

Package ‘gammSlice’

January 27, 2015

Type Package

Title Generalized additive mixed model analysis via slice sampling

Version 1.3

Date 2015-01-21

Author Tung Pham and Matt Wand

Maintainer Tung Pham <pham.t@unimelb.edu.au>

Description Uses a slice sampling-based Markov chain Monte Carlo to conduct Bayesian fitting and inference for generalized additive mixed models (GAMM). Generalized linear mixed models and generalized additive models are also handled as special cases of GAMM.

Depends R(>= 2.13), KernSmooth, lattice, mgcv

License GPL (>= 2)

NeedsCompilation yes

Repository CRAN

Date/Publication 2015-01-21 08:24:52

R topics documented:

gSlc	2
gSlc.control	4
gSlcSim	5
indonRespir	7
plot.gSlc	7
summary.gSlc	8
toenail	9

Index	10
--------------	-----------

gSlc

*Generalized additive mixed model analysis via slice sampling***Description**

Use slice sampling-based Markov chain Monte Carlo to fit a generalized additive mixed model.

Usage

```
gSlc(formula, data = NULL, random = NULL, family, control = gSlc.control())
```

Arguments

formula	Formula describing the generalized additive mixed model.
data	Data frame containing the input data.
random	List describing random effects structure. This argument is optional.
family	Distribution family of the response variable. Options are "binomial" and "poisson".
control	Control options specified by gSlc.control .

Details

A Bayesian generalized additive mixed model is fitted to the input data according to specified formula. Such models are special cases of the general design generalized linear mixed models of Zhao, Staudenmayer, Coull and Wand (2003). Markov chain Monte Carlo, with slice sampling for the fixed and random effects, is used to obtain samples from the posterior distributions of the model parameters. Full details of the sampling scheme are in the appendix of Pham and Wand (2012).

Value

nu	Matrix containing the MCMC samples for the combined fixed effects and random effects vectors. Each column of nu is a separate MCMC sample.
beta	Matrix containing the MCMC samples for the fixed effects vector.
u	Matrix containing the MCMC samples for the random effects vector. If the model contains smooth function components then u includes both random intercept and spline coefficient MCMC samples.
sigmaSquared	Matrix contain of variances.
scaledData	The scaled data set was used to fit in.
formulaInfor	Information obtained from the formula.
timeTaken	Time in seconds taken by the MCMC sampling.
Xmin	The minimum values of each predictor variable.
Xmax	The maximum values of each predictor variable.
Xrange	The difference between Xmax and Xmin.

Author(s)

Tung Pham <tung.pham@epfl.ch> and Matt Wand <matt.wand@uts.edu.au>

References

- Neal, R.M. (2003).
Slice sampling (with discussion).
The Annals of Statistics, **31**, 705-767.
- Pham, T. and Wand, M.P. (2012).
Generalized additive mixed model analysis via gammSlice.
Submitted.
- Zhao, Y., Staudenmayer, J., Coull, B.A. and Wand, M.P. (2003).
General design Bayesian generalized linear mixed models.
Statistical Science, **21**, 35-51.

See Also

[gSlc.control](#), [plot.gSlc](#), [summary.gSlc](#)

Examples

```
## Not run:
library(mgcv)
dat0 <- gamSim(eg=1, n=500, scale = 0.2, dist = "poisson")
fit0 <- gSlc( y~s(x0) + s(x1) + s(x2) + s(x3), family = "poisson", data = dat0)
plot(fit0,pages = 1)
summary(fit0)

dat1 <- gamSim(eg=6, n = 400,scale = 0.1, dist = "poisson")
fit1 <- gSlc(y ~ s(x0) + s(x1) + s(x2) + s(x3), family = "poisson",
            data = dat1, random = list(fac=~1))
plot(fit1,pages=2)
summary(fit1)

dat2 <- gSlcSim(eg = 2, numGrp = 200, family = "poisson",
              randomFactor = FALSE)
fit2 <- gSlc(y~x1 + x2, family = "poisson", data = dat2)
summary(fit2)

dat3 <- gSlcSim(eg = 3,numGrp = 1000, family = "binomial",
              randomFactor = FALSE)
fit3 <- gSlc(y~s(x1),family = "binomial", data = dat3)
plot(fit3)
summary(fit3)

fit3a <- gSlc(y~s(x1,nBasis=10),family = "binomial",
            data = dat3)
plot(fit3a)
summary(fit3a)
```

```

dat4 <- gSlcSim(eg = 4, numGrp = 400, family = "poisson",
               randomFactor = FALSE)
fit4 <- gSlc(y~x1 + s(x2), family = "poisson", data = dat4)
plot(fit4)
summary(fit4)

dat5 <- gSlcSim(eg=6,family = "poisson", randomFactor = TRUE)
fit5 <- gSlc(y~x1 + x2 + s(x3) + s(x4), random = list(idnum=~1),
             family = "poisson", data = dat5)
plot(fit5)
summary(fit5)

## End(Not run)

```

gSlc.control

Modification of the gSlc defaults

Description

The fitting of a generalized additive mixed model in `gammSlice` via the core function `gSlc` entails various fitting options to be set to default values. The `gScl.control` function supports modification of these options.

Usage

```

gSlc.control(nBurnin = 5000, nIter = 5000, nThin = 5, fixedEffPriorVar = 1e10,
             sdPriorScale = 1e5)

```

Arguments

<code>nBurnin</code>	The length of the burnin. The first <code>nBurnin</code> Markov chain Monte Carlo samples are discarded. Its default value of <code>nBurnin</code> is 5000.
<code>nIter</code>	The number of retained Markov chain Monte Carlo samples after the burnin period. The default value of <code>nIter</code> is 5000.
<code>nThin</code>	Thinning factor applied to the retained Markov chain Monte Carlo samples. Setting <code>nIter</code> to be an integer greater than 1 results in every <code>nIter</code> th value in the post-burnin samples being retained. The final Markov chain Monte Carlo sample size is an integer close to <code>nIter</code> divided by <code>nIter</code> . The default value of <code>nThin</code> is 5.
<code>fixedEffPriorVar</code>	The variance in the independent zero mean Normal priors of the fixed effect parameters after the predictor data have been transformed to the interval [0,1]. The default value of <code>fixedEffPriorVar</code> is 1e10.
<code>sdPriorScale</code>	The scale parameter in the Half Cauchy priors on standard deviation parameters after the predictor data have been transformed to the interval [0,1]. The default value of <code>sdPriorScale</code> is 1e5.

Author(s)

Tung Pham <tung.pham@epfl.ch> and Matt Wand <matt.wand@uts.edu.au>.

References

- Pham, T. and Wand, M.P. (2012).
Generalized additive mixed model analysis via gammSlice.
Submitted.
- Zhao, Y., Staudenmayer, J., Coull, B.A. and Wand, M.P. (2003).
General design Bayesian generalized linear mixed models.
Statistical Science, **21**, 35-51.

See Also

[gSlc](#)

Examples

```
## Not run:
dat <- gSlcSim(eg=3, num.rep = 10, num.gps = 100, family = "binomial",
              random.factor = FALSE)

fitDefault <- gSlc(y~s(x1), family = "binomial", data = data)

fitMyPriors <- gSlc(y~s(x1), family = "binomial", data = data,
                  control = gSlc.control(fixedEffPriorVar=1e13,
                                         sdPriorScale=1e3))

fitBigMCMC <- gSlc(y~s(x1), family = "binomial", data = data,
                  control = gSlc.control(nBurnin=10000, nIter=8000,
                                         nThin=10))

## End(Not run)
```

gSlcSim

Simulate data from a generalized additive mixed model

Description

Six types of generalized additive mixed model structures can be simulated. The user has the option to specify the response distribution and sample sizes.

Usage

```
gSlcSim(eg, family, numRep = 10, numGrp = 100, randomFactor)
```

Arguments

eg	An integer between 1 and 6 that specifies the type of example. Details are given below.
family	Distribution family of the response variable. Options are "binomial" and "poisson".
numRep	The number of repeated measures within each group.
numGrp	The number of groups.
randomFactor	Boolean flag that indicates whether or not the the model has a random intercept. If randomFactor is FALSE then the random intercept is omitted and numRep is automatically set to 1.

Details

The example types are (as specified by the value of eg:

1. Example contains only one linear function.
2. Example contains two linear functions.
3. Example has only one smooth function.
4. Example contains one linear function and one smooth function.
5. Example contains only two smooth functions.
6. Example contains two linear functions and two smooth functions.

Value

A data frame containing the response and predictors as columns. If randomFactor is true then a column of containing group labels, and named idnum, is also included.

Author(s)

Tung Pham <tung.pham@epfl.ch> and Matt Wand <matt.wand@uts.edu.au>.

References

Pham, T. and Wand, M.P. (2012).
Generalized additive mixed model analysis via gammSlice.
Submitted.

See Also

[gSlc](#)

Examples

```
dat1 <- gSlcSim(eg = 6, family = "binomial", randomFactor = TRUE)

dat2 <- gSlcSim(eg = 4, numGrp = 500, family = "poisson",
               randomFactor = FALSE)
```

indonRespir	<i>The Indonesian Children's Health Study data</i>
-------------	--

Description

The Indonesian Children's Health Study data, corresponding to a cohort of 275 Indonesian children. The response variable is respiratory infection whilst potential predictors are age, indicator of vitamin A deficiency, sex, height, indicator of being stunted and the number of clinic visits for each child.

plot.gS1c	<i>Plot smooth function components of gS1c fits</i>
-----------	---

Description

Smooth function components of generalized additive mixed model fits obtained via gS1c are plotted.

Usage

```
## S3 method for class 'gS1c'
plot(x,pages=0,responseScale = FALSE,xlab = NULL,ylab = NULL,main=NULL,
      bty = NULL,...)
```

Arguments

x	gS1c object.
pages	The number of pages used to display the smooth function fits. The default value of pages is 0. Set to 0 to have the routine leave the graphic settings as they are.
responseScale	Boolean flag indicating whether or the smooth function fits are plotted on the same scale as the response variable. If responseScale is set to FALSE then the the smooth function fits are plotted on the link scale. The default value of responseScale is FALSE.
xlab	They are used as the x label for plots if supplied.
ylab	They are used as the y labels for plots if supplied.
main	They are used as the title for plots if supplied.
bty	A character string which determined the type of box which is drawn about plots. See par for reference.
...	Other graphic parameters.

Details

For each smooth function component of the generalized additive mixed model specified in the call to gS1c the pointwise posterior mean is plotted along with a shaded polygon corresponding to pointwise 95% credible sets.

Author(s)

Tung Pham <tung.pham@epfl.ch> and Matt Wand <matt.wand@uts.edu.au>.

References

Pham, T. and Wand, M.P. (2012).
Generalized additive mixed model analysis via gammSlice.
Submitted.

See Also

[gSlc](#), [summary.gSlc](#)

Examples

```
## Not run:
dat1 <- gSlcSim(eg=3, num.rep = 10, num.gps = 100, family = "binomial",
              random.factor = FALSE)
fit1 <- gSlc(y~s(x1),family = "binomial", data = dat1)
plot(fit1)
plot(fit1,responseScale=TRUE)

dat2 <- gSlcSim(eg=6,family = "poisson", random.factor = TRUE)
fit2 <- gSlc(y~x1 + x2 + s(x3) + s(x4), random = list(idnum=~1),
            family = "poisson", data = dat2)
plot(fit2,pages=2)

## End(Not run)
```

summary.gSlc

Summary of the generalized additive mixed model fit produced by gSlc

Description

A graphical table showing,for key model parameters, the Markov chain Monte Carlo (MCMC) samples, diagnostic plots and meaningful summaries.

Usage

```
## S3 method for class 'gSlc'
summary(object,pages = 1,...)
```

Arguments

object	A gSlc object.
pages	The number of pages used to display summary. The default value of pages is 1.
...	Other parameters.

Details

The columns of the graphical table are:

1. parameter name,
2. trace plot of the MCMC sample,
3. plot of MCMC sample against its lag 1 sample,
4. sample autocorrelation function,
5. kernel density estimate of posterior density function,
6. numerical summaries of posterior density function.

Author(s)

Tung Pham <tung.pham@epfl.ch> and Matt Wand <matt.wand@uts.edu.au>.

References

Pham, T. and Wand, M.P. (2012).
Generalized additive mixed model analysis via gammSlice.
Submitted.

See Also

[gSlc](#), [plot.gSlc](#)

Examples

```
## Not run:
dat1 <- gSlcSim(eg=3, num.rep = 10, num.gps = 100, family = "binomial",
              random.factor = FALSE)
fit1 <- gSlc(y~s(x1),family = "binomial", data = dat1)
summary(fit1)

dat2 <- gSlcSim(eg=6,family = "poisson", random.factor = TRUE)
fit2 <- gSlc(y~x1 + x2 + s(x3) + s(x4), random = list(idnum=~1),
            family = "poisson", data = dat2)
summary(fit2,pages=2)

## End(Not run)
```

toenail

A toenail data set

Description

The toenail data, the response measurement is onycholysis. The predictors variables are term and month.

Index

*Topic **models**

gSlc, [2](#)
gSlc.control, [4](#)
gSlcSim, [5](#)
plot.gSlc, [7](#)
summary.gSlc, [8](#)

*Topic **regression**

gSlc, [2](#)
gSlc.control, [4](#)
gSlcSim, [5](#)
plot.gSlc, [7](#)
summary.gSlc, [8](#)

box, [7](#)

gSlc, [2](#), [5](#), [6](#), [8](#), [9](#)
gSlc.control, [2](#), [3](#), [4](#)
gSlcSim, [5](#)

indonRespir, [7](#)

par, [7](#)
plot.gSlc, [3](#), [7](#), [9](#)

summary.gSlc, [3](#), [8](#), [8](#)

toenail, [9](#)