

Package ‘CoMiRe’

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Description Posterior inference under the convex mixture regression (CoMiRe) models intro-
duced by Canale, Durante, and Dunson (2018) <[doi:10.1111/biom.12917](https://doi.org/10.1111/biom.12917)>.

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CoMiRe-package	<i>Convex Mixture Regression</i>
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Description

Posterior inference under the convex mixture regression (CoMiRe) models introduced by Canale, Durante, and Dunson (2018) <doi:10.1111/biom.12917>.

Details

The CoMiRe package implements the convex mixture regression approach of Canale, Durante, and Dunson (2018) and some extensions to deal with binary response variables or to account for the presence of continuous and categorical confounders. Estimation is conducted via Gibbs sampler. Posterior plots for inference and goodness-of-fit tests are also available.

Author(s)

Antonio Canale [aut, cre], Daniele Durante [ctb], Arianna Falcioni [aut], Luisa Galtarossa [aut], Tommaso Rigon [ctb] Maintainer: Antonio Canale <canale@stat.unipd.it>

References

Canale, A., Durante, D., and Dunson, D. (2018), Convex Mixture Regression for Quantitative Risk Assessment, *Biometrics*, 74, 1331-1340

add.risk	<i>Additional risk function</i>
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Description

Additional risk function estimated from the object fit

Usage

```
add.risk(y, x, fit, mcmc, a, alpha=0.05,
x.grid=NULL, y.grid=NULL)
```

Arguments

<code>y</code>	optional numeric vector for the response used in <code>comire.gibbs</code> . If <code>y</code> is missing, <code>y.grid</code> must be provided.
<code>x</code>	numeric vector for the covariate relative to the dose of exposure used in <code>comire.gibbs</code> .
<code>fit</code>	the output of <code>comire.gibbs</code> . an object of the class <code>classCoMiRe</code> .
<code>mcmc</code>	a list giving the MCMC parameters.
<code>a</code>	threshold of clinical interest for the response variable
<code>alpha</code>	level of the credible bands.
<code>x.grid</code>	optional numerical vector giving the actual values of the grid for <code>x</code> for plotting the additional risk function. If <code>x.grid</code> is not provided, standard grids are automatically used.
<code>y.grid</code>	optional numerical vector giving the actual values of the grid for <code>y</code> for plotting the additional risk function. If <code>y.grid</code> is not provided, standard grids are automatically used.

Value

A list of arguments for generating posterior output. It contains:

- `mcmc.risk` a matrix containing in the lines the MCMC chains, after thinning, of the additional risk function over `x.grid`, in the columns.
- `summary.risk` a data frame with four variables: the posterior means of the additional risk function over `x.grid`, the respective $\alpha/2$ and $1 - \alpha/2$ quantiles, and `x.grid`.

Author(s)

Antonio Canale, Arianna Falcioni

Examples

```
{
data(CPP)
attach(CPP)

n <- NROW(CPP)
J <- H <- 10

premature <- as.numeric(gestage<=37)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## too few iterations to be meaningful. see below for safer and more comprehensive results

mcmc <- list(nrep=10, nb=2, thin=1, ndisplay=4)

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)
```

```

fit.dummy <- comire.gibbs(gestage, dde, family="continuous",
                        mcmc=mcmc, prior=prior, seed=1, max.x=180)

risk.data <- add.risk(y = gestage, x = dde, fit = fit.dummy, mcmc = mcmc,
                    a = 37, x.grid = seq(0, max(dde), length = 100))
riskplot(risk.data$summary.risk, xlab="DDE", x = dde, xlim = c(0,150))

## safer procedure with more iterations (it may take some time)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## Fit the model for continuous y

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit1 <- comire.gibbs(gestage, dde, family="continuous",
                   mcmc=mcmc, prior=prior, seed=5, max.x=180)

risk.data <- add.risk(y = gestage, x = dde, fit = fit1, mcmc = mcmc,
                    a = 37, x.grid = seq(0, max(dde), length = 100))
riskplot(risk.data$summary.risk, xlab="DDE", x = dde, xlim = c(0,150))

}

```

as.classCoMiRe

classCoMiRe class constructor

Description

A constructor for the classCoMiRe class. The class classCoMiRe is a named list containing the output of the posterior estimation of CoMiRe model implemented in comire.gibbs

Usage

```
as.classCoMiRe(call = NULL, out = NULL, z = NULL, z.val = NULL, f0 = NULL, f1 = NULL,
              nrep, nb, bin = FALSE, univariate = TRUE)
```

Arguments

call	a formula for comire.gibbs.
out	an output of comire.gibbs.
z	optional numeric vector or matrix for the confounding covariates.
z.val	optional numeric vector containing a fixed value of interest for each of the confounding covariates to be used for the plots. Default value is mean(z) for numeric covariates or the mode for factorial covariates.

<code>f0, f1</code>	optional matrices containing simulated values of the mixture densities at low and high dose exposure; default values are simulated with <code>comire.gibbs</code> . It is possible to change these for different fixed values of <code>z</code> : see <code>predict_new_z</code> function.
<code>nrep</code>	integer giving the total number of iterations used in <code>comire.gibbs</code> .
<code>nb</code>	integer giving the number of burn-in iterations used in <code>comire.gibbs</code> .
<code>bin</code>	logical. It is TRUE if <code>y</code> is drawn for a binomial distribution.
<code>univariate</code>	logical. It is TRUE if the model is univariate.

Author(s)

Antonio Canale, Arianna Falcioni

betaplot $\beta(x)$ plot

Description

Posterior mean (continuous lines) and pointwise credible bands (shaded areas) for $\beta(x)$.

Usage

```
betaplot(x, fit, x.grid = NULL, xlim = c(0, max(x)), xlab = "x")
```

Arguments

<code>x</code>	numeric vector for the covariate relative to the dose of exposure used in <code>comire.gibbs</code> .
<code>fit</code>	the output of <code>comire.gibbs</code> opportunely trasformed in <code>classCoMiRe</code> class.
<code>x.grid</code>	optional numerical vector giving the actual values of the grid for <code>x</code> for plotting $\beta(x)$. If <code>x.grid</code> is not provided, standard grids are automatically used.
<code>xlim</code>	numeric vectors of length 2, giving the <code>x</code> coordinates ranges for the plot.
<code>xlab</code>	the title of the <code>x</code> axis.

Author(s)

Antonio Canale

Examples

```
{
data(CPP)
attach(CPP)

n <- NROW(CPP)
J <- H <- 10
```

```

premature <- as.numeric(gestage<=37)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## too few iterations to be meaningful. see below for safer and more comprehensive results

mcmc <- list(nrep=10, nb=2, thin=1, ndisplay=4)

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
              alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit.dummy <- comire.gibbs(gestage, dde, family="continuous",
                          mcmc=mcmc, prior=prior, seed=1, max.x=180)

betaplot(x=dde, fit=fit.dummy, x.grid=seq(0,180, length=100), xlim=c(0,150))

## safer procedure with more iterations (it may take some time)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## Fit the model for continuous y

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
              alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit1 <- comire.gibbs(gestage, dde, family="continuous",
                    mcmc=mcmc, prior=prior, seed=5, max.x=180)

betaplot(x=dde, fit=fit1, x.grid=seq(0,180, length=100), xlim=c(0,150))

}

```

BMD

Benchmark dose

Description

Benchmark dose associated to a particular risk

Usage

```
BMD(level, risk, x, alpha=0.05)
```

Arguments

level	dose level of interest.
risk	summary.risk\$mcmc.risk from the output of add.risk function.

x numeric vector for the covariate relative to the dose of exposure used in `comire.gibbs`.
 alpha level of the credible bands.

Value

A dataframe containing as variables:

- q the dose level of interest.
- BMD the benchmark dose.
- low lower credible limit.
- upp upper credible limit.
- BMDL a more conservative benchmark dose.

Author(s)

Antonio Canale

Examples

```
{
data(CPP)
attach(CPP)

n <- NROW(CPP)
J <- H <- 10

premature <- as.numeric(gestage<=37)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## too few iterations to be meaningful. see below for safer and more comprehensive results

mcmc <- list(nrep=10, nb=2, thin=1, ndisplay=4)

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit.dummy <- comire.gibbs(gestage, dde, family="continuous",
                        mcmc=mcmc, prior=prior, seed=1, max.x=180)

risk.data <- add.risk(y = gestage, x = dde, fit = fit.dummy, mcmc = mcmc,
                    a = 37, x.grid = seq(0, max(dde), length = 100))
bmd.data <- BMD(seq(0,.20, length=50), risk.data$mcmc.risk,
               x=seq(0,max(dde), length=100), alpha=0.05)
bmd.plot(bmd.data)

## safer procedure with more iterations (it may take some time)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)
```

```

## Fit the model for continuous y

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit <- comire.gibbs(gestage, dde, family="continuous",
                  mcmc=mcmc, prior=prior, seed=5, max.x=180)

risk.data <- add.risk(y = gestage, x = dde, fit = fit, mcmc = mcmc,
                    a = 37, x.grid = seq(0, max(dde), length = 100))
bmd.data <- BMD(seq(0,.20, length=50), risk.data$mcmc.risk,
               x=seq(0,max(dde), length=100), alpha=0.05)
bmd.plot(bmd.data)

}

```

bmd.plot

Benchmark dose plot

Description

Posterior mean (continuous lines) and pointwise credible bands (shaded areas) for the benchmark dose in function of the increase in risk.

Usage

```
bmd.plot(bmd.data)
```

Arguments

bmd.data output of BMD function.

Author(s)

Antonio Canale

Examples

```

{
data(CPP)
attach(CPP)

n <- NROW(CPP)
J <- H <- 10

premature <- as.numeric(gestage<=37)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

```



```

## too few iterations to be meaningful. see below for safer and more comprehensive results

mcmc <- list(nrep=10, nb=2, thin=1, ndisplay=4)

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit.dummy <- comire.gibbs(gestage, dde, family="continuous",
                        mcmc=mcmc, prior=prior, seed=1, max.x=180)

risk.data <- add.risk(y = gestage, x = dde, fit = fit.dummy, mcmc = mcmc,
                    a = 37, x.grid = seq(0, max(dde), length = 100))
bmd.data <- BMD(seq(0,.20, length=50), risk.data$mcmc.risk,
               x=seq(0,max(dde), length=100), alpha=0.05)
bmd.plot(bmd.data)

## safer procedure with more iterations (it may take some time)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## Fit the model for continuous y

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit <- comire.gibbs(gestage, dde, family="continuous",
                  mcmc=mcmc, prior=prior, seed=5, max.x=180)

risk.data <- add.risk(y = gestage, x = dde, fit = fit, mcmc = mcmc,
                    a = 37, x.grid = seq(0, max(dde), length = 100))
bmd.data <- BMD(seq(0,.20, length=50), risk.data$mcmc.risk,
               x=seq(0,max(dde), length=100), alpha=0.05)
bmd.plot(bmd.data)

}

```

comire.gibbs

Gibbs sampler for CoMiRe model

Description

Posterior inference via Gibbs sampler for CoMiRe model

Usage

```

comire.gibbs(y, x, z = NULL, family = 'continuous',
            grid = NULL, mcmc, prior,
            state = NULL, seed, max.x = max(x), z.val = NULL, verbose = TRUE)

```

Arguments

- y** numeric vector for the response: when family="continuous" y must be a numeric vector; if family="binary" y must assume values 0 or 1.
- x** numeric vector for the covariate relative to the dose of exposure.
- z** numeric vector for the confounders; a vector if there is only one confounder or a matrix for two or more confounders
- family** type of y. This can be "continuous" or "binary". Default "continuous".
- grid** a list giving the parameters for plotting the posterior mean density and the posterior mean $\beta(x)$ over finite grids if family="continuous" and z=NULL. It must include the following values:
- grids, logical value (if TRUE the provided grids are used, otherwise standard grids are automatically used);
 - xgrid and ygrid, numerical vectors with the actual values of the grid for y and x.
- mcmc** a list giving the MCMC parameters. It must include the following integers: nb giving the number of burn-in iterations, nrep giving the total number of iterations, thin giving the thinning interval, ndisplay giving the multiple of iterations to be displayed on screen while the algorithm is running (a message will be printed every ndisplay iterations).
- prior** a list containing the values of the hyperparameters.
- If family = "continuous", it must include the following values:
- mu.theta, the prior mean μ_θ for each location parameter θ_{0h} and θ_1 ,
 - k.theta, the prior variance k_θ for each location parameter θ_{0h} and θ_1 ,
 - mu.gamma (if p confounding covariates are included in the model) a p-dimensional vector of prior means μ_γ of the parameters γ corresponding to the confounders,
 - k.gamma, the prior variance k_γ for parameter corresponding to the confounding covariate (if p=1) or sigma.gamma (if p>1), that is the covariance matrix Σ_γ for the parameters corresponding to the p confounding covariates; this must be a symmetric positive definite matrix.
 - eta, numeric vector of size J for the Dirichlet prior on the beta basis weights,
 - alpha, prior for the mixture weights,
 - a and b, prior scale and shape parameter for the gamma distribution of each precision parameter,
 - J, parameter controlling the number of elements of the I-spline basis,
 - H, total number of components in the mixture at x_0 .
- If family="binary" it must include the following values:
- eta, numeric vector of size J for the Dirichlet prior on the beta basis weights,
 - a.pi0 and b.pi0, the prior parameters of the prior beta distribution for π_0 ,
 - J, parameter controlling the number of elements of the Ispline basis.

state	if family="continuous", a list giving the current value of the parameters. This list is used if the current analysis is the continuation of a previous analysis or if we want to start the MCMC algorithm from some particular value of the parameters.
seed	seed for random initialization.
max.x	maximum value allowed for x.
z.val	optional numeric vector containing a fixed value of interest for each of the confounding covariates to be used for the plots. Default value is mean(z) for numeric covariates or the mode for factorial covariates.
verbose	logical, if TRUE a message on the status of the MCMC algorithm is printed to the console. Default is TRUE.

Details

The function fit a convex mixture regression (CoMiRe) model (Canale, Durante, Dunson, 2018) via Gibbs sampler. For continuous outcome $y \in \mathcal{Y}$, adverse exposure level $x \in \mathcal{X}$ and no confounding variables, one can set family = 'continuous' and z = NULL and fit model

$$f_x(y) = \{1 - \beta(x)\} \sum_{h=1}^H \nu_{0h} \phi(y; \theta_{0h}, \tau_{0h}^{-1}) + \beta(x) \phi(y; \theta_{\infty}, \tau_{\infty}^{-1});$$

where $\beta(x) = \sum_{j=1}^J \omega_j \psi_j(x)$, $x \geq 0$, is a monotone nondecreasing interpolation function, constrained between 0 and 1 and ψ_1, \dots, ψ_J are monotone nondecreasing I-splines basis.

If $p \geq 1$ confounding covariates $z \in \mathcal{Z}$ are available, passing the argument z the function fits model

$$f(y; x, z) = \{1 - \beta(x)\} f_0(y; z) + \beta(x) f_{\infty}(y; z);$$

where:

$$f_0(y; z) = \sum_{h=1}^H \nu_{0h} \phi(y; \theta_{0h} + z^T \gamma, \tau_{0h}^{-1}), \text{ and } f_{\infty}(y; z) = \phi(y; \theta_{\infty} + z^T \gamma, \tau_{\infty}^{-1}).$$

Finally, if y is a binary response, one can set family = 'binary' and fit model

$$p_x(y) = (\pi_x)^y (1 - \pi_x)^{1-y};$$

where $\pi_x = P(Y = 1|x)$ is $\pi_x = \{1 - \beta(x)\} \pi_0 + \beta(x) \pi_{\infty}$.

Value

An object of the class classCoMiRe, i.e. a list of arguments for generating posterior output. It contains:

- call the model formula
- post.means a list containing the posterior mean density beta over the grid, of all the mixture parameters and, if family = "continuous" and z = NULL, of f_0 and f_{inf} over the y.grid.
- ci a list containing the 95% credible intervals for all the quantities stored in post.means.
- mcmc a list containing all the MCMC chains.
- z the same of the input
- z.val the same of the input

- f_0, f_1 MCMC replicates of the density in the two extremes (only if family = 'continuous')
- nrep, nb the same values of the list mcmc in the input arguments
- bin logical, equal to TRUE if family = 'binary'
- univariate logical, equal to TRUE if z is null or a vector

Author(s)

Antonio Canale [aut, cre], Daniele Durante [ctb], Arianna Falcioni [aut], Luisa Galtarossa [aut], Tommaso Rigon [ctb]

References

- Canale, A., Durante, D., and Dunson, D. (2018), Convex Mixture Regression for Quantitative Risk Assessment, *Biometrics*, 74, 1331-1340
- Galtarossa, L., Canale, A., (2019), A Convex Mixture Model for Binomial Regression, *Book of Short Papers SIS 2019*

Examples

```
{
data(CPP)
attach(CPP)

n <- NROW(CPP)
J <- H <- 10

premature <- as.numeric(gestage<=37)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## too few iterations to be meaningful. see below for safer and more comprehensive results
mcmc <- list(nrep=10, nb=2, thin=1, ndisplay=4)

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
              alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit.dummy <- comire.gibbs(gestage, dde, family="continuous",
                         mcmc=mcmc, prior=prior, seed=1, max.x=180)

summary(fit.dummy)

## safer procedure with more iterations (it may take some time)
mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## 1. binary case ##
```

```

prior <- list(pi0=mean(gestage), eta=rep(1, J)/J,
             a.pi0=27, b.pi0=360, J=J)

fit_binary<- comire.gibbs(premature, dde, family="binary",
                        mcmc=mcmc, prior=prior, seed=5, max.x=180)

## 2. continuous case ##

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit1 <- comire.gibbs(gestage, dde, family="continuous",
                   mcmc=mcmc, prior=prior, seed=5, max.x=180)

## 2.2 One confunder ##

mage_std <- scale(mage, center = TRUE, scale = TRUE)

prior <- list(mu.theta=mean(gestage), k.theta=10, mu.gamma=0, k.gamma=10,
             eta=rep(1, J)/J, alpha=1/H, a=2, b=2, H=H, J=J)

fit2 <- comire.gibbs(gestage, dde, mage_std, family="continuous",
                   mcmc=mcmc, prior=prior, seed=5, max.x=180)

## 2.3 More confunders ##

Z <- cbind(mage, mbmi, sei)
Z <- scale(Z, center = TRUE, scale = TRUE)
Z <- as.matrix(cbind(Z, CPP$smoke))
colnames(Z) <- c("age", "BMI", "sei", "smoke")

mod <- lm(gestage ~ dde + Z)
prior <- list(mu.theta = mod$coefficients[1], k.theta = 10,
             mu.gamma = mod$coefficients[-c(1, 2)], sigma.gamma = diag(rep(10, 4)),
             eta = rep(1, J)/J, alpha = 1/H, a = 2, b = 2, H = H, J = J)

fit3 <- comire.gibbs(y = gestage, x = dde, z = Z, family = "continuous", mcmc = mcmc,
                   prior = prior, seed = 5)

}

```

Description

Pointwise posterior mean (continuous blue lines), and credible bands (shaded blue areas) for $f(y | x, z)$ calculated in `x.val` under the the model fitted in `fit`.

Usage

```
fit.pdf.mcmc(y, x, fit, mcmc, J=10, H = 10, alpha = 0.05,
max.x = max(x), x.val, y.grid = NULL, xlim = c(0, max(x)),
ylim = c(0, 1), xlab = NULL)
```

Arguments

<code>y</code>	optional numeric vector for the response used in <code>comire.gibbs</code> . If <code>y</code> is missing, <code>y.grid</code> must be provided.
<code>x</code>	numeric vector for the covariate relative to the dose of exposure used in <code>comire.gibbs</code> .
<code>fit</code>	the output of <code>comire.gibbs</code> opportunely trasformed in <code>classCoMiRe</code> class.
<code>mcmc</code>	a list giving the MCMC parameters.
<code>J</code>	parameter controlling the number of elements of the I-spline basis
<code>H</code>	total number of components in the mixture at x_0 .
<code>alpha</code>	level of the credible bands.
<code>max.x</code>	maximum value allowed for <code>x</code> .
<code>x.val</code>	central points of each dose interval to be used in the posterior estimation of the probability density function.
<code>y.grid</code>	optional numerical vector giving the actual values of the grid for <code>y</code> for plotting the posterior mean density. If <code>y.grid</code> is not provided, standard grids are automatically used.
<code>xlim, ylim</code>	numeric vectors of length 2, giving the <code>x</code> and <code>y</code> coordinates ranges for the plot.
<code>xlab</code>	the title of the <code>x</code> axis.

Author(s)

Antonio Canale, Arianna Falcioni

Examples

```
{
data(CPP)
attach(CPP)

n <- NROW(CPP)
J <- H <- 10

premature <- as.numeric(gestage<=37)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)
```

```

## too few iterations to be meaningful. see below for safer and more comprehensive results

mcmc <- list(nrep=10, nb=2, thin=1, ndisplay=4)

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit.dummy <- comire.gibbs(gestage, dde, family="continuous",
                        mcmc=mcmc, prior=prior, seed=1, max.x=180)

fit.pdf.mcmc(y = gestage, x = dde, fit = fit.dummy, mcmc = mcmc, J = 10, H = 10,
            alpha = 0.05, max.x = max(dde), x.val = 125,
            xlim = c(25,48), ylim = c(0,0.25),
            xlab = "Gest. age. for DDE = 125")

## safer procedure with more iterations (it may take some time)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## Fit the model for continuous y

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit1 <- comire.gibbs(gestage, dde, family="continuous",
                   mcmc=mcmc, prior=prior, seed=5, max.x=180)

fit.pdf.mcmc(y = gestage, x = dde, fit = fit1, mcmc = mcmc, J = 10, H = 10,
            alpha = 0.05, max.x = max(dde), x.val = 125,
            xlim = c(25,48), ylim = c(0,0.25),
            xlab = "Gest. age. for DDE = 125")

}

```

plot.classCoMiRe

CoMiRe plot

Description

An S3 plot method for an object of classCoMiRe class.

Usage

```

## S3 method for class 'classCoMiRe'
plot(
  x,
  y,
  xobs,

```

```

mcmc,
J = 10,
H = 10,
a = NULL,
max.x = max(xobs),
bandwidth = 20,
x.grid = NULL,
xlim = c(0, max(xobs)),
ylim = c(0, 1),
xlab = "x",
alpha = 0.05,
risk = TRUE,
bmd = TRUE,
level,
oneevery = 20,
...
)

```

Arguments

x	the output of <code>comire.gibbs</code> , an object of the <code>classCoMiRe</code> class.
y	numeric vector for the response used in <code>comire.gibbs</code> .
xobs	numeric vector for the covariate relative to the dose of exposure used in <code>comire.gibbs</code> .
mcmc	a list giving the MCMC parameters.
J	parameter controlling the number of elements of the I-spline basis
H	total number of components in the mixture at x_0 .
a	optional threshold of clinical interest for the response variable.
max.x	maximum value allowed for x.
bandwidth	the kernel bandwidth smoothing parameter for the <code>post.pred.check</code> plot.
x.grid	optional numerical vector giving the actual values of the grid for x for plotting the additional risk function. If <i>x.grid</i> is not provided, standard grids are automatically used.
xlim, ylim	numeric vectors of length 2, giving the x and y coordinates ranges for the plot.
xlab	the title of the x axis.
alpha	level of the credible bands, default 0.05
risk	if TRUE the additional risk plot via <code>riskplot</code> is computed.
bmd	if TRUE the benchmark dose plot via <code>bmd.plot</code> is computed.
level	if <code>bmd=TRUE</code> , dose levels of interest for BMD plot.
oneevery	integer number representing how many MCMC draws to plot in the posterior predictive check. It draws one sample every <code>oneevery</code> .
...	additional arguments to be passed.

Details

The output is a list of ggplot2 plots containing the result of the betaplot function and, if the threshold `a` is provided, of `post.pred.check`, `riskplot`, `bmd.plot`.

Value

If `a=NULL` returns only `betaplot` otherwise, if `risk=FALSE` and `bmd=FALSE` returns a list containing `betaplot` (which is automatically plotted) and `post.pred.check` plot. Finally, if `a` is provided, `risk=TRUE` and `bmd=TRUE` returns a list with `betaplot`, `post.pred.check`, `riskplot` and `bmd.plot`.

Author(s)

Antonio Canale, Arianna Falcioni

<code>post.pred.check</code>	<i>Posterior predictive check plot</i>
------------------------------	--

Description

A plot for an object of `classCoMiRe` class. The plot is a goodness-of-fit assessment of CoMiRe model. If `family = 'continuous'`, a smoothed empirical estimate of $F(a|x,z) = \text{pr}(y < a | x,z)$ is computed from the observed data (black line) and from some of the data sets simulated from the posterior predictive distribution in the `fit` object (grey lines). If `family = 'binary'`, a smoothed empirical estimate of the proportion of events (black line) and of the smoothed empirical proportion of data simulated from the posterior predictive distribution in the `fit` object (grey lines). In the `x` axis are reported the observed exposures.

Usage

```
post.pred.check(y, x, z, fit, mcmc, J=10, H=10, a, max.x=max(x),
xlim=c(0, max(x)), bandwidth = 20, oneevery = 20)
```

Arguments

<code>y</code>	numeric vector for the response used in <code>comire.gibbs</code>
<code>x</code>	numeric vector for the covariate relative to the dose of exposure used in <code>comire.gibbs</code>
<code>z</code>	optional numeric vector or matrix for the confounding covariates.
<code>fit</code>	the output of <code>comire.gibbs</code> opportunely trasformed in <code>classCoMiRe</code> class
<code>mcmc</code>	a list giving the MCMC parameters
<code>J</code>	parameter controlling the number of elements of the I-spline basis
<code>H</code>	total number of components in the mixture at x_0
<code>a</code>	threshold of clinical interest to compute the $F(a x,z)$
<code>max.x</code>	maximum value allowed for <code>x</code>

`xlim` numeric vectors of length 2, giving the x coordinates ranges for the plot
`bandwidth` the kernel bandwidth smoothing parameter
`oneevery` integer number representing how many MCMC draws to plot in the posterior predictive check. It draws one sample every `oneevery`.

Author(s)

Antonio Canale, Arianna Falcioni

Examples

```
{
data(CPP)
attach(CPP)

n <- NROW(CPP)
J <- H <- 10

premature <- as.numeric(gestage<=37)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## too few iterations to be meaningful. see below for safer and more comprehensive results

mcmc <- list(nrep=10, nb=2, thin=1, ndisplay=4)

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit.dummy <- comire.gibbs(gestage, dde, family="continuous",
                        mcmc=mcmc, prior=prior, seed=1, max.x=180)

post.pred.check(y = gestage, x = dde, fit = fit.dummy, mcmc = mcmc, J = 10, H = 10, a = 37,
               max.x = max(dde), xlim = c(0,150), oneevery = 4)

## safer procedure with more iterations (it may take some time)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## Fit the model for continuous y

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit1 <- comire.gibbs(gestage, dde, family="continuous",
                   mcmc=mcmc, prior=prior, seed=5, max.x=180)

post.pred.check(y = gestage, x = dde, fit = fit1, mcmc = mcmc, J = 10, H = 10, a = 37,
               max.x = max(dde), xlim = c(0,150))
```

```
}

```

```
predict_new_z      comire.gibbs for different fixed values of z
```

Description

This function computes the predicted values of the density at low dose f_0 and of the density at high dose f_{∞} , for fixed values of the confounders z .

Usage

```
predict_new_z(fit, y, z.val)
```

Arguments

<code>fit</code>	the output of <code>comire.gibbs</code> opportunely transformed in <code>classCoMiRe</code> class
<code>y</code>	numeric vector for the response used in <code>comire.gibbs</code>
<code>z.val</code>	optional numeric vector containing a fixed value of interest for each of the confounding covariates to be used for the plots. Default value is <code>mean(z)</code> for numeric covariates or the mode for factorial covariates.

Value

An object of class `classCoMiRe`.

Author(s)

Antonio Canale, Arianna Falcioni

```
print.classCoMiRe  CoMiRe print
```

Description

The `print.classCoMiRe` method prints the type of a `classCoMiRe` object.

Usage

```
## S3 method for class 'classCoMiRe'
print(x, ...)
```

Arguments

<code>x</code>	an object of class <code>classCoMiRe</code> ;
<code>...</code>	additional arguments.

Author(s)

Antonio Canale, Arianna Falcioni

riskplot

Additional risk function plot

Description

Posterior mean (continuous lines) and pointwise credible bands (shaded areas) for $Ra(x, a)$.

Usage

```
riskplot(risk.data, xlab = NULL, x = NULL, ylim=c(0,1), xlim=c(0, max(x)))
```

Arguments

risk.data	output of add.risk function.
xlab	the title of the x axis.
x	numeric vector for the covariate relative to the dose of exposure used in comire.gibbs.
xlim, ylim	numeric vectors of length 2, giving the x and y coordinates ranges for the plot.

Author(s)

Antonio Canale

Examples

```
{
data(CPP)
attach(CPP)

n <- NROW(CPP)
J <- H <- 10

premature <- as.numeric(gestage<=37)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## too few iterations to be meaningful. see below for safer and more comprehensive results

mcmc <- list(nrep=10, nb=2, thin=1, ndisplay=4)

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
             alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit.dummy <- comire.gibbs(gestage, dde, family="continuous",
                        mcmc=mcmc, prior=prior, seed=1, max.x=180)
```

```

risk.data <- add.risk(y = gestage, x = dde, fit = fit.dummy, mcmc = mcmc,
  a = 37, x.grid = seq(0, max(dde), length = 100))
riskplot(risk.data$summary.risk, xlab="DDE", x = dde, xlim = c(0,150))

## safer procedure with more iterations (it may take some time)

mcmc <- list(nrep=5000, nb=2000, thin=5, ndisplay=4)

## Fit the model for continuous y

prior <- list(mu.theta=mean(gestage), k.theta=10, eta=rep(1, J)/J,
  alpha=rep(1,H)/H, a=2, b=2, J=J, H=H)

fit <- comire.gibbs(gestage, dde, family="continuous",
  mcmc=mcmc, prior=prior, seed=5, max.x=180)

risk.data <- add.risk(y = gestage, x = dde, fit = fit, mcmc = mcmc,
  a = 37, x.grid = seq(0, max(dde), length = 100))
riskplot(risk.data$summary.risk, xlab="DDE",
  x = dde, xlim = c(0,150))

}

```

summary.classCoMiRe *CoMiRe summary*

Description

The `summary.classCoMiRe` method provides summary information on `classCoMiRe` objects.

Usage

```
## S3 method for class 'classCoMiRe'
summary(object, ...)
```

Arguments

<code>object</code>	an object of class <code>classCoMiRe</code> ;
<code>...</code>	additional arguments

Author(s)

Antonio Canale Arianna Falcioni

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