

# 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      *Noncompartmental Analysis for Pharmacokinetic Data*

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## 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 then  $1e-4$ , it pickes 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 Phoneix 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. Pheonix 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)**

Kyun-Seop Bae <k@acr.kr>

**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

*Determine slope for the log(y) and x regression manually*


---

**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"])
```

---

IntAUC *Calculate interval AUC*

---

**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)**

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**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**Interpolate y value*

---

**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

*Area Under the Curve(AUC) and Area Under the first Moment Curve(AUMC) by linear trapezoidal method*

---

**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, Clast   |
| CLSTP   | last positive concentration predicted, Clast_pred                                       |
| TLST    | time of last positive concentration, Tlast  |
| 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)**

Kyun-Seop Bae <k@acr.kr>

**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, 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")
```

---

**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

*Display CDISC standard units and multiplied factor of NCA results***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 PPTTESTCD      |
| timeUnit | unit of time             |
| concUnit | unit of concentration    |
| doseUnit | unit of dose             |
| MW       | molecular weight of drug |

**Value**

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

**Author(s)**

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**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 |
|--------|--|

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### 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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