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DESCRIPTION

```
Package: TGRmodel
Title: Functions to predict Tumor Growth Rate inhibition using in vitro data
Version: 0.0.1.0
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Description: Functions to predict Tumor Growth Rate inhibition using in vitro data.
    Model described in the manuscript "Growth-rate model predicts in vivo tumor response from in vitro
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```

.integration_step

step for the numerical integration

Description

step for the numerical integration

Usage

```
.integration_step()
```

GR_inVitro_integration

GR_inVitro_integration Calculate relative tumor growth inhibition (TGR) based on conc_profile

Description

Calculate the serum concentration profile based on the drug PK, dose, and schedule. The concentration (in µM) is calculated based on one-compartment PK model with parameters k_a and k_e provided in the input variable PK_para.

Usage

```
GR_inVitro_integration(conc_profile, GR_para, int_method = "mean")
```

Arguments

Argument	Description
`conc_profile`	data.frame with `Time` (in days) and relative growth rate `k` over time can be the output of `PK_to_conc_profile`

Argument	Description
GR_para	numeric array for the in vitro GR parameters of the drug (required fields: GR_inf, GEC50, h_GR) Can calculate the average of multiple parameters at the same time given multiple rows in GR_para
int_method	string to define the type of integration

Value

numeric value for relative tumor growth rate (TGR)

Examples

```
## regular QD treatment

PK_para = data.frame(k_a = 2, k_e = 0.25, MW = 450, VF = 1)
GR_para = data.frame(GR_inf = -0.5, GEC50 = 0.3, h_GR = 1.5)
Schedule = "QD"
Duration = 21
Dose = 5
conc_profile = PK_to_conc_profile(PK_para, Dose, Schedule, Duration)
relk_1 = relk_over_time(GR_para, conc_profile)
GR_predicted = GR_inVitro_integration(conc_profile, GR_para)
```

logistic_4parameters

logistic function for fitting drug-dose response curve

Description

logistic_4parameters returns values based on concentration and fit parameters

Usage

```
logistic_4parameters(c, Vinf, V0, EC50, h)
```

Arguments

Argument	Description
c	concentration (can be an array)
Vinf	asymptotic value at high concentration
V0	asymptotic value at low concentration
EC50	mid-point of the curve
h	Hill coefficient

Details

returns values based on concentration and fit parameters

Value

array of response values

logisticFit

Actual fitting function

Description

`logisticFit` returns fit parameters for an IC or GR curve

Usage

```
logisticFit(
  concs,
  normValues,
  x_0 = 1,
  curve_type = c("IC", "GR"),
  force = FALSE,
  cap = 0.1
)
```

Arguments

Argument	Description
`concs`	concentration values
`normValues`	normalized response values
`x_0`	upper limit; (=1 by default)
`curve_type`	response curve: either IC (0,1) or GR(-1,1)
`force`	force a sigmoidal fit even if the fit is not significantly better than a flat fit
`cap`	cap values at (x_0 + cap)

Details

returns fit parameters

Value

vector of parameters

PK_to_conc_profile

PK_to_conc_profile Calculate the serum concentration profile based on the drug PK, dose, and schedule

Description

Calculate the serum concentration profile based on the drug PK, dose, and schedule. The concentration (in µM) is calculated based on one-compartment PK model with parameters k_a and k_e provided in the input variable PK_para.

Usage

```
PK_to_conc_profile(PK_para, Dose, Schedule, Duration, Dose_uM_0 = 0)
```

Arguments

Argument	Description
`PK_para`	numeric array for the PK properties of the drug (required fields: MW, VF, k_a, k_e)

- 'MW' molecular weight in g/mol
- 'VF' distribution volume in L/kg
- 'k_a' absoption rate in 1/h
- 'k_e' elimination rate in 1/h `Dose` | numeric values for the dose of the drug given in mg/kg `Schedule` | string for the frequency of the treatment given (QC, BID or EOD) `Duration` | numeric value for the duration of the treatment (in days) `Dose_uM_0` | numeric value for the initial serum concentration (in µM) Defaults to `0` .

Value

list with `Time` (in days) and `Conc` serum concentration (in µM) and `dose_period` for the dosing schedule

relk_fct

expanding GR function for rate based on concentration

Description

expanding GR function for rate based on concentration

Usage

```
relk_fct(c, GR_para)
```

relk_over_time

relk_over_time Calculate the serum concentration profile based on the drug PK, dose, and schedule

Description

Calculate the serum concentration profile based on the drug PK, dose, and schedule. The concentration (in µM) is calculated based on one-compartment PK model with parameters k_a and k_e provided in the input variable PK_para.

Usage

```
relk_over_time(GR_para, conc_profile)
```

Arguments

Argument	Description
`GR_para`	numeric array for the in vitro GR parameters of the drug (required fields: `GR_inf` , `GEC50` , `h_GR`)
`conc_profile`	data.frame with `Time` (in days) and `Conc` (serum concentration in µM) can be the output of PK_to_conc_profile

Value

data.frame with `Time` (in days) and relative growth rate `k` over time