Package 'radir'

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Type Package

Title Inverse-Regression Estimation of Radioactive Doses

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Description Radioactive doses estimation using individual chromosomal aberrations information. See Higueras M, Puig P, Ainsbury E, Rothkamm K. (2015) <doi:10.1088/0952-4746/35/3/557>.

Depends R (>= 3.1.1), hermite

License GPL (>= 2)

NeedsCompilation no

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radir-package *Inverse regression model for radiation biodosimetry*

Description

The package implements a new inverse regression model with applications to radiation biodosimetry.

Details

Package:	radir
Type:	Package
Version:	1.0.5
Date:	2026-07-27
License:	GPL version 2 or newer
LazyLoad:	yes

The package implements a new inverse regression model with applications to radiation biodosimetry by means of the function `dose.distr`. It allows for several distributions for the dose prior including `uniform` and `gamma`, and for the mean prior, including `gamma` and `normal` distributions. A summary containing the most relevant information about the estimated doses can be obtained via `summary` and graphics can be obtained in a standard way by means of `plot` or `lines` functions.

Author(s)

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References

Higueras M, Puig P, Ainsbury EA, Rothkamm K. A new inverse regression model applied to radiation biodosimetry. Proc R Soc A 2015;**471**, http://dx.doi.org/10.1098/rspa.2014.0588

See Also

`dose.distr`

Examples

```
f <- expression(b1*x+b2*x^2)
pars <- c("b1","b2")
beta <- c(3.126e-3, 2.537e-2)
cov  <- matrix(c(7.205e-06,-3.438e-06,-3.438e-06,2.718e-06),nrow=2)

ex1.a <- dose.distr(f, pars, beta, cov, cells=1811, dics=102,
```

```
m.prior="normal", d.prior="uniform", prior.param=c(0, Inf))
summary(ex1.a)
plot(ex1.a)
```

`ci.dose.radir` *Credible intervals for radiation dose*

Description

The function allows the user to compute credible intervals for radiation doses objects of class `radir`.

Usage

```
ci.dose.radir(object, cr=0.95)
```

Arguments

`object`	the doses estimated by `dose.distr` function, an object of class `radir`.
`cr`	size of the credibility region. Its default value is 0.95.

Value

A vector with two elements containing the lower and upper bounds of the credible region.

Author(s)

David Moriña (Barcelona Graduate School of Mathematics), Manuel Higueras (Basque Center for Applied Mathematics) and Pedro Puig (Universitat Autònoma de Barcelona)

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References

Higueras M, Puig P, Ainsbury EA, Rothkamm K. A new inverse regression model applied to radiation biodosimetry. Proc R Soc A 2015;**471**, http://dx.doi.org/10.1098/rspa.2014.0588

See Also

`radir-package`, `dose.distr`, `pr.dose.radir`

Examples

```
### Example 3 (a)
f <- expression(b1*x+b2*x^2)
pars <- c("b1","b2")
beta <- c(3.126e-3, 2.537e-2)
cov  <- matrix(c(7.205e-06,-3.438e-06,-3.438e-06,2.718e-06),nrow=2)

### (a)
```

```
ex1.a <- dose.distr(f, pars, beta, cov, cells=1811, dics=102,
m.prior="normal", d.prior="uniform", prior.param=c(0, Inf))

ci.dose.radir(ex1.a, 0.90)
```

`dose.distr` *Inverse regression model for radiation biodosimetry*

Description

The function allows the user to estimate radiation doses distribution using the methodology described in Higueras et al. (2014).

Usage

```
dose.distr(f, pars, beta, cov, cells, dics, m.prior="gamma",
d.prior="uniform", prior.param=c(0,"Inf"), stdf=6, nsim=1000)
```

Arguments

`f`	dose-response function, as an `expression`. Must be differenciable in the domain of parameters.
`pars`	string vector containing the parameters in `f`.
`beta`	estimates of the parameters.
`cov`	variance-covariance matrix.
`cells`	patient information, number of cells examined.
`dics`	patient information, observed number of aberrations.
`m.prior`	string containing the prior distribution of the mean. It can be `gamma` (the default value) or `normal`.
`d.prior`	string containing the prior distribution of the dose. It can be `gamma` or `uniform` (the default value).
`prior.param`	vector of length 2 containing the parameters of the distribution of the dose prior. The parametrization for the `uniform` distribution is the usual, based on the support, and an improper uniform distribution is allowed, setting the second parameter to `Inf`. Its default value is the non-informative prior. The `gamma` distribution is parametrized in terms of the mean and standard deviation.
`stdf`	Approximated standard deviation factor. This input is useful to control the ends of the calibrative density; i.e. in case the tails of the calibrative dose density are very long this value could be reduced, or viceversa. Its default value is 6.
`nsim`	Number of simulations to base the results on. Its default value is 1000.

Value

An object of class `dose.radir` containing the distribution of the estimated doses.

Author(s)

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References

Higueras M, Puig P, Ainsbury EA, Rothkamm K. A new inverse regression model applied to radiation biodosimetry. Proc R Soc A 2015;**471**, http://dx.doi.org/10.1098/rspa.2014.0588

See Also

radir-package, ci.dose.radir, pr.dose.radir

Examples

```
### Example 3 (a)
f <- expression(b1*x+b2*x^2)
pars <- c("b1","b2")
beta <- c(3.126e-3, 2.537e-2)
cov  <- matrix(c(7.205e-06,-3.438e-06,-3.438e-06,2.718e-06),nrow=2)

### (a)
ex1.a <- dose.distr(f, pars, beta, cov, cells=1811, dics=102,
m.prior="normal", d.prior="uniform", prior.param=c(0, Inf))
```

`pr.dose.radir` *Probability between doses*

Description

This function allows the user to compute the probability between two radiation doses.

Usage

```
pr.dose.radir(object, lod = 0, upd = object[[2]][length(object[[2]])])
```

Arguments

`object`	An object of class `radir` containing the estimated doses.
`lod`	Lower dose considered. Its default value is 0.
`upd`	Upper dose considered. Its default value is the maximum dose in `object`.

Value

The probability that the real dose is between `lod` and upd.

Author(s)

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References

Higueras M, Puig P, Ainsbury EA, Rothkamm K. A new inverse regression model applied to radiation biodosimetry. Proc R Soc A 2015;**471**, http://dx.doi.org/10.1098/rspa.2014.0588

See Also

radir-package, dose.distr, ci.dose.radir

Examples

```
### Example 3 (a)
f <- expression(b1*x+b2*x^2)
pars <- c("b1","b2")
beta <- c(3.126e-3, 2.537e-2)
cov  <- matrix(c(7.205e-06,-3.438e-06,-3.438e-06,2.718e-06),nrow=2)

### (a)
ex1.a <- dose.distr(f, pars, beta, cov, cells=1811, dics=102,
m.prior="normal", d.prior="uniform", prior.param=c(0, Inf))

pr.dose.radir(ex1.a, 1, 1.4)
```

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