

Package ‘RandomForestsGLS’

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Title Random Forests for Dependent Data

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Imports BRISC, parallel, stats, matrixStats, randomForest, pbapply

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Description Fits non-linear regression models on dependant data with Generalised Least Square (GLS) based Random Forest (RF-GLS) detailed in Saha, Basu and Datta (2021) <doi:10.1080/01621459.2021.1950003>.

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URL <https://github.com/ArkajyotiSaha/RandomForestsGLS>

BugReports <https://github.com/ArkajyotiSaha/RandomForestsGLS/issues>

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RFGLS_estimate_spatial

Function for estimation in spatial data with RF-GLS

Description

The function `RFGLS_estimate_spatial` fits univariate non-linear spatial regression models for spatial data using RF-GLS in Saha et al. 2020. `RFGLS_estimate_spatial` uses the sparse Cholesky representation of Vecchia's likelihood (Vecchia, 1988) developed in Datta et al., 2016 and Saha & Datta, 2018. The fitted Random Forest (RF) model is used later for prediction via the `RFGLS_predict` and `RFGLS_predict_spatial`.

Some code blocks are borrowed from the R packages: `spNNGP`: Spatial Regression Models for Large Datasets using Nearest Neighbor Gaussian Process

<https://CRAN.R-project.org/package=spNNGP> and `randomForest`: Breiman and Cutler's Random Forests for Classification and Regression

<https://CRAN.R-project.org/package=randomForest> .

Usage

```
RFGLS_estimate_spatial(coords, y, X, Xtest = NULL,
                        nrnodes = NULL, nthsize = 20,
                        mtry = 1, pinv_choice = 1,
                        n_omp = 1, ntree = 50, h = 1,
                        sigma.sq = 1, tau.sq = 0.1,
                        phi = 5, nu = 0.5,
                        n.neighbors = 15,
                        cov.model = "exponential",
                        search.type = "tree",
                        param_estimate = FALSE,
                        verbose = FALSE)
```

Arguments

<code>coords</code>	an $n \times 2$ matrix of the observation coordinates in R^2 (e.g., easting and northing).
<code>y</code>	an n length vector of response at the observed coordinates.
<code>X</code>	an $n \times p$ matrix of the covariates in the observation coordinates.
<code>Xtest</code>	an $ntest \times p$ matrix of covariates for prediction locations. Its Structure should be identical (including intercept) with that of covariates provided for estimation purpose in <code>X</code> . If <code>NULL</code> , will use <code>X</code> as <code>Xtest</code> . Default value is <code>NULL</code> .
<code>nrnodes</code>	the maximum number of nodes a tree can have. Default choice leads to the deepest tree contingent on <code>nthsize</code> . For significantly large n , one needs to bound it for growing shallow trees which trades off efficiency for computation time.
<code>nthsize</code>	minimum size of leaf nodes. We recommend not setting this value too small, as that will lead to very deep trees that takes a lot of time to be built and can produce unstable estimates. Default value is 20.

mtry	number of variables randomly sampled at each partition as a candidate split direction. We recommend using the value $p/3$ where p is the number of variables in X . Default value is 1.
pinv_choice	dictates the choice of method for obtaining the pseudoinverse involved in the cost function and node representative evaluation. if <code>pinv_choice = 0</code> , SVD is used (slower but more stable), if <code>pinv_choice = 1</code> , orthogonal decomposition (faster, may produce unstable results if <code>nthsize</code> is too low) is used. Default value is 1.
n_omp	number of threads to be used, value can be more than 1 if source code is compiled with OpenMP support. Default is 1.
ntree	number of trees to be grown. This value should not be too small. Default value is 50.
h	number of core to be used in parallel computing setup for bootstrap samples. If <code>h = 1</code> , there is no parallelization. Default value is 1.
sigma.sq	value of sigma square. Default value is 1.
tau.sq	value of tau square. Default value is 0.1.
phi	value of phi. Default value is 5.
nu	value of nu, only required for matern covariance model. Default value is 0.5.
n.neighbors	number of neighbors used in the NNGP. Default value is 15.
cov.model	keyword that specifies the covariance function to be used in modelling the spatial dependence structure among the observations. Supported keywords are: "exponential", "matern", "spherical", and "gaussian" for exponential, matern, spherical and gaussian covariance function respectively. Default value is "exponential".
search.type	keyword that specifies type of nearest neighbor search algorithm to be used. Supported keywords are: "tree" and "brute". Both of them provide the same result, though "tree" should be faster. Default value is "tree".
param_estimate	if TRUE, using the residuals obtained from fitting a classical RF with default options and <code>nodesize = nthsize</code> , will estimate the coefficients corresponding to <code>cov.model</code> from <code>BRISC_estimate</code> with the default options. Default value is FALSE.
verbose	if TRUE, model specifications along with information regarding OpenMP support and progress of the algorithm is printed to the screen. Otherwise, nothing is printed to the screen. Default value is FALSE.

Value

A list comprising:

P_matrix	an $n \times ntree$ matrix of zero indexed resamples. t -th column denote the n resamples used in the t -th tree.
predicted_matrix	an $ntest \times ntree$ matrix of predictions. t -th column denote the predictions at $ntest$ datapoints obtained from the t -th tree.

predicted predicted values at the *ntest* prediction points. Average (rowMeans) of the
 treewise predictions in *predicted_matrix*,
 X the matrix X.
 y the vector y.
 RFGLS_Object object required for prediction.

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References

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<https://CRAN.R-project.org/package=randomForest>

Examples

```

rmvn <- function(n, mu = 0, V = matrix(1)){
  p <- length(mu)
  if(any(is.na(match(dim(V),p))))
    stop("Dimension not right!")
  D <- chol(V)
  t(matrix(rnorm(n*p), ncol=p)%*%D + rep(mu,rep(n,p)))
}

set.seed(1)
n <- 200
coords <- cbind(runif(n,0,1), runif(n,0,1))

set.seed(2)
x <- as.matrix(rnorm(n),n,1)

sigma.sq = 1
phi = 5
tau.sq = 0.1

```

```

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

y <- rnorm(n, 10*sin(pi * x) + w, sqrt(tau.sq))

estimation_result <- RFGLS_estimate_spatial(coords, y, x, ntree = 10)

```

RFGLS_estimate_timeseries

Function for estimation in time-series data with RF-GLS

Description

The function `RFGLS_estimate_spatial` fits univariate non-linear regression models for time-series data using a RF-GLS in Saha et al. 2020. `RFGLS_estimate_spatial` uses the sparse Cholesky representation corresponding to AR(q) process. The fitted Random Forest (RF) model is used later for prediction via the `RFGLS-predict`.

Some code blocks are borrowed from the R packages: `spNNGP`: Spatial Regression Models for Large Datasets using Nearest Neighbor Gaussian Processes

<https://CRAN.R-project.org/package=spNNGP> and `randomForest`: Breiman and Cutler's Random Forests for Classification and Regression

<https://CRAN.R-project.org/package=randomForest> .

Usage

```

RFGLS_estimate_timeseries(y, X, Xtest = NULL, nrnodes = NULL,
                           nthsize = 20, mtry = 1,
                           pinv_choice = 1, n_omp = 1,
                           ntree = 50, h = 1, lag_params = 0.5,
                           variance = 1,
                           param_estimate = FALSE,
                           verbose = FALSE)

```

Arguments

<code>y</code>	an n length vector of response at the observed time points.
<code>X</code>	an $n \times p$ matrix of the covariates in the observation time points.
<code>Xtest</code>	an $ntest \times p$ matrix of covariates for prediction. Its Structure should be identical (including intercept) with that of covariates provided for estimation purpose in <code>X</code> . If <code>NULL</code> , will use <code>X</code> as <code>Xtest</code> . Default value is <code>NULL</code> .
<code>nrnodes</code>	the maximum number of nodes a tree can have. Default choice leads to the deepest tree contingent on <code>nthsize</code> . For significantly large n , one needs to bound it for growing shallow trees which trades off efficiency for computation time.

nthesize	minimum size of leaf nodes. We recommend not setting this value too small, as that will lead to very deep trees that takes a lot of time to be built and can produce unstable estimates. Default value is 20.
mtry	number of variables randomly sampled at each partition as a candidate split direction. We recommend using the value $p/3$ where p is the number of variables in X . Default value is 1.
pinv_choice	dictates the choice of method for obtaining the pseudoinverse involved in the cost function and node representative evaluation. if <code>pinv_choice = 0</code> , SVD is used (slower but more stable), if <code>pinv_choice = 1</code> , orthogonal decomposition (faster, may produce unstable results if <code>nthesize</code> is too low) is used. Default value is 1.
n_omp	number of threads to be used, value can be more than 1 if source code is compiled with OpenMP support. Default is 1.
ntree	number of trees to be grown. This value should not be too small. Default value is 50.
h	number of core to be used in parallel computing setup for bootstrap samples. If $h = 1$, there is no parallelization. Default value is 1.
lag_params	q length vector of AR coefficients. If the parameters need to be estimated from AR(q) process, should be any numeric vector of length q . For notations please see <code>arima</code> . Default value is 0.5.
variance	variance of the white noise in temporal error. The function estimate is not affected by this. Default value is 1.
param_estimate	if TRUE, using the residuals obtained from fitting a classical RF default options and <code>nodesize = nthesize</code> , will estimate the coefficients corresponding to $AR(q)$ from <code>arima</code> with the option, <code>include.mean = FALSE</code> . Default value is FALSE.
verbose	if TRUE, model specifications along with information regarding OpenMP support and progress of the algorithm is printed to the screen. Otherwise, nothing is printed to the screen. Default value is FALSE.

Value

A list comprising:

P_matrix	an $n \times ntree$ matrix of zero indexed resamples. t -th column denote the n resamples used in the t -th tree.
predicted_matrix	an $ntest \times ntree$ matrix of predictions. t -th column denote the predictions at $ntest$ datapoints obtained from the t -th tree.
predicted	predicted values at the $ntest$ prediction points. Average (<code>rowMeans</code>) of the tree-wise predictions in <code>predicted_matrix</code> ,
X	the matrix X .
y	the vector y .
RFGLS_Object	object required for prediction.

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References

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<https://CRAN.R-project.org/package=randomForest>

Andrew Finley, Abhirup Datta and Sudipto Banerjee (2017). spNNGP: Spatial Regression Models for Large Datasets using Nearest Neighbor Gaussian Processes. R package version 0.1.1.
<https://CRAN.R-project.org/package=spNNGP>

Examples

```
rmvn <- function(n, mu = 0, V = matrix(1)){
  p <- length(mu)
  if(any(is.na(match(dim(V),p))))
    stop("Dimension not right!")
  D <- chol(V)
  t(matrix(rnorm(n*p), ncol=p)%*%D + rep(mu,rep(n,p)))
}

set.seed(2)
n <- 200
x <- as.matrix(rnorm(n),n,1)

sigma.sq <- 1
rho <- 0.5

set.seed(3)
b <- rho
s <- sqrt(sigma.sq)
eps = arima.sim(list(order = c(1,0,0), ar = b),
                 n = n, rand.gen = rnorm, sd = s)

y <- eps + 10*sin(pi * x)

estimation_result <- RFGLS_estimate_timeseries(y, x, ntree = 10)
```

RFGLS_predict

*Prediction of mean function with RF-GLS***Description**

The function `RFGLS_predict` predicts the mean function at a given set of covariates. It uses a fitted RF-GLS model in Saha et al. 2020 to obtain the predictions.

Some code blocks are borrowed from the R package: `randomForest`: Breiman and Cutler's Random Forests for Classification and Regression
<https://CRAN.R-project.org/package=randomForest> .

Usage

```
RFGLS_predict(RFGLS_out, Xtest, h = 1, verbose = FALSE)
```

Arguments

<code>RFGLS_out</code>	an object obtained from <code>RFGLS_estimate_spatial</code> or <code>RFGLS_estimate_timeseries</code> .
<code>Xtest</code>	an $n_{test} \times p$ matrix of covariates for prediction. Its Structure should be identical (including intercept) with that of covariates provided for estimation purpose in <code>X</code> in <code>RFGLS_out</code> .
<code>h</code>	number of core to be used in parallel computing setup for bootstrap samples. If <code>h = 1</code> , there is no parallelization. Default value is 1.
<code>verbose</code>	if <code>TRUE</code> , model specifications along with information regarding OpenMP support and progress of the algorithm is printed to the screen. Otherwise, nothing is printed to the screen. Default value is <code>FALSE</code> .

Value

A list comprising:

<code>predicted_matrix</code>	an $n_{test} \times n_{tree}$ matrix of predictions. <code>t</code> -th column denote the predictions at n_{test} datapoints obtained from the <code>t</code> -th tree.
<code>predicted</code>	predicted values at the n_{test} prediction points. Average (<code>rowMeans</code>) of the tree-wise predictions in <code>predicted_matrix</code>

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References

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Andy Liaw, and Matthew Wiener (2015). randomForest: Breiman and Cutler's Random Forests for Classification and Regression. R package version 4.6-14.
<https://CRAN.R-project.org/package=randomForest>

Examples

```
rmvn <- function(n, mu = 0, V = matrix(1)){
  p <- length(mu)
  if(any(is.na(match(dim(V),p))))
    stop("Dimension not right!")
  D <- chol(V)
  t(matrix(rnorm(n*p), ncol=p)%*%D + rep(mu,rep(n,p)))
}

set.seed(2)
n <- 200
x <- as.matrix(rnorm(n),n,1)

sigma.sq <- 1
rho <- 0.5

set.seed(3)
b <- rho
s <- sqrt(sigma.sq)
eps = arima.sim(list(order = c(1,0,0), ar = b),
                 n = n, rand.gen = rnorm, sd = s)

y <- eps + 10*sin(pi * x[,1])

estimation_result <- RFGLS_estimate_timeseries(y, x, ntree = 10)
Xtest <- matrix(seq(0,1, by = 1/1000), 1001, 1)
RFGLS_predict <- RFGLS_predict(estimation_result, Xtest)
```

RFGLS_predict_spatial *Spatial response prediction at new location with RF-GLS*

Description

The function `RFGLS_predict_spatial` performs fast prediction on a set of new locations by combining non-linear mean estimate from a fitted RF-GLS model in Saha et al. 2020 with spatial kriging estimate obtained by using Nearest Neighbor Gaussian Processes (NNGP) (Datta et al., 2016).

Some code blocks are borrowed from the R packages: `spNNGP`: Spatial Regression Models for Large Datasets using Nearest Neighbor Gaussian Processes
<https://CRAN.R-project.org/package=spNNGP> and `randomForest`: Breiman and Cutler's Random

Forests for Classification and Regression
<https://CRAN.R-project.org/package=randomForest> .

Usage

```
RFGLS_predict_spatial(RFGLS_out, coords.0, Xtest,
                      h = 1, verbose = FALSE)
```

Arguments

RFGLS_out	an object obtained from RFGLS_estimate_spatial.
coords.0	the spatial coordinates corresponding to prediction locations. Its structure should be same as that of coords in BRISC_estimation. Default covariate value is a column of 1 to adjust for the mean (intercept).
Xtest	an $n_{test} \times p$ matrix of covariates for prediction. Its Structure should be identical (including intercept) with that of covariates provided for estimation purpose in X in RFGLS_out.
h	number of core to be used in parallel computing setup for bootstrap samples. If $h = 1$, there is no parallelization. Default value is 1.
verbose	if TRUE, model specifications along with information regarding OpenMP support and progress of the algorithm is printed to the screen. Otherwise, nothing is printed to the screen. Default value is FALSE.

Value

A list comprising:

prediction	predicted spatial response corresponding to Xtest and coords.0.
------------	---

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References

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Saha, A., & Datta, A. (2018). BRISC: bootstrap for rapid inference on spatial covariances. Stat, e184, DOI: 10.1002/sta4.184.

Datta, A., S. Banerjee, A.O. Finley, and A.E. Gelfand. (2016) Hierarchical Nearest-Neighbor Gaussian process models for large geostatistical datasets. Journal of the American Statistical Association, 111:800-812.

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Andy Liaw, and Matthew Wiener (2015). randomForest: Breiman and Cutler's Random Forests for Classification and Regression. R package version 4.6-14.
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Examples

```
rmvn <- function(n, mu = 0, V = matrix(1)){
  p <- length(mu)
  if(any(is.na(match(dim(V),p))))
    stop("Dimension not right!")
  D <- chol(V)
  t(matrix(rnorm(n*p), ncol=p)%*%D + rep(mu,rep(n,p)))
}

set.seed(1)
n <- 250
coords <- cbind(runif(n,0,1), runif(n,0,1))

set.seed(2)
x <- as.matrix(rnorm(n),n,1)

sigma.sq = 1
phi = 5
tau.sq = 0.1

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

y <- rnorm(n, 10*sin(pi * x) + w, sqrt(tau.sq))

estimation_result <- RFGLS_estimate_spatial(coords[1:200,], y[1:200],
                                             matrix(x[1:200,],200,1), ntree = 10)
prediction_result <- RFGLS_predict_spatial(estimation_result,
                                           coords[201:250,], matrix(x[201:250,],50,1))
```

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