

# Package ‘NonCompart’

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**Title** Noncompartmental Analysis for Pharmacokinetic Data

**Description** Conduct a noncompartmental analysis with industrial strength.

Some features are

- 1) Use of CDISC SDTM terms
- 2) Automatic or manual slope selection
- 3) Supporting both 'linear-up linear-down' and 'linear-up log-down' method
- 4) Interval(partial) AUCs with 'linear' or 'log' interpolation method

\* Reference: Gabrielsson J, Weiner D. Pharmacokinetic and Pharmacodynamic Data Analysis - Concepts and Applications. 5th ed. 2016. (ISBN:9198299107).

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## R topics documented:

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|                    |                                                           |
|--------------------|-----------------------------------------------------------|
| NonCompart-package | <i>Noncompartmental Analysis for Pharmacokinetic Data</i> |
|--------------------|-----------------------------------------------------------|

---

## Description

It conducts a noncompartmental analysis(NCA) with industrial strength.

## Details

The main functions are

tblNCA to perform NCA for many subjects.

sNCA to perform NCA for one subject.

## Author(s)

Kyun-Seop Bae <k@acr.kr>

## References

1. Gabrielsson J, Weiner D. Pharmacokinetic and Pharmacodynamic Data Analysis - Concepts and Applications. 5th ed. 2016.
2. Shargel L, Yu A. Applied Biopharmaceutics and Pharmacokinetics. 7th ed. 2015.
3. Rowland M, Tozer TN. Clinical Pharmacokinetics and Pharmacodynamics - Concepts and Applications. 4th ed. 2011.
4. Gibaldi M, Perrier D. Pharmacokinetics. 2nd ed. revised and expanded. 1982.

## Examples

```
# Theoph and Indometh data: dose in mg, conc in mg/L, time in h
tblNCA(Theoph, key="Subject", colTime="Time", colConc="conc", dose=320,
      adm="Extravascular", doseUnit="mg", concUnit="mg/L")

tblNCA(Indometh, key="Subject", colTime="time", colConc="conc", dose=25,
      adm="Infusion", dur=0.5, doseUnit="mg", concUnit="mg/L", R2ADJ=0.9)
```

```
# For individual NCA
iAUC = data.frame(Name=c("AUC[0-12h]", "AUC[0-24h]"), Start=c(0,0), End=c(12,24)) ; iAUC

x = Theoph[Theoph$Subject=="1", "Time"]
y = Theoph[Theoph$Subject=="1", "conc"]

sNCA(x, y, dose=320, doseUnit="mg", concUnit="mg/L", timeUnit="h", iAUC=iAUC)
sNCA(x, y, dose=320, concUnit="mg/L", iAUC=iAUC)
```

---

|     |                                                                                                            |
|-----|------------------------------------------------------------------------------------------------------------|
| AUC | <i>Calculate Area Under the Curve (AUC) and Area Under the first Moment Curve (AUMC) in a table format</i> |
|-----|------------------------------------------------------------------------------------------------------------|

---

### Description

Calculate Area Under the Curve(AUC) and the first Moment Curve(AUMC) in two ways; 'linear trapezoidal method' or 'linear-up and log-down' method. Return a table of cumulative values.

### Usage

```
AUC(x, y, down = "Linear")
```

### Arguments

|      |                                                                           |
|------|---------------------------------------------------------------------------|
| x    | vector values of independent variable, usually time                       |
| y    | vector values of dependent variable, usually concentration                |
| down | either of "Linear" or "Log" to indicate the way to calculate AUC and AUMC |

### Details

down="Linear" means linear trapezoidal rule with linear interpolation. down="Log" means linear-up and log-down method.

### Value

Table with two columns, AUC and AUMC; the first column values are cumulative AUCs and the second column values cumulative AUMCs.

### Author(s)

Kyun-Seop Bae <k@acr.kr>

### References

Rowland M, Tozer TN. Clinical Pharmacokinetics and Pharmacodynamics - Concepts and Applications. 4th ed. pp687-689. 2011.

**See Also**

[LinAUC](#), [LogAUC](#)

**Examples**

```
AUC(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"])
AUC(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"], down="Log")
```

---

|           |                                                                                                        |
|-----------|--------------------------------------------------------------------------------------------------------|
| BestSlope | <i>Choose the best-fit slope for the log(y) and x regression by the criteria of adjusted R-square.</i> |
|-----------|--------------------------------------------------------------------------------------------------------|

---

**Description**

It sequentially fits  $\log(y) \sim x$  from the last point of x to the previous points with at least 3 points. It chooses a slope the highest adjusted R-square. If the difference is less than  $1e-4$ , it picks longer slope.

**Usage**

```
BestSlope(x, y, adm = "Extravascular", TOL=1e-4, excludeDelta = 1)
```

**Arguments**

|              |                                                                                                                                         |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| x            | vector values of x-axis, usually time                                                                                                   |
| y            | vector values of y-axis, usually concentration                                                                                          |
| adm          | one of "Bolus" or "Infusion" or "Extravascular" to indicate drug administration mode                                                    |
| TOL          | tolerance. See Phoenix WinNonlin 6.4 User's Guide p33 for the detail.                                                                   |
| excludeDelta | Improvement of R2ADJ larger than this value could exclude the last point. Default value 1 is for the compatibility with other software. |

**Details**

Choosing the best terminal slope (y in log scale) in pharmacokinetic analysis is somewhat challenging, and it could vary by analysis performer. Phoenix WinNonlin chooses a slope with highest adjusted R-squared and the longest one. The difference of adjusted R-Squared less than TOL considered to be 0. This function uses ordinary least square method (OLS). Author recommends to use excludeDelta option with about 0.3.

Value

|         |                                                                                      |
|---------|--------------------------------------------------------------------------------------|
| R2      | R-squared                                                                            |
| R2ADJ   | adjusted R-squared                                                                   |
| LAMZNPT | number of points used for slope                                                      |
| LAMZ    | negative of the slope, lambda_z                                                      |
| b0      | intercept of the regression line                                                     |
| CORRXY  | correlation of log(y) and x                                                          |
| LAMZLL  | earliest x for lambda_z                                                              |
| LAMZUL  | last x for lambda_z                                                                  |
| CLSTP   | predicted y value at the last point, predicted concentration for the last time point |

Author(s)

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See Also

[Slope](#)

Examples

```
BestSlope(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"])
BestSlope(Indometh[Indometh$Subject==1, "time"], Indometh[Indometh$Subject==1, "conc"],
          adm="Bolus")
```

---

|          |                                                                 |
|----------|-----------------------------------------------------------------|
| DetSlope | <i>Determine slope for the log(y) and x regression manually</i> |
|----------|-----------------------------------------------------------------|

---

Description

You choose a slope for terminal half-life.

Usage

```
DetSlope(x, y, SubTitle="", sel.1=0, sel.2=0)
```

Arguments

|          |                                                |
|----------|------------------------------------------------|
| x        | vector values of x-axis, usually time          |
| y        | vector values of y-axis, usually concentration |
| SubTitle | subtitle to be shown on the plot               |
| sel.1    | default index of the first element to use      |
| sel.2    | default index of the last element to use       |

Details

Sometimes BestSlope cannot find terminal slope satisfactorily. Then you can use this function to choose manually. It returns the same format result with BestSlope with an attribute indicating used points.

Value

|         |                                                                                      |
|---------|--------------------------------------------------------------------------------------|
| R2      | R-squared                                                                            |
| R2ADJ   | adjusted R-squared                                                                   |
| LAMZNPT | number of points used for the slope                                                  |
| LAMZ    | negative of the slope, lambda_z                                                      |
| b0      | intercept of the regression line                                                     |
| CORRXY  | correlation of log(y) and x                                                          |
| LAMZLL  | earliest x for lambda_z                                                              |
| LAMZUL  | last x for lambda_z                                                                  |
| CLSTP   | predicted y value at the last point, predicted concentration for the last time point |

Author(s)

Kyun-Seop Bae <k@acr.kr>

See Also

[Slope](#)

Examples

```
DetSlope(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"])
DetSlope(Indometh[Indometh$Subject==2, "time"], Indometh[Indometh$Subject==2, "conc"])
```

---

|      |                                     |
|------|-------------------------------------|
| gAUC | <i>General Area Under the Curve</i> |
|------|-------------------------------------|

---

Description

General AUC function for Emax, TEmax and AUCs

Usage

```
gAUC(x, y, Ymax = "Emax", XofYmax = "TEmax", AUCname = "AUEClast", iAUC = "",
      Outer = "NEAREST")
```

**Arguments**

|         |                                                        |
|---------|--------------------------------------------------------|
| x       | usually time                                           |
| y       | usually concentration or effect. This can be negative/ |
| Ymax    | usually Cmax or Emax                                   |
| XofYmax | usually Tmax or TEmax                                  |
| AUCname | usually AUClast or AUEClast                            |
| iAUC    | a data.frame to calculate interval AUCs                |
| Outer   | indicates how to do the out of x range point           |

**Details**

This is a general purpose AUC function. It calculates only Cmax(Emax), Tmax(TEmax) and AUCs(AUECs). This can be used for effect(pharmacodynamic) data which has negative values. For concentration data, use IntAUC.

**Value**

Column names can vary according to the options.

|          |                                 |
|----------|---------------------------------|
| Emax     | maximum y value                 |
| TEmax    | x value at the maximum y value  |
| AUEClast | Area under the y versus x curve |
| iAUCs    | Columns from iAUC input         |

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**Examples**

```
# For one subject
x = Theoph[Theoph$Subject=="1", "Time"]
y = Theoph[Theoph$Subject=="1", "conc"]
gAUC(x, y)

iAUC = data.frame(Name=c("AUC[0-12h]", "AUC[0-24h]"), Start=c(0,0), End=c(12,24))
gAUC(x, y, iAUC=iAUC)
```

gIntAUC

*Calculate interval AUC of general form***Description**

It calculates interval AUC of general form. This is useful for pharmacodynamic data.

**Usage**

```
gIntAUC(x, y, t1, t2, Outer = "NEAREST")
```

**Arguments**

|       |                                                            |
|-------|------------------------------------------------------------|
| x     | vector values of independent variable, usually time        |
| y     | vector values of dependent variable, usually concentration |
| t1    | start time for AUC                                         |
| t2    | end time for AUC                                           |
| Outer | indicates how to do the out of x range point               |

**Details**

This calculates an interval (partial) AUC (from t1 to t2) with the given series of x and y. If t1 and/or t2 cannot be found within x vector, it interpolates. If t1 and/or t2 are out of x range, it uses the nearest value. For concentration data, use IntAUC.

**Value**

return interval AUC value (scalar)

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**See Also**

[gAUC](#), [gInterpol](#), [tblAUC](#)

**Examples**

```
gIntAUC(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"], t1=0.5, t2=11)
```



---

`gInterpol`*Interpolate y value for general y value not for concentration*

---

**Description**

It interpolates y value when a corresponding x value (xnew) does not exist within x vector

**Usage**

```
gInterpol(x, y, xnew, Outer="NEAREST")
```

**Arguments**

|       |                                                        |
|-------|--------------------------------------------------------|
| x     | vector values of x-axis, usually time                  |
| y     | vector values of y-axis, usually concentration         |
| xnew  | new x point to be interpolated, usually new time point |
| Outer | indicates how to do the out of x range point           |

**Details**

This function interpolate y value, if xnew is not in x vector. If xnew is in the x vector, it just returns the given x and y vector. This function usually is called by gIntAUC function. Returned vector is sorted in the order of increasing x values.

**Value**

new x and y vector containing xnew and ynew point

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**See Also**

[gIntAUC](#)

**Examples**

```
x = 1:10 + 0.1
y = -2*x + 40.2
gInterpol(x, y, 1.5)
gInterpol(x, y, 0.5) # Out of range, Left
gInterpol(x, y, 11) # Out of range, Left
```

---

|        |                               |
|--------|-------------------------------|
| IntAUC | <i>Calculate interval AUC</i> |
|--------|-------------------------------|

---

**Description**

It calculates interval AUC

**Usage**

```
IntAUC(x, y, t1, t2, Res, down = "Linear")
```

**Arguments**

|      |                                                                  |
|------|------------------------------------------------------------------|
| x    | vector values of independent variable, usually time              |
| y    | vector values of dependent variable, usually concentration       |
| t1   | start time for AUC                                               |
| t2   | end time for AUC                                                 |
| Res  | result from sNCA function                                        |
| down | either of "Linear" or "Log" to indicate the way to calculate AUC |

**Details**

This calculates an interval (partial) AUC (from t1 to t2) with the given series of x and y. If t1 and/or t2 cannot be found within x vector, it interpolates according to the down option.

**Value**

return interval AUC value (scalar)

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**References**

1. Gabrielsson J, Weiner D. Pharmacokinetic and Pharmacodynamic Data Analysis - Concepts and Applications. 5th ed. 2016.
2. Shargel L, Yu A. Applied Biopharmaceutics and Pharmacokinetics. 7th ed. 2015.
3. Rowland M, Tozer TN. Clinical Pharmacokinetics and Pharmacodynamics - Concepts and Applications. 4th ed. 2011.
4. Gibaldi M, Perrier D. Pharmacokinetics. 2nd ed. revised and expanded. 1982.

**See Also**

[AUC](#), [Interpol](#)

**Examples**

```
Res = sNCA(Theoph[Theoph$Subject==1,"Time"], Theoph[Theoph$Subject==1, "conc"],
           dose=320, concUnit="mg/L")
IntAUC(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"], t1=0.5, t2=11, Res)
```

---

|          |                            |
|----------|----------------------------|
| Interpol | <i>Interpolate y value</i> |
|----------|----------------------------|

---

**Description**

It interpolates y value when a corresponding x value (xnew) does not exist within x vector

**Usage**

```
Interpol(x, y, xnew, Slope, b0, down = "Linear")
```

**Arguments**

|       |                                                                |
|-------|----------------------------------------------------------------|
| x     | vector values of x-axis, usually time                          |
| y     | vector values of y-axis, usually concentration                 |
| xnew  | new x point to be interpolated, usually new time point         |
| Slope | slope of regression $\log(y) \sim x$                           |
| b0    | y value of just left point of xnew                             |
| down  | either of "Linear" or "Log" to indicate the way to interpolate |

**Details**

This function interpolate y value, if xnew is not in x vector. If xnew is in x vector, it just returns the given x and y vector. This function usually is called by IntAUC function. Returned vector is sorted in the order of increasing x values.

**Value**

new x and y vector containing xnew and ynew point

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**See Also**

[IntAUC](#)

**Examples**

```
x = 10:1 + 0.1
y = -2*x + 40.2
Interpol(x, y, 1.5)
Interpol(x, y, 1.5, down="Log")
```

---

|        |                                                                                                           |
|--------|-----------------------------------------------------------------------------------------------------------|
| LinAUC | <i>Area Under the Curve(AUC) and Area Under the first Moment Curve(AUMC) by linear trapezoidal method</i> |
|--------|-----------------------------------------------------------------------------------------------------------|

---

**Description**

It calculates AUC and AUMC using the linear trapezoidal method

**Usage**

```
LinAUC(x, y)
```

**Arguments**

|   |                                                                |
|---|----------------------------------------------------------------|
| x | vector values of the independent variable, usually time        |
| y | vector values of the dependent variable, usually concentration |

**Details**

This function returns AUC and AUMC by the linear trapezoidal method.

**Value**

|      |                                   |
|------|-----------------------------------|
| AUC  | area under the curve              |
| AUMC | area under the first moment curve |

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**References**

1. Gabrielsson J, Weiner D. Pharmacokinetic and Pharmacodynamic Data Analysis - Concepts and Applications. 5th ed. 2016.
2. Shargel L, Yu A. Applied Biopharmaceutics and Pharmacokinetics. 7th ed. 2015.
3. Rowland M, Tozer TN. Clinical Pharmacokinetics and Pharmacodynamics - Concepts and Applications. 4th ed. 2011.
4. Gibaldi M, Perrier D. Pharmacokinetics. 2nd ed. revised and expanded. 1982.

**See Also**

[LogAUC](#), [AUC](#)

**Examples**

```
LinAUC(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"])
AUC(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"]) # compare the last line
```

---

|        |                                                                                                           |
|--------|-----------------------------------------------------------------------------------------------------------|
| LogAUC | <i>Area Under the Curve(AUC) and Area Under the first Moment Curve(AUMC) by linear-up log-down method</i> |
|--------|-----------------------------------------------------------------------------------------------------------|

---

**Description**

It calculates AUC and AUMC using the linear-up log-down method

**Usage**

```
LogAUC(x, y)
```

**Arguments**

|   |                                                                |
|---|----------------------------------------------------------------|
| x | vector values of the independent variable, usually time        |
| y | vector values of the dependent variable, usually concentration |

**Details**

This function returns AUC and AUMC by the linear-up log-down method.

**Value**

|      |                                   |
|------|-----------------------------------|
| AUC  | area under the curve              |
| AUMC | area under the first moment curve |

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**References**

1. Gabrielsson J, Weiner D. Pharmacokinetic and Pharmacodynamic Data Analysis - Concepts and Applications. 5th ed. 2016.
2. Shargel L, Yu A. Applied Biopharmaceutics and Pharmacokinetics. 7th ed. 2015.
3. Rowland M, Tozer TN. Clinical Pharmacokinetics and Pharmacodynamics - Concepts and Applications. 4th ed. 2011.
4. Gibaldi M, Perrier D. Pharmacokinetics. 2nd ed. revised and expanded. 1982.

**See Also**

[LinAUC,AUC](#)

**Examples**

```
LogAUC(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"])
# Compare the last line with the above
AUC(Theoph[Theoph$Subject==1, "Time"], Theoph[Theoph$Subject==1, "conc"], down="Log")
```

---

Slope*Get the Slope of regression  $\log(y) \sim x$* 

---

**Description**

It calculates the slope with linear regression of  $\log(y) \sim x$

**Usage**

Slope(x, y)

**Arguments**

|   |                                                                |
|---|----------------------------------------------------------------|
| x | vector values of the independent variable, usually time        |
| y | vector values of the dependent variable, usually concentration |

**Details**

With time-concentration curve, you frequently need to estimate slope in  $\log(\text{concentration}) \sim \text{time}$ . This function is usually called by BestSlope function, and you seldom need to call this function directly.

**Value**

|         |                                  |
|---------|----------------------------------|
| R2      | R-squared                        |
| R2ADJ   | adjusted R-squared               |
| LAMZNPT | number of points used for slope  |
| LAMZ    | negative of the slope, lambda_z  |
| b0      | intercept of the regression line |
| CORRXY  | correlation of $\log(y)$ and x   |
| LAMZLL  | earliest x for lambda_z          |
| LAMZUL  | last x for lambda_z              |

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**See Also**

[BestSlope](#)

**Examples**

```
Slope(Indometh[Indometh$Subject==1, "time"], Indometh[Indometh$Subject==1, "conc"])
```

sNCA

*Simplest NCA***Description**

This is the work-horse function for NCA.

**Usage**

```
sNCA(x, y, dose = 0, adm = "Extravascular", dur = 0, doseUnit = "mg", timeUnit = "h",
     concUnit = "ug/L", iAUC = "", down = "Linear", R2ADJ = 0.7, MW = 0, Keysting="",
     excludeDelta = 1)
```

**Arguments**

|              |                                                                                                                                         |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| x            | usually time                                                                                                                            |
| y            | usually concentration                                                                                                                   |
| dose         | given amount, not amount per body weight                                                                                                |
| adm          | one of "Bolus" or "Infusion" or "Extravascular" to indicate drug administration mode                                                    |
| dur          | duration of infusion                                                                                                                    |
| doseUnit     | unit of dose                                                                                                                            |
| timeUnit     | unit of time                                                                                                                            |
| concUnit     | unit of concentration                                                                                                                   |
| iAUC         | interval AUCs to calculate                                                                                                              |
| down         | either of "Linear" or "Log" to indicate the way to calculate AUC and AUMC                                                               |
| R2ADJ        | Minimum adjusted R-square value to determine terminal slope automatically                                                               |
| MW           | molecular weight of the drug                                                                                                            |
| Keysting     | a text string to be shown at the plot in case of manual selection of terminal slope                                                     |
| excludeDelta | Improvement of R2ADJ larger than this value could exclude the last point. Default value 1 is for the compatibility with other software. |

**Details**

This replaced previous IndiNCA. Author recommends to use excludeDelta option with about 0.3.

**Value**

|       |                                                                                         |
|-------|-----------------------------------------------------------------------------------------|
| CMAx  | maximum concentration, Cmax                                                             |
| CMAxD | dose normalized Cmax, CMAx / Dose, Cmax / Dose                                          |
| TMAx  | time of maximum concentration, Tmax                                                     |
| TLAG  | time to observe the first non-zero concentration, for extravascular administration only |

|          |                                                                                        |
|----------|----------------------------------------------------------------------------------------|
| CLST     | last positive concentration observed, $C_{last}$                                       |
| CLSTP    | last positive concentration predicted, $C_{last\_pred}$                                |
| TLST     | time of last positive concentration, $T_{last}$                                        |
| LAMZHL   | half-life by lambda z, $\ln(2)/LAMZ$                                                   |
| LAMZ     | lambda_z negative of the best-fit terminal slope                                       |
| LAMZLL   | earliest time for LAMZ                                                                 |
| LAMZUL   | last time for LAMZ                                                                     |
| LAMZNPT  | number of points for LAMZ                                                              |
| CORRXY   | correlation of log(concentration) and time                                             |
| R2       | R-squared                                                                              |
| R2ADJ    | R-squared adjusted                                                                     |
| C0       | back extrapolated concentration at time 0, for intravascular bolus administration only |
| AUCLST   | AUC from 0 to TLST                                                                     |
| AUCALL   | AUC using all the given points, including trailing zero concentrations                 |
| AUCIFO   | AUC infinity observed                                                                  |
| AUCIFOD  | AUCIFO / Dose                                                                          |
| AUCIFP   | AUC infinity predicted using CLSTP instead of CLST                                     |
| AUCIFPD  | AUCIFP / Dose                                                                          |
| AUCPEO   | AUC % extrapolation observed                                                           |
| AUCPEP   | AUC % extrapolated for AUCIFP                                                          |
| AUCPBEO  | AUC % back extrapolation observed, for bolus IV administration only                    |
| AUCPBEP  | AUC % back extrapolation predicted with AUCIFP, for bolus IV administration only       |
| AUMCLST  | AUMC to the TLST                                                                       |
| AUMCIFO  | AUMC infinity observed using CLST                                                      |
| AUMCIFP  | AUMC infinity determined by CLSTP                                                      |
| AUMCPEO  | AUMC % extrapolated observed                                                           |
| AUMCPEP  | AUMC % extrapolated predicted                                                          |
| MRTIVLST | mean residence time (MRT) to TLST, for intravascular administration                    |
| MRTIVIFO | mean residence time (MRT) infinity using CLST, for intravascular administration        |
| MRTIVIFP | mean residence time (MRT) infinity using CLSTP, for intravascular administration       |
| MRTEVLST | mean residence time (MRT) to TLST, for extravascular administration                    |
| MRTEVIFO | mean residence time (MRT) infinity using CLST, for extravascular administration        |
| MRTEVIFP | mean residence time (MRT) infinity using CLSTP, for extravascular administration       |



|      |                                                                                           |
|------|-------------------------------------------------------------------------------------------|
| VZO  | volume of distribution determined by LAMZ and AUCIFO, for intravascular administration    |
| VZP  | volume of distribution determined by LAMZ and AUCIFP, for intravascular administration    |
| VZFO | VZO for extravascular administration, VZO/F, F is bioavailability                         |
| VZFP | VZP for extravascular administration, VZP/F, F is bioavailability                         |
| CLO  | clearance using AUCIFO, for intravascular administration                                  |
| CLP  | clearance using AUCIFP, for intravascular administration                                  |
| CLFO | CLO for extravascular administration, CLO/F, F is bioavailability                         |
| CLFP | CLP for extravascular administration, CLP/F, F is bioavailability                         |
| VSSO | volume of distribution at steady state using CLST, for intravascular administration only  |
| VSSP | volume of distribution at steady state using CLSTP, for intravascular administration only |

**Author(s)**

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**References**

Gabrielsson J, Weiner D. Pharmacokinetic and Pharmacodynamic Data Analysis - Concepts and Applications. 5th ed. 2016.

**See Also**

[help](#), [tblNCA](#)

**Examples**

```
# For one subject
x = Theoph[Theoph$Subject=="1","Time"]
y = Theoph[Theoph$Subject=="1","conc"]

sNCA(x, y, dose=320, doseUnit="mg", concUnit="mg/L", timeUnit="h")
sNCA(x, y, dose=320, concUnit="mg/L")

iAUC = data.frame(Name=c("AUC[0-12h]", "AUC[0-24h]"), Start=c(0,0), End=c(12,24))
sNCA(x, y, dose=320, doseUnit="mg", concUnit="mg/L", timeUnit="h", iAUC=iAUC)

MW = 180.164 # Molecular weight of theophylline

sNCA(x, y/MW, dose=320, doseUnit="mg", concUnit="mmol/L", timeUnit="h")
sNCA(x, y/MW, dose=320, doseUnit="mg", concUnit="mmol/L", timeUnit="h", MW=MW)
sNCA(x, y, dose=320/MW, doseUnit="mmol", concUnit="mg/L", timeUnit="h", MW=MW)
sNCA(x, y/MW, dose=320/MW, doseUnit="mmol", concUnit="mmol/L", timeUnit="h", MW=MW)

sNCA(x, y/MW, dose=320/MW, doseUnit="mmol", concUnit="mmol/L", timeUnit="h", MW=MW)
```

```

sNCA(x, y/MW, doseUnit="mmol", concUnit="mmol/L", timeUnit="h", MW=MW)
sNCA(x, y/MW, dose=as.numeric(NA), doseUnit="mmol", concUnit="mmol/L", timeUnit="h",
      MW=MW)

sNCA(x, y, dose=320, concUnit="mg/L", timeUnit="hr")
sNCA(x*60, y, dose=320, concUnit="mg/L", timeUnit="min")

```

tblAUC

*Table output of gAUCs***Description**

Do multiple AUCs and returns a result table. See gNCA for more detail i.e. iAUC

**Usage**

```
tblAUC(Data, key = "Subject", colX = "Time", colY = "Y", iAUC = "",
        Ymax = "Emax", XofYmax = "TEmax", AUCname = "AUEclast", Outer = "NEAREST")
```

**Arguments**

|         |                                                      |
|---------|------------------------------------------------------|
| Data    | data table name                                      |
| key     | column names of Data to be shown in the output table |
| colX    | column name for x axis                               |
| colY    | column name for y axis                               |
| iAUC    | a data.frame to calculate interval AUCs              |
| Ymax    | usually Cmax or Emax                                 |
| XofYmax | usually Tmax or TEmax                                |
| AUCname | usually AUClast or AUEclast                          |
| Outer   | indicates how to do the out of x range point         |

**Details**

Tabular output of AUC with many subjects. This calculates only Cmax(Emax), Tmax(TEmax), AUCs

**Value**

Basically same with [gAUC](#)

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**See Also**

[help](#), [gAUC](#)

### Examples

```
tblAUC(Theoph, key="Subject", colX="Time", colY="conc")

iAUC = data.frame(Name=c("AUC[0-12h]", "AUC[0-24h]"), Start=c(0,0), End=c(12,24))
tblAUC(Indometh, key="Subject", colX="time", colY="conc", iAUC=iAUC)
```

tblNCA

*Table output NCA*

### Description

Do multiple NCA and returns a result table. See sNCA for more detail i.e. iAUC

### Usage

```
tblNCA(concData, key = "Subject", colTime = "Time", colConc = "conc", dose = 0,
      adm = "Extravascular", dur = 0, doseUnit = "mg", timeUnit = "h",
      concUnit = "ug/L", down = "Linear", R2ADJ = 0, MW = 0, iAUC="",
      excludeDelta = 1)
```

### Arguments

|              |                                                                                                                                         |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| concData     | concentration data table                                                                                                                |
| key          | column names of concData to be shown in the output table                                                                                |
| colTime      | column name for time                                                                                                                    |
| colConc      | column name for concentration                                                                                                           |
| dose         | administered dose                                                                                                                       |
| adm          | one of "Bolus" or "Infusion" or "Extravascular" to indicate drug administration mode                                                    |
| dur          | duration of infusion                                                                                                                    |
| doseUnit     | unit of dose                                                                                                                            |
| timeUnit     | unit of time                                                                                                                            |
| concUnit     | unit of concentration                                                                                                                   |
| down         | method to calculate AUC, "Linear" or "Log"                                                                                              |
| R2ADJ        | Lowest threshold of adjusted R-square value to do manual slope determination                                                            |
| MW           | molecular weight of drug                                                                                                                |
| iAUC         | data.frame for interval AUC                                                                                                             |
| excludeDelta | Improvement of R2ADJ larger than this value could exclude the last point. Default value 1 is for the compatibility with other software. |

### Details

Tabular output of NCA with many subjects. Author recommends to use excludeDelta option with about 0.3.

**Value**

Basically same with [sNCA](#)

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**See Also**

[help](#), [sNCA](#)

**Examples**

```
tblNCA(Theoph, key="Subject", dose=320, concUnit="mg/L")
tblNCA(Indometh, key="Subject", colTime="time", colConc="conc", dose=25,
      adm="Infusion", dur=0.5, concUnit="mg/L")
```

---

|      |                                                                          |
|------|--------------------------------------------------------------------------|
| Unit | <i>Display CDISC standard units and multiplied factor of NCA results</i> |
|------|--------------------------------------------------------------------------|

---

**Description**

It displays CDISC PP output units and multiplication factor for them.

**Usage**

```
Unit(code = "", timeUnit = "h", concUnit = "ng/mL", doseUnit = "mg", MW = 0)
```

**Arguments**

|          |                          |
|----------|--------------------------|
| code     | vector of PPTESTCD       |
| timeUnit | unit of time             |
| concUnit | unit of concentration    |
| doseUnit | unit of dose             |
| MW       | molecular weight of drug |

**Value**

|           |                                |
|-----------|--------------------------------|
| row names | PPTESTCD                       |
| Unit      | unit                           |
| Factor    | internal multiplication factor |

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**Examples**

```

Unit(concUnit="ug/L", doseUnit="mg")
Unit(concUnit="ng/L", doseUnit="mg")

Unit(concUnit="umol/L", doseUnit="mmol")
Unit(concUnit="nmol/L", doseUnit="mmol")

Unit(concUnit="mmol/L", doseUnit="mg", MW=500)
Unit(concUnit="umol/L", doseUnit="mg", MW=500)
Unit(concUnit="nmol/L", doseUnit="mg", MW=500)
Unit(concUnit="nmol/mL", doseUnit="mg", MW=500)

Unit(concUnit="ug/L", doseUnit="mmol", MW=500)
Unit(concUnit="ug/L", doseUnit="mol", MW=500)
Unit(concUnit="ng/L", doseUnit="mmol", MW=500)
Unit(concUnit="ng/mL", doseUnit="mmol", MW=500)

Unit(concUnit="nmol/L", doseUnit="mg")
Unit(concUnit="ug/L", doseUnit="mmol")

```

---

|           |                                                                                                   |
|-----------|---------------------------------------------------------------------------------------------------|
| UnitUrine | <i>Returns a conversion factor for the amount calculation from urine concentration and volume</i> |
|-----------|---------------------------------------------------------------------------------------------------|

---

**Description**

You can get a conversion factor for the multiplication:  $\text{conc} * \text{vol} * \text{factor} = \text{amount}$  in the given unit.

**Usage**

```
UnitUrine(conU = "ng/mL", volU = "mL", amtU = "mg", MW = 0)
```

**Arguments**

|      |                    |
|------|--------------------|
| conU | concentration unit |
| volU | volume unit        |
| amtU | amount unit        |
| MW   | molecular weight   |

**Value**

|        |                                                            |
|--------|------------------------------------------------------------|
| Factor | conversion factor for multiplication with the unit in name |
|--------|------------------------------------------------------------|

**Author(s)**

Kyun-Seop Bae <k@acr.kr>

**Examples**

```
UnitUrine()  
UnitUrine("ng/mL", "mL", "mg")  
UnitUrine("ug/L", "mL", "mg")  
UnitUrine("ug/L", "L", "mg")  
  
UnitUrine("ng/mL", "mL", "g")  
  
UnitUrine("ng/mL", "mL", "mol", MW=500)  
UnitUrine("ng/mL", "mL", "mmol", MW=500)  
UnitUrine("ng/mL", "mL", "umol", MW=500)
```

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