

Package: radir (via r-universe)

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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 Higuera 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: 1.0.4
Date: 2019-6-30
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

Higuera 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

<code>object</code>	the doses estimated by <code>dose.distr</code> function, an object of class <code>radir</code> .
<code>cr</code>	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)

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References

Higuera 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 Higuera 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 differentiable 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.

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References

Higuera 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 <code>radir</code> 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`.

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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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