

Package ‘spBayes’

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Title Univariate and Multivariate Spatial Modeling

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Depends R (>= 1.8.0), coda, magic, lattice, abind

Suggests MBA, geoR, MASS

Description spBayes fits univariate and multivariate models with Markov chain Monte Carlo (MCMC).

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adaptMetropGibbs	<i>Adaptive Metropolis within Gibbs algorithm</i>
------------------	---

Description

Markov chain Monte Carlo for continuous random vector using an adaptive Metropolis within Gibbs algorithm.

Usage

```
adaptMetropGibbs(ltd, starting, tuning=1, accept.rate=0.44,
                 batch = 1, batch.length=25, report=100,
                 verbose=TRUE, ...)
```

Arguments

ltd	an R function that evaluates the log target density of the desired equilibrium distribution of the Markov chain. First argument is the starting value vector of the Markov chain. Pass variables used in the ltd via the ...argument of aMetropGibbs.
starting	a real vector of parameter starting values.
tuning	a scalar or vector of initial Metropolis tuning values. The vector must be of length(starting). If a scalar is passed then it is expanded to length(starting).
accept.rate	a scalar or vector of target Metropolis acceptance rates. The vector must be of length(starting). If a scalar is passed then it is expanded to length(starting).
batch	the number of batches.
batch.length	the number of sampler iterations in each batch.
report	the number of batches between acceptance rate reports.
verbose	if TRUE, progress of the sampler is printed to the screen. Otherwise, nothing is printed to the screen.
...	currently no additional arguments.

Value

A list with the following tags:

```
p.samples      a coda object of posterior samples for the parameters.
acceptance     the Metropolis acceptance rate at the end of each batch.
ltd            ltd
accept.rate    accept.rate
batch          batch
batch.length   batch.length
```

Note

This function is a rework of Rosenthal (2007) with some added niceties.

Author(s)

Andrew O. Finley (finleya@msu.edu),
Sudipto Banerjee (sudiptob@biostat.umn.edu)

References

Roberts G.O. and Rosenthal J.S. (2006). Examples of Adaptive MCMC. <http://probability.ca/jeff/ftpdir/adaptex.pdf> Preprint.

Rosenthal J.S. (2007). AMCMC: An R interface for adaptive MCMC. *Computational Statistics and Data Analysis*. 51:5467-5470.

Examples

```
## Not run:
## Not run:
#####
##Example of fitting a
##a non-linear model
#####
set.seed(1)

##Simulate some data
par <- c(0.1,0.1,3,1)
tau.sq <- 0.01

fn <- function(par,x){
  par[1]+par[2]^(1-(log(x/par[3])/par[4])^2)
}

n <- 200
x <- seq(1,10,0.1)
y <- rnorm(length(x), fn(par,x), sqrt(tau.sq))

##Define the log target density
```

```

ltd <- function(theta, x, y, fn, IG.a, IG.b){

  theta[2:5] <- exp(theta[2:5])
  tau.sq <- theta[5]

  y.hat <- fn(theta[1:4],x)

  ##likelihood
  logl <- -(n/2)*log(tau.sq)-(1/(2*tau.sq))*sum((y-y.hat)^2)

  ##priors IG on tau.sq and the rest flat
  logl <- logl-(IG.a+1)*log(tau.sq)-IG.b/tau.sq

  ##Jacobian adjustments
  logl <- logl+sum(log(theta[2:5]))

  return(logl)
}

##Give some reasonable starting values,
##note the transformation
starting <- c(0.5, log(0.5), log(5), log(3), log(1))

m.1 <- adaptMetropGibbs(ltd, starting=starting,
                       batch=1200, batch.length=25,
                       x=x, y=y, fn=fn, IG.a=2, IG.b=0.01)

##Back transform
m.1$p.samples[,2:5] <- exp(m.1$p.samples[,2:5])

##Summary with 95
burn.in <- 10000

fn.pred <- function(par,x){
  rnorm(length(x), fn(par[1:4],x), sqrt(par[5]))
}

post.curves <-
  t(apply(m.1$p.samples[burn.in:nrow(m.1$p.samples)], 1, fn.pred, x))

post.curves.quantiles <- summary(mcmc(post.curves))$quantiles

plot(x, y, pch=19, xlab="x", ylab="f(x)")
lines(x, post.curves.quantiles[,1], lty="dashed", col="blue")
lines(x, post.curves.quantiles[,3])
lines(x, post.curves.quantiles[,5], lty="dashed", col="blue")

#####
##Now some real data. There are way too
##few data for this model so we use a
##slightly informative normal prior on
##the parameters.
#####

```

```

fn <- function(par,x){
  par[1]-(par[2]^(1-(log(x/par[3])/par[4])^2))
}

x <- c(5,6,7,17,17,18,39,55,60)
y <- c(47.54,62.10,37.29,24.74,22.64,32.60,11.16,9.65,14.83)
n <- length(x)

##Define the log target density
ltd <- function(theta, x, y, fn, IG.a, IG.b){

  theta[2:5] <- exp(theta[2:5])
  tau.sq <- theta[5]

  y.hat <- fn(theta[1:4],x)

  ##likelihood
  logl <- -(n/2)*log(tau.sq)-(1/(2*tau.sq))*sum((y-y.hat)^2)

  ##priors IG on tau.sq and the rest normal
  logl <- logl-(IG.a+1)*log(tau.sq)-IG.b/tau.sq+
    sum(dnorm(theta[1:4], rep(0,4), 500, log = TRUE))

  ##Jacobian adjustments
  logl <- logl+sum(log(theta[2:5]))

  return(logl)
}

##Give some reasonable starting values,
##note the transformation
starting <- c(50, log(40), log(40), log(2), log(0.1))

m.1 <- adaptMetropGibbs(ltd, starting=starting,
  batch=1500, batch.length=25,
  x=x, y=y, fn=fn, IG.a=2, IG.b=10)

##Back transform
m.1$p.samples[,2:5] <- exp(m.1$p.samples[,2:5])

##Summary with 95
burn.in <- 20000

x.pred <- seq(0, 60, seq=0.1)

fn.pred <- function(par,x){
  rnorm(length(x), fn(par[1:4],x), sqrt(par[5]))
}

post.curves <-
  t(apply(m.1$p.samples[burn.in:nrow(m.1$p.samples)], 1, fn.pred, x.pred))

```

```

post.curves.quantiles <- summary(mcmc(post.curves))$quantiles

plot(x, y, pch=19, xlab="x", ylab="f(x)", xlim=c(0,60), ylim=c(0,100))
lines(x.pred, post.curves.quantiles[,1], lty="dashed", col="blue")
lines(x.pred, post.curves.quantiles[,3])
lines(x.pred, post.curves.quantiles[,5], lty="dashed", col="blue")

## End(Not run)

## End(Not run)

```

bayesGeostatExact *Simple Bayesian spatial linear model with fixed semivariogram parameters*

Description

Given a observation coordinates and fixed semivariogram parameters the bayesGeostatExact function fits a simple Bayesian spatial linear model.

Usage

```

bayesGeostatExact(formula, data = parent.frame(), n.samples,
                  beta.prior.mean, beta.prior.precision,
                  coords, cov.model="exponential", phi, nu, alpha,
                  sigma.sq.prior.shape, sigma.sq.prior.rate,
                  sp.effects=TRUE, verbose=TRUE, ...)

```

Arguments

formula	for a univariate model, this is a symbolic description of the regression model to be fit. See example below.
data	an optional data frame containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which spLM is called.
n.samples	the number of posterior samples to collect.
beta.prior.mean	β multivariate normal mean vector hyperprior.
beta.prior.precision	β multivariate normal precision matrix hyperprior.
coords	an $n \times 2$ matrix of the observation coordinates in R^2 (e.g., easting and northing).
cov.model	a quoted key word that specifies the covariance function used to model the spatial dependence structure among the observations. Supported covariance model key words are: "exponential", "matern", "spherical", and "gaussian". See below for details.

<code>phi</code>	the fixed value of the spatial range.
<code>nu</code>	if <code>cov.model</code> is "matern" then the fixed value of the spatial process smoothness must be specified.
<code>alpha</code>	the fixed value of the ratio between the nugget τ^2 and partial-sill σ^2 parameters from the specified <code>cov.model</code> .
<code>sigma.sq.prior.shape</code>	σ^2 (i.e., partial-sill) inverse-Gamma shape hyperprior.
<code>sigma.sq.prior.rate</code>	σ^2 (i.e., partial-sill) inverse-Gamma 1/scale hyperprior.
<code>sp.effects</code>	a logical value indicating if spatial random effects should be recovered.
<code>verbose</code>	if TRUE, model specification and progress of the sampler is printed to the screen. Otherwise, nothing is printed to the screen.
<code>...</code>	currently no additional arguments.

Value

An object of class `bayesGeostatExact`, which is a list with the following tags:

<code>p.samples</code>	a coda object of posterior samples for the defined parameters.
<code>sp.effects</code>	a matrix that holds samples from the posterior distribution of the spatial random effects. The rows of this matrix correspond to the n point observations and the columns are the posterior samples.
<code>args</code>	a list with the initial function arguments.

Author(s)

Sudipto Banerjee <sudiptob@biostat.umn.edu>
 Andrew O. Finley <finleya@msu.edu>

Examples

```
## Not run:

data(FBC07.dat)
Y <- FBC07.dat[1:150,"Y.2"]
coords <- as.matrix(FBC07.dat[1:150,c("coord.X", "coord.Y")])

n.samples <- 500
n = length(Y)
p = 1

phi <- 0.15
nu <- 0.5

beta.prior.mean <- as.matrix(rep(0, times=p))
beta.prior.precision <- matrix(0, nrow=p, ncol=p)

alpha <- 5/5
```

```

sigma.sq.prior.shape <- 2.0
sigma.sq.prior.rate <- 5.0

#####
##Simple linear model with
##the default exponential
##spatial decay function
#####
set.seed(1)
m.1 <- bayesGeostatExact(Y~1, n.samples=n.samples,
                          beta.prior.mean=beta.prior.mean,
                          beta.prior.precision=beta.prior.precision,
                          coords=coords, phi=phi, alpha=alpha,
                          sigma.sq.prior.shape=sigma.sq.prior.shape,
                          sigma.sq.prior.rate=sigma.sq.prior.rate)

print(summary(m.1$sp.samples))

##Requires MBA package to
##make surfaces
library(MBA)
par(mfrow=c(1,2))
obs.surf <-
  mba.surf(cbind(coords, Y), no.X=100, no.Y=100, extend=T)$xyz.est
image(obs.surf, xaxs = "r", yaxs = "r", main="Observed response")
points(coords)
contour(obs.surf, add=T)

w.hat <- rowMeans(m.1$sp.effects)
w.surf <-
  mba.surf(cbind(coords, w.hat), no.X=100, no.Y=100, extend=T)$xyz.est
image(w.surf, xaxs = "r", yaxs = "r", main="Estimated random effects")
points(coords)
contour(w.surf, add=T)

#####
##Simple linear model with
##the matern spatial decay
##function. Note, nu=0.5 so
##should produce the same
##estimates as m.1
#####
set.seed(1)
m.2 <- bayesGeostatExact(Y~1, n.samples=n.samples,
                          beta.prior.mean=beta.prior.mean,
                          beta.prior.precision=beta.prior.precision,
                          coords=coords, cov.model="matern",
                          phi=phi, nu=nu, alpha=alpha,
                          sigma.sq.prior.shape=sigma.sq.prior.shape,
                          sigma.sq.prior.rate=sigma.sq.prior.rate)

```

```

print(summary(m.2$p.samples))

#####
##This time with the
##spherical just for fun
#####
m.3 <- bayesGeostatExact(Y~1, n.samples=n.samples,
                        beta.prior.mean=beta.prior.mean,
                        beta.prior.precision=beta.prior.precision,
                        coords=coords, cov.model="spherical",
                        phi=phi, alpha=alpha,
                        sigma.sq.prior.shape=sigma.sq.prior.shape,
                        sigma.sq.prior.rate=sigma.sq.prior.rate)

print(summary(m.3$p.samples))

#####
##Another example but this
##time with covariates
#####
data(FORMGMT.dat)

n = nrow(FORMGMT.dat)
p = 5 ##an intercept an four covariates

n.samples <- 50

phi <- 0.0012

coords <- cbind(FORMGMT.dat$Longi, FORMGMT.dat$Lat)
coords <- coords*(pi/180)*6378

beta.prior.mean <- rep(0, times=p)
beta.prior.precision <- matrix(0, nrow=p, ncol=p)

alpha <- 1/1.5

sigma.sq.prior.shape <- 2.0
sigma.sq.prior.rate <- 10.0

m.4 <-
  bayesGeostatExact(Y~X1+X2+X3+X4, data=FORMGMT.dat, n.samples=n.samples,
                  beta.prior.mean=beta.prior.mean,
                  beta.prior.precision=beta.prior.precision,
                  coords=coords, phi=phi, alpha=alpha,
                  sigma.sq.prior.shape=sigma.sq.prior.shape,
                  sigma.sq.prior.rate=sigma.sq.prior.rate)

print(summary(m.4$p.samples))

##Requires MBA package to
##make surfaces

```

```

library(MBA)
par(mfrow=c(1,2))
obs.surf <-
  mba.surf(cbind(coords, resid(lm(Y~X1+X2+X3+X4, data=FORMGMT.dat))),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(obs.surf, xaxs = "r", yaxs = "r", main="Observed response")
points(coords)
contour(obs.surf, add=T)

w.hat <- rowMeans(m.4$sp.effects)
w.surf <-
  mba.surf(cbind(coords, w.hat), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(w.surf, xaxs = "r", yaxs = "r", main="Estimated random effects")
contour(w.surf, add=T)
points(coords, pch=1, cex=1)

#####
##Now with synthetic data
#####
data(rf.n1000.dat)

Y <- rf.n1000.dat$Y
coords <- as.matrix(rf.n1000.dat[,c("x.coords","y.coords")])
w <- rf.n1000.dat$w
p <- 1
alpha <- 1/10
phi <- 3/6

beta.prior.mean <- rep(0, times=p)
beta.prior.precision <- matrix(0, nrow=p, ncol=p)

sigma.sq.prior.shape <- 2.0
sigma.sq.prior.rate <- 1/10.0

n.samples <- 50

m.5 <-
  bayesGeostatExact(Y~1, n.samples=n.samples,
                    beta.prior.mean=beta.prior.mean,
                    beta.prior.precision=beta.prior.precision,
                    coords=coords, phi=phi, alpha=alpha,
                    sigma.sq.prior.shape=sigma.sq.prior.shape,
                    sigma.sq.prior.rate=sigma.sq.prior.rate)

print(summary(m.5$p.samples))

##Requires MBA package to
##make surfaces
library(MBA)
par(mfrow=c(1,2))
obs.surf <-
  mba.surf(cbind(coords, w),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est

```

```

image(obs.surf, xaxs = "r", yaxs = "r", main="Observed response")
points(coords)
contour(obs.surf, add=T)

w.hat <- rowMeans(m.5$sp.effects)
w.surf <-
  mba.surf(cbind(coords, w.hat), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(w.surf, xaxs = "r", yaxs = "r", main="Estimated random effects")
contour(w.surf, add=T)
points(coords, pch=1, cex=1)

## End(Not run)

```

bayesLMConjugate *Simple Bayesian linear model via the Normal/inverse-Gamma conjugate*

Description

Given an `lm` object, the `bayesLMConjugate` function fits a simple Bayesian linear model with Normal and inverse-Gamma priors.

Usage

```

bayesLMConjugate(formula, data = parent.frame(), n.samples,
                 beta.prior.mean, beta.prior.precision,
                 prior.shape, prior.rate, ...)

```

Arguments

<code>formula</code>	for a univariate model, this is a symbolic description of the regression model to be fit. See example below.
<code>data</code>	an optional data frame containing the variables in the model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>spLM</code> is called.
<code>n.samples</code>	the number of posterior samples to collect.
<code>beta.prior.mean</code>	β multivariate normal mean vector hyperprior.
<code>beta.prior.precision</code>	β multivariate normal precision matrix hyperprior.
<code>prior.shape</code>	σ^2 inverse-Gamma shape hyperprior.
<code>prior.rate</code>	σ^2 inverse-Gamma 1/scale hyperprior.
<code>...</code>	currently no additional arguments.

Value

An object of class `bayesLMConjugate`, which is a list with at least the following tag:

`p.samples` a coda object of posterior samples for the defined parameters.

Author(s)

Sudipto Banerjee (sudiptob@biostat.umn.edu),
Andrew O. Finley (finleya@msu.edu)

Examples

```
## Not run:

data(FORMGMT.dat)

n = nrow(FORMGMT.dat)
p = 7 ##an intercept and six covariates

n.samples <- 500

## Below we demonstrate the conjugate function in the special case
## with improper priors. The results are the same as for the above,
## up to MC error.
beta.prior.mean <- rep(0, times=p)
beta.prior.precision <- matrix(0, nrow=p, ncol=p)

prior.shape <- -p/2
prior.rate <- 0

m.1 <-
  bayesLMConjugate(Y ~ X1+X2+X3+X4+X5+X6, data = FORMGMT.dat,
                  n.samples, beta.prior.mean,
                  beta.prior.precision,
                  prior.shape, prior.rate)

summary(m.1$p.samples)
## End(Not run)
```

 bayesLMRef

Simple Bayesian linear model with non-informative priors

Description

Given an `lm` object, the `bayesLMRef` function fits a simple Bayesian linear model with reference (non-informative) priors.

Usage

```
bayesLMRef(lm.obj, n.samples, ...)
```

Arguments

`lm.obj` an object returned by `lm`.
`n.samples` the number of posterior samples to collect.
`...` currently no additional arguments.

Details

See page 355 in Gelman et al. (2004).

Value

An object of class `bayesLMRef`, which is a list with at least the following tag:

`p.samples` a coda object of posterior samples for the defined parameters.

Author(s)

Sudipto Banerjee (sudiptob@biostat.umn.edu),
Andrew O. Finley (finleya@msu.edu)

References

Gelman, A., Carlin, J.B., Stern, H.S., and Rubin, D.B. (2004). Bayesian Data Analysis. 2nd ed. Boca Raton, FL: Chapman and Hall/CRC Press.

Examples

```
data(FORMGMT.dat)

lm.obj <- lm(Y ~ X1+X2+X3+X4+X5+X6, data = FORMGMT.dat)

summary(lm.obj)

##Now with bayesLMRef
n.samples <- 500

m.1 <- bayesLMRef(lm.obj, n.samples)

summary(m.1$p.sample)
```

 BEF.dat

Bartlett Experimental Forest inventory data

Description

Data generated in long-term research studies on the Bartlett Experimental Forest, Bartlett, NH funded by the U.S. Department of Agriculture, Forest Service, Northeastern Research Station.

This dataset holds 1991 and 2002 forest inventory data for 437 points on the BEF.dat. Variables include species specific basal area and biomass; inventory plot coordinates; slope; elevation; and tasseled cap brightness (TC1), greenness (TC2), and wetness (TC3) components from spring, summer, and fall 2002 Landsat images.

Species specific basal area and biomass are recorded as a fraction of totals.

Usage

```
data(BEF.dat)
```

Format

A data frame containing 437 rows and 208 columns.

Source

BEF.dat inventory data provided by:

Marie-Louise Smith USDA Forest Service Northeastern Research Station <marielouisesmith@fs.fed.us>

Additional variables provided by:

Andrew Lister USDA Forest Service Northeastern Research Station <alister@fs.fed.us>

 covGivens

Returns covariance matrix C given components of P and L in C=PLP'

Description

Given components of P and Λ in $C = P\Lambda P^T$, covGivens returns C .

Usage

```
covGivens(theta, lambda, p, strict=TRUE)
```

Arguments

theta	a $p(p-1)/2$ vector of Givens angles that are restricted to lie in the interval $(-\pi/2, \pi/2)$ for uniqueness and positive definiteness of the covariance matrix. These are arranged in column major order in P.
lambda	a vector of length p of positive eigenvalues which form the diagonal matrix Λ .
p	refers to the dimension of the desired $p \times p$ covariance matrix.
strict	checks that theta elements lie in the interval $(-\pi/2, \pi/2)$ and the lambda elements are positive.

Details

The spectral decomposition of a matrix C is given by $P\Lambda P^T$, where P is an orthogonal matrix of eigenvectors and Λ is a diagonal matrix of positive eigenvalues. In the case of distinct eigenvalues, P can be expressed as $P = G_{12}, G_{13}, G_{23}, \dots, G_{p-1,p}$ where G_{ij} is a $p \times p$ matrix with $\cos(\theta_{tl})$ in the tl th and tl th diagonal elements, $\sin(\theta_{tl})$ in the tl th and $-\sin(\theta_{tl})$ in the tl th elements, zeros on the rest of the off-diagonal elements and 1's on the rest of the diagonal. The $p(p-1)/2$ angles are called Givens angles and are restricted to lie in the interval $(-\pi/2, \pi/2)$ for uniqueness and positive definiteness of the resulting covariance matrix.

Value

A list with the following tags:

C	$p \times p$ covariance matrix.
P	$p \times p$ P matrix.
Lambda	diagonal elements of the $p \times p$ Λ matrix.

Author(s)

Andrew O. Finley (finleya@msu.edu),
Sudipto Banerjee (sudiptob@biostat.umn.edu),

References

Daniels, M.J and R.E. Kass (1999) Nonconjugate Bayesian estimation of covariance matrices and its use in hierarchical models, J. Amer. Statist. Assoc. 94:1254-1263.

Examples

```
## Not run:
#####
##Syntetic covariance matrix IIIR_1 from
##Daniels, M.J. and R.E. Kass (1999)
##JASA 94(448):1254-1263.
#####
p <- 5
theta <- rep(pi/4, p*(p-1)/2)
```

```
lambda <- c(1, 0.75, 0.56, 0.06, 0.003)

cov <- covGivens(theta, lambda, p)$C
cov2cor(cov)
## End(Not run)
```

covInvLogDet *Utility function for constructing predictive process covariance matrices*

Description

Utility function for constructing predictive process covariance matrices

Usage

```
covInvLogDet(coords, knots, cov.model, sigma.sq,
              tau.sq, theta, modified.pp=TRUE, SWM=TRUE, ...)
```

Arguments

coords	a $n \times 2$ matrix of the observation coordinates in R^2 (e.g., easting and northing).
knots	a $m \times 2$ matrix of knot coordinates.
sigma.sq	partial sill value.
tau.sq	nugget value.
theta	if <code>cov.model</code> is <code>matern</code> then <code>theta</code> is a vector of the spatial range and smoothness parameters; otherwise, <code>theta</code> is the spatial range.
modified.pp	a logical value indicating if the <i>modified predictive process</i> should be used.
cov.model	a quoted key word that specifies the covariance function used to model the spatial dependence structure among the observations. Supported covariance model key words are: "exponential", "matern", "spherical", and "gaussian". See below for details.
SWM	a logical value indicating if the Sherman-Woodbury-Morrison equation should be used for computing the inverse (this is ignored if <code>modified.pp</code> is <code>FALSE</code>).
...	currently no additional arguments.

Value

Returns the covariance matrix, log-determinant, and inverse.

Author(s)

Andrew O. Finley (finleya@msu.edu),
Sudipto Banerjee (baner009@umn.edu)

Examples

```

set.seed(1)

n <- 100
coords <- cbind(runif(n), runif(n))

m <- 50
knots <- cbind(runif(m), runif(m))

theta <- c(6, 2)
sigma.sq <- 1
tau.sq <- 1
tol <- 1.0e-5

##
##non bias-adjusted predictive process
##
c1 <- covInvLogDet(coords=coords, knots=knots, cov.model="exponential",
                  sigma.sq=sigma.sq, tau.sq=tau.sq, theta=theta,
                  modified.pp=FALSE, SWM=FALSE)

if(max(abs(chol2inv(chol(c1$C)) - c1$C.inv)) > tol) stop("test-1 failed")
if(max(abs(2*sum(log(diag(chol(c1$C)))) - c1$log.det)) > tol)
stop("test-1 failed")

c2 <- covInvLogDet(coords=coords, knots=knots, cov.model="matern",
                  sigma.sq=sigma.sq, tau.sq=tau.sq, theta=theta,
                  modified.pp=FALSE, SWM=FALSE)

if(max(abs(chol2inv(chol(c2$C)) - c2$C.inv)) > tol) stop("test-2 failed")
if(max(abs(2*sum(log(diag(chol(c2$C)))) - c2$log.det)) > tol)
stop("test-2 failed")

##
##bias-adjusted predictive process
##
c3 <- covInvLogDet(coords=coords, knots=knots, cov.model="exponential",
                  sigma.sq=sigma.sq, tau.sq=tau.sq, theta=theta,
                  modified.pp=TRUE, SWM=FALSE)

if(max(abs(chol2inv(chol(c3$C)) - c3$C.inv)) > tol) stop("test-3 failed")
if(max(abs(2*sum(log(diag(chol(c3$C)))) - c3$log.det)) > tol)
stop("test-3 failed")

c4 <- covInvLogDet(coords=coords, knots=knots, cov.model="matern",
                  sigma.sq=sigma.sq, tau.sq=tau.sq, theta=theta,
                  modified.pp=TRUE, SWM=FALSE)

if(max(abs(chol2inv(chol(c4$C)) - c4$C.inv)) > tol) stop("test-4 failed")
if(max(abs(2*sum(log(diag(chol(c4$C)))) - c4$log.det)) > tol)
stop("test-4 failed")

```

```

##
##non bias-adjusted predictive process using SWM
##
c5 <- covInvLogDet(coords=coords, knots=knots, cov.model="exponential",
                  sigma.sq=sigma.sq, tau.sq=tau.sq, theta=theta,
                  modified.pp=FALSE, SWM=TRUE)

if(max(abs(chol2inv(chol(c5$C)) - c5$C.inv)) > tol) stop("test-5 failed")
if(max(abs(2*sum(log(diag(chol(c5$C)))) - c5$log.det)) > tol)
stop("test-5 failed")

c6 <- covInvLogDet(coords=coords, knots=knots, cov.model="matern",
                  sigma.sq=sigma.sq, tau.sq=tau.sq, theta=theta,
                  modified.pp=FALSE, SWM=TRUE)

if(max(abs(chol2inv(chol(c6$C)) - c6$C.inv)) > tol) stop("test-6 failed")
if(max(abs(2*sum(log(diag(chol(c6$C)))) - c6$log.det)) > tol)
stop("test-6 failed")

##
##Check SWM
##
##c.str <- sigma.sq*exp(-theta[1]*iDist(knots))
##ct <- sigma.sq*exp(-theta[1]*iDist(coords,knots))
##C.inv.swm <- diag(1/tau.sq,n)-diag(1/tau.sq,n)/
## chol2inv(chol(c.str+t(ct)/
## t(ct)/
##if(max(abs(C.inv.swm - c5$C.inv)) > tol) stop("test-5a failed")

##
##bias-adjusted predictive process using SWM
##
c7 <- covInvLogDet(coords=coords, knots=knots, cov.model="exponential",
                  sigma.sq=sigma.sq, tau.sq=tau.sq, theta=theta,
                  modified.pp=TRUE, SWM=TRUE)

if(max(abs(chol2inv(chol(c7$C)) - c7$C.inv)) > tol) stop("test-7 failed")
if(max(abs(2*sum(log(diag(chol(c7$C)))) - c7$log.det)) > tol)
stop("test-7 failed")

c8 <- covInvLogDet(coords=coords, knots=knots, cov.model="matern",
                  sigma.sq=sigma.sq, tau.sq=tau.sq, theta=theta,
                  modified.pp=TRUE, SWM=TRUE)

if(max(abs(chol2inv(chol(c8$C)) - c8$C.inv)) > tol) stop("test-8 failed")
if(max(abs(2*sum(log(diag(chol(c8$C)))) - c8$log.det)) > tol)
stop("test-8 failed")

```

FBC07.dat *Synthetic multivariate data with spatial and non-spatial variance structures*

Description

The synthetic dataset describes a stationary and isotropic bivariate process. Please refer to the vignette Section 4.2 for specifics.

Usage

```
data(FBC07.dat)
```

Format

A data frame of 250 rows and 4 columns. Columns 1 and 2 are coordinates and columns 3 and 4 are response variables.

Source

Finley A.O., S. Banerjee, and B.P. Carlin (2007) spBayes: R package for Univariate and Multivariate Hierarchical Point-referenced Spatial Models. Journal of Statistical Software.

Examples

```
## Not run:

data(FBC07.dat)
library(geoR)

max <- 40
bins <- 20
pts <- 1:150

vario.1 <- variog(coords=FBC07.dat[pts,1:2], data=FBC07.dat[pts,3],
                 uvec=(seq(0, max, length=bins)))

vario.2 <- variog(coords=FBC07.dat[pts,1:2], data=FBC07.dat[pts,4],
                 uvec=(seq(0,max, length=bins)))

vario.fit.1 <- variofit(vario.1, ini.cov.pars=c(5.0, 1.0),
                      cov.model="exponential",
                      minimisation.function="nls",
                      weights="equal")

vario.fit.2 <- variofit(vario.2, ini.cov.pars=c(5.0, 10.0),
                      cov.model="exponential",
                      minimisation.function="nls",
                      weights="equal")
```

```

par(mfrow=c(1,2))

plot(vario.1$u, vario.1$v, axes=FALSE, type = "n",
      ylim=c(0,15), xlab="Distance", ylab="Semivariance")
points(vario.1$u, vario.1$v, pch=19, cex=0.5)
axis(1, seq(0,max,10))
axis(2, seq(0,15,5))
abline(h=vario.fit.1$nugget)
abline(h=vario.fit.1$cov.pars[1]+vario.fit.1$nugget)
abline(v=3/(1/vario.fit.1$cov.pars[2]))
lines(vario.fit.1)

plot(vario.2$u, vario.2$v, axes=FALSE, type = "n",
      ylim=c(0,15), xlab="Distance", ylab="")
points(vario.2$u, vario.2$v, pch=19, cex=0.5)
axis(1, seq(0,max,10))
abline(h=vario.fit.2$nugget)
abline(h=vario.fit.2$cov.pars[1]+vario.fit.2$nugget)
abline(v=3/(1/vario.fit.2$cov.pars[2]))
lines(vario.fit.2)
## End(Not run)

```

FORMGMT.dat

Data used for illustrations

Description

Data used for illustrations.

Usage

```
data(FORMGMT.dat)
```

hexGrid

Generates a hexagon tessellation within a bounding box

Description

This function generates a hexagon tessellation within a bounding box.

Usage

```
hexGrid(nodes.per.layer, b.box, ...)
```

Arguments

<code>nodes.per.layer</code>	the number of hexagons from <code>min.x</code> to <code>max.x</code> at <code>min.y</code> .
<code>b.box</code>	the domain's bounding box defined with a vector of length four and elements ordered <code>min.x, min.y, max.x, max.y</code> .
<code>...</code>	currently no additional arguments.

Value

A list with the following tags:

<code>hx.hy</code>	a vector of length two that holds the height and width, respectively, between hexagon centroids.
<code>layers</code>	the number of hexagon layers within the domain.
<code>nodes.per.layer</code>	the number of hexagons from <code>min.x</code> to <code>max.x</code> at <code>min.y</code> .
<code>hex.centroids</code>	an $n \times 2$ matrix with rows corresponding to the x and y coordinates of the n hexagons within the domain.
<code>hex.polygons</code>	a list with 6×2 matrices which hold the hexagons' x and y vertices coordinates.

Author(s)

Andrew O. Finley <finleya@msu.edu>
Sudipto Banerjee <baner009@umn.edu>

Examples

```
## Not run:

##Define the bounding box and make the call
b.box <- c(0,0,10,10)

out <- hexGrid(20, b.box)

##Plot using lapply
par(mfrow=c(1,2))

plot(out$hex.centroids, pch=19, cex=0.5,
      ylab="Northing", xlab="Easting")
lapply(out$hex.polygons, polygon, col="blue")

##Now color hexagons based on value
my.col.ramp <- function(z){
  zlim <- range(z)
  zlen <- zlim[2]-zlim[1]+1
  colorlut <- heat.colors(as.integer(zlen))
  col <- colorlut[z-zlim[1]+1]
  col
}
```

```

}

n <- nrow(out$hex.centroids)
col <- my.col.ramp(rnorm(n))

plot(out$hex.centroids, typ="n", ylab="", xlab="Easting")
for(i in 1:n){
  polygon(out$hex.polygons[[i]], col=col[i], border=col[i])
}

## End(Not run)

```

iDist

Euclidean distance matrix

Description

Computes the inter-site Euclidean distance matrix for one or two sets of points.

Usage

```
iDist(coords.1, coords.2, ...)
```

Arguments

coords.1	an $n \times p$ matrix with each row corresponding to a point in p dimensional space.
coords.2	an $m \times p$ matrix with each row corresponding to a point in p dimensional space. If this is missing then <code>coords.1</code> is used.
...	currently no additional arguments.

Value

The $n \times m$ inter-site Euclidean distance matrix.

Author(s)

Andrew O. Finley (finleya@msu.edu),
Sudipto Banerjee (sudiptob@biostat.umn.edu),

Examples

```

n <- 10
p1 <- cbind(runif(n), runif(n))

m <- 5
p2 <- cbind(runif(m), runif(m))

```

```
D <- iDist(p1, p2)
```

mkMvX

Make a multivariate design matrix

Description

Given m univariate design matrices, the function `mkMvX` creates a multivariate design matrix suitable for use in `spPredict`.

Usage

```
mkMvX(X)
```

Arguments

`X` a list of m univariate design matrices. The matrices must have the same number of rows (i.e., observations) but may have different number of columns (i.e., regressors).

Value

A multivariate design matrix suitable for use in `spPredict`.

Author(s)

Andrew O. Finley (finleya@msu.edu),
Sudipto Banerjee (sudiptob@biostat.umn.edu).

See Also

`spPredict`

Examples

```
##Define some univariate model design matrices
##with intercepts.
X.1 <- cbind(rep(1, 10), matrix(rnorm(50), nrow=10))
X.2 <- cbind(rep(1, 10), matrix(rnorm(20), nrow=10))
X.3 <- cbind(rep(1, 10), matrix(rnorm(30), nrow=10))

##Make a multivariate design matrix suitable
##for use in spPredict.
X.mv <- mkMvX(list(X.1, X.2, X.3))
```

mvCovInvLogDet	<i>Utility function for constructing multivariate predictive process covariance matrices</i>
----------------	--

Description

Utility function for constructing multivariate predictive process covariance matrices

Usage

```
mvCovInvLogDet(coords, knots, cov.model, V,
               Psi, theta, modified.pp=TRUE, SWM=TRUE, ...)
```

Arguments

<code>coords</code>	a $n \times 2$ matrix of the observation coordinates in R^2 (e.g., easting and northing).
<code>knots</code>	a $m \times 2$ matrix of knot coordinates.
<code>V</code>	spatial cross-covariance matrix.
<code>Psi</code>	residual cross-covariance matrix.
<code>theta</code>	if <code>cov.model</code> is <code>matern</code> then <code>theta</code> is a vector of the multivariate spatial ranges followed by the associated smoothness parameters; otherwise, <code>theta</code> is the spatial range vector.
<code>modified.pp</code>	a logical value indicating if the <i>modified predictive process</i> should be used.
<code>cov.model</code>	a quoted key word that specifies the covariance function used to model the spatial dependence structure among the observations. Supported covariance model key words are: "exponential", "matern", "spherical", and "gaussian". See below for details.
<code>SWM</code>	a logical value indicating if the Sherman-Woodbury-Morrison equation should be used for computing the inverse (this is ignored if <code>modified.pp</code> is <code>FALSE</code>).
<code>...</code>	currently no additional arguments.

Value

Returns the covariance matrix, log-determinant, and inverse.

Author(s)

Andrew O. Finley (finleya@msu.edu),
Sudipto Banerjee (baner009@umn.edu)

Examples

```

set.seed(1)

n <- 100 ##number of coords
m <- 25  ##number of knots
q <- 5   ##number of response variables

coords <- cbind(runif(n),runif(n))
knots <- cbind(runif(m), runif(m))

theta <- c(rep(6,q),rep(0.5,q)) #phi and nu

A <- matrix(0,q,q)
A[lower.tri(A,TRUE)] <- rnorm(q*(q-1)/2+q)

V <- A%*%t(A)

P <- matrix(0,q,q)
P[lower.tri(A,TRUE)] <- rnorm(q*(q-1)/2+q)

Psi <- P%*%t(P)

tol <- 1.0e-8

##
##non bias-adjusted predictive process
##
c1 <- mvCovInvLogDet(coords=coords, knots=knots, cov.model="exponential",
                     V=V, Psi=Psi, theta=theta,
                     modified.pp=FALSE, SWM=FALSE)

if(max(abs(chol2inv(chol(c1$C)) - c1$C.inv)) > tol) stop("test-1 failed")
if(max(abs(2*sum(log(diag(chol(c1$C)))) - c1$log.det)) > tol)
stop("test-1 failed")

c2 <- mvCovInvLogDet(coords=coords, knots=knots, cov.model="matern",
                     V=V, Psi=Psi, theta=theta,
                     modified.pp=FALSE, SWM=FALSE)

if(max(abs(chol2inv(chol(c2$C)) - c2$C.inv)) > tol) stop("test-2 failed")
if(max(abs(2*sum(log(diag(chol(c2$C)))) - c2$log.det)) > tol)
stop("test-2 failed")

##
##bias-adjusted predictive process
##
c3 <- mvCovInvLogDet(coords=coords, knots=knots, cov.model="exponential",
                     V=V, Psi=Psi, theta=theta,
                     modified.pp=TRUE, SWM=FALSE)

if(max(abs(chol2inv(chol(c3$C)) - c3$C.inv)) > tol) stop("test-3 failed")
if(max(abs(2*sum(log(diag(chol(c3$C)))) - c3$log.det)) > tol)

```

```

stop("test-3 failed")

c4 <- mvCovInvLogDet(coords=coords, knots=knots, cov.model="matern",
                    V=V, Psi=Psi, theta=theta,
                    modified.pp=TRUE, SWM=FALSE)

if(max(abs(chol2inv(chol(c4$C)) - c4$C.inv)) > tol) stop("test-4 failed")
if(max(abs(2*sum(log(diag(chol(c4$C)))) - c4$log.det)) > tol)
stop("test-4 failed")

##
##non bias-adjusted predictive process using SWM
##
c5 <- mvCovInvLogDet(coords=coords, knots=knots, cov.model="exponential",
                    V=V, Psi=Psi, theta=theta,
                    modified.pp=FALSE, SWM=TRUE)

if(max(abs(chol2inv(chol(c5$C)) - c5$C.inv)) > tol) stop("test-5 failed")
if(max(abs(2*sum(log(diag(chol(c5$C)))) - c5$log.det)) > tol)
stop("test-5 failed")

c6 <- mvCovInvLogDet(coords=coords, knots=knots, cov.model="matern",
                    V=V, Psi=Psi, theta=theta,
                    modified.pp=FALSE, SWM=TRUE)

if(max(abs(chol2inv(chol(c6$C)) - c6$C.inv)) > tol) stop("test-6 failed")
if(max(abs(2*sum(log(diag(chol(c6$C)))) - c6$log.det)) > tol)
stop("test-6 failed")

##
##bias-adjusted predictive process using SWM
##
c7 <- mvCovInvLogDet(coords=coords, knots=knots, cov.model="exponential",
                    V=V, Psi=Psi, theta=theta,
                    modified.pp=TRUE, SWM=TRUE)

if(max(abs(chol2inv(chol(c7$C)) - c7$C.inv)) > tol) stop("test-7 failed")
if(max(abs(2*sum(log(diag(chol(c7$C)))) - c7$log.det)) > tol)
stop("test-7 failed")

c8 <- mvCovInvLogDet(coords=coords, knots=knots, cov.model="matern",
                    V=V, Psi=Psi, theta=theta,
                    modified.pp=TRUE, SWM=TRUE)

if(max(abs(chol2inv(chol(c8$C)) - c8$C.inv)) > tol) stop("test-8 failed")
if(max(abs(2*sum(log(diag(chol(c8$C)))) - c8$log.det)) > tol)
stop("test-8 failed")

```

Description

Given a polygon and a set of points this function returns the subset of points that are within the polygon.

Usage

```
pointsInPoly(poly, points, ...)
```

Arguments

<code>poly</code>	an $n \times 2$ matrix of polygon vertices. Matrix columns correspond to vertices' x and y coordinates, respectively.
<code>points</code>	an $m \times 2$ matrix of points. Matrix columns correspond to points' x and y coordinates, respectively.
<code>...</code>	currently no additional arguments.

Details

It is assumed that the polygon is to be closed by joining the last vertex to the first vertex.

Value

If points are found with the polygon, then a vector is returned with elements corresponding to the row indices of `points`, otherwise NA is returned.

Author(s)

Andrew O. Finley <finleya@msu.edu>,
Sudipto Banerjee <sudiptob@biostat.umn.edu>.

Examples

```
## Not run:
##Example 1
points <- cbind(runif(1000, 0, 10),runif(1000, 0, 10))

poly <- cbind(c(1:9,8:1), c(1,2*(5:3),2,-1,17,9,8,2:9))

point.indx <- pointsInPoly(poly, points)

plot(points, pch=19, cex=0.5, xlab="x", ylab="y", col="red")
points[points[point.indx,], pch=19, cex=0.5, col="blue"]
polygon(poly)

##Example 2
##a function to partition the domain
tiles <- function(points, x.cnt, y.cnt, tol = 1.0e-10){
```

```

x.min <- min(points[,1])-tol
x.max <- max(points[,1])+tol
y.min <- min(points[,2])-tol
y.max <- max(points[,2])+tol

x.cnt <- x.cnt+1
y.cnt <- y.cnt+1

x <- seq(x.min, x.max, length.out=x.cnt)
y <- seq(y.min, y.max, length.out=y.cnt)

tile.list <- vector("list", (length(y)-1)*(length(x)-1))

l <- 1
for(i in 1:(length(y)-1)){
  for(j in 1:(length(x)-1)){
    tile.list[[l]] <- rbind(c(x[j], y[i]),
                          c(x[j+1], y[i]),
                          c(x[j+1], y[i+1]),
                          c(x[j], y[i+1]))
    l <- l+1
  }
}

tile.list
}

n <- 1000
points <- cbind(runif(n, 0, 10), runif(n, 0, 10))

grd <- tiles(points, x.cnt=10, y.cnt=10)

plot(points, pch=19, cex=0.5, xlab="x", ylab="y")

sum.points <- 0
for(i in 1:length(grd)){
  polygon(grd[[i]], border="red")

  point.indx <- pointsInPoly(grd[[i]], points)

  if(!is.na(point.indx[1])){
    sum.points <- length(point.indx)+sum.points

    text(mean(grd[[i]][,1]), mean(grd[[i]][,2]), length(point.indx), col="red")
  }
}
sum.points

## End(Not run)

```

`prior` *Creates prior distribution definitions*

Description

The function `prior` creates a valid prior definition for use in `spGGT`.

Usage

```
prior(dist, ...)
```

Arguments

`dist` a quoted key word that identifies the prior distribution. The choices are inverse-gamma "IG", uniform "UNIF", half-Cauchy "HC", normal "NORMAL", flat "FLAT", inverse-Wishart "IWISH", and fixed scalar or matrix "FIXED".

`...` the hyperparameters of the chosen prior distribution, passed as quoted key words with associated values. See details below.

Details

Up to a proportionality constant the possible priors are:

- Uniform: $1/(b - a), b > a$, where $b > a$. Use key words "a", and "b".
- Inverse-gamma: $x^{-(a+1)} \exp(-b/x)$, where a is shape > 0 and b is scale > 0 . Use key words "shape", and "scale".
- Half-Cauchy: $(x + a^2)^{-1}$. Use key word "a".
- Normal: $\exp(-1/2(\beta - \mu)^t V^{-1}(\beta - \mu))$, where μ is the mean vector of length p and V^{-1} is the $p \times p$ precision matrix. Use key words "mu" and "precision".
- Inverse-Wishart: $\det(S)^{df/2} \det(W)^{-(df+m+1)/2} \exp(-1/2 \text{tr}(SW^{-1}))$, where W is the $m \times m$ covariance matrix, df is the degrees of freedom, and S is the positive definite $m \times m$ scale matrix. Use key words "df" and "S".

The normal and flat priors can only be used for the regressors specified in `spGGT`.

Value

`prior` a list object of class `ggt.prior` which is used for the value portion of the `prior` tag in the `spGGT` function.

Author(s)

Andrew O. Finley (finleya@msu.edu),
Sudipto Banerjee (sudiptob@biostat.umn.edu).

References

- Banerjee, S., Carlin, B.P., and Gelfand, A.E. (2004). Hierarchical modeling and analysis for spatial data. Chapman and Hall/CRC Press, Boca Raton, Fla.
- Gelman, A. (2006). Prior distributions for variance parameters in hierarchical models 1(3):515-533, Bayesian Analysis.

See Also

[spGGT](#)

spDIC	<i>Calculates model DIC and associated statistics given a bayesLMRef, bayesLMConjugate, spGGT, spLM, spMvLM, bayesGeostatExact object</i>
-------	---

Description

The function `spDIC` calculates model DIC and associated statistics given a [bayesLMRef](#), [bayesLMConjugate](#), [spGGT](#), [spLM](#), [spMvLM](#), or [bayesGeostatExact](#) object.

Usage

```
spDIC(sp.obj, DIC.marg=TRUE, DIC.unmarg=TRUE,
      start=1, end, thin=1, verbose=TRUE, ...)
```

Arguments

sp.obj	an object returned by bayesLMRef , bayesLMConjugate , spGGT , spLM , spMvLM , or bayesGeostatExact
DIC.marg	a logical value indicating if marginalized DIC and associated statistics should be calculated. Note, this argument is ignored when <code>sp.obj</code> specifies a non-spatial model.
DIC.unmarg	a logical value indicating if unmarginalized DIC and associated statistics should be calculated. Note, this argument is ignored when <code>sp.obj</code> specifies a non-spatial model.
start	specifies the first sample included in the DIC calculation. This is useful for those who choose to acknowledge chain burn-in.
end	specifies the last sample included in the prediction calculation. The default is to use all posterior samples in <code>sp.obj</code> .
thin	a sample thinning factor. The default of 1 considers all samples between <code>start</code> and <code>end</code> . For example, if <code>thin = 10</code> then 1 in 10 samples are considered between <code>start</code> and <code>end</code> .
verbose	if TRUE calculation progress is printed to the screen; otherwise, nothing is printed to the screen.
...	currently no additional arguments.

Details

Please refer to Section 3.3 in the vignette.

Value

A list with some of the following tags:

DIC	a matrix holding DIC and associated statistics when <code>sp.obj</code> specifies a non-spatial model.
DIC.marg	a matrix holding marginalized DIC and associated statistics.
DIC.unmarg	a matrix holding unmarginalized DIC and associated statistics.
sp.effects	if DIC.unmarg is true and if <code>sp.obj</code> specifies a spatial model without pre-calculated spatial effects then <code>spDIC</code> calculates the spatial effects.

Author(s)

Andrew O. Finley (finleya@msu.edu),
Sudipto Banerjee (sudiptob@biostat.umn.edu).

References

Banerjee, S., Carlin, B.P., and Gelfand, A.E. (2004). Hierarchical modeling and analysis for spatial data. Chapman and Hall/CRC Press, Boca Raton, Fla.

See Also

[bayesLMRef](#), [bayesLMConjugate](#), [spGGT](#), [bayesGeostatExact](#), [spLM](#)

Examples

```
## Not run:
#####
##          DIC for spLM
#####

##Use some more observations
data(rf.n200.dat)

Y <- rf.n200.dat$Y
coords <- as.matrix(rf.n200.dat[,c("x.coords", "y.coords")])

#####
##With and without predictive
##process
#####
m.la <- spLM(Y~1, coords=coords, knots=c(5, 5, 0),
             starting=list("phi"=0.6, "sigma.sq"=1, "tau.sq"=1),
             sp.tuning=list("phi"=0.01, "sigma.sq"=0.05, "tau.sq"=0.05),
             priors=list("phi.Unif"=c(0.3, 3), "sigma.sq.IG"=c(2, 1),
                        "tau.sq.IG"=c(2, 1)),
```

```

        cov.model="exponential",
        n.samples=1000, verbose=TRUE, n.report=100)

print(spDIC(m.1a, start=100, thin=2, DIC.marg=TRUE, DIC.unmarg=TRUE))

m.1b <- spLM(Y~1, coords=coords, knots=c(7, 7, 0),
            starting=list("phi"=0.6,"sigma.sq"=1, "tau.sq"=1),
            sp.tuning=list("phi"=0.01, "sigma.sq"=0.05, "tau.sq"=0.05),
            priors=list("phi.Unif"=c(0.3, 3), "sigma.sq.IG"=c(2, 1),
                       "tau.sq.IG"=c(2, 1)),
            cov.model="exponential",
            n.samples=1000, verbose=TRUE, n.report=100)

print(spDIC(m.1b, start=100, thin=2, DIC.marg=TRUE, DIC.unmarg=TRUE))

m.2 <- spLM(Y~1, coords=coords,
            starting=list("phi"=0.6,"sigma.sq"=1, "tau.sq"=1),
            sp.tuning=list("phi"=0.01, "sigma.sq"=0.05, "tau.sq"=0.05),
            priors=list("phi.Unif"=c(0.3, 3), "sigma.sq.IG"=c(2, 1),
                       "tau.sq.IG"=c(2, 1)),
            cov.model="exponential",
            n.samples=1000, verbose=TRUE, n.report=100)

print(spDIC(m.2, start=100, thin=2, DIC.marg=TRUE, DIC.unmarg=TRUE))

#####
##    DIC for bayesGeostatExact
#####
data(FORMGMT.dat)

n = nrow(FORMGMT.dat)
p = 5 ##an intercept an four covariates

n.samples <- 10

coords <- cbind(FORMGMT.dat$Longi, FORMGMT.dat$Lat)

phi <- 3/0.07

beta.prior.mean <- rep(0, times=p)
beta.prior.precision <- matrix(0, nrow=p, ncol=p)

alpha <- 1/1.5

sigma.sq.prior.shape <- 2.0
sigma.sq.prior.rate <- 10.0

##With covariates
m.3 <-
  bayesGeostatExact(Y~X1+X2+X3+X4, data=FORMGMT.dat,
                    n.samples=n.samples,
                    beta.prior.mean=beta.prior.mean,
                    beta.prior.precision=beta.prior.precision,

```

```

        coords=coords, phi=phi, alpha=alpha,
        sigma.sq.prior.shape=sigma.sq.prior.shape,
        sigma.sq.prior.rate=sigma.sq.prior.rate,
        sp.effects=FALSE)

print(spDIC(m.3, DIC.marg=TRUE, DIC.unmarg=FALSE))

##Without covariates
p <- 1 ##intercept only
beta.prior.mean <- 0
beta.prior.precision <- 0

m.4 <-
  bayesGeostatExact(Y~1, data=FORMGMT.dat,
                    n.samples=n.samples,
                    beta.prior.mean=beta.prior.mean,
                    beta.prior.precision=beta.prior.precision,
                    coords=coords, phi=phi, alpha=alpha,
                    sigma.sq.prior.shape=sigma.sq.prior.shape,
                    sigma.sq.prior.rate=sigma.sq.prior.rate,
                    sp.effects=FALSE)

print(spDIC(m.4, DIC.marg=TRUE, DIC.unmarg=FALSE))

##Lower DIC is better, so go with the covariates.

#####
##          DIC for spGGT
#####
data(FBC07.dat)

Y.2 <- FBC07.dat[1:100,"Y.2"]
coords <- as.matrix(FBC07.dat[1:100,c("coord.X", "coord.Y")])

##m.5 some model with spGGT.
K.prior <- prior(dist="IG", shape=2, scale=5)
Psi.prior <- prior(dist="IG", shape=2, scale=5)
phi.prior <- prior(dist="UNIF", a=0.06, b=3)

var.update.control <-
  list("K"=list(starting=5, tuning=0.1, prior=K.prior),
       "Psi"=list(starting=5, tuning=0.1, prior=Psi.prior),
       "phi"=list(starting=0.1, tuning=0.5, prior=phi.prior)
       )

beta.control <- list(update="GIBBS", prior=prior(dist="FLAT"))

run.control <- list("n.samples"=1000, "sp.effects"=TRUE)

m.5 <-
  spGGT(formula=Y.2~1, run.control=run.control,
        coords=coords, var.update.control=var.update.control,
        beta.update.control=beta.control,

```

```

cov.model="exponential")

##Now with the spGGT object, m.5, calculate the DIC
##for both the unmarginalized and marginalized models.
##The likelihoods for these models are given by equation 6 and 7
##within the vignette.

DIC <- spDIC(m.5)
print(DIC)

#####
##      Compare DIC between non-spatial
##      and spatial models
#####

data(FBC07.dat)
Y.2 <- FBC07.dat[1:150,"Y.2"]
coords <- as.matrix(FBC07.dat[1:150,c("coord.X", "coord.Y")])

#####
##Non-spatial model
#####
m.1 <- bayesLMConjugate(Y.2~1, n.samples = 2000,
                        beta.prior.mean=0, beta.prior.precision=0,
                        prior.shape=-0.5, prior.rate=0)

summary(m.1$p.samples)

dic.m1 <- spDIC(m.1)

##> dic.m1
##           [,1]
##bar.D      503.023678
##D.bar.Omega 501.059965
##pD         1.963713
##DIC        504.987392

#####
##Spatial model
#####
m.2 <- spLM(Y.2~1, coords=coords, knots=c(6,6,0),
             starting=list("phi "=0.1, "sigma.sq "=5, "tau.sq "=5),
             sp.tuning=list("phi "=0.03, "sigma.sq "=0.03, "tau.sq "=0.03),
             priors=list("phi.Unif "=c(0.06, 3), "sigma.sq.IG "=c(2, 5),
                          "tau.sq.IG "=c(2, 5)),
             cov.model="exponential",
             n.samples=2000, verbose=TRUE, n.report=100)

summary(m.2$p.samples)

dic.m2 <- spDIC(m.2)

##> dic.m2

```

```

##$DIC.marg
##          value
##bar.D      479.904433
##D.bar.Omega 476.856815
##pD         3.047617
##DIC        482.952050

##$DIC.unmarg
##          value
##bar.D      330.50408
##D.bar.Omega 258.64266
##pD         71.86142
##DIC        402.36550

## End(Not run)

## End(Not run)

```

spGGT	<i>Function for fitting univariate and multivariate Bayesian spatial regression models</i>
-------	--

Description

The function `spGGT` fits Gaussian univariate and multivariate stationary Bayesian spatial regression models.

Usage

```

spGGT(formula, data = parent.frame(), coords, run.control,
       var.update.control, beta.update.control, cov.model,
       verbose=TRUE, ...)

```

Arguments

<code>formula</code>	for a univariate model, this is a symbolic description of the regression model to be fit. For a multivariate model, this is a list of univariate formulas. See example below.
<code>data</code>	an optional data frame containing the variables in the model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>spGGT</code> is called.
<code>coords</code>	an $n \times 2$ matrix of the observation coordinates in R^2 (e.g., easting and northing).
<code>run.control</code>	a list with tags: <code>n.samples</code> the value of which is the number of MCMC iterations; <code>sp.effects</code> a logical value indicating if spatial random effects should be recovered; <code>DIC</code> a logical value indicating if marginalized DIC and associated statistics should be computed; <code>DIC.start</code> and <code>DIC.end</code> the MCMC iteration interval over which DIC should be calculated; and <code>linpack</code> a logical value indicating if LINPACK or LAPACK should be used for matrix algebra operations. The default is to use LINPACK.

`var.update.control`

a list with each tag corresponding to a parameter name used to define the variance structure of the model. Valid list tags are `K`, `Psi`, `phi`, and `nu`. The value portion of each of these tags is another list with tags `sample.order`, `starting`, `tuning`, and `prior`. The positive scalar value of the optional tag `sample.order` determines the order in which parameters are updated by sequential Metropolis-Hastings steps. The `sample.order` value is relative to the sample order specified for the other parameters. The value of the `starting` tag defines the starting value of the parameter in the Metropolis-Hastings sampling. If the list element defines a vector or matrix of parameters, then the starting value should be set accordingly. If a scalar starting value is given for a vector or matrix of parameters then the scalar value is recycled. If the model defines `K` or `Psi` as a full cross-covariance matrix, opposed to a diagonal matrix or scalar, then the starting value should be the lower-triangle of the Cholesky square root of the desired starting matrix value. If `K` or `Psi` is a diagonal matrix, then the starting values should be passed as a vector or scalar. The value associated with the `tuning` tag defines the step size of the proposal used in the Metropolis-Hastings sampling. Again the tuning value is recycled if needed. If the parameter element is a matrix, i.e., `K` or `Psi`, then the diagonal elements in the tuning matrix correspond to the column major lower-triangle elements in the parameter matrix. The value of the `prior` tag is a valid `prior` object which describes the prior distribution of the parameter. Any parameter in the specified model can be fixed by using the `FIXED prior` with the `starting` value set to the desired fixed value. See example below.

`beta.update.control`

a list with tags `update`, `tuning`, `starting`, `prior`, and `sample.order`. The value of `update` is either "GIBBS" or "MH". With the "MH" option, the value of the optional tag `tuning` is the upper-triangle of the Cholesky decomposed $p \times p$ tuning matrix, where p is the number of regression parameters. The tuning matrix controls the proposal step size in the Metropolis-Hastings sampling. The tuning values along the diagonal of this matrix correspond to the order of the regressors in the model formula. Off-diagonal elements are the covariance among the terms. The optional tag `starting` receives a vector of length p , whose elements define the starting values of the regressors used in the MCMC sampling. The order of the starting values in this vector corresponds to the order of the regressors in the model formula. The optional tag `prior` is a valid `prior` object that defines either a normal or flat distribution. If `prior` is not included in the `beta.update.control` list then the prior distribution on the regressors is assumed flat (i.e., proportional to 1.0). With the "MH" option, the value of the optional tag `sample.order` determines the order in which parameters are updated by sequential Metropolis-Hastings steps, see below for details.

`cov.model`

a quoted key word that specifies the covariance function used to model the spatial dependence structure among the observations. Supported covariance model key words are: "exponential", "matern", "spherical", and "gaussian". See below for details.

`verbose`

if TRUE, model specification and progress of the sampler is printed to the screen. Otherwise, nothing is printed to the screen.

... currently no additional arguments.

Details

Please refer to Section 3.1 in the vignette.

Value

An object of class `spGGT`, which is a list with the following tags:

<code>cov.model</code>	the covariance model specified by <code>cov.model</code> .
<code>no.Psi</code>	a logical value indicating if the parameter <code>Psi</code> was used.
<code>coords</code>	the $n \times 2$ matrix specified by <code>coords</code> .
<code>X</code>	the $n \times p$ matrix of regressors specified by <code>formula</code> .
<code>Y</code>	the $n \times 1$ response variable vector specified by <code>formula</code> .
<code>p.samples</code>	a matrix of posterior samples for the defined parameters. If <code>K</code> or <code>Psi</code> is specified as a full cross-covariance matrix then the corresponding samples in <code>p.samples</code> are column major lower-triangle elements of the matrix.
<code>acceptance</code>	a matrix of the Metropolis-Hastings sampling acceptance rate. Row names correspond to the parameters updated with Metropolis-Hastings.
<code>DIC</code>	a matrix that holds marginalized DIC and associated values is returned if <code>DIC</code> is true in the <code>run.control</code> list.
<code>sp.effects</code>	a matrix that holds samples from the posterior distribution of the response specific spatial random effects. The rows of this matrix correspond to the n point observations and the columns are the posterior samples. If a multivariate model is fit to m response variables, the <code>sp.effects</code> matrix has mn rows. The random effects samples for points are held in rows $1:m$, $(m+1):2m$, ..., $((i-1)m+1):im$, ..., $((n-1)m+1):nm$, where $i = 1 \dots n$ (e.g., the samples for the first point are in rows $1:m$, second point in rows $(m+1):2m$, etc.).

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References

Banerjee, S., Carlin, B.P., and Gelfand, A.E. (2004). Hierarchical modeling and analysis for spatial data. Chapman and Hall/CRC Press, Boca Raton, Fla.

See Also

[prior](#), [spPredict](#), [spDIC](#)

Examples

```

## Not run:

data(FBC07.dat)
Y.1 <- FBC07.dat[1:100,"Y.1"]
Y.2 <- FBC07.dat[1:100,"Y.2"]
coords <- as.matrix(FBC07.dat[1:100,c("coord.X", "coord.Y")])

#####
##   Univariate models
#####

##Fit some competing models.
##Full model with nugget (Psi), partial sill (K),
##and spatial range (Phi).
K.prior <- prior(dist="IG", shape=2, scale=5)
Psi.prior <- prior(dist="IG", shape=2, scale=5)
phi.prior <- prior(dist="UNIF", a=0.06, b=3)

var.update.control <-
  list("K"=list(starting=5, tuning=0.5, prior=K.prior),
       "Psi"=list(starting=5, tuning=0.5, prior=Psi.prior),
       "phi"=list(starting=0.1, tuning=0.5, prior=phi.prior)
       )

beta.control <- list(update="GIBBS", prior=prior(dist="FLAT"))

run.control <- list("n.samples"=1000, "sp.effects"=TRUE)

Fit.m1 <- spGGT(formula=Y.2~1, run.control=run.control,
                coords=coords, var.update.control=var.update.control,
                beta.update.control=beta.control,
                cov.model="exponential")

plot(Fit.m1$p.samples)
summary(Fit.m1$p.samples)

##First reduced model with no nugget just partial sill and range.
var.update.control <-
  list("K"=list(starting=5, tuning=0.5, prior=K.prior),
       "phi"=list(starting=0.1, tuning=0.5, prior=phi.prior)
       )

Fit.m2 <- spGGT(formula=Y.2~1, run.control=run.control,
                coords=coords, var.update.control=var.update.control,
                beta.update.control=beta.control,
                cov.model="exponential")

plot(Fit.m2$p.samples)

##Second reduced model with no nugget just partial sill and fixed
##range at the WRONG value, which forces the wrong estimate of K.

```

```

phi.prior <- prior(dist="FIXED")

var.update.control <-
  list("K"=list(starting=5, tuning=0.5, prior=K.prior),
       "phi"=list(starting=0.1, prior=phi.prior)
       )

Fit.m3 <- spGGT(formula=Y.2~1, run.control=run.control,
               coords=coords, var.update.control=var.update.control,
               beta.update.control=beta.control,
               cov.model="exponential")
plot(Fit.m3$sp.samples)

##For this data, DIC cannot distinguish between the first two
##models but does show that the third model is clearly
##wrong. An empirical semivariogram is useful
##for recognizing that the full model is the correct choice
##over the second model.
print(spDIC(Fit.m1, DIC.unmarg=FALSE))
print(spDIC(Fit.m2, DIC.unmarg=FALSE))
print(spDIC(Fit.m3, DIC.unmarg=FALSE))

##Use akima or MBA to produce interpolated surfaces of
##estimated random spatial effects.

m1.surf <- mba.surf(cbind(coords, rowMeans(Fit.m1$sp.effects)),
                  no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(m1.surf, xaxs="r", yaxs="r",
      main="Y.2 random spatial effects")
points(coords, pch=19)

##Now the full model using the Matern spatial correlation function.
##Also, for fun, update the spatial range parameters
##phi and nu in a separate MH block. This provides finer control
##on the parameters' acceptance rate, but takes a bit longer to
##run.
phi.prior <- prior(dist="UNIF", a=0.06, b=3)
nu.prior <- prior(dist="UNIF", a=0.01, b=2)

var.update.control <-
  list("K"=list(starting=5, tuning=0.5, prior=K.prior),
       "Psi"=list(starting=5, tuning=0.5, prior=Psi.prior),
       "phi"=list(sample.order=1, starting=0.1,
                  tuning=0.5, prior=phi.prior),
       "nu"=list(sample.order=1, starting=0.1,
                  tuning=0.5, prior=nu.prior)
       )

run.control <- list("n.samples"=1000, "sp.effects"=FALSE)

Fit.m4 <-
  spGGT(formula=Y.2~1, run.control=run.control,
        coords=coords, var.update.control=var.update.control,

```

```

        beta.update.control=beta.control,
        cov.model="matern")

plot(Fit.m4$p.samples)

##Solve the Matern correlation function for the estimated
##95% CI for effective range (e.g., distance at which the
##correlation drops to 0.05).
phi.hat <- quantile(Fit.m4$p.samples[, "Phi"], c(0.50,0.025,0.975))
nu.hat <- quantile(Fit.m4$p.samples[, "Nu"], c(0.50,0.025,0.975))

matern <- function(cor, eff.d, phi, nu){
  cor - (eff.d*phi)^nu/(2^(nu-1)*gamma(nu))*besselK(x=eff.d*phi, nu=nu)
}

##50
print(uniroot(matern, interval=c(1, 50),
             cor=0.05, phi=phi.hat[1], nu=nu.hat[1])$root)
print(uniroot(matern, interval=c(1, 50),
             cor=0.05, phi=phi.hat[2], nu=nu.hat[2])$root)
print(uniroot(matern, interval=c(1, 50),
             cor=0.05, phi=phi.hat[3], nu=nu.hat[3])$root)

##Finally, the full model again but this time update the Beta
##using MH. Using the default of sample.order=0, this sampling
##scheme is simply a single block MH proposal of all model parameters.
##Also, the first run uses the default tuning value for the Beta
##(i.e., chol(vcov(lm(Y~X))). Both chains use a normal prior on Beta;
##however, the first chain allows for a vague prior, where as the
##second is much too strict.
var.update.control <-
  list("K"=list(starting=5, tuning=0.5, prior=K.prior),
       "Psi"=list(starting=5, tuning=0.5, prior=Psi.prior),
       "phi"=list(starting=0.1, tuning=0.5, prior=phi.prior)
  )

##Chain 1: vague prior normal variance of 1/0.001 = 1000
beta.prior <- prior(dist="NORMAL", mu=5, precision=0.001)
beta.control <- list(update="MH", prior=beta.prior)

Fit.m5.a <-
  spGGT(formula=Y.2~1, run.control=run.control,
        coords=coords, var.update.control=var.update.control,
        beta.update.control=beta.control,
        cov.model="exponential")

##Chain 2: restrictive prior normal variance of 1/5 = 0.2
##(i.e., crazy strict)
beta.prior <- prior(dist="NORMAL", mu=5, precision=5)
beta.control <- list(update="MH", prior=beta.prior, tuning=0.75)

Fit.m5.b <-
  spGGT(formula=Y.2~1, run.control=run.control,

```

```

        coords=coords, var.update.control=var.update.control,
        beta.update.control=beta.control,
        cov.model="exponential")

plot(mcmc.list(Fit.m5.a$p.samples, Fit.m5.b$p.samples))

##Now just for fun, here is the full model but using the weakly
##informative half-Cauchy for the nugget (Psi) and partial sill (K).

K.prior <- prior(dist="HC", a=50)
Psi.prior <- prior(dist="HC", a=50)
phi.prior <- prior(dist="UNIF", a=0.06, b=3)

var.update.control <-
  list("K"=list(starting=5, tuning=0.5, prior=K.prior),
       "Psi"=list(starting=5, sample.order=1, tuning=2, prior=Psi.prior),
       "phi"=list(starting=0.1, sample.order=2, tuning=1, prior=phi.prior)
  )

beta.control <- list(update="GIBBS", prior=prior(dist="FLAT"))

run.control <- list("n.samples"=3000, "sp.effects"=TRUE)

Fit.m1 <- spGGT(formula=Y.2~1, run.control=run.control,
               coords=coords, var.update.control=var.update.control,
               beta.update.control=beta.control,
               cov.model="exponential")

plot(Fit.m1$p.samples)
summary(Fit.m1$p.samples)

#####
##  Multivariate models
#####

##Full model with non-spatial cross-covariance
##(Psi) matrix, spatial cross-covariance matrix (K),
##and response specific spatial range parameter (Phi)
##(i.e., a non-separable model).

##These chains really need to be run for several thousand
##samples (e.g., 10,000). Also note that it is much easier to maintain
##a healthy acceptance rate for each parameter if they
##are updated individually using the sample.order
##directive, as shown in the second example below.
K.prior <- prior(dist="IWISH", df=2, S=diag(c(3, 6)))
Psi.prior <- prior(dist="IWISH", df=2, S=diag(c(7, 5)))
phi.prior <- prior(dist="UNIF", a=0.06, b=3)

##The matrix starting values for K and Psi are actually
##passed as the sqrt of the desired starting values.
##This is only done if K or Psi are full cross-covariance
##matrices and serve to insure that the true starting value

```

```

##matrix is positive definite.
K.starting <- matrix(c(2,-3, 0, 1), 2, 2)
Psi.starting <- diag(c(3, 2))

var.update.control <-
  list("K"=list(starting=K.starting, tuning=diag(c(0.08, 0.3, 0.08)),
    prior=K.prior),
    "Psi"=list(starting=Psi.starting, tuning=diag(c(0.08, 0.3, 0.08)),
    prior=Psi.prior),
    "phi"=list(starting=0.1, tuning=0.5,
    prior=list(phi.prior, phi.prior))
  )

beta.control <- list(update="GIBBS", prior=prior(dist="FLAT"))

run.control <- list("n.samples"=2000, "sp.effects"=FALSE)

Fit.mv.m1 <-
  spGGT(formula=list(Y.1~1, Y.2~1), run.control=run.control,
    coords=coords, var.update.control=var.update.control,
    beta.update.control=beta.control,
    cov.model="exponential")

plot(Fit.mv.m1$p.samples)

##Calculate the mean K correlation matrix. Note that since K is
##specified as a full cross-covariance matrix, the posterior
##samples are returned for the lower triangle of the symmetric K,
##in column major order.
K <- matrix(0, 2, 2)
K[lower.tri(K, diag=TRUE)] <-
  colMeans(Fit.mv.m1$p.samples[,c("K_1", "K_2", "K_3")])
K[upper.tri(K, diag=FALSE)] <- t(K)[upper.tri(K, diag=FALSE)]
print(cov2cor(K))

##Now using sample order. Note this takes ~3 times as long
##to run, but provides much finer control of acceptance rates.
var.update.control <-
  list("K"=list(sample.order=0, starting=K.starting,
    tuning=diag(c(0.3, 0.5, 0.2)), prior=K.prior),
    "Psi"=list(sample.order=1, starting=Psi.starting,
    tuning=diag(c(0.2, 0.5, 0.2)), prior=Psi.prior),
    "phi"=list(sample.order=2, starting=0.1,
    tuning=0.5, prior=list(phi.prior, phi.prior))
  )

run.control <- list("n.samples"=2000, "sp.effects"=TRUE)

Fit.mv.m2 <-
  spGGT(formula=list(Y.1~1, Y.2~1), run.control=run.control,
    coords=coords, var.update.control=var.update.control,
    beta.update.control=beta.control,
    cov.model="exponential")

```

```

plot(Fit.mv.m2$sp.samples)

##Now again check out the random spatial effects. Recall,
##these are stored in the sp.effects matrix, which is organized
##as m consecutive rows for each point.
rand.effect.Y.1 <-
  Fit.mv.m2$sp.effects[seq(1, nrow(Fit.mv.m2$sp.effects), 2),]

rand.effect.Y.2 <-
  Fit.mv.m2$sp.effects[seq(2, nrow(Fit.mv.m2$sp.effects), 2),]

rand.effect.Y.1.surf <-
  mba.surf(cbind(coords, rowMeans(rand.effect.Y.1)),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est

rand.effect.Y.2.surf <-
  mba.surf(cbind(coords, rowMeans(rand.effect.Y.2)),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est

##The estimated negative value of off-diagonal element in K is
##clearly seen in the map of random spatial effects.
par(mfrow=c(1,2))
image(rand.effect.Y.1.surf, xaxs="r", yaxs="r",
      main="Y.1 random spatial effects")
contour(rand.effect.Y.1.surf, add=TRUE)
image(rand.effect.Y.2.surf, xaxs="r", yaxs="r",
      main="Y.2 random spatial effects")
contour(rand.effect.Y.2.surf, add=TRUE)

##Now a simpler model. Specifically, the full model shows that
##there is negligible non-spatial cross-covariance, therefore,
##Psi might just be modeled with a diagonal covariance matrix.
##This is actually the model which gave rise to this synthetic
##data set.
K.prior <- prior(dist="IWISH", df=2, S=diag(c(3, 6)))
Psi.prior <- prior(dist="IG", shape=2, scale=5)
phi.prior <- prior(dist="UNIF", a=0.06, b=3)

var.update.control <-
  list("K"=list(sample.order=0, starting=K.starting,
               tuning=diag(c(0.3, 0.5, 0.2)), prior=K.prior),
       "Psi"=list(sample.order=1, starting=5,
                  tuning=0.5, prior=list(Psi.prior, Psi.prior)),
       "phi"=list(sample.order=2, starting=0.1,
                  tuning=0.5, prior=list(phi.prior, phi.prior))
  )

run.control <- list("n.samples"=2000)

Fit.mv.m3 <-
  spGGT(formula=list(Y.1~1, Y.2~1), run.control=run.control,
        coords=coords, var.update.control=var.update.control,

```

```

        beta.update.control=beta.control,
        cov.model="exponential")

plot(Fit.mv.m3$p.samples)
summary(Fit.mv.m3$p.samples)

##Finally, a really simple model which we know makes no sense
##for this data set. Specifically, a single variance parameter
##for the diagonal elements of K and Psi and common spatial range,
##phi. Also, we use a spherical spatial covariance function, just
##because we can.
K.prior <- prior(dist="IG", shape=2, scale=5)
Psi.prior <- prior(dist="IG", shape=2, scale=5)
phi.prior <- prior(dist="UNIF", a=0.06, b=3)

var.update.control <-
  list("K"=list(starting=5, tuning=0.5, prior=K.prior),
       "Psi"=list(starting=5, tuning=0.5, prior=Psi.prior),
       "phi"=list(starting=0.1, tuning=0.5, prior=phi.prior)
      )

Fit.mv.m4 <-
  spGGT(formula=list(Y.1~1, Y.2~1), run.control=run.control,
        coords=coords, var.update.control=var.update.control,
        beta.update.control=beta.control,
        cov.model="spherical")

plot(Fit.mv.m4$p.samples)

## End(Not run)

```

spGLM

Function for fitting univariate Bayesian generalized linear spatial regression models

Description

The function `spGLM` fits univariate stationary Bayesian generalized linear spatial regression models. Given a set of knots, `spGLM` fits a *predictive process* model (see references below).

Usage

```

spGLM(formula, family="binomial", data = parent.frame(), coords, knots,
       starting, tuning, priors, cov.model,
       n.samples, sub.samples, verbose=TRUE, n.report=100, ...)

```

Arguments

`formula` a symbolic description of the regression model to be fit. See example below.

family	currently only supports <code>binomial</code> and <code>poisson</code> data using the logit and log link functions, respectively.
data	an optional data frame containing the variables in the model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>spGLM</code> is called.
coords	an $n \times 2$ matrix of the observation coordinates in R^2 (e.g., easting and northing).
knots	either a $m \times 2$ matrix of the <i>predictive process</i> knot coordinates in R^2 (e.g., easting and northing) or a vector of length two or three with the first and second elements recording the number of columns and rows in the desired knot grid. The third, optional, element sets the offset of the outermost knots from the extent of the <code>coords</code> extent.
starting	a list with each tag corresponding to a parameter name. Valid list tags are <code>beta</code> , <code>sigma.sq</code> , <code>phi</code> , <code>nu</code> , and <code>w</code> . The value portion of each tag is the parameter's starting value. If the predictive process is used then <code>w</code> must be of length m ; otherwise, it must be of length n . Alternatively, <code>w</code> can be set as a scalar, in which case the value is repeated.
tuning	a list with each tag corresponding to a parameter name. Valid list tags are <code>beta</code> , <code>sigma.sq</code> , <code>phi</code> , <code>nu</code> , and <code>w</code> . The value portion of each tag defines the variance of the Metropolis normal proposal distribution. The tuning value for <code>beta</code> can be a vector of length p or the lower-triangle of the $p \times p$ Cholesky square-root of the desired proposal variance matrix. If the predictive process is used then <code>w</code> must be of length m ; otherwise, it must be of length n . Alternatively, <code>w</code> can be set as a scalar, in which the value is repeated.
priors	a list with each tag corresponding to a parameter name. Valid list tags are <code>beta.flat</code> , <code>beta.normal</code> , <code>sigma.sq.ig</code> , <code>phi.unif</code> , and <code>nu.unif</code> . <code>sigma.sq</code> is assumed to follow an inverse-Gamma distribution, whereas the spatial range <code>phi</code> and smoothness <code>nu</code> parameters are assumed to follow Uniform distributions. If <code>beta.normal</code> then covariate specific mean and variance hyperparameters are passed as the first and second list elements, respectively. The hyperparameters of the inverse-Gamma are passed as a vector of length two, with the first and second elements corresponding to the <i>shape</i> and <i>scale</i> , respectively. The hyperparameters of the Uniform are also passed as a vector of length two with the first and second elements corresponding to the lower and upper support, respectively.
cov.model	a quoted key word that specifies the covariance function used to model the spatial dependence structure among the observations. Supported covariance model key words are: <code>"exponential"</code> , <code>"matern"</code> , <code>"spherical"</code> , and <code>"gaussian"</code> . See below for details.
n.samples	the number of MCMC iterations.
sub.samples	a vector of length 3 that specifies <i>start</i> , <i>end</i> , and <i>thin</i> , respectively, of the MCMC samples. The default is <code>c(1, n.samples, 1)</code> (i.e., all samples).
verbose	if <code>TRUE</code> , model specification and progress of the sampler is printed to the screen. Otherwise, nothing is printed to the screen.
n.report	the interval to report Metropolis acceptance and MCMC progress.
...	currently no additional arguments.

Value

An object of class `spGLM`, which is a list with the following tags:

<code>coords</code>	the $n \times 2$ matrix specified by <code>coords</code> .
<code>knot.coords</code>	the $m \times 2$ matrix as specified by <code>knots</code> .
<code>p.samples</code>	a coda object of posterior samples for the defined parameters.
<code>acceptance</code>	the Metropolis sampling acceptance rate.
<code>sp.effects</code>	a matrix that holds samples from the posterior distribution of the spatial random effects. The rows of this matrix correspond to the n point observations and the columns are the posterior samples.

The return object might include additional data used for subsequent prediction and/or model fit evaluation.

Author(s)

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References

- Finley, A.O., S. Banerjee, and R.E. McRoberts. (2008) A Bayesian approach to quantifying uncertainty in multi-source forest area estimates. *Environmental and Ecological Statistics*, 15:241–258.
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- Banerjee, S., Carlin, B.P., and Gelfand, A.E. (2004). Hierarchical modeling and analysis for spatial data. Chapman and Hall/CRC Press, Boca Raton, Fla.

See Also

[spGGT](#), [spMvLM](#), [spMvGLM](#)

Examples

```
## Not run:
#####
##Spatial poisson
#####

##Generate count data
n <- 100

coords <- cbind(runif(n,1,100),runif(n,1,100))

phi <- 3/75
```

```

sigma.sq <- 2

R <- sigma.sq*exp(-phi*as.matrix(dist(coords)))
w <- mvrnorm(1, rep(0,n), R)

x <- as.matrix(rep(1,n))
beta <- 0.1
y <- rpois(n, exp(x%*%beta+w))

##Collect samples
beta.starting <- coefficients(glm(y~x-1, family="poisson"))
beta.tuning <- t(chol(vcov(glm(y~x-1, family="poisson"))))

n.samples <- 25000

m.1 <- spGLM(y~1, family="poisson", coords=coords,
             starting=
             list("beta"=beta.starting, "phi"=0.06,"sigma.sq"=1, "w"=0),
             tuning=
             list("beta"=0.1, "phi"=0.01, "sigma.sq"=0.01, "w"=0.005),
             priors=
             list("beta.Flat", "phi.Unif"=c(0.03, 0.3), "sigma.sq.IG"=c(2, 1)),
             cov.model="exponential",
             n.samples=n.samples, sub.samples=c(10000,n.samples,10),
             verbose=TRUE, n.report=500)

m.1$p.samples[,"phi"] <- 3/m.1$p.samples[,"phi"]

print(summary(mcmc(m.1$p.samples)))

beta.hat <- mean(m.1$p.samples[,"(Intercept)"])
w.hat <- rowMeans(m.1$sp.effects)

y.hat <-exp(x%*%beta.hat+w.hat)

##Take a look
par(mfrow=c(1,2))
surf <- mba.surf(cbind(coords,y),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="obs")
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=y, cex=1, col="blue")

surf <- mba.surf(cbind(coords,y.hat),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Fitted counts")
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=round(y.hat,0), cex=1, col="blue")

#####
##Spatial logistic
#####

##Generate binary data
n <- 50

```

```

coords <- cbind(runif(n,1,100),runif(n,1,100))

phi <- 3/50
sigma.sq <- 1

R <- sigma.sq*exp(-phi*as.matrix(dist(coords)))
w <- mvrnorm(1, rep(0,n), R)

x <- as.matrix(rep(1,n))
beta <- 0.1
p <- 1/(1+exp(-(x%*%beta+w)))
y <- rbinom(n, 1, prob=p)

##Collect samples
beta.starting <- coefficients(glm(y~x-1, family="binomial"))
beta.tuning <- t(chol(vcov(glm(y~x-1, family="binomial"))))

n.samples <- 50000

m.1 <- spGLM(y~1, family="binomial", coords=coords,
             starting=
             list("beta"=beta.starting, "phi"=0.06,"sigma.sq"=1, "w"=0),
             tuning=
             list("beta"=beta.tuning, "phi"=0.1, "sigma.sq"=0.1, "w"=0.01),
             priors=
             list("beta.Normal"=list(0,10), "phi.Unif"=c(0.03, 0.3),
                  "sigma.sq.IG"=c(2, 1)),
             cov.model="exponential",
             n.samples=n.samples, sub.samples=c(25000,n.samples,10),
             verbose=TRUE, n.report=500)

m.1$p.samples[, "phi"] <- 3/m.1$p.samples[, "phi"]

print(summary(mcmc(m.1$p.samples)))

beta.hat <- mean(m.1$p.samples[, "(Intercept)"])
w.hat <- rowMeans(m.1$sp.effects)

y.hat <- 1/(1+exp(-(x%*%beta.hat+w.hat)))

##Take a look
par(mfrow=c(1,2))
surf <- mba.surf(cbind(coords,y),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Observed")
contour(surf, add=TRUE)
points(coords[y==1,], pch=19, cex=1)
points(coords[y==0,], cex=1)

surf <- mba.surf(cbind(coords,y.hat),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Fitted probabilities")
contour(surf, add=TRUE)
points(coords[y==1,], pch=19, cex=1)

```

```

points(coords[y==0,], cex=1)

#####
##Predictive process
#####

##Generate binary data
n <- 500

coords <- cbind(runif(n,1,100),runif(n,1,100))

phi <- 3/50
sigma.sq <- 1

R <- sigma.sq*exp(-phi*as.matrix(dist(coords)))
w <- mvrnorm(1, rep(0,n), R)

x <- as.matrix(rep(1,n))
beta <- 0.1
p <- 1/(1+exp(-(x*%*beta+w)))
y <- rbinom(n, 1, prob=p)

##Collect samples
beta.starting <- coefficients(glm(y~x-1, family="binomial"))
beta.tuning <- t(chol(vcov(glm(y~x-1, family="binomial"))))

n.samples <- 25000

m.2 <- spGLM(y~1, family="binomial", coords=coords, knots=c(8,8,0),
  starting=
  list("beta"=beta.starting, "phi"=0.06, "sigma.sq"=1, "w"=0),
  tuning=
  list("beta"=beta.tuning, "phi"=0.1, "sigma.sq"=0.1, "w"=0.01),
  priors=
  list("beta.Normal"=list(0,10), "phi.Unif"=c(0.03, 0.3),
    "sigma.sq.IG"=c(2, 1)),
  cov.model="exponential",
  n.samples=n.samples, sub.samples=c(15000,n.samples,10),
  verbose=TRUE, n.report=500)

m.2$p.samples[, "phi"] <- 3/m.2$p.samples[, "phi"]

print(summary(mcmc(m.2$p.samples)))

beta.hat <- mean(m.2$p.samples[, "(Intercept)"])
w.hat <- rowMeans(m.2$sp.effects)

y.hat <- 1/(1+exp(-(x*%*beta.hat+w.hat)))

##Take a look
par(mfrow=c(1,2))
surf <- mba.surf(cbind(coords,y),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Observed")

```

```

contour(surf, add=TRUE)
points(coords[y==1,], pch=19, cex=1)
points(coords[y==0,], cex=1)

surf <- mba.surf(cbind(coords,y.hat),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Fitted probabilities")
contour(surf, add=TRUE)
points(coords[y==1,], pch=19, cex=1)
points(coords[y==0,], cex=1)
points(m.2$knot.coords, pch=15, cex=1, col="blue")

## End(Not run)

```

spLM

Function for fitting univariate Bayesian spatial regression models

Description

The function `spLM` fits Gaussian univariate stationary Bayesian spatial regression models. Given a set of knots, `spLM` fits a *predictive process* model (see references below).

Usage

```

spLM(formula, data = parent.frame(), coords, knots,
      starting, sp.tuning, priors, cov.model,
      modified.pp = TRUE, n.samples, sub.samples,
      verbose=TRUE, n.report=100, ...)

```

Arguments

<code>formula</code>	a symbolic description of the regression model to be fit. See example below.
<code>data</code>	an optional data frame containing the variables in the model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>spLM</code> is called.
<code>coords</code>	an $n \times 2$ matrix of the observation coordinates in R^2 (e.g., easting and northing).
<code>knots</code>	either a $m \times 2$ matrix of the <i>predictive process</i> knot coordinates in R^2 (e.g., easting and northing) or a vector of length two or three with the first and second elements recording the number of columns and rows in the desired knot grid. The third, optional, element sets the offset of the outermost knots from the extent of the <code>coords</code> extent.
<code>starting</code>	a list with each tag corresponding to a parameter name. Valid list tags are <code>beta</code> , <code>sigma.sq</code> , <code>tau.sq</code> , <code>phi</code> , and <code>nu</code> . The value portion of each of each tag is the parameter's starting value.
<code>sp.tuning</code>	a list with each tag corresponding to a parameter name. Valid list tags are <code>sigma.sq</code> , <code>tau.sq</code> , <code>phi</code> , and <code>nu</code> . The value portion of each of each tag defines the variance of the Metropolis normal proposal distribution.

<code>modified.pp</code>	a logical value indicating if the <i>modified predictive process</i> should be used (see references below for details). Note, if a predictive process model is not used (i.e., <code>knots</code> is not specified) then this argument is ignored.
<code>priors</code>	a list with each tag corresponding to a parameter name. Valid list tags are <code>sigma.sq.ig</code> , <code>tau.sq.ig</code> , <code>phi.unif</code> , and <code>nu.unif</code> (Beta priors are assumed <i>flat</i>). Variance parameters, <code>sigma.sq</code> and <code>tau.sq</code> , are assumed to follow an inverse-Gamma distribution, whereas the spatial range <code>phi</code> and smoothness <code>nu</code> parameters are assumed to follow Uniform distributions. The hyperparameters of the inverse-Gamma are passed as a vector of length two, with the first and second elements corresponding to the <i>shape</i> and <i>scale</i> , respectively. The hyperparameters of the Uniform are also passed as a vector of length two with the first and second elements corresponding to the lower and upper support, respectively.
<code>cov.model</code>	a quoted key word that specifies the covariance function used to model the spatial dependence structure among the observations. Supported covariance model key words are: "exponential", "matern", "spherical", and "gaussian". See below for details.
<code>n.samples</code>	the number of MCMC iterations.
<code>sub.samples</code>	a vector of length 3 that specifies <i>start</i> , <i>end</i> , and <i>thin</i> , respectively, of the MCMC samples. The default is <code>c(1, n.samples, 1)</code> (i.e., all samples).
<code>verbose</code>	if TRUE, model specification and progress of the sampler is printed to the screen. Otherwise, nothing is printed to the screen.
<code>n.report</code>	the interval to report Metropolis acceptance and MCMC progress.
<code>...</code>	currently no additional arguments.

Value

An object of class `spLM`, which is a list with the following tags:

<code>coords</code>	the $n \times 2$ matrix specified by <code>coords</code> .
<code>knot.coords</code>	the $m \times 2$ matrix as specified by <code>knots</code> .
<code>p.samples</code>	a coda object of posterior samples for the defined parameters.
<code>acceptance</code>	the Metropolis sampling acceptance rate.
<code>sp.effects</code>	a matrix that holds samples from the posterior distribution of the spatial random effects. The rows of this matrix correspond to the n point observations and the columns are the posterior samples.

The return object might include additional data used for subsequent prediction and/or model fit evaluation.

Author(s)

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References

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- Banerjee, S., Carlin, B.P., and Gelfand, A.E. (2004). Hierarchical modeling and analysis for spatial data. Chapman and Hall/CRC Press, Boca Raton, Fla.

See Also

[spGGT](#), [spMvLM](#)

Examples

```
## Not run:
data(rf.n200.dat)

Y <- rf.n200.dat$Y
coords <- as.matrix(rf.n200.dat[,c("x.coords", "y.coords")])
w <- rf.n200.dat$w

#####
##Simple spatial regression
#####
m.1 <- spLM(Y~1, coords=coords,
            starting=list("phi"=0.6, "sigma.sq"=1, "tau.sq"=1),
            sp.tuning=list("phi"=0.01, "sigma.sq"=0.05, "tau.sq"=0.05),
            priors=list("phi.Unif"=c(0.3, 3), "sigma.sq.IG"=c(2, 1),
                       "tau.sq.IG"=c(2, 1)),
            cov.model="exponential",
            n.samples=1000, verbose=TRUE, n.report=100)

print(summary(m.1$sp.samples))
plot(m.1$sp.samples)

##Requires MBA package to
##make surfaces
library(MBA)
par(mfrow=c(1,2))
obs.surf <-
  mba.surf(cbind(coords, Y), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(obs.surf, xaxs = "r", yaxs = "r", main="Observed response")
points(coords)
contour(obs.surf, add=T)

w.hat <- rowMeans(m.1$sp.effects)
```

```

w.surf <-
  mba.surf(cbind(coords, w.hat), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(w.surf, xaxs = "r", yaxs = "r", main="Estimated random effects")
points(coords)
points(m.1$knot.coords, pch=19, cex=1)
contour(w.surf, add=T)

#####
##Predictive process
#####
##Use some more observations
data(rf.n500.dat)

Y <- rf.n500.dat$Y
coords <- as.matrix(rf.n500.dat[,c("x.coords", "y.coords")])
w <- rf.n500.dat$w

m.2 <- spLM(Y~1, coords=coords, knots=c(6,6,0),
  starting=list("phi"=0.6, "sigma.sq"=1, "tau.sq"=1),
  sp.tuning=list("phi"=0.01, "sigma.sq"=0.01, "tau.sq"=0.01),
  priors=list("phi.Unif"=c(0.3, 3), "sigma.sq.IG"=c(2, 1),
    "tau.sq.IG"=c(2, 1)),
  cov.model="exponential",
  modified.pp=FALSE, n.samples=2000, verbose=TRUE, n.report=100)

print(summary(m.2$p.samples))
plot(m.2$p.samples)

##Requires MBA package to
##make surfaces
library(MBA)
par(mfrow=c(1,2))
obs.surf <-
  mba.surf(cbind(coords, w), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(obs.surf, xaxs = "r", yaxs = "r", main="Observed response")
points(coords)
contour(obs.surf, add=T)

w.hat <- rowMeans(m.2$sp.effects)
w.surf <-
  mba.surf(cbind(coords, w.hat), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(w.surf, xaxs = "r", yaxs = "r", main="Estimated random effects")
contour(w.surf, add=T)
points(coords, pch=1, cex=1)
points(m.2$knot.coords, pch=19, cex=1)
legend(1.5,2.5, legend=c("Obs.", "Knots"), pch=c(1,19), bg="white")

#####
##Modified predictive process
#####
m.3 <- spLM(Y~1, coords=coords, knots=c(6,6,0),
  starting=list("phi"=0.6, "sigma.sq"=1, "tau.sq"=1),
  sp.tuning=list("phi"=0.01, "sigma.sq"=0.01, "tau.sq"=0.01),

```

```

priors=list("phi.Unif"=c(0.3, 3), "sigma.sq.IG"=c(2, 1),
            "tau.sq.IG"=c(2, 1)),
cov.model="exponential",
n.samples=2000, verbose=TRUE, n.report=100)

print(summary(m.3$p.samples))
plot(m.3$p.samples)

##Requires MBA package to
##make surfaces
library(MBA)
par(mfrow=c(1,2))
obs.surf <-
  mba.surf(cbind(coords, w), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(obs.surf, xaxs = "r", yaxs = "r", main="Observed response")
points(coords)
contour(obs.surf, add=T)

w.hat <- rowMeans(m.3$sp.effects)
w.surf <-
  mba.surf(cbind(coords, w.hat), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(w.surf, xaxs = "r", yaxs = "r", main="Estimated random effects")
contour(w.surf, add=T)
points(coords, pch=1, cex=1)
points(m.3$knot.coords, pch=19, cex=1)
legend(1.5,2.5, legend=c("Obs.", "Knots"), pch=c(1,19), bg="white")

## End(Not run)

```

spMvGLM

Function for fitting multivariate Bayesian generalized linear spatial regression models

Description

The function `spMvGLM` fits multivariate stationary Bayesian generalized linear spatial regression models. Given a set of knots, `spMvGLM` fits a *predictive process* model (see references below).

Usage

```

spMvGLM(formula, family="binomial", data = parent.frame(), coords, knots,
         starting, tuning, priors, cov.model, n.samples, sub.samples,
         verbose=TRUE, n.report=100, ...)

```

Arguments

<code>formula</code>	for a multivariate model with q response variables, this is a list of univariate formulas. See example below.
<code>family</code>	currently only supports <code>binomial</code> and <code>poisson</code> data using the logit and log link functions, respectively.

<code>data</code>	an optional data frame containing the variables in the model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>spMvGLM</code> is called.
<code>coords</code>	an $n \times 2$ matrix of the observation coordinates in R^2 (e.g., easting and northing).
<code>knots</code>	either a $m \times 2$ matrix of the <i>predictive process</i> knot coordinates in R^2 (e.g., easting and northing) or a vector of length two or three with the first and second elements recording the number of columns and rows in the desired knot grid. The third, optional, element sets the offset of the outermost knots from the extent of the <code>coords</code> extent.
<code>starting</code>	a list with each tag corresponding to a parameter name. Valid list tags are <code>beta</code> , <code>A</code> , <code>phi</code> , and <code>nu</code> . The value portion of each tag is a vector of parameter's starting value. For <code>A</code> the vector is of length $\frac{q(q-q)}{2} + q$ and <code>phi</code> and <code>nu</code> are of length q . Here, <code>A</code> holds the the lower-triangle elements in column major ordering of the Cholesky square root of the spatial cross-covariance matrix. If the predictive process is used then <code>w</code> must be of length qm ; otherwise, it must be of length qn . Alternatively, <code>w</code> can be set as a scalar, in which case the value is repeated.
<code>tuning</code>	a list with each tag corresponding to a parameter name. Valid list tags are <code>beta</code> , <code>A</code> , <code>phi</code> , <code>nu</code> , and <code>w</code> . The value portion of each tag defines the variance of the Metropolis normal proposal distribution. The tuning value for <code>beta</code> can be a vector of length p or the lower-triangle of the $p \times p$ Cholesky square-root of the desired proposal variance matrix. For <code>A</code> , the vector is of length $\frac{q(q-q)}{2} + q$ and <code>phi</code> and <code>nu</code> are of length q . If the predictive process is used then <code>w</code> must be of length m ; otherwise, it must be of length n . Alternatively, <code>w</code> can be set as a scalar, in which the value is repeated.
<code>priors</code>	a list with each tag corresponding to a parameter name. Valid list tags are <code>beta.flat</code> , <code>beta.normal</code> , <code>K.IW</code> , <code>Psi.IW</code> , <code>phi.unif</code> , and <code>nu.unif</code> . If <code>beta.normal</code> then covariate specific mean and variance hyperparameters are passed as the first and second list elements, respectively. <code>K</code> is assumed to follow an inverse-Wishart distribution, whereas the spatial range <code>phi</code> and smoothness <code>nu</code> parameters are assumed to follow Uniform distributions. The hyperparameters of the inverse-Wishart are passed as a list of length two, with the first and second elements corresponding to the <i>df</i> and $q \times q$ <i>scale</i> matrix, respectively. The hyperparameters of the Uniform are also passed as a vector of length $2 \times q$ with consecutive elements representing the first and second elements corresponding to the lower and upper support in the order of the univariate models given in <code>formula</code> .
<code>cov.model</code>	a quoted key word that specifies the covariance function used to model the spatial dependence structure among the observations. Supported covariance model key words are: "exponential", "matern", "spherical", and "gaussian". See below for details.
<code>n.samples</code>	the number of MCMC iterations.
<code>sub.samples</code>	a vector of length 3 that specifies <i>start</i> , <i>end</i> , and <i>thin</i> , respectively, of the MCMC samples. The default is <code>c(1, n.samples, 1)</code> (i.e., all samples).
<code>verbose</code>	if TRUE, model specification and progress of the sampler is printed to the screen. Otherwise, nothing is printed to the screen.
<code>n.report</code>	the interval to report Metropolis acceptance and MCMC progress.

... currently no additional arguments.

Value

An object of class `spMvGLM`, which is a list with the following tags:

<code>coords</code>	the $n \times 2$ matrix specified by <code>coords</code> .
<code>knot.coords</code>	the $m \times 2$ matrix as specified by <code>knots</code> .
<code>p.samples</code>	a coda object of posterior samples for the defined parameters.
<code>acceptance</code>	the Metropolis sampling acceptance rate.
<code>sp.effects</code>	a matrix that holds samples from the posterior distribution of the spatial random effects. The rows of this matrix correspond to the n point observations and the columns are the posterior samples.

The return object might include additional data used for subsequent prediction and/or model fit evaluation.

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References

- Finley, A.O., S. Banerjee, and R.E. McRoberts. (2008) A Bayesian approach to quantifying uncertainty in multi-source forest area estimates. *Environmental and Ecological Statistics*, 15:241–258.
- Banerjee, S., A.E. Gelfand, A.O. Finley, and H. Sang. (2008) Gaussian Predictive Process Models for Large Spatial Datasets. *Journal of the Royal Statistical Society Series B*, 70:825–848.
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See Also

[spGGT](#), [spMvLM](#), [spMvGLM](#)

Examples

```
## Not run:
#####
##Spatial multivariate poisson
#####
##Generate some data
```

```

n <- 100
q <- 3
nltr <- q*(q-1)/2+q

coords <- cbind(runif(n,1,100),runif(n,1,100))

theta <- rep(3/50,q)

A <- matrix(0,q,q)
A[lower.tri(A,TRUE)] <- rnorm(nltr,1,1)
K <- A%*%t(A)

Psi <- diag(0,q)

c1 <- mvCovInvLogDet(coords=coords, knots=coords,
                     cov.model="exponential",
                     V=K, Psi=Psi, theta=theta,
                     modified.pp=TRUE, SWM=FALSE)

w <- mvrnorm(1,rep(0,nrow(c1$C)),c1$C)

X <- mkMvX(list(matrix(1,n,1), matrix(1,n,1), matrix(1,n,1)))
beta <- c(-1,0,1)
y <- rpois(n*q, exp(X%*%beta+w))

y.1 <- y[seq(1,length(y),q)]
y.2 <- y[seq(2,length(y),q)]
y.3 <- y[seq(3,length(y),q)]

##Specify starting values and collect samples. For
##a true analysis, several longer chains should be
##run.
A.starting <- diag(1,q)[lower.tri(diag(1,q), TRUE)]

beta.starting <- coefficients(glm(y~X-1, family="poisson"))
beta.tuning <- t(chol(vcov(glm(y~X-1, family="poisson"))))

n.samples <- 15000

m.1 <- spMvGLM(list(y.1~1,y.2~1,y.3~1), family="poisson", coords=coords,
                 knots=c(8,8,0),
                 starting=
                 list("beta"=beta.starting, "phi"=rep(0.06,q),
                      "A"=A.starting, "w"=0),
                 tuning=
                 list("beta"=beta.tuning, "phi"=rep(0.01,q),
                      "A"=rep(0.005,nltr), "w"=0.001),
                 priors=
                 list("beta.Flat", "phi.Unif"=rep(c(0.03, 0.3),q),
                      "K.IW"=list(q+1, diag(0.1,q))),
                 cov.model="exponential",
                 n.samples=n.samples, sub.sample=c(5000,n.samples,10),
                 verbose=TRUE, n.report=500)

```

```

m.1$p.samples[,paste("phi_",1:q,sep="")] <-
  3/m.1$p.samples[,paste("phi_",1:q,sep="")]

print(summary(mcmc(m.1$p.samples)))

beta.hat <- colMeans(m.1$p.samples[,1:q])
w.hat <- rowMeans(m.1$sp.effects)

y.hat <- exp(X%*%beta.hat+w.hat)

y.hat.1 <- y.hat[seq(1,length(y.hat),q)]
y.hat.2 <- y.hat[seq(2,length(y.hat),q)]
y.hat.3 <- y.hat[seq(3,length(y.hat),q)]

##Take a look
par(mfrow=c(3,2))
surf <- mba.surf(cbind(coords,y.1),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Observed counts")
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=y.1, cex=1, col="blue")

surf <- mba.surf(cbind(coords,y.hat.1),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Fitted counts")
contour(surf, add=TRUE)
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=round(y.hat.1,0), cex=1, col="blue")

surf <- mba.surf(cbind(coords,y.2),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf)
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=y.2, cex=1, col="blue")

surf <- mba.surf(cbind(coords,y.hat.2),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf)
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=round(y.hat.2,0), cex=1, col="blue")

surf <- mba.surf(cbind(coords,y.3),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf)
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=y.3, cex=1, col="blue")

surf <- mba.surf(cbind(coords,y.hat.3),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf)
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=round(y.hat.3,0), cex=1, col="blue")
## End(Not run)

```

Description

The function `spMvLM` fits Gaussian multivariate stationary Bayesian spatial regression models. Given a set of knots, `spMvLM` fits a *predictive process* model (see references below).

Usage

```
spMvLM(formula, data = parent.frame(), coords, knots,
        starting, sp.tuning, priors, cov.model,
        modified.pp = TRUE, n.samples, sub.samples,
        verbose=TRUE, n.report=100, ...)
```

Arguments

<code>formula</code>	for a multivariate model with q response variables, this is a list of univariate formulas. See example below.
<code>data</code>	an optional data frame containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>spMvLM</code> is called.
<code>coords</code>	an $n \times 2$ matrix of the observation coordinates in R^2 (e.g., easting and northing).
<code>knots</code>	either a $m \times 2$ matrix of the <i>predictive process</i> knot coordinates in R^2 (e.g., easting and northing) or a vector of length two or three with the first and second elements recording the number of columns and rows in the desired knot grid. The third, optional, element sets the offset of the outermost knots from the extent of the <code>coords</code> extent.
<code>starting</code>	a list with each tag corresponding to a parameter name. Valid list tags are <code>beta</code> , <code>A</code> , <code>L</code> , <code>phi</code> , and <code>nu</code> . The value portion of each tag is a vector of parameter's starting value. For <code>A</code> and <code>L</code> the vectors are of length $\frac{q(q-q)}{2} + q$ and <code>phi</code> and <code>nu</code> are of length q . Here, <code>A</code> and <code>L</code> hold the the lower-triangle elements in column major ordering of the Cholesky square root of the spatial and non-spatial cross-covariance matrices, respectively.
<code>sp.tuning</code>	a list with each tag corresponding to a parameter name. Valid list tags are <code>A</code> , <code>L</code> , <code>phi</code> , and <code>nu</code> . The value portion of each of each tag defines the step size of the proposal used in the Metropolis sampling. For <code>A</code> and <code>L</code> the vectors are of length $\frac{q(q-q)}{2} + q$ and <code>phi</code> and <code>nu</code> are of length q .
<code>modified.pp</code>	a logical value indicating if the <i>modified predictive process</i> should be used (see references below for details). Note, if a predictive process model is not used (i.e., <code>knots</code> is not specified) then this argument is ignored.
<code>priors</code>	a list with each tag corresponding to a parameter name. Valid list tags are <code>K.IW</code> , <code>Psi.IW</code> , <code>phi.unif</code> , and <code>nu.unif</code> (Beta priors are assumed <i>flat</i>). Variance parameters, <code>K</code> and <code>Psi</code> , are assumed to follow an inverse-Wishart distribution, whereas the spatial range <code>phi</code> and smoothness <code>nu</code> parameters are assumed to follow Uniform distributions. The hyperparameters of the inverse-Wishart are passed as a list of length two, with the first and second elements corresponding to the <i>df</i> and $q \times q$ <i>scale</i> matrix, respectively. The hyperparameters of the Uniform are also passed as a vector of length $2 \times q$ with consecutive elements representing the first and second elements corresponding to the lower and upper support in the order of the univariate models given in <code>formula</code> .

<code>cov.model</code>	a quoted key word that specifies the covariance function used to model the spatial dependence structure among the observations. Supported covariance model key words are: "exponential", "matern", "spherical", and "gaussian". See below for details.
<code>n.samples</code>	the number of MCMC iterations.
<code>sub.samples</code>	a vector of length 3 that specifies <i>start</i> , <i>end</i> , and <i>thin</i> , respectively, of the MCMC samples. The default is <code>c(1, n.samples, 1)</code> (i.e., all samples).
<code>verbose</code>	if TRUE, model specification and progress of the sampler is printed to the screen. Otherwise, nothing is printed to the screen.
<code>n.report</code>	the interval to report Metropolis acceptance and MCMC progress.
<code>...</code>	currently no additional arguments.

Value

An object of class `spMvLM`, which is a list with the following tags:

<code>coords</code>	the $n \times 2$ matrix specified by <code>coords</code> .
<code>knot.coords</code>	the $m \times 2$ matrix as specified by <code>knots</code> .
<code>p.samples</code>	a coda object of posterior samples for the defined parameters.
<code>acceptance</code>	the Metropolis sampling acceptance rate.
<code>sp.effects</code>	a matrix that holds samples from the posterior distribution of the spatial random effects. The rows of this matrix correspond to the n point observations and the columns are the posterior samples.

The return object might include additional data used for subsequent prediction and/or model fit evaluation.

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References

- Banerjee, S., A.E. Gelfand, A.O. Finley, and H. Sang. (2008) Gaussian Predictive Process Models for Large Spatial Datasets. *Journal of the Royal Statistical Society Series B*, 70:825–848.
- Finley, A.O., S. Banerjee, P. Waldmann, and T. Ericsson. (2008). Hierarchical spatial modeling of additive and dominance genetic variance for large spatial trial datasets. *Biometrics*. DOI: 10.1111/j.1541-0420.2008.01115.x
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- Banerjee, S., Carlin, B.P., and Gelfand, A.E. (2004). Hierarchical modeling and analysis for spatial data. Chapman and Hall/CRC Press, Boca Raton, Fla.

See Also

[spMvLM](#), [spGGT](#)

Examples

```
## Not run:
#####
##Multivariate spatial regression
#####

##Generate some data
n <- 50 ##observed
q <- 3
nltr <- q*(q-1)/2+q

coords <- cbind(runif(n),runif(n))
theta <- rep(3/0.5,q)

A <- matrix(0,q,q)
A[lower.tri(A,TRUE)] <- rnorm(nltr, 5, 1)
K <- A%*%t(A)

Psi <- diag(1,q)

c1 <- mvCovInvLogDet(coords=coords, knots=coords,
                    cov.model="exponential",
                    V=K, Psi=Psi, theta=theta,
                    modified.pp=FALSE, SWM=FALSE)

w <- mvrnorm(1,rep(0,nrow(c1$C)),c1$C)

w.1 <- w[seq(1,length(w),q)]
w.2 <- w[seq(2,length(w),q)]
w.3 <- w[seq(3,length(w),q)]

##Specify starting values and collect samples
K.starting <- diag(1,q)[lower.tri(diag(1,q), TRUE)]
Psi.starting <- diag(1,q)[lower.tri(diag(1,q), TRUE)]

n.samples <- 5000

m.1 <- spMvLM(list(w.1~1,w.2~1,w.3~1), coords=coords,
               starting=list("beta"=rep(1,q), "phi"=rep(3/0.5,q),
                             "A"=K.starting, "L"=Psi.starting),
               sp.tuning=list("phi"=rep(0.1,q),
                              "A"=rep(0.1,nltr), "L"=rep(0.1,nltr)),
               priors=list("phi.Unif"=rep(c(3/1,3/0.1),q),
                           "K.IW"=list(q+1, diag(1,q)), "Psi.IW"=list(q+1, diag(1,q))),
               modified.pp=TRUE, cov.model="exponential",
               n.samples=n.samples, sub.samples=c(2500,n.samples,5), verbose=TRUE, n.report=1)

m.1$p.samples[,paste("phi_",1:q,sep="")] <-
```

```

3/m.1$sp.samples[,paste("phi_",1:q,sep="")]

print(summary(mcmc(m.1$sp.samples)))

w.hat <- rowMeans(m.1$sp.effects)
w.hat.1 <- w.hat[seq(1,length(w.hat),q)]
w.hat.2 <- w.hat[seq(2,length(w.hat),q)]
w.hat.3 <- w.hat[seq(3,length(w.hat),q)]

##Take a look
par(mfrow=c(3,2))
surf <- mba.surf(cbind(coords,w.1),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf, main="Observed 1"); contour(surf, add=TRUE)

surf <- mba.surf(cbind(coords,w.hat.1),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf, main="Fitted 1"); contour(surf, add=TRUE)
points(m.1$knot.coords, pch=19, cex=1)

surf <- mba.surf(cbind(coords,w.2),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf, main="Observed 2"); contour(surf, add=TRUE)

surf <- mba.surf(cbind(coords,w.hat.2),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf, main="Fitted 2"); contour(surf, add=TRUE)
points(m.1$knot.coords, pch=19, cex=1)

surf <- mba.surf(cbind(coords,w.3),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf, main="Observed 3"); contour(surf, add=TRUE)

surf <- mba.surf(cbind(coords,w.hat.3),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf, main="Fitted 3"); contour(surf, add=TRUE)
points(m.1$knot.coords, pch=19, cex=1)
## End(Not run)

```

spPredict

Prediction for new points given a spGGT, spLM, spMvLM, spGLM, spMvGLM, or bayesGeostatExact object

Description

The function `spPredict` collects a posterior predictive sample for a set of new points given a `spGGT`, `spLM`, `spMvLM`, `spGLM`, `spMvGLM`, or `bayesGeostatExact` object.

Usage

```
spPredict(sp.obj, pred.coords, pred.covars,
          start=1, end, thin=1, verbose=TRUE, ...)
```

Arguments

sp.obj	an object returned by <code>spGGT</code> , <code>bayesGeostatExact</code> , <code>spLM</code> , <code>spMvLM</code> , <code>spGLM</code> , or <code>spMvGLM</code>
pred.coords	an $n \times 2$ matrix of m prediction point coordinates in R^2 (e.g., easting and northing). The first column is assumed to be easting coordinates and the second column northing coordinates.
pred.covars	an $n \times p$ design matrix associated with the new points. If this is a multivariate prediction defined by m models, the multivariate design matrix can be created by passing a list of the m univariate design matrices to the <code>mkMvX</code> function.
start	specifies the first sample included in the prediction calculation. This is useful for those who choose to acknowledge chain burn-in.
end	specifies the last sample included in the prediction calculation. The default is to use all posterior samples in <code>sp.obj</code> .
thin	a sample thinning factor. The default of 1 considers all samples between <code>start</code> and <code>end</code> . For example, if <code>thin = 10</code> then 1 in 10 samples are considered between <code>start</code> and <code>end</code> .
verbose	if TRUE calculation progress is printed to the screen; otherwise, nothing is printed to the screen.
...	currently no additional arguments.

Value

obs.coords	the matrix of the observation coordinates.
pred.coords	the matrix of prediction point coordinates specified by <code>pred.coords</code> .
pp.samples	a matrix that holds samples from the posterior predictive distribution(s). For multivariate models the rows of this matrix correspond to the predicted points and the columns are the posterior predictive samples. If prediction is for m response variables the <code>pp.samples</code> matrix has mn rows. The predictions for points are held in rows 1:m, (m+1):2m, ..., ((i-1)m+1):im, ..., ((n-1)m+1):nm, where $i = 1 \dots n$ (e.g., the samples for the first point are in rows 1:m, second point in rows (m+1):2m, etc.). For <code>bayesGeostatExact</code> , the rows of this matrix correspond to the predicted points and the columns are the posterior predictive samples.

Author(s)

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References

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See Also

[spGGT](#), [bayesGeostatExact](#), [spLM](#), [spMvLM](#), [spGLM](#), [spMvGLM](#)

Examples

```
## Not run:
##Portions of this example requires MBA package to make surfaces
library(MBA)

#####
##Prediction for spMvGLM
#####

##Generate some count data
n <- 100
q <- 3
nltr <- q*(q-1)/2+q

coords <- cbind(runif(n,1,100),runif(n,1,100))

theta <- rep(3/50,q)

A <- matrix(0,q,q)
A[lower.tri(A,TRUE)] <- rnorm(nltr,1,1)
K <- A%*%t(A)

Psi <- diag(0,q)

c1 <- mvCovInvLogDet(coords=coords, knots=coords,
                     cov.model="exponential",
                     V=K, Psi=Psi, theta=theta,
                     modified.pp=TRUE, SWM=FALSE)

w <- mvrnorm(1,rep(0,nrow(c1$C)),c1$C)

X <- mkMvX(list(matrix(1,n,1), matrix(1,n,1), matrix(1,n,1)))
beta <- c(-1,0,1)
y <- rpois(n*q, exp(X%*%beta+w))
```

```

y.1 <- y[seq(1,length(y),q)]
y.2 <- y[seq(2,length(y),q)]
y.3 <- y[seq(3,length(y),q)]

##Specify starting values and collect samples. For
##a true analysis, several longer chains should be
##run.
A.starting <- diag(1,q)[lower.tri(diag(1,q), TRUE)]

beta.starting <- coefficients(glm(y~X-1, family="poisson"))
beta.tuning <- t(chol(vcov(glm(y~X-1, family="poisson"))))

n.samples <- 5000

m.1 <- spMvGLM(list(y.1~1,y.2~1,y.3~1), family="poisson", coords=coords,
                 knots=c(8,8,0),
                 starting=
                 list("beta"=beta.starting, "phi"=rep(0.06,q),
                      "A"=A.starting, "w"=0),
                 tuning=
                 list("beta"=beta.tuning, "phi"=rep(0.01,q),
                      "A"=rep(0.005,nltr), "w"=0.001),
                 priors=
                 list("beta.Flat", "phi.Unif"=rep(c(0.03, 0.3),q),
                      "K.IW"=list(q+1, diag(0.1,q))),
                 cov.model="exponential",
                 n.samples=n.samples, sub.samples=c(2000,n.samples,10),
                 verbose=TRUE, n.report=500)

pred.coords <- expand.grid(seq(0,100,10), seq(0,100,10))
m <- nrow(pred.coords)
pred.covars <- mkMvX(list(matrix(1,m,1), matrix(1,m,1), matrix(1,m,1)))

out <-
  spPredict(m.1, pred.coords=pred.coords, pred.covars=pred.covars)

y.hat <- rowMeans(out$y.pred)

y.hat.1 <- y.hat[seq(1,length(y.hat),q)]
y.hat.2 <- y.hat[seq(2,length(y.hat),q)]
y.hat.3 <- y.hat[seq(3,length(y.hat),q)]

##Take a look
par(mfrow=c(3,2))
surf <- mba.surf(cbind(coords,y.1),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Observed counts")
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=y.1, cex=1, col="blue")

surf <- mba.surf(cbind(pred.coords,y.hat.1),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Predicted counts")
contour(surf, add=TRUE)

```

```

contour(surf, drawlabels=FALSE, add=TRUE)
text(pred.coords, labels=round(y.hat.1,0), cex=1, col="green")

surf <- mba.surf(cbind(coords,y.2),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf)
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=y.2, cex=1, col="blue")

surf <- mba.surf(cbind(pred.coords,y.hat.2),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf)
contour(surf, drawlabels=FALSE, add=TRUE)
text(pred.coords, labels=round(y.hat.2,0), cex=1, col="green")

surf <- mba.surf(cbind(coords,y.3),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf)
contour(surf, drawlabels=FALSE, add=TRUE)
text(coords, labels=y.3, cex=1, col="blue")

surf <- mba.surf(cbind(pred.coords,y.hat.3),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf)
contour(surf, drawlabels=FALSE, add=TRUE)
text(pred.coords, labels=round(y.hat.3,0), cex=1, col="green")

#####
##Prediction for spGLM
#####

##Generate count data
n <- 300

coords <- cbind(runif(n,1,100),runif(n,1,100))

phi <- 3/75
sigma.sq <- 3

R <- sigma.sq*exp(-phi*as.matrix(dist(coords)))
w <- mvrnorm(1, rep(0,n), R)

x <- as.matrix(rep(1,n))
beta <- 0.1
y <- rpois(n, exp(x%*%beta+w))

##Collect samples
beta.starting <- coefficients(glm(y~x-1, family="poisson"))
beta.tuning <- t(chol(vcov(glm(y~x-1, family="poisson"))))

n.samples <- 15000

m.1 <- spGLM(y~1, family="poisson", coords=coords, knots=c(8,8,0),
            starting=
            list("beta"=beta.starting, "phi"=0.06,
                "sigma.sq"=1, "w"=0),
            tuning=

```

```

list("beta"=beta.tuning, "phi"=0.1,
     "sigma.sq"=0.1, "w"=0.001),
priors=
list("beta.Flat", "phi.Unif"=c(0.03, 0.3),
     "sigma.sq.IG"=c(2, 1)),
cov.model="exponential",
n.samples=n.samples, sub.samples=c(10000,n.samples,5),
verbose=TRUE, n.report=500)

##Make prediction grid
pred.coords <- expand.grid(seq(0,100,5), seq(0,100,5))
out <- spPredict(m.1, pred.coords=pred.coords,
                pred.covars=as.matrix(rep(1,nrow(pred.coords))))

y.pred <- rowMeans(out$y.pred)

##Take a look
par(mfrow=c(1,2))
surf <-
  mba.surf(cbind(coords,y),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Observed counts")
contour(surf, add=TRUE)

surf <-
  mba.surf(cbind(pred.coords, y.pred),no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(surf, main="Predicted counts")
contour(surf, add=TRUE)
points(pred.coords, pch=19, cex=0.5, col="blue")

#####
##Prediction for spMvLM
#####

##Generate some data
n <- 100 ##observed
m <- 50  ##predict
N <- n+m
q <- 3
nltr <- q*(q-1)/2+q

coords <- cbind(runif(N),runif(N))
theta <- rep(3/0.5,q)

A <- matrix(0,q,q)
A[lower.tri(A,TRUE)] <- rnorm(nltr, 5, 1)
V <- A%*%t(A)

Psi <- diag(1,q)

cl <- mvCovInvLogDet(coords=coords, knots=coords,
                    cov.model="exponential",
                    V=V, Psi=Psi, theta=theta)

```

```

w <- mvrnorm(1, rep(0, nrow(c1$C)), c1$C)
obs.w <- w[1:(n*q)]

w.1 <- obs.w[seq(1, length(obs.w), q)]
w.2 <- obs.w[seq(2, length(obs.w), q)]
w.3 <- obs.w[seq(3, length(obs.w), q)]

##Specify starting values and collect samples
A.starting <- diag(1, q) [lower.tri(diag(1, q), TRUE)]
L.starting <- diag(1, q) [lower.tri(diag(1, q), TRUE)]

n.samples <- 1000

obs.coords <- coords[1:n,]

m.1 <- spMvLM(list(w.1~1, w.2~1, w.3~1), coords=obs.coords,
  knots=c(8, 8, 0),
  starting=list("beta"=rep(1, q), "phi"=rep(3/0.5, q),
    "nu"=rep(1, q), "A"=A.starting, "L"=L.starting),
  sp.tuning=list("phi"=rep(0.1, q), "nu"=rep(0.1, q),
    "A"=rep(0.1, nltr), "L"=rep(0.1, nltr)),
  priors=list("phi.Unif"=rep(c(3/1, 3/0.1), q),
    "nu.Unif"=rep(c(0.1, 2), q),
    "K.IW"=list(q+1, diag(1, q)), "Psi.IW"=list(q+1, diag(1, q))),
  modified.pp=FALSE, cov.model="matern",
  n.samples=n.samples, verbose=TRUE, n.report=100)

##Predict for holdout set
pred.coords <- coords[(n+1):nrow(coords),]
pred.covars <- mkMvX(list(matrix(1, m, 1), matrix(1, m, 1), matrix(1, m, 1)))

pred <- spPredict(m.1, pred.coords, pred.covars)

ho.w <- w[(n*q+1):length(w)]
ho.w.1 <- ho.w[seq(1, length(ho.w), q)]
ho.w.2 <- ho.w[seq(2, length(ho.w), q)]
ho.w.3 <- ho.w[seq(3, length(ho.w), q)]

burn.in <- 500

pred.w <- rowMeans(pred$y.pred[, burn.in:ncol(pred$y.pred)])
pred.w.1 <- pred.w[seq(1, length(pred.w), q)]
pred.w.2 <- pred.w[seq(2, length(pred.w), q)]
pred.w.3 <- pred.w[seq(3, length(pred.w), q)]

##Take a look
par(mfrow=c(3, 2))
surf <- mba.surf(cbind(obs.coords, w.1),
  no.X=100, no.Y=100, extend=T)$xyz.est
image(surf, main="Observed"); contour(surf, add=TRUE)

surf <- mba.surf(cbind(pred.coords, pred.w.1),
  no.X=100, no.Y=100, extend=T)$xyz.est

```

```

image(surf, main="Predicted"); contour(surf, add=TRUE)
points(m.1$knot.coords, pch=19, cex=1)

surf <- mba.surf(cbind(obs.coords,w.2),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf); contour(surf, add=TRUE)

surf <- mba.surf(cbind(pred.coords,pred.w.2),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf); contour(surf, add=TRUE)
points(m.1$knot.coords, pch=19, cex=1)

surf <- mba.surf(cbind(obs.coords,w.3),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf); contour(surf, add=TRUE)

surf <- mba.surf(cbind(pred.coords,pred.w.3),
                no.X=100, no.Y=100, extend=T)$xyz.est
image(surf); contour(surf, add=TRUE)
points(m.1$knot.coords, pch=19, cex=1)

#####
## Prediction for bayesGeostatExact
#####
data(FBC07.dat)
Y <- FBC07.dat[1:150,"Y.2"]
coords <- as.matrix(FBC07.dat[1:150,c("coord.X", "coord.Y")])

n.samples <- 1000
n = length(Y)
p = 1

phi <- 0.15
nu <- 0.5

beta.prior.mean <- as.matrix(rep(0, times=p))
beta.prior.precision <- matrix(0, nrow=p, ncol=p)

alpha <- 5/5

sigma.sq.prior.shape <- 2.0
sigma.sq.prior.rate <- 5.0

#####
##Simple linear model with
##the default exponential
##spatial decay function
#####
m.1 <- bayesGeostatExact(Y~1, n.samples=n.samples,
                        beta.prior.mean=beta.prior.mean,
                        beta.prior.precision=beta.prior.precision,
                        coords=coords, phi=phi, alpha=alpha,
                        sigma.sq.prior.shape=sigma.sq.prior.shape,

```

```

sigma.sq.prior.rate=sigma.sq.prior.rate,
sp.effects=TRUE)

##Now prediction
set.seed(1)
pred.coords <- expand.grid(seq(0,100,length=10),seq(0,100,length=10))
pred.covars <- as.matrix(rep(1,nrow(pred.coords)))

m.l.pred <- spPredict(m.l, pred.coords=pred.coords,
                    pred.covars=pred.covars, thin=5)

par(mfrow=c(2,2))
obs.surf <-
  mba.surf(cbind(coords, Y), no.X=100, no.Y=100, extend=T)$xyz.est
image(obs.surf, xaxs = "r", yaxs = "r", main="Observed response")
points(coords, pch=19, cex=1, col="green")
contour(obs.surf, add=T)

w.hat <- rowMeans(m.l$sp.effects)
w.surf <-
  mba.surf(cbind(coords, w.hat), no.X=100, no.Y=100, extend=T)$xyz.est
image(w.surf, xaxs = "r", yaxs = "r", main="Random effects")
points(coords, pch=19, cex=1, col="green")
contour(w.surf, add=T)

y.hat <- rowMeans(m.l.pred)
y.surf <-
  mba.surf(cbind(pred.coords, y.hat), no.X=100, no.Y=100, extend=T)$xyz.est
image(y.surf, xaxs = "r", yaxs = "r", main="Predicted response")
points(pred.coords, pch=19, cex=1, col="black")
rect(0, 0, 50, 50, col=NA, border="green")
contour(y.surf, add=T)

y.var <- apply(m.l.pred, 1, var)
y.surf <-
  mba.surf(cbind(pred.coords, y.var), no.X=100, no.Y=100, extend=T)$xyz.est
image(y.surf, xaxs = "r", yaxs = "r", main="Predicted response\nvariance")
points(coords, pch=19, cex=1, col="green")
points(pred.coords, pch=19, cex=1, col="black")
rect(0, 0, 50, 50, col=NA, border="green")
contour(y.surf, add=T)

#####
## Prediction for spLM
#####
data(rf.n200.dat)

Y <- rf.n200.dat$Y
coords <- as.matrix(rf.n200.dat[,c("x.coords","y.coords")])
w <- rf.n200.dat$w

pred.coords <- expand.grid(seq(1,10,1), seq(1,10,1))
n.pred <- nrow(pred.coords)

```

```
#####
##Prediction with a spLM model
#####
m.2 <- spLM(Y~1, coords=coords,
            starting=list("phi"=0.6,"sigma.sq"=1, "tau.sq"=1),
            sp.tuning=list("phi"=0.01, "sigma.sq"=0.05, "tau.sq"=0.05),
            priors=list("phi.Unif"=c(0.3, 3), "sigma.sq.IG"=c(2, 1),
                       "tau.sq.IG"=c(2, 1)),
            cov.model="exponential",
            n.samples=1000, verbose=TRUE, n.report=100)

pred <- spPredict(m.2, pred.coords,
                  pred.covars=as.matrix(rep(1,n.pred)))

par(mfrow=c(1,2))
obs.surf <-
  mba.surf(cbind(coords, Y), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(obs.surf, xaxs = "r", yaxs = "r", main="Observed response")
points(coords)
contour(obs.surf, add=T)

y.hat <- rowMeans(pred$y.pred)
y.pred.surf <-
  mba.surf(cbind(pred.coords, y.hat), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(y.pred.surf, xaxs = "r", yaxs = "r", main="Predicted response")
points(coords, pch=1, cex=1)
points(pred.coords, pch=19, cex=1)
contour(y.pred.surf, add=T)
legend(1.5,2.5, legend=c("Obs.", "Pred."), pch=c(1,19), bg="white")

#####
##Prediction with a spLM
##predictive process model
#####
m.3 <- spLM(Y~1, coords=coords, knots=c(6,6,0),
            starting=list("phi"=0.6,"sigma.sq"=1, "tau.sq"=1),
            sp.tuning=list("phi"=0.01, "sigma.sq"=0.01, "tau.sq"=0.01),
            priors=list("phi.Unif"=c(0.3, 3), "sigma.sq.IG"=c(2, 1),
                       "tau.sq.IG"=c(2, 1)),
            cov.model="exponential",
            n.samples=2000, verbose=TRUE, n.report=100)

print(summary(m.3$p.samples))
plot(m.3$p.samples)

pred <- spPredict(m.3, pred.coords,
                  pred.covars=as.matrix(rep(1,n.pred)))

par(mfrow=c(1,2))
obs.surf <-
  mba.surf(cbind(coords, Y), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(obs.surf, xaxs = "r", yaxs = "r", main="Observed response")
```

```

points(coords)
contour(obs.surf, add=T)

y.hat <- rowMeans(pred$y.pred)
y.pred.surf <-
  mba.surf(cbind(pred.coords, y.hat), no.X=100, no.Y=100, extend=TRUE)$xyz.est
image(y.pred.surf, xaxs = "r", yaxs = "r", main="Predicted response")
points(coords, pch=1, cex=1)
points(m.3$knot.coords, pch=3, cex=1)
points(pred.coords, pch=19, cex=1)
contour(y.pred.surf, add=T)
legend(1.5,2.5, legend=c("Obs.", "Knots", "Pred."),
      pch=c(1,3,19), bg="white")

#####
##      Prediction for spGGT
#####
data(FBC07.dat)

##Divide the data into model and prediction sets
Y.1 <- FBC07.dat[1:100,"Y.1"]
Y.2 <- FBC07.dat[1:100,"Y.2"]
model.coords <- as.matrix(FBC07.dat[1:100,c("coord.X", "coord.Y")])
pred.coords <- as.matrix(FBC07.dat[151:200,c("coord.X", "coord.Y")])

#####
##      Univariate model
#####

##Fit some model with spGGT.
K.prior <- prior(dist="IG", shape=2, scale=5)
Psi.prior <- prior(dist="IG", shape=2, scale=5)
phi.prior <- prior(dist="UNIF", a=0.06, b=3)

var.update.control <-
  list("K"=list(starting=5, tuning=0.5, prior=K.prior),
       "Psi"=list(starting=5, tuning=0.5, prior=Psi.prior),
       "phi"=list(starting=0.1, tuning=0.5, prior=phi.prior)
      )

beta.control <- list(update="GIBBS", prior=prior(dist="FLAT"))

run.control <- list("n.samples"=1000)

Fit <- spGGT(formula=Y.2~1, run.control=run.control,
             coords=model.coords,
             var.update.control=var.update.control,
             beta.update.control=beta.control,
             cov.model="exponential")

##Now make predictions for the holdout set.
##Step 1. make the design matrix for the prediction points.
pred.covars <- as.matrix(rep(1, nrow(pred.coords)))

```

```

##Step 2. call spPredict.
Pred <- spPredict(Fit, pred.covars=pred.covars,
                 pred.coords=pred.coords)

##Step 3. check out the predicted random effects and
##predicted response variable.

Pred.sp.effects.surf <-
  mba.surf(cbind(pred.coords, rowMeans(Pred$pred.sp.effects)),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est

Pred.Y.surf <-
  mba.surf(cbind(pred.coords, rowMeans(Pred$pred.y)),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est

par(mfrow=c(1,2))
image(Pred.sp.effects.surf, xaxs="r", yaxs="r",
      main="Predicted random spatial effects")
contour(Pred.sp.effects.surf, add=TRUE)

image(Pred.Y.surf, xaxs="r", yaxs="r",
      main="Predicted Y.2")
contour(Pred.Y.surf, add=TRUE)

#####
##  Multivariate models
#####

##Fit some model with spGGT.
K.prior <- prior(dist="IWISH", df=2, S=diag(c(3, 6)))
Psi.prior <- prior(dist="IWISH", df=2, S=diag(c(7, 5)))
phi.prior <- prior(dist="UNIF", a=0.06, b=3)

K.starting <- matrix(c(2,-3, 0, 1), 2, 2)
Psi.starting <- diag(c(3, 2))

var.update.control <-
  list("K"=list(starting=K.starting, tuning=diag(c(0.1, 0.5, 0.1)),
              prior=K.prior),
       "Psi"=list(starting=Psi.starting, tuning=diag(c(0.1, 0.5, 0.1)),
                 prior=Psi.prior),
       "phi"=list(starting=0.1, tuning=0.5,
                 prior=list(phi.prior, phi.prior))
  )

beta.control <- list(update="GIBBS", prior=prior(dist="FLAT"))

run.control <- list("n.samples"=1000, "sp.effects"=FALSE)

Fit.mv <-
  spGGT(formula=list(Y.1~1, Y.2~1), run.control=run.control,
        coords=model.coords,

```

```

var.update.control=var.update.control,
beta.update.control=beta.control,
cov.model="exponential")

##Now make predictions for the holdout set.
##Step 1. make the design matrix for the prediction points using
##the mkMvX function.
pred.covars.1 <- as.matrix(rep(1, nrow(pred.coords)))
pred.covars.2 <- as.matrix(rep(1, nrow(pred.coords)))

pred.covars.mv <- mkMvX(list(pred.covars.1, pred.covars.2))

##Step 2. call spPredict.
Pred.mv <- spPredict(Fit.mv, pred.covars=pred.covars.mv,
                    pred.coords=pred.coords)

##Step 3. check out the predicted random effects and
##predicted response variables. Recall, these are
##organized as m consecutive rows for each point.
Pred.sp.effects.1 <-
  Pred.mv$pred.sp.effects[seq(1, nrow(Pred.mv$pred.sp.effects), 2),]

Pred.sp.effects.2 <-
  Pred.mv$pred.sp.effects[seq(2, nrow(Pred.mv$pred.sp.effects), 2),]

Pred.Y.1 <-
  Pred.mv$pred.sp.effects[seq(1, nrow(Pred.mv$pred.y), 2),]

Pred.Y.2 <-
  Pred.mv$pred.sp.effects[seq(2, nrow(Pred.mv$pred.y), 2),]

##Then map.
Pred.sp.effects.1.surf <-
  mba.surf(cbind(pred.coords, rowMeans(Pred.sp.effects.1)),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est

Pred.sp.effects.2.surf <-
  mba.surf(cbind(pred.coords, rowMeans(Pred.sp.effects.2)),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est

Pred.Y.1.surf <-
  mba.surf(cbind(pred.coords, rowMeans(Pred.Y.1)),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est

Pred.Y.2.surf <-
  mba.surf(cbind(pred.coords, rowMeans(Pred.Y.2)),
           no.X=100, no.Y=100, extend=TRUE)$xyz.est

par(mfrow=c(2,2))
image(Pred.sp.effects.surf, xaxs="r", yaxs="r",
      main="Predicted random spatial effects Y.1")
contour(Pred.sp.effects.1.surf, add=TRUE)

```

```

image(Pred.sp.effects.surf, xaxs="r", yaxs="r",
      main="Predicted random spatial effects Y.2")
contour(Pred.sp.effects.2.surf, add=TRUE)

image(Pred.sp.effects.surf, xaxs="r", yaxs="r",
      main="Predicted Y.1")
contour(Pred.Y.1.surf, add=TRUE)

image(Pred.sp.effects.surf, xaxs="r", yaxs="r",
      main="Predicted Y.2")
contour(Pred.Y.2.surf, add=TRUE)

## End(Not run)

```

```
synthetic.dat      Synthetic univariate data used for illustrations
```

Description

The synthetic datasets were generated from a stationary and isotropic spatial process using an exponential correlation function (code below).

Usage

```

data(rf.n200.dat)
data(rf.n500.dat)
data(rf.n1000.dat)

```

Format

The rf.n200.dat, rf.n500.dat, rf.n1000.dat files contain n rows (i.e., points) and 4 columns. Column 1, Y, is the response variable. Column 2, w, is the vector of random spatial effects. Columns 4 and 5 are the x and y coordinates.

Examples

```

## Not run:

##These synthetic data were generated with the following:

##n <- 200
##n <- 500
n <- 1000

coords <- cbind(runif(n, 1, 10), runif(n, 1, 10))

sigma.sq <- 10
tau.sq <- 1
phi <- 3/5

```

```

C <- sigma.sq*exp(-phi*as.matrix(dist(coords)))
w <- mvrnorm(1, rep(0,n), C)

Y <- w+rnorm(n, 0, sqrt(tau.sq))

## End(Not run)

```

WEF.dat

Western Experimental Forest inventory data

Description

Data generated as part of a long-term research study on an experimental forest in central Oregon. This dataset holds the coordinates for all trees in the experimental forest. The typical stem measurements are recorded for each tree. Crown radius was measured at the cardinal directions for a subset of trees. Mean crown radius was calculated for all trees using a simple relationship between DBH, Height, and observed crown dimension.

Usage

```
data(WEF.dat)
```

Format

A data frame containing 2422 rows and 15 columns.

Zurich.dat

Zurichberg Forest inventory data

Description

Inventory data of the Zurichberg Forest, Switzerland (see Mandallaz 2008 for details). These data are provided with the kind authorization of the Forest Service of the Canton of Zurich.

This dataset holds the coordinates for all trees in the Zurichberg Forest. Species (SPP), basal area (BAREA) diameter at breast height (DBH), and volume (VOL) are recorded for each tree. See species codes below.

Usage

```
data(Zurich.dat)
```

Format

A data frame containing 4954 rows and 6 columns.

Examples

```
## Not run:
data(Zurich.dat)

coords <- Zurich.dat[,c("X_TREE", "Y_TREE")]

spp.name <- c("beech", "maple", "ash", "other broadleaves",
             "spruce", "silver fir", "larch", "other coniferous")

spp.col <- c("yellow", "red", "orange", "pink",
            "green", "dark green", "black", "gray")

plot(coords, col=spp.col[Zurich.dat$SPP+1],
      pch=19, cex=0.5, ylab="Northing", xlab="Easting")

legend.coords <- c(23,240)

legend(legend.coords, pch=19, legend=spp.name,
      col=spp.col, bty="n")

## End(Not run)
```

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