

Package ‘bayescopulareg’

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Type Package

Title Bayesian Copula Regression

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Description Tools for Bayesian copula generalized linear models (GLMs).

The sampling scheme is based on Pitt, Chan, and Kohn (2006) <[doi:10.1093/biomet/93.3.537](https://doi.org/10.1093/biomet/93.3.537)>.

Regression parameters (including coefficients and dispersion parameters) are estimated via the adaptive random walk Metropolis approach developed by Haario, Saksman, and Tamminen (1999) <[doi:10.1007/s001800050022](https://doi.org/10.1007/s001800050022)>.

The prior for the correlation matrix is based on Hoff (2007) <[doi:10.1214/07-AOAS107](https://doi.org/10.1214/07-AOAS107)>.

Depends R (>= 3.6.0)

License GPL (>= 2)

Imports Rcpp (>= 1.0.3), stats

LinkingTo Rcpp, RcppArmadillo, RcppDist, mvtnorm

RoxygenNote 7.1.1

Encoding UTF-8

URL <https://github.com/ethan-alt/bayescopulareg>

BugReports <https://github.com/ethan-alt/bayescopulareg/issues>

NeedsCompilation yes

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 bayescopulaglm

Sample from Bayesian copula GLM

Description

Sample from a GLM via Bayesian copula regression model. Uses random-walk Metropolis to update regression coefficients and dispersion parameters. Assumes Inverse Wishart prior on augmented data.

Usage

```
bayescopulaglm(
  formula.list,
  family.list,
  data,
  histdata = NULL,
  b0 = NULL,
  c0 = NULL,
  alpha0 = NULL,
  gamma0 = NULL,
  Gamma0 = NULL,
  S0beta = NULL,
  sigma0logphi = NULL,
  v0 = NULL,
  V0 = NULL,
  beta0 = NULL,
  phi0 = NULL,
  M = 10000,
  burnin = 2000,
  thin = 1,
  adaptive = TRUE
)
```

Arguments

<code>formula.list</code>	A J -dimensional list of formulas giving how the endpoints are related to the covariates
<code>family.list</code>	A J -dimensional list of families giving how each endpoint is distributed. See <code>help(family)</code>
<code>data</code>	A data frame containing all response variables and covariates. Variables must be named.
<code>histdata</code>	<i>Optional</i> historical data set for power prior on β, ϕ
<code>b0</code>	<i>Optional</i> power prior hyperparameter. Ignored if <code>is.null(histdata)</code> . Must be a number between $(0, 1]$ if <code>histdata</code> is not NULL
<code>c0</code>	A J -dimensional vector for $\beta \phi$ prior covariance. If NULL, sets $c_0 = 10000$ for each endpoint

alpha0	A J -dimensional vector giving the shape hyperparameter for each dispersion parameter on the prior on ϕ . If NULL sets $\alpha_0 = .01$ for each dispersion parameter
gamma0	A J -dimensional vector giving the rate hyperparameter for each dispersion parameter on the prior on ϕ . If NULL sets $\alpha_0 = .01$ for each dispersion parameter
Gamma0	Initial value for correlation matrix. If NULL defaults to the correlation matrix from the responses.
S0beta	A J -dimensional list for the covariance matrix for random walk metropolis on beta. Each matrix must have the same dimension as the corresponding regression coefficient. If NULL, uses <code>solve(crossprod(X))</code>
sigma0logphi	A J -dimensional vector giving the standard deviation on $\log(\phi)$ for random walk metropolis. If NULL defaults to $\theta.1$
v0	An integer scalar giving degrees of freedom for Inverse Wishart prior. If NULL defaults to $J + 2$
V0	An integer giving inverse scale parameter for Inverse Wishart prior. If NULL defaults to <code>diag(.001, J)</code>
beta0	A J -dimensional list giving starting values for random walk Metropolis on the regression coefficients. If NULL, defaults to the GLM MLE
phi0	A J -dimensional vector giving initial values for dispersion parameters. If NULL. Dispersion parameters will always return 1 for binomial and Poisson models
M	Number of desired posterior samples after burn-in and thinning
burnin	burn-in parameter
thin	post burn-in thinning parameter
adaptive	logical indicating whether to use adaptive random walk MCMC to estimate parameters. This takes longer, but generally has a better acceptance rate

Value

A named list. ["betasample"] gives a J -dimensional list of sampled coefficients as matrices. ["phisample"] gives a $M \times J$ matrix of sampled dispersion parameters. ["Gammasample"] gives a $J \times J \times M$ array of sampled correlation matrices. ["betaaccept"] gives a $M \times J$ matrix where each row indicates whether the proposal for the regression coefficient was accepted. ["phiaccept"] gives a $M \times J$ matrix where each row indicates whether the proposal for the dispersion parameter was accepted

Examples

```
set.seed(1234)
n <- 100
M <- 100

x <- runif(n, 1, 2)
y1 <- 0.25 * x + rnorm(100)
y2 <- rpois(n, exp(0.25 * x))

formula.list <- list(y1 ~ 0 + x, y2 ~ 0 + x)
```

```

family.list <- list(gaussian(), poisson())
data = data.frame(y1, y2, x)

## Perform copula regression sampling with default
## (noninformative) priors
sample <- bayescopulaglm(
  formula.list, family.list, data, M = M, burnin = 0, adaptive = F
)
## Regression coefficients
summary(do.call(cbind, sample$betasample))

## Dispersion parameters
summary(sample$phisample)

## Posterior mean correlation matrix
apply(sample$Gammasample, c(1,2), mean)

## Fraction of accepted betas
colMeans(sample$betaaccept)

## Fraction of accepted dispersion parameters
colMeans(sample$phiaccept)

```

predict.bayescopulaglm

Predictive posterior sample from copula GLM

Description

Sample from the predictive posterior density of a copula generalized linear model regression

Usage

```

## S3 method for class 'bayescopulaglm'
predict(object, newdata, nsims = 1, ...)

```

Arguments

object	Result from calling bayescopulaglm
newdata	data.frame of new data
nsims	number of posterior draws to take. The default and minimum is 1. The maximum is the number of simulations in object
...	further arguments passed to or from other methods

Value

array of dimension $c(n, J, nsims)$ of predicted values, where J is the number of endpoints

Examples

```
set.seed(1234)
n <- 100
M <- 1000

x <- runif(n, 1, 2)
y1 <- 0.25 * x + rnorm(100)
y2 <- rpois(n, exp(0.25 * x))

formula.list <- list(y1 ~ 0 + x, y2 ~ 0 + x)
family.list <- list(gaussian(), poisson())
data = data.frame(y1, y2, x)

## Perform copula regression sampling with default
## (noninformative) priors
sample <- bayescopulaglm(
  formula.list, family.list, data, M = M
)
predict(sample, newdata = data)
```

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