

Package ‘Rivivc’

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Type Package

Title In vitro in vivo correlation linear level A

Version 0.9

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Depends signal, compiler

Suggests graphics

Description This package is devoted to the IVIVC linear level A with numerical deconvolution method. The latter is working for unequal and incompatible timepoints between impulse and response curves. A numerical convolution method is also available. Application domains include pharmaceutical industry QA/QC and R&D together with academic research.

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Author Aleksander Mendyk [aut, cre], Sebastian Polak [aut]

Maintainer Aleksander Mendyk <mfmendyk@cyf-kr.edu.pl>

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Rivivc-package

IVIVC LEVEL A

Description

This package performs linear iv vitro in vivo correlation of linear level A. It provides numerical convolution/deconvolution procedures with unequal time steps and no assumptions about the function shapes.

Details

Package: Rivivc
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License: GPLv3

Author(s)

Aleksander Mendyk and Sebastian Polak

Maintainer: Aleksander Mendyk <mfmendyk@cyf-kr.edu.pl>

References

Langenbucher (2003) F. Handling of computational in vitro/in vivo correlation problems by Microsoft Excel: III. Convolution and deconvolution. *Eur J Pharm Biopharm.* **56**, 429-37.

impulse

PK profile after drug intravenous administration

Description

This data set gives the time and concentration of the hypothetical drug after its intravenous administration. This is the simulated data set.

Usage

impulse

Format

matrix

input	<i>In vivo absorption of the drug</i>
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Description

This data set gives the time and cumulative amount of the hypothetical drug absorbed. It is also used as in vitro dissolution for Rivivc example of IVIVC level A. This is the simulated data set.

Usage

input

Format

matrix

NumConv	<i>Numerical convolution</i>
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Description

Performs numerical convolution independent of the sampling points but requiring the same timescale of the input and impulse profiles.

Usage

```
NumConv(impulse.matrix, input.matrix, conv.timescale = NULL, explicit.interpolation = 1000)
```

Arguments

`impulse.matrix` matrix of the PK profile after the drug intravenous (i.v.) administration

`input.matrix` cumulative in vivo absorption profile

`conv.timescale` a timescale of convolution defined either as a whole vector with specific time-points $c(t_1, t_2, \dots, t_N)$ or two-element vector containing only lower and upper boundary of the required prediction timescale $c(\text{lower}, \text{upper})$; in the latter case system creates the time vector based on the parameter `explicit.interpolation`; if omitted it computes convolution timescale based on the input matrix

`explicit.interpolation` sampling accuracy used by the interpolation method to find the same timepoints for input and impulse profiles

Value

Output values are:

`$par` convolved time profile based on the original timescale

`$par_explicit` provides convolution with the explicit interpolation

Author(s)

Aleksander Mendyk and Sebastian Polak

See Also

[NumDeconv](#),

Examples

```
require(Rivivc)
require(graphics)

#i.v. data
data("impulse")
#p.o. PK profile
data("resp")
#in vitro dissolution for correlation purposes
data("input")

#preparing data matrices
input_mtx<-as.matrix(input)
impulse_mtx<-as.matrix(impulse)
resp_mtx<-as.matrix(resp)

#setting interpolation accuracy
accur_explic<-1000

#run convolution
result<-NumConv(impulse_mtx,input_mtx,explicit.interp=accur_explic)

print("Raw results")
print(result$par)

print("Raw results explicit")
print(result$par_explicit)

dev.new()
plot(resp_mtx)
lines(result$par, type="l", col="blue")

dev.new()
plot(resp_mtx)
lines(result$par_explicit, type="l", col="blue")
```

Description

Numerical deconvolution method based on the convolution and the `optim()` BFGS method to find in vivo absorption profile through the convolution approach. The function works iteratively with the cumulative in vivo absorption profile optimization performed by the BFGS method in regard to the convolved PK profile and its proximity to the real known p.o. profile.

Usage

```
NumDeconv(impulse.matrix, resp.matrix, dose_iv=NULL, dose_po=NULL,  
          deconv.timescale = NULL, explicit.interpolation = 20,  
          implicit.interpolation = 10, optim.maxit = 200)
```

Arguments

`impulse.matrix` matrix of the PK profile after the drug intravenous (i.v.) administration

`resp.matrix` PK profile after oral (p.o.) administration of the drug

`dose_iv` drug dose after i.v. administration; not obligatory but if provided must be in the same units like the dose p.o.

`dose_po` drug dose after p.o. administration; not obligatory but if provided must be in the same units like the dose i.v.

`deconv.timescale` a timescale of deconvolution defined either as a whole vector with specific time-points `c(t1, t2, ... tN)` or two-element vector containing only lower and upper boundary of the required prediction timescale `c(lower, upper)`; in the latter case system creates the time vector based on the parameter `explicit.interpolation`; if omitted it computes deconvolution timescale based on the impulse matrix

`explicit.interpolation` deconvolution explicit interpolation parameter, namely number of the curve interpolation points used directly by the `optim()` method

`implicit.interpolation` implicit interpolation - a factor multiplying `explicit.interpolation` for better accuracy

`optim.maxit` maximum number of iterations used by `optim()` method

Details

This method is an empirical approach to the deconvolution method with minimum mechanistic assumptions. Yet the latter involve kinetics linearity when the doses of i.v. and p.o. are different, thus the i.v. profile is scaled by multiplication with the factor of `dose_po/dose_iv`. It is also important to know that large values of explicit and/or implicit accuracy lead to the long execution times. The recommended values are `explicit = 20` and `implicit = 10`, however this is only a rule of thumb used here. When looking for higher accuracy it is advisable to increase implicit interpolation prior to the explicit.

Value

Three matrices are returned at the output of the function:

`$par` represents original timescale provided at the input
`$par_explicit` provides deconvolution with the explicit interpolation
`$par_implicit` provides deconvolution with the implicit interpolation

Author(s)

Aleksander Mendyk and Sebastian Polak

See Also

[RivivcA](#)

Examples

```
require(Rivivc)
require(graphics)

#i.v. data
data("impulse")
#p.o. PK profile
data("resp")
#in vitro dissolution for correlation purposes
data("input")

#preparing data matrices
input_mtx<-as.matrix(input)
impulse_mtx<-as.matrix(impulse)
resp_mtx<-as.matrix(resp)

#setting accuracy for both interpolation modes
accur_explic<-10
accur_implicit<-5

#for deconvolution
result<-NumDeconv(impulse_mtx,resp_mtx,explicit.interp=accur_explic,implicit.interp=accur_implicit)

print("Raw results")
print(result$par)

print("Explicit interpolation")
print(result$par_explicit)

print("Implicit interpolation")
print(result$par_implicit)
```

```
#let's compare the deconvolved curve with known input
dev.new()
plot(input_mtx)
lines(result$par, type="l", col="blue")
```

resp *PK profile after drug oral administration*

Description

This data set gives the time and concentration of the hypothetical drug after its oral administration. This is the simulated data set.

Usage

```
resp
```

Format

```
matrix
```

RivivcA *Level A linear correlation for a single formulation*

Description

This is the major function to be called where numerical convolution ad/or deconvolution might be used for a linear in vitro in vivo correlation level A. It performs either numerical convolution via `/codeNumConv()` or deconvolution via `/codeNumDeconv()` and correlates their results with the `known.data` object via linear regression `lm()`. If you just want raw results of convolution/deconvolution then call explicitly `NumConv` or `link{NumDeconv}`

Usage

```
RivivcA(known.data, impulse.data, second.profile.data, dose_iv=NULL, dose_po=NULL,
mode = "deconv", explicit.interp = 20, implicit.interp = 10,
optimization.maxit = 200)
```

Arguments

<code>known.data</code>	the data matrix to be correlated with; depending on the state of the mode variable it represents either in vitro dissolution profile (mode = "deconv") or PK profile after oral administration of the drug (mode="conv")
<code>impulse.data</code>	matrix of the PK profile after the drug i.v. administration
<code>second.profile.data</code>	matrix of the second PK profile; depending on the mode variable it represents either PK profile after oral administration of the drug (mode = "deconv") or a drug cumulative absorption profile (mode="conv"), sometimes substituted directly by the in vitro dissolution profile
<code>dose_iv</code>	drug dose after i.v. administration; not obligatory but if provided must be in the same units like the dose p.o.
<code>dose_po</code>	drug dose after p.o. administration; not obligatory but if provided must be in the same units like the dose i.v.
<code>mode</code>	represents the method used here; two states are allowed: mode="conv" for numerical convolution method or mode="deconv" for numerical deconvolution (default)
<code>explicit.interp</code>	convolution and deconvolution explicit interpolation parameter, namely number of the curve interpolation points
<code>implicit.interp</code>	implicit interpolation - a factor multiplying <code>explicit.interp</code> for better accuracy; applies to the deconvolution procedure only
<code>optimization.maxit</code>	maximum number of iterations used by <code>optim()</code> method; applies to the deconvolution procedure only

Details

The function represents either convolution or deconvolution data together with linear regression of the above functions outputs and known data supplied as a parameter. Please bear in mind that `NumDeconv()` procedure is iterative and therefore depending on the parameters might require substantial amount of time to converge. Please refer to the [NumDeconv](#) description.

Value

<code>\$regression</code>	returns a whole object of the linear regression - a result from the <code>lm()</code> procedure
<code>\$numeric</code>	returns results from <code>NumConv()</code> or <code>NumDeconv()</code> functions

Author(s)

Aleksander Mendyk and Sebastian Polak

See Also

[NumConv](#), [NumDeconv](#)

Examples

```
require(Rivivc)
require(graphics)

#i.v. data
data("impulse")
#p.o. PK profile
data("resp")
#in vitro dissolution for correlation purposes
data("input")

#preparing data matrices
input_mtx<-as.matrix(input)
impulse_mtx<-as.matrix(impulse)
resp_mtx<-as.matrix(resp)

#setting accuracy
accur_explic<-20
accur_implic<-5

#run deconvolution
result<-RivivcA(input_mtx,impulse_mtx,resp_mtx,explicit.interp=accur_explic,implicit.interp=accur_implic)

summary(result$regression)

print("Raw results of deconvolution")
print(result$numeric$par)

predicted<-predict(result$regression)
deconvolved_data<-unname(predicted)
orig_data<-input_mtx[,2]

dev.new()
plot(orig_data,result$numeric$par[,2])
lines(orig_data,deconvolved_data, type="l", col="blue")
dev.new()
plot(input_mtx)
lines(result$numeric$par, type="l", col="blue")
```

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