
ruv	residual error (list)

Examples

```
pk_2cmt_bolus_ss(dose = 1000, tau = 12, CL = 5, V = 50, Q = 20, V2 = 200)
```

pk_2cmt_inf — *Concentration predictions for 1-compartmental PK model, single or multiple infusions*

Description

Concentration predictions for 1-compartmental PK model, single or multiple infusions

Usage

```
pk_2cmt_inf(t = c(0:24), dose = 100, tau = 12, t_inf = 1, CL = 3,
  V = 30, Q = 2, V2 = 20, ruv = NULL)
```

Arguments

t	vector of time
dose	dose
tau	dosing interval
t_inf	infusion time
CL	clearance
V	volume of central compartment
Q	inter-compartimental clearance
V2	volume of peripheral compartment
ruv	residual error (list)

pk_2cmt_inf_cmax_ss — *Cmax (trough) for 2-compartmental PK model, bolus dosing at steady state*

Description

Cmax (trough) for 2-compartmental PK model, bolus dosing at steady state

Usage

```
pk_2cmt_inf_cmax_ss(dose = 100, tau = 12, t_inf = 1, CL = 3, V = 30,
  Q = 2, V2 = 20, ruv = NULL)
```

Arguments

dose	dose
tau	dosing interval
t_inf	infusion time
CL	clearance
V	volume of central compartment
Q	inter-compartimental clearance
V2	volume of peripheral compartment
ruv	residual error (list)

Examples

```
pk_2cmt_inf_cmax_ss(
  dose = 1000, tau = 12, t_inf = 2,
  CL = 5, V = 50, Q = 20, V2 = 200)
```

---

pk_2cmt_inf_cmin_ss *Cmin (trough) for 2-compartmental PK model, bolus dosing at steady state*

Description

Cmin (trough) for 2-compartmental PK model, bolus dosing at steady state

Usage

```
pk_2cmt_inf_cmin_ss(dose = 100, tau = 12, t_inf = 1, CL = 3, V = 30,
  Q = 2, V2 = 20, ruv = NULL)
```

Arguments

dose	dose
tau	dosing interval
t_inf	infusion time
CL	clearance
V	volume of central compartment
Q	inter-compartimental clearance
V2	volume of peripheral compartment
ruv	residual error (list)

Examples

```
pk_2cmt_inf_cmin_ss(
  dose = 1000, tau = 12, t_inf = 2,
  CL = 5, V = 50, Q = 20, V2 = 200)
```

pk_2cmt_inf_dose_from_cmax

Calculate dose to achieve steady state Cmax for 2-compartmental PK model with infusion dosing at steady state

Description

Calculate dose to achieve steady state Cmax for 2-compartmental PK model with infusion dosing at steady state

Usage

```
pk_2cmt_inf_dose_from_cmax(cmax = 1, tau = 12, t_inf = 1, CL = 3,
  V = 30, Q = 2, V2 = 20)
```

Arguments

cmax	desired trough concentration
tau	dosing interval
t_inf	infusion time
CL	clearance
V	volume of distribution
Q	inter-compartimental clearance
V2	volume of peripheral compartment

Examples

```
dos <- pk_2cmt_inf_dose_from_cmax(
  cmax = 25, tau = 12, t_inf = 2,
  CL = 5, V = 50, Q = 20, V2 = 200)
find_nearest_dose(dos, 100)
```

pk_2cmt_inf_dose_from_cmin

Calculate dose to achieve steady state trough for 2-compartmental PK model with infusion dosing at steady state

Description

Calculate dose to achieve steady state trough for 2-compartmental PK model with infusion dosing at steady state

Usage

```
pk_2cmt_inf_dose_from_cmin(cmin = 1, tau = 12, t_inf = 1, CL = 3,
  V = 30, Q = 2, V2 = 20)
```

Arguments

cmin	desired trough concentration
tau	dosing interval
t_inf	infusion time
CL	clearance
V	volume of distribution
Q	inter-compartimental clearance
V2	volume of peripheral compartment

Examples

```
dos <- pk_2cmt_inf_dose_from_cmin(
  cmin = 10, tau = 12, t_inf = 2,
  CL = 5, V = 50, Q = 20, V2 = 200)
find_nearest_dose(dos, 100)
```

---

pk_2cmt_inf_ss *Concentration predictions for 1-compartmental PK model with infusion dosing at steady state*

Description

Concentration predictions for 1-compartmental PK model with infusion dosing at steady state

Usage

```
pk_2cmt_inf_ss(t = c(0:24), dose = 100, t_inf = 1, tau = 12, CL = 3,
  V = 30, Q = 2, V2 = 20, ruv = NULL)
```

Arguments

t	vector of time
dose	dose
t_inf	infusion time
tau	dosing interval
CL	clearance
V	volume of distribution
Q	inter-compartimental clearance
V2	volume of peripheral compartment
ruv	residual variability, specified as list with optional arguments for proportional, additive, or exponential components, e.g. ‘list(prop=0.1, add=1, exp=0)‘

Examples

```
pk_2cmt_inf_ss(
  dose = 1000, tau = 12, t_inf = 2,
  CL = 5, V = 50, Q = 20, V2 = 200)
```

---

pk_2cmt_t12 *Calculate half-life(s) for 2-compartment model*

Description

Calculate half-life(s) for 2-compartment model

Usage

```
pk_2cmt_t12(CL = 3, V = 30, Q = 2, V2 = 20, phase = "both")
```

Arguments

CL	clearance
V	volume of central compartment
Q	inter-compartimental clearance
V2	volume of peripheral compartment
phase	'alpha', 'beta' (default) or 'both' to indicate initial (distribution) or terminal (elimination) phase.

Examples

```
pk_2cmt_t12(CL = 5, V = 50, Q = 20, V2 = 200)
```

---

pk_2cmt_t12_interval *Calculate average half-life for 2-compartment model during a specific interval*

Description

Calculate average half-life for 2-compartment model during a specific interval

Usage

```
pk_2cmt_t12_interval(CL = 3, V = 30, Q = 2, V2 = 20, tau = 12,
  t_inf = NULL)
```

Arguments

CL	clearance
V	volume of central compartment
Q	inter-compartimental clearance
V2	volume of peripheral compartment
tau	interval (hours)
t_inf	infusion time (hours)

Examples

```
pk_2cmt_t12_interval(CL = 5, V = 50, Q = 20, V2 = 200, tau = 12, t_inf = 2)
```

---

read_who_table *Internal function to read WHO growth tables from package or download from WHO*

Description

Internal function to read WHO growth tables from package or download from WHO

Usage

```
read_who_table(sex = NULL, age = NULL, type = "wfa",
  who_url = "http://www.who.int/entity/childgrowth/standards",
  download = FALSE)
```

Arguments

sex,	either ‘male‘ or ‘female‘
age	age in years
type	table type, choose from ‘wfa‘ (weight for age), ‘lhfa‘ (length for age)
who_url	base URL for WHO growth tables
download	download current tables from WHO?

`weight2kg` *Convert any weight unit to kg*

Description

Convert any weight unit to kg

Usage

```
weight2kg(value = NULL, unit = NULL)
```

Arguments

`value`	weight in any allowed unit
`unit`	unit of weight, one of "lbs", "pound", "pounds", "oz", "ounce", "ounces"

Examples

```
weight2kg(250, unit = "oz")
weight2kg(250, unit = "pounds")
weight2kg(250, unit = "lbs")
```

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