

# Package ‘gpboost’

February 19, 2025

**Type** Package

**Title** Combining Tree-Boosting with Gaussian Process and Mixed Effects Models

**Version** 1.5.6

**Date** 2025-02-19

**Description** An R package that allows for combining tree-boosting with Gaussian process and mixed effects models. It also allows for independently doing tree-boosting as well as inference and prediction for Gaussian process and mixed effects models. See <<https://github.com/fabsig/GPBoost>> for more information on the software and Sigrist (2022, JMLR) <<https://www.jmlr.org/papers/v23/20-322.html>> and Sigrist (2023, TPAMI) <[doi:10.1109/TPAMI.2022.3168152](https://doi.org/10.1109/TPAMI.2022.3168152)> for more information on the methodology.

**Encoding** UTF-8

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**URL** <https://github.com/fabsig/GPBoost>

**BugReports** <https://github.com/fabsig/GPBoost/issues>

**NeedsCompilation** yes

**Biarch** true

**Suggests** testthat

**Depends** R (>= 3.5), R6 (>= 2.0)

**Imports** data.table (>= 1.9.6), graphics, RJSONIO, Matrix (>= 1.1-0), methods, utils

**SystemRequirements** C++17

**RoxygenNote** 6.0.1

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**Repository** CRAN

**Date/Publication** 2025-02-19 07:20:02 UTC

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agaricus.test      *Test part from Mushroom Data Set*

### Description

This data set is originally from the Mushroom data set, UCI Machine Learning Repository. This data set includes the following fields:

- label: the label for each record
- data: a sparse Matrix of dgCMatrx class, with 126 columns.

### Usage

```
data(agaricus.test)
```

### Format

A list containing a label vector, and a dgCMatrx object with 1611 rows and 126 variables

### References

<https://archive.ics.uci.edu/ml/datasets/Mushroom>

Bache, K. & Lichman, M. (2013). UCI Machine Learning Repository [<http://archive.ics.uci.edu/ml>]. Irvine, CA: University of California, School of Information and Computer Science.

agaricus.train      *Training part from Mushroom Data Set*

### Description

This data set is originally from the Mushroom data set, UCI Machine Learning Repository. This data set includes the following fields:

- label: the label for each record
- data: a sparse Matrix of dgCMatrx class, with 126 columns.

### Usage

```
data(agaricus.train)
```

### Format

A list containing a label vector, and a dgCMatrx object with 6513 rows and 127 variables

**References**

<https://archive.ics.uci.edu/ml/datasets/Mushroom>

Bache, K. & Lichman, M. (2013). UCI Machine Learning Repository [<http://archive.ics.uci.edu/ml>]. Irvine, CA: University of California, School of Information and Computer Science.

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bank

*Bank Marketing Data Set*

---

**Description**

This data set is originally from the Bank Marketing data set, UCI Machine Learning Repository.

It contains only the following: bank.csv with 10 randomly selected from 3 (older version of this dataset with less inputs).

**Usage**

```
data(bank)
```

**Format**

A data.table with 4521 rows and 17 variables

**References**

<http://archive.ics.uci.edu/ml/datasets/Bank+Marketing>

S. Moro, P. Cortez and P. Rita. (2014) A Data-Driven Approach to Predict the Success of Bank Telemarketing. Decision Support Systems

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coords

*Example data for the GPBoost package*

---

**Description**

A matrix with spatial coordinates for the example data of the GPBoost package

**Usage**

```
data(GPBoost_data)
```

coords\_test                    *Example data for the GPBoost package*

---

**Description**

A matrix with spatial coordinates for predictions for the example data of the GPBoost package

**Usage**

```
data(GPBoost_data)
```

---

dim.gpb.Dataset                *Dimensions of an gpb.Dataset*

---

**Description**

Returns a vector of numbers of rows and of columns in an gpb.Dataset.

**Usage**

```
## S3 method for class 'gpb.Dataset'  
dim(x, ...)
```

**Arguments**

x                    Object of class gpb.Dataset  
...                   other parameters

**Details**

Note: since nrow and ncol internally use dim, they can also be directly used with an gpb.Dataset object.

**Value**

a vector of numbers of rows and of columns

**Examples**

```
data(agaricus.train, package = "gpboost")  
train <- agaricus.train  
dtrain <- gpb.Dataset(train$data, label = train$label)  
  
stopifnot(nrow(dtrain) == nrow(train$data))  
stopifnot(ncol(dtrain) == ncol(train$data))  
stopifnot(all(dim(dtrain) == dim(train$data)))
```

---

dimnames.gpb.Dataset    *Handling of column names of gpb.Dataset*

---

## Description

Only column names are supported for `gpb.Dataset`, thus setting of row names would have no effect and returned row names would be `NULL`.

## Usage

```
## S3 method for class 'gpb.Dataset'
dimnames(x)

## S3 replacement method for class 'gpb.Dataset'
dimnames(x) <- value
```

## Arguments

<code>x</code>	object of class <code>gpb.Dataset</code>
<code>value</code>	a list of two elements: the first one is ignored and the second one is column names

## Details

Generic `dimnames` methods are used by `colnames`. Since row names are irrelevant, it is recommended to use `colnames` directly.

## Value

A list with the dimension names of the dataset

A list with the dimension names of the dataset

## Examples

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
gpb.Dataset.construct(dtrain)
dimnames(dtrain)
colnames(dtrain)
colnames(dtrain) <- make.names(seq_len(ncol(train$data)))
print(dtrain, verbose = TRUE)
```

---

fit	<i>Generic 'fit' method for a GPMoDel</i>
-----	---

---

**Description**

Generic 'fit' method for a GPMoDel

**Usage**

```
fit(gp_model, y, X, params, offset = NULL, fixed_effects = NULL)
```

**Arguments**

- |          |  |
|----------|--|
| gp_model | a GPMoDel  |
| y        | A vector with response variable data   |
| X        | A matrix with numeric covariate data for the fixed effects linear regression term (if there is one)  |
| params   | <p>A list with parameters for the estimation / optimization</p> <ul style="list-style-type: none"> <li>• optimizer_cov: string (default = "lbfgs"). Optimizer used for estimating covariance parameters. Options: "gradient_descent", "lbfgs", "fisher_scoring", "newton", "nelder_mead". If there are additional auxiliary parameters for non-Gaussian likelihoods, 'optimizer_cov' is also used for those</li> <li>• optimizer_coef: string (default = "wls" for Gaussian likelihoods and "lbfgs" for other likelihoods). Optimizer used for estimating linear regression coefficients, if there are any (for the GPBoost algorithm there are usually none). Options: "gradient_descent", "lbfgs", "wls", "nelder_mead". Gradient descent steps are done simultaneously with gradient descent steps for the covariance parameters. "wls" refers to doing coordinate descent for the regression coefficients using weighted least squares. If 'optimizer_cov' is set to "nelder_mead" or "lbfgs", 'optimizer_coef' is automatically also set to the same value.</li> <li>• maxit: integer (default = 1000). Maximal number of iterations for optimization algorithm</li> <li>• delta_rel_conv: numeric (default = 1E-6 except for "nelder_mead" for which the default is 1E-8). Convergence tolerance. The algorithm stops if the relative change in either the (approximate) log-likelihood or the parameters is below this value. If &lt; 0, internal default values are used</li> <li>• convergence_criterion: string (default = "relative_change_in_log_likelihood"). The convergence criterion used for terminating the optimization algorithm. Options: "relative_change_in_log_likelihood" or "relative_change_in_parameters"</li> <li>• init_coef: vector with numeric elements (default = NULL). Initial values for the regression coefficients (if there are any, can be NULL)</li> <li>• init_cov_pars: vector with numeric elements (default = NULL). Initial values for covariance parameters of Gaussian process and random effects (can be NULL). The order is the same as the order of the parameters in</li> </ul> |



the summary function: first is the error variance (only for "gaussian" likelihood), next follow the variances of the grouped random effects (if there are any, in the order provided in 'group\_data'), and then follow the marginal variance and the range of the Gaussian process. If there are multiple Gaussian processes, then the variances and ranges follow alternately. If 'init\_cov\_pars = NULL', an internal choice is used that depends on the likelihood and the random effects type and covariance function. If you select the option 'trace = TRUE' in the 'params' argument, you will see the first initial covariance parameters in iteration 0.

- lr\_coef: numeric (default = 0.1). Learning rate for fixed effect regression coefficients if gradient descent is used
- lr\_cov: numeric (default = 0.1 for "gradient\_descent" and 1. otherwise). Initial learning rate for covariance parameters if a gradient-based optimization method is used
  - If lr\_cov < 0, internal default values are used (0.1 for "gradient\_descent" and 1. otherwise)
  - If there are additional auxiliary parameters for non-Gaussian likelihoods, 'lr\_cov' is also used for those
  - For "lbfgs", this is divided by the norm of the gradient in the first iteration
- use\_nesterov\_acc: boolean (default = TRUE). If TRUE Nesterov acceleration is used. This is used only for gradient descent
- acc\_rate\_coef: numeric (default = 0.5). Acceleration rate for regression coefficients (if there are any) for Nesterov acceleration
- acc\_rate\_cov: numeric (default = 0.5). Acceleration rate for covariance parameters for Nesterov acceleration
- momentum\_offset: integer (Default = 2). Number of iterations for which no momentum is applied in the beginning.
- trace: boolean (default = FALSE). If TRUE, information on the progress of the parameter optimization is printed
- std\_dev: boolean (default = TRUE). If TRUE, approximate standard deviations are calculated for the covariance and linear regression parameters (= square root of diagonal of the inverse Fisher information for Gaussian likelihoods and square root of diagonal of a numerically approximated inverse Hessian for non-Gaussian likelihoods)
- init\_aux\_pars: vector with numeric elements (default = NULL). Initial values for additional parameters for non-Gaussian likelihoods (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- estimate\_aux\_pars: boolean (default = TRUE). If TRUE, additional parameters for non-Gaussian likelihoods are also estimated (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- cg\_max\_num\_it: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithms
- cg\_max\_num\_it\_tridiag: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithm when being run as Lanczos algorithm for tridiagonalization

- `cg_delta_conv`: numeric (default = 1E-2). Tolerance level for L2 norm of residuals for checking convergence in conjugate gradient algorithm when being used for parameter estimation
- `num_rand_vec_trace`: integer (default = 50). Number of random vectors (e.g., Rademacher) for stochastic approximation of the trace of a matrix
- `reuse_rand_vec_trace`: boolean (default = TRUE). If true, random vectors (e.g., Rademacher) for stochastic approximations of the trace of a matrix are sampled only once at the beginning of the parameter estimation and reused in later trace approximations. Otherwise they are sampled every time a trace is calculated
- `seed_rand_vec_trace`: integer (default = 1). Seed number to generate random vectors (e.g., Rademacher)
- `piv_chol_rank`: integer (default = 50). Rank of the pivoted Cholesky decomposition used as preconditioner in conjugate gradient algorithms
- `cg_preconditioner_type`: string. Type of preconditioner used for conjugate gradient algorithms.
  - Options for likelihood != "gaussian" and `gp_approx == "vecchia"` or `likelihood == "gaussian"` and `gp_approx == "vecchia_latent"`:
    - \* "vadu" (= default):  $(B^T * (D^{-1} + W) * B)$  as preconditioner for inverting  $(B^T * D^{-1} * B + W)$ , where  $B^T * D^{-1} * B \approx \Sigma^{-1}$
    - \* "fitc": modified predictive process preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$
    - \* "pivoted\_cholesky":  $(Lk * Lk^T + W^{-1})$  as preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$ , where  $Lk$  is a low-rank pivoted Cholesky approximation for  $\Sigma$  and  $B^{-1} * D * B^{-T} \approx \Sigma$
    - \* "incomplete\_cholesky": zero fill-in incomplete (reverse) Cholesky factorization of  $(B^T * D^{-1} * B + W)$  using the sparsity pattern of  $B^T * D^{-1} * B \approx \Sigma^{-1}$
  - Options for likelihood == "gaussian" and `gp_approx == "full_scale_tapering"`:
    - \* "fitc" (= default): modified predictive process preconditioner
    - \* "none": no preconditioner

`offset` A numeric vector with additional fixed effects contributions that are added to the linear predictor (= offset). The length of this vector needs to equal the number of training data points.

`fixed_effects` This is discontinued. Use the renamed equivalent argument `offset` instead

### Author(s)

Fabio Sigrist

fit.GPModel

*Fits a GPModel***Description**

Estimates the parameters of a GPModel by maximizing the marginal likelihood

**Usage**

```
## S3 method for class 'GPModel'
fit(gp_model, y, X = NULL, params = list(),
    offset = NULL, fixed_effects = NULL)
```

**Arguments**

- |          |   |
|----------|---|
| gp_model | a GPModel   |
| y        | A vector with response variable data  |
| X        | A matrix with numeric covariate data for the fixed effects linear regression term (if there is one)   |
| params   | A list with parameters for the estimation / optimization <ul style="list-style-type: none"> <li>• optimizer_cov: string (default = "lbfgs"). Optimizer used for estimating covariance parameters. Options: "gradient_descent", "lbfgs", "fisher_scoring", "newton", "nelder_mead". If there are additional auxiliary parameters for non-Gaussian likelihoods, 'optimizer_cov' is also used for those</li> <li>• optimizer_coef: string (default = "wls" for Gaussian likelihoods and "lbfgs" for other likelihoods). Optimizer used for estimating linear regression coefficients, if there are any (for the GPBoost algorithm there are usually none). Options: "gradient_descent", "lbfgs", "wls", "nelder_mead". Gradient descent steps are done simultaneously with gradient descent steps for the covariance parameters. "wls" refers to doing coordinate descent for the regression coefficients using weighted least squares. If 'optimizer_cov' is set to "nelder_mead" or "lbfgs", 'optimizer_coef' is automatically also set to the same value.</li> <li>• maxit: integer (default = 1000). Maximal number of iterations for optimization algorithm</li> <li>• delta_rel_conv: numeric (default = 1E-6 except for "nelder_mead" for which the default is 1E-8). Convergence tolerance. The algorithm stops if the relative change in either the (approximate) log-likelihood or the parameters is below this value. If &lt; 0, internal default values are used</li> <li>• convergence_criterion: string (default = "relative_change_in_log_likelihood"). The convergence criterion used for terminating the optimization algorithm. Options: "relative_change_in_log_likelihood" or "relative_change_in_parameters"</li> <li>• init_coef: vector with numeric elements (default = NULL). Initial values for the regression coefficients (if there are any, can be NULL)</li> </ul> |

- `init_cov_pars`: vector with numeric elements (default = NULL). Initial values for covariance parameters of Gaussian process and random effects (can be NULL). The order is the same as the order of the parameters in the summary function: first is the error variance (only for "gaussian" likelihood), next follow the variances of the grouped random effects (if there are any, in the order provided in 'group\_data'), and then follow the marginal variance and the range of the Gaussian process. If there are multiple Gaussian processes, then the variances and ranges follow alternately. If 'init\_cov\_pars = NULL', an internal choice is used that depends on the likelihood and the random effects type and covariance function. If you select the option 'trace = TRUE' in the 'params' argument, you will see the first initial covariance parameters in iteration 0.
- `lr_coef`: numeric (default = 0.1). Learning rate for fixed effect regression coefficients if gradient descent is used
- `lr_cov`: numeric (default = 0.1 for "gradient\_descent" and 1. otherwise). Initial learning rate for covariance parameters if a gradient-based optimization method is used
  - If `lr_cov < 0`, internal default values are used (0.1 for "gradient\_descent" and 1. otherwise)
  - If there are additional auxiliary parameters for non-Gaussian likelihoods, 'lr\_cov' is also used for those
  - For "lbfgs", this is divided by the norm of the gradient in the first iteration
- `use_nesterov_acc`: boolean (default = TRUE). If TRUE Nesterov acceleration is used. This is used only for gradient descent
- `acc_rate_coef`: numeric (default = 0.5). Acceleration rate for regression coefficients (if there are any) for Nesterov acceleration
- `acc_rate_cov`: numeric (default = 0.5). Acceleration rate for covariance parameters for Nesterov acceleration
- `momentum_offset`: integer (Default = 2). Number of iterations for which no momentum is applied in the beginning.
- `trace`: boolean (default = FALSE). If TRUE, information on the progress of the parameter optimization is printed
- `std_dev`: boolean (default = TRUE). If TRUE, approximate standard deviations are calculated for the covariance and linear regression parameters (= square root of diagonal of the inverse Fisher information for Gaussian likelihoods and square root of diagonal of a numerically approximated inverse Hessian for non-Gaussian likelihoods)
- `init_aux_pars`: vector with numeric elements (default = NULL). Initial values for additional parameters for non-Gaussian likelihoods (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- `estimate_aux_pars`: boolean (default = TRUE). If TRUE, additional parameters for non-Gaussian likelihoods are also estimated (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- `cg_max_num_it`: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithms

- `cg_max_num_it_tridiag`: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithm when being run as Lanczos algorithm for tridiagonalization
- `cg_delta_conv`: numeric (default = 1E-2). Tolerance level for L2 norm of residuals for checking convergence in conjugate gradient algorithm when being used for parameter estimation
- `num_rand_vec_trace`: integer (default = 50). Number of random vectors (e.g., Rademacher) for stochastic approximation of the trace of a matrix
- `reuse_rand_vec_trace`: boolean (default = TRUE). If true, random vectors (e.g., Rademacher) for stochastic approximations of the trace of a matrix are sampled only once at the beginning of the parameter estimation and reused in later trace approximations. Otherwise they are sampled every time a trace is calculated
- `seed_rand_vec_trace`: integer (default = 1). Seed number to generate random vectors (e.g., Rademacher)
- `piv_chol_rank`: integer (default = 50). Rank of the pivoted Cholesky decomposition used as preconditioner in conjugate gradient algorithms
- `cg_preconditioner_type`: string. Type of preconditioner used for conjugate gradient algorithms.
  - Options for likelihood != "gaussian" and `gp_approx` == "vecchia" or likelihood == "gaussian" and `gp_approx` == "vecchia\_latent":
    - \* "vadu" (= default):  $(B^T * (D^{-1} + W) * B)$  as preconditioner for inverting  $(B^T * D^{-1} * B + W)$ , where  $B^T * D^{-1} * B \approx \Sigma^{-1}$
    - \* "fitc": modified predictive process preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$
    - \* "pivoted\_cholesky":  $(Lk * Lk^T + W^{-1})$  as preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$ , where  $Lk$  is a low-rank pivoted Cholesky approximation for  $\Sigma$  and  $B^{-1} * D * B^{-T} \approx \Sigma$
    - \* "incomplete\_cholesky": zero fill-in incomplete (reverse) Cholesky factorization of  $(B^T * D^{-1} * B + W)$  using the sparsity pattern of  $B^T * D^{-1} * B \approx \Sigma^{-1}$
  - Options for likelihood == "gaussian" and `gp_approx` == "full\_scale\_tapering":
    - \* "fitc" (= default): modified predictive process preconditioner
    - \* "none": no preconditioner

`offset` A numeric vector with additional fixed effects contributions that are added to the linear predictor (= offset). The length of this vector needs to equal the number of training data points.

`fixed_effects` This is discontinued. Use the renamed equivalent argument `offset` instead

### Value

A fitted GPModel

**Author(s)**

Fabio Sigrist

**Examples**

```
# See https://github.com/fabsig/GPBoost/tree/master/R-package for more examples

data(GPBoost_data, package = "gpboost")
# Add intercept column
X1 <- cbind(rep(1,dim(X)[1]),X)
X_test1 <- cbind(rep(1,dim(X_test)[1]),X_test)

#-----Grouped random effects model: single-level random effect-----
gp_model <- GPMoDel(group_data = group_data[,1], likelihood="gaussian")
fit(gp_model, y = y, X = X1, params = list(std_dev = TRUE))
summary(gp_model)
# Make predictions
pred <- predict(gp_model, group_data_pred = group_data_test[,1],
               X_pred = X_test1, predict_var = TRUE)
pred$mu # Predicted mean
pred$var # Predicted variances
# Also predict covariance matrix
pred <- predict(gp_model, group_data_pred = group_data_test[,1],
               X_pred = X_test1, predict_cov_mat = TRUE)
pred$mu # Predicted mean
pred$cov # Predicted covariance

#-----Gaussian process model-----
gp_model <- GPMoDel(gp_coords = coords, cov_function = "matern", cov_fct_shape = 1.5,
                  likelihood="gaussian")
fit(gp_model, y = y, X = X1, params = list(std_dev = TRUE))
summary(gp_model)
# Make predictions
pred <- predict(gp_model, gp_coords_pred = coords_test,
               X_pred = X_test1, predict_cov_mat = TRUE)
pred$mu # Predicted (posterior) mean of GP
pred$cov # Predicted (posterior) covariance matrix of GP
```

---

fitGPMoDel

*Fits a GPMoDel*


---

**Description**

Estimates the parameters of a GPMoDel by maximizing the marginal likelihood

**Usage**

```
fitGPMModel(likelihood = "gaussian", group_data = NULL,
  group_rand_coef_data = NULL, ind_effect_group_rand_coef = NULL,
  drop_intercept_group_rand_effect = NULL, gp_coords = NULL,
  gp_rand_coef_data = NULL, cov_function = "matern", cov_fct_shape = 1.5,
  gp_approx = "none", num_parallel_threads = NULL,
  cov_fct_taper_range = 1, cov_fct_taper_shape = 1, num_neighbors = 20L,
  vecchia_ordering = "random", ind_points_selection = "kmeans++",
  num_ind_points = 500L, cover_tree_radius = 1,
  matrix_inversion_method = "cholesky", seed = 0L, cluster_ids = NULL,
  free_raw_data = FALSE, y, X = NULL, params = list(),
  vecchia_approx = NULL, vecchia_pred_type = NULL,
  num_neighbors_pred = NULL, offset = NULL, fixed_effects = NULL,
  likelihood_additional_param = NULL)
```

**Arguments**

likelihood	<p>A string specifying the likelihood function (distribution) of the response variable. Available options:</p> <ul style="list-style-type: none"> <li>• "gaussian"</li> <li>• "bernoulli_probit": binary data with Bernoulli likelihood and a probit link function</li> <li>• "bernoulli_logit": binary data with Bernoulli likelihood and a logit link function</li> <li>• "gamma": gamma distribution with a with log link function</li> <li>• "poisson": Poisson distribution with a with log link function</li> <li>• "negative_binomial": negative binomial distribution with a with log link function</li> <li>• "t": t-distribution (e.g., for robust regression)</li> <li>• "t_fix_df": t-distribution with the degrees-of-freedom (df) held fixed and not estimated. The df can be set via the likelihood_additional_param parameter</li> <li>• Note: other likelihoods could be implemented upon request</li> </ul>
group_data	<p>A vector or matrix whose columns are categorical grouping variables. The elements being group levels defining grouped random effects. The elements of 'group_data' can be integer, double, or character. The number of columns corresponds to the number of grouped (intercept) random effects</p>
group_rand_coef_data	<p>A vector or matrix with numeric covariate data for grouped random coefficients</p>
ind_effect_group_rand_coef	<p>A vector with integer indices that indicate the corresponding categorical grouping variable (=columns) in 'group_data' for every covariate in 'group_rand_coef_data'. Counting starts at 1. The length of this index vector must equal the number of covariates in 'group_rand_coef_data'. For instance, c(1,1,2) means that the first</p>

two covariates (=first two columns) in 'group\_rand\_coef\_data' have random coefficients corresponding to the first categorical grouping variable (=first column) in 'group\_data', and the third covariate (=third column) in 'group\_rand\_coef\_data' has a random coefficient corresponding to the second grouping variable (=second column) in 'group\_data'

drop_intercept_group_rand_effect	A vector of type logical (boolean). Indicates whether intercept random effects are dropped (only for random coefficients). If drop_intercept_group_rand_effect[k] is TRUE, the intercept random effect number k is dropped / not included. Only random effects with random slopes can be dropped.
gp_coords	A matrix with numeric coordinates (= inputs / features) for defining Gaussian processes
gp_rand_coef_data	A vector or matrix with numeric covariate data for Gaussian process random coefficients
cov_function	A string specifying the covariance function for the Gaussian process. Available options: <ul style="list-style-type: none"> <li>• "exponential": Exponential covariance function (using the parametrization of Diggle and Ribeiro, 2007)</li> <li>• "gaussian": Gaussian, aka squared exponential, covariance function (using the parametrization of Diggle and Ribeiro, 2007)</li> <li>• "matern": Matern covariance function with the smoothness specified by the cov_fct_shape parameter (using the parametrization of Rasmussen and Williams, 2006)</li> <li>• "powered_exponential": powered exponential covariance function with the exponent specified by the cov_fct_shape parameter (using the parametrization of Diggle and Ribeiro, 2007)</li> <li>• "wendland": Compactly supported Wendland covariance function (using the parametrization of Bevilacqua et al., 2019, AOS)</li> <li>• "matern_space_time": Spatio-temporal Matern covariance function with different range parameters for space and time. Note that the first column in gp_coords must correspond to the time dimension</li> <li>• "matern_ard": anisotropic Matern covariance function with Automatic Relevance Determination (ARD), i.e., with a different range parameter for every coordinate dimension / column of gp_coords</li> <li>• "gaussian_ard": anisotropic Gaussian, aka squared exponential, covariance function with Automatic Relevance Determination (ARD), i.e., with a different range parameter for every coordinate dimension / column of gp_coords</li> </ul>
cov_fct_shape	A numeric specifying the shape parameter of the covariance function (=smoothness parameter for Matern covariance) This parameter is irrelevant for some covariance functions such as the exponential or Gaussian
gp_approx	A string specifying the large data approximation for Gaussian processes. Available options: <ul style="list-style-type: none"> <li>• "none": No approximation</li> <li>• "vecchia": A Vecchia approximation; see Sigrist (2022, JMLR) for more details</li> </ul>



- "tapering": The covariance function is multiplied by a compactly supported Wendland correlation function
- "fitc": Fully Independent Training Conditional approximation aka modified predictive process approximation; see Gyger, Furrer, and Sigrist (2024) for more details
- "full\_scale\_tapering": A full scale approximation combining an inducing point / predictive process approximation with tapering on the residual process; see Gyger, Furrer, and Sigrist (2024) for more details
- "vecchia\_latent": similar as "vecchia" but a Vecchia approximation is applied to the latent Gaussian process for likelihood == "gaussian". For likelihood != "gaussian", "vecchia" and "vecchia\_latent" are equivalent

num\_parallel\_threads

An integer specifying the number of parallel threads for OMP. If num\_parallel\_threads = NULL, all available threads are used

cov\_fct\_taper\_range

A numeric specifying the range parameter of the Wendland covariance function and Wendland correlation taper function. We follow the notation of Bevilacqua et al. (2019, AOS)

cov\_fct\_taper\_shape

A numeric specifying the shape (=smoothness) parameter of the Wendland covariance function and Wendland correlation taper function. We follow the notation of Bevilacqua et al. (2019, AOS)

num\_neighbors

An integer specifying the number of neighbors for the Vecchia approximation. Note: for prediction, the number of neighbors can be set through the 'num\_neighbors\_pred' parameter in the 'set\_prediction\_data' function. By default, num\_neighbors\_pred = 2 \* num\_neighbors. Further, the type of Vecchia approximation used for making predictions is set through the 'vecchia\_pred\_type' parameter in the 'set\_prediction\_data' function

vecchia\_ordering

A string specifying the ordering used in the Vecchia approximation. Available options:

- "none": the default ordering in the data is used
- "random": a random ordering
- "time": ordering according to time (only for space-time models)
- "time\_random\_space": ordering according to time and randomly for all spatial points with the same time points (only for space-time models)

ind\_points\_selection

A string specifying the method for choosing inducing points Available options:

- "kmeans++": the k-means++ algorithm
- "cover\_tree": the cover tree algorithm
- "random": random selection from data points

num\_ind\_points

An integer specifying the number of inducing points / knots for, e.g., a predictive process approximation

cover\_tree\_radius

A numeric specifying the radius (= "spatial resolution") for the cover tree algorithm

matrix_inversion_method	<p>A string specifying the method used for inverting covariance matrices. Available options:</p> <ul style="list-style-type: none"> <li>• "cholesky": Cholesky factorization</li> <li>• "iterative": iterative methods. A combination of conjugate gradient, Lanczos algorithm, and other methods.</li> </ul> <p>This is currently only supported for the following cases:</p> <ul style="list-style-type: none"> <li>– likelihood != "gaussian" and gp_approx == "vecchia" (non-Gaussian likelihoods with a Vecchia-Laplace approximation)</li> <li>– likelihood == "gaussian" and gp_approx == "full_scale_tapering" (Gaussian likelihood with a full-scale tapering approximation)</li> </ul>
seed	An integer specifying the seed used for model creation (e.g., random ordering in Vecchia approximation)
cluster_ids	A vector with elements indicating independent realizations of random effects / Gaussian processes (same values = same process realization). The elements of 'cluster_ids' can be integer, double, or character.
free_raw_data	A boolean. If TRUE, the data (groups, coordinates, covariate data for random coefficients) is freed in R after initialization
y	A vector with response variable data
X	A matrix with numeric covariate data for the fixed effects linear regression term (if there is one)
params	<p>A list with parameters for the estimation / optimization</p> <ul style="list-style-type: none"> <li>• optimizer_cov: string (default = "lbfgs"). Optimizer used for estimating covariance parameters. Options: "gradient_descent", "lbfgs", "fisher_scoring", "newton", "nelder_mead". If there are additional auxiliary parameters for non-Gaussian likelihoods, 'optimizer_cov' is also used for those</li> <li>• optimizer_coef: string (default = "wls" for Gaussian likelihoods and "lbfgs" for other likelihoods). Optimizer used for estimating linear regression coefficients, if there are any (for the GPBoost algorithm there are usually none). Options: "gradient_descent", "lbfgs", "wls", "nelder_mead". Gradient descent steps are done simultaneously with gradient descent steps for the covariance parameters. "wls" refers to doing coordinate descent for the regression coefficients using weighted least squares. If 'optimizer_cov' is set to "nelder_mead" or "lbfgs", 'optimizer_coef' is automatically also set to the same value.</li> <li>• maxit: integer (default = 1000). Maximal number of iterations for optimization algorithm</li> <li>• delta_rel_conv: numeric (default = 1E-6 except for "nelder_mead" for which the default is 1E-8). Convergence tolerance. The algorithm stops if the relative change in either the (approximate) log-likelihood or the parameters is below this value. If &lt; 0, internal default values are used</li> <li>• convergence_criterion: string (default = "relative_change_in_log_likelihood"). The convergence criterion used for terminating the optimization algorithm. Options: "relative_change_in_log_likelihood" or "relative_change_in_parameters"</li> <li>• init_coef: vector with numeric elements (default = NULL). Initial values for the regression coefficients (if there are any, can be NULL)</li> </ul>

- `init_cov_pars`: vector with numeric elements (default = NULL). Initial values for covariance parameters of Gaussian process and random effects (can be NULL). The order is the same as the order of the parameters in the summary function: first is the error variance (only for "gaussian" likelihood), next follow the variances of the grouped random effects (if there are any, in the order provided in 'group\_data'), and then follow the marginal variance and the range of the Gaussian process. If there are multiple Gaussian processes, then the variances and ranges follow alternately. If 'init\_cov\_pars = NULL', an internal choice is used that depends on the likelihood and the random effects type and covariance function. If you select the option 'trace = TRUE' in the 'params' argument, you will see the first initial covariance parameters in iteration 0.
- `lr_coef`: numeric (default = 0.1). Learning rate for fixed effect regression coefficients if gradient descent is used
- `lr_cov`: numeric (default = 0.1 for "gradient\_descent" and 1. otherwise). Initial learning rate for covariance parameters if a gradient-based optimization method is used
  - If `lr_cov < 0`, internal default values are used (0.1 for "gradient\_descent" and 1. otherwise)
  - If there are additional auxiliary parameters for non-Gaussian likelihoods, 'lr\_cov' is also used for those
  - For "lbfgs", this is divided by the norm of the gradient in the first iteration
- `use_nesterov_acc`: boolean (default = TRUE). If TRUE Nesterov acceleration is used. This is used only for gradient descent
- `acc_rate_coef`: numeric (default = 0.5). Acceleration rate for regression coefficients (if there are any) for Nesterov acceleration
- `acc_rate_cov`: numeric (default = 0.5). Acceleration rate for covariance parameters for Nesterov acceleration
- `momentum_offset`: integer (Default = 2). Number of iterations for which no momentum is applied in the beginning.
- `trace`: boolean (default = FALSE). If TRUE, information on the progress of the parameter optimization is printed
- `std_dev`: boolean (default = TRUE). If TRUE, approximate standard deviations are calculated for the covariance and linear regression parameters (= square root of diagonal of the inverse Fisher information for Gaussian likelihoods and square root of diagonal of a numerically approximated inverse Hessian for non-Gaussian likelihoods)
- `init_aux_pars`: vector with numeric elements (default = NULL). Initial values for additional parameters for non-Gaussian likelihoods (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- `estimate_aux_pars`: boolean (default = TRUE). If TRUE, additional parameters for non-Gaussian likelihoods are also estimated (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- `cg_max_num_it`: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithms

- `cg_max_num_it_tridiag`: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithm when being run as Lanczos algorithm for tridiagonalization
- `cg_delta_conv`: numeric (default = 1E-2). Tolerance level for L2 norm of residuals for checking convergence in conjugate gradient algorithm when being used for parameter estimation
- `num_rand_vec_trace`: integer (default = 50). Number of random vectors (e.g., Rademacher) for stochastic approximation of the trace of a matrix
- `reuse_rand_vec_trace`: boolean (default = TRUE). If true, random vectors (e.g., Rademacher) for stochastic approximations of the trace of a matrix are sampled only once at the beginning of the parameter estimation and reused in later trace approximations. Otherwise they are sampled every time a trace is calculated
- `seed_rand_vec_trace`: integer (default = 1). Seed number to generate random vectors (e.g., Rademacher)
- `piv_chol_rank`: integer (default = 50). Rank of the pivoted Cholesky decomposition used as preconditioner in conjugate gradient algorithms
- `cg_preconditioner_type`: string. Type of preconditioner used for conjugate gradient algorithms.
  - Options for likelihood != "gaussian" and `gp_approx` == "vecchia" or likelihood == "gaussian" and `gp_approx` == "vecchia\_latent":
    - \* "vadu" (= default):  $(B^T * (D^{-1} + W) * B)$  as preconditioner for inverting  $(B^T * D^{-1} * B + W)$ , where  $B^T * D^{-1} * B \approx \Sigma^{-1}$
    - \* "fitc": modified predictive process preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$
    - \* "pivoted\_cholesky":  $(Lk * Lk^T + W^{-1})$  as preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$ , where  $Lk$  is a low-rank pivoted Cholesky approximation for  $\Sigma$  and  $B^{-1} * D * B^{-T} \approx \Sigma$
    - \* "incomplete\_cholesky": zero fill-in incomplete (reverse) Cholesky factorization of  $(B^T * D^{-1} * B + W)$  using the sparsity pattern of  $B^T * D^{-1} * B \approx \Sigma^{-1}$
  - Options for likelihood == "gaussian" and `gp_approx` == "full\_scale\_tapering":
    - \* "fitc" (= default): modified predictive process preconditioner
    - \* "none": no preconditioner

`vecchia_approx` Discontinued. Use the argument `gp_approx` instead

`vecchia_pred_type`

A string specifying the type of Vecchia approximation used for making predictions. This is discontinued here. Use the function 'set\_prediction\_data' to specify this

`num_neighbors_pred`

an integer specifying the number of neighbors for making predictions. This is discontinued here. Use the function 'set\_prediction\_data' to specify this

`offset`

A numeric vector with additional fixed effects contributions that are added to the linear predictor (= offset). The length of this vector needs to equal the number of training data points.

`fixed_effects` This is discontinued. Use the renamed equivalent argument `offset` instead  
`likelihood_additional_param`

A numeric specifying an additional parameter for the likelihood which cannot be estimated for this likelihood (e.g., degrees of freedom for likelihood = "t\_fix\_df"). This is not to be confused with any auxiliary parameters that can be estimated and accessed through the function `get_aux_pars` after estimation. Note that this `likelihood_additional_param` parameter is irrelevant for many likelihoods. If `likelihood_additional_param = NULL`, the following internal default values are used:

- `df = 2` for likelihood = "t\_fix\_df"

### Value

A fitted GPMoDel

### Author(s)

Fabio Sigrist

### Examples

# See <https://github.com/fabsig/GPBoost/tree/master/R-package> for more examples

```
data(GPBoost_data, package = "gpboost")
# Add intercept column
X1 <- cbind(rep(1,dim(X)[1]),X)
X_test1 <- cbind(rep(1,dim(X_test)[1]),X_test)

#-----Grouped random effects model: single-level random effect-----
gp_model <- fitGPMoDel(group_data = group_data[,1], y = y, X = X1,
                      likelihood="gaussian", params = list(std_dev = TRUE))
summary(gp_model)
# Make predictions
pred <- predict(gp_model, group_data_pred = group_data_test[,1],
               X_pred = X_test1, predict_var = TRUE)
pred$mu # Predicted mean
pred$var # Predicted variances
# Also predict covariance matrix
pred <- predict(gp_model, group_data_pred = group_data_test[,1],
               X_pred = X_test1, predict_cov_mat = TRUE)
pred$mu # Predicted mean
pred$cov # Predicted covariance

#-----Two crossed random effects and a random slope-----
gp_model <- fitGPMoDel(group_data = group_data, likelihood="gaussian",
                      group_rand_coef_data = X[,2],
                      ind_effect_group_rand_coef = 1,
                      y = y, X = X1, params = list(std_dev = TRUE))
summary(gp_model)
```

```

#-----Gaussian process model-----
gp_model <- fitGPMModel(gp_coords = coords, cov_function = "matern", cov_fct_shape = 1.5,
                      likelihood="gaussian", y = y, X = X1, params = list(std_dev = TRUE))
summary(gp_model)
# Make predictions
pred <- predict(gp_model, gp_coords_pred = coords_test,
               X_pred = X_test1, predict_cov_mat = TRUE)
pred$mu # Predicted (posterior) mean of GP
pred$cov # Predicted (posterior) covariance matrix of GP

#-----Gaussian process model with Vecchia approximation-----
gp_model <- fitGPMModel(gp_coords = coords, cov_function = "matern", cov_fct_shape = 1.5,
                      gp_approx = "vecchia", num_neighbors = 20,
                      likelihood="gaussian", y = y)
summary(gp_model)

#-----Gaussian process model with random coefficients-----
gp_model <- fitGPMModel(gp_coords = coords, cov_function = "matern", cov_fct_shape = 1.5,
                      gp_rand_coef_data = X[,2], y=y,
                      likelihood = "gaussian", params = list(std_dev = TRUE))
summary(gp_model)

#-----Combine Gaussian process with grouped random effects-----
gp_model <- fitGPMModel(group_data = group_data,
                      gp_coords = coords, cov_function = "matern", cov_fct_shape = 1.5,
                      likelihood = "gaussian", y = y, X = X1, params = list(std_dev = TRUE))
summary(gp_model)

```

---

getinfo

*Get information of an gpb.Dataset object*


---

## Description

Get one attribute of a gpb.Dataset

## Usage

```
getinfo(dataset, ...)
```

```
## S3 method for class 'gpb.Dataset'
getinfo(dataset, name, ...)
```

## Arguments

dataset	Object of class gpb.Dataset
...	other parameters
name	the name of the information field to get (see details)

**Details**

The name field can be one of the following:

- `label`: label gpboost learn from ;
- `weight`: to do a weight rescale ;
- `group`: used for learning-to-rank tasks. An integer vector describing how to group rows together as ordered results from the same set of candidate results to be ranked. For example, if you have a 100-document dataset with `group = c(10, 20, 40, 10, 10, 10)`, that means that you have 6 groups, where the first 10 records are in the first group, records 11-30 are in the second group, etc.
- `init_score`: initial score is the base prediction gpboost will boost from.

**Value**

info data

info data

**Examples**

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
gpb.Dataset.construct(dtrain)
```

```
labels <- gpboost::getinfo(dtrain, "label")
gpboost::setinfo(dtrain, "label", 1 - labels)
```

```
labels2 <- gpboost::getinfo(dtrain, "label")
stopifnot(all(labels2 == 1 - labels))
```

---

get\_aux\_pars

*Get (estimated) auxiliary (additional) parameters of the likelihood*

---

**Description**

Get (estimated) auxiliary (additional) parameters of the likelihood such as the shape parameter of a gamma or a negative binomial distribution. Some likelihoods (e.g., `bernoulli_logit` or `poisson`) have no auxiliary parameters

**Usage**

```
get_aux_pars(gp_model)
```

**Arguments**

`gp_model`      A `GPMoDel`

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
X1 <- cbind(rep(1,dim(X)[1]),X) # Add intercept column
y_pos <- exp(y)
gp_model <- fitGPModel(group_data = group_data[,1], y = y_pos, X = X1, likelihood="gamma")
get_aux_pars(gp_model)
```

---

get\_aux\_pars.GPModel    *Get (estimated) auxiliary (additional) parameters of the likelihood*

---

**Description**

Get (estimated) auxiliary (additional) parameters of the likelihood such as the shape parameter of a gamma or a negative binomial distribution. Some likelihoods (e.g., bernoulli\_logit or poisson) have no auxiliary parameters

**Usage**

```
## S3 method for class 'GPModel'
get_aux_pars(gp_model)
```

**Arguments**

gp\_model            A GPModel

**Value**

A GPModel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
X1 <- cbind(rep(1,dim(X)[1]),X) # Add intercept column
y_pos <- exp(y)
gp_model <- fitGPModel(group_data = group_data[,1], y = y_pos, X = X1, likelihood="gamma")
get_aux_pars(gp_model)
```



---

get_coef	<i>Get (estimated) linear regression coefficients</i>
----------	---

---

**Description**

Get (estimated) linear regression coefficients and standard deviations (if `std_dev=TRUE` was set in `fit`)

**Usage**

```
get_coef(gp_model)
```

**Arguments**

`gp_model`          A GPMoel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
X1 <- cbind(rep(1,dim(X)[1]),X) # Add intercept column
gp_model <- fitGPMoel(group_data = group_data[,1], y = y, X = X1, likelihood="gaussian")
get_coef(gp_model)
```

---

get_coef.GPMoel	<i>Get (estimated) linear regression coefficients</i>
-----------------	---

---

**Description**

Get (estimated) linear regression coefficients and standard deviations (if `std_dev=TRUE` was set in `fit`)

**Usage**

```
## S3 method for class 'GPMoel'
get_coef(gp_model)
```

**Arguments**

`gp_model`          A GPMoel

**Value**

A GPModel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
X1 <- cbind(rep(1,dim(X)[1]),X) # Add intercept column
gp_model <- fitGPModel(group_data = group_data[,1], y = y, X = X1, likelihood="gaussian")
get_coef(gp_model)
```

---

get\_cov\_pars

*Get (estimated) covariance parameters*

---

**Description**

Get (estimated) covariance parameters and standard deviations (if std\_dev=TRUE was set in fit)

**Usage**

```
get_cov_pars(gp_model)
```

**Arguments**

gp\_model            A GPModel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
X1 <- cbind(rep(1,dim(X)[1]),X) # Add intercept column
gp_model <- fitGPModel(group_data = group_data[,1], y = y, X = X1, likelihood="gaussian")
get_cov_pars(gp_model)
```

---

get\_cov\_pars.GPModel *Get (estimated) covariance parameters*

---

**Description**

Get (estimated) covariance parameters and standard deviations (if std\_dev=TRUE was set in fit)

**Usage**

```
## S3 method for class 'GPModel'  
get_cov_pars(gp_model)
```

**Arguments**

gp\_model            A GPModel

**Value**

A GPModel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")  
X1 <- cbind(rep(1,dim(X)[1]),X) # Add intercept column  
gp_model <- fitGPModel(group_data = group_data[,1], y = y, X = X1, likelihood="gaussian")  
get_cov_pars(gp_model)
```

---

get\_nested\_categories *Auxiliary function to create categorical variables for nested grouped random effects*

---

**Description**

Auxiliary function to create categorical variables for nested grouped random effects

**Usage**

```
get_nested_categories(outer_var, inner_var)
```

**Arguments**

`outer_var` A vector containing the outer categorical grouping variable within which the `inner_var` is nested in. Can be of type integer, double, or character.

`inner_var` A vector containing the inner nested categorical grouping variable

**Value**

A vector containing a categorical variable such that `inner_var` is nested in `outer_var`

**Author(s)**

Fabio Sigrist

**Examples**

```
# Fit a model with Time as categorical fixed effects variables and Diet and Chick
# as random effects, where Chick is nested in Diet using lme4
chick_nested_diet <- get_nested_categories(ChickWeight$Diet, ChickWeight$Chick)
fixed_effects_matrix <- model.matrix(weight ~ as.factor(Time), data = ChickWeight)
mod_gpb <- fitGPModel(X = fixed_effects_matrix,
                     group_data = cbind(diet=ChickWeight$Diet, chick_nested_diet),
                     y = ChickWeight$weight, params = list(std_dev = TRUE))

summary(mod_gpb)
# This does (almost) the same thing as the following code using lme4:
# mod_lme4 <- lmer(weight ~ as.factor(Time) + (1 | Diet/Chick), data = ChickWeight, REML = FALSE)
# summary(mod_lme4)
```

---

`gpb.convert_with_rules`

*Data preparator for GPBoost datasets with rules (integer)*

---

**Description**

Attempts to prepare a clean dataset to prepare to put in a `gpb.Dataset`. Factor, character, and logical columns are converted to integer. Missing values in factors and characters will be filled with 0L. Missing values in logicals will be filled with -1L.

This function returns and optionally takes in "rules" the describe exactly how to convert values in columns.

Columns that contain only NA values will be converted by this function but will not show up in the returned rules.

**Usage**

```
gpb.convert_with_rules(data, rules = NULL)
```

**Arguments**

`data` A data.frame or data.table to prepare.

`rules` A set of rules from the data preparator, if already used. This should be an R list, where names are column names in data and values are named character vectors whose names are column values and whose values are new values to replace them with.

**Value**

A list with the cleaned dataset (`data`) and the rules (`rules`). Note that the data must be converted to a matrix format (`as.matrix`) for input in `gpb.Dataset`.

**Examples**

```
data(iris)

str(iris)

new_iris <- gpb.convert_with_rules(data = iris)
str(new_iris$data)

data(iris) # Erase iris dataset
iris$Species[1L] <- "NEW FACTOR" # Introduce junk factor (NA)

# Use conversion using known rules
# Unknown factors become 0, excellent for sparse datasets
newer_iris <- gpb.convert_with_rules(data = iris, rules = new_iris$rules)

# Unknown factor is now zero, perfect for sparse datasets
newer_iris$data[1L, ] # Species became 0 as it is an unknown factor

newer_iris$data[1L, 5L] <- 1.0 # Put back real initial value

# Is the newly created dataset equal? YES!
all.equal(new_iris$data, newer_iris$data)

# Can we test our own rules?
data(iris) # Erase iris dataset

# We remapped values differently
personal_rules <- list(
  Species = c(
    "setosa" = 3L
    , "versicolor" = 2L
    , "virginica" = 1L
  )
)
newest_iris <- gpb.convert_with_rules(data = iris, rules = personal_rules)
str(newest_iris$data) # SUCCESS!
```

gpb.cv

*CV function for number of boosting iterations***Description**

Cross validation function for determining number of boosting iterations

**Usage**

```
gpb.cv(params = list(), data, gp_model = NULL, nrounds = 1000L,
       early_stopping_rounds = NULL, folds = NULL, nfold = 5L, metric = NULL,
       verbose = 1L, use_gp_model_for_validation = TRUE,
       fit_GP_cov_pars_OOS = FALSE, train_gp_model_cov_pars = TRUE,
       label = NULL, weight = NULL, obj = NULL, eval = NULL, record = TRUE,
       eval_freq = 1L, showsd = FALSE, stratified = TRUE, init_model = NULL,
       colnames = NULL, categorical_feature = NULL, callbacks = list(),
       reset_data = FALSE, delete_boosters_folds = FALSE, ...)
```

**Arguments**

- params list of "tuning" parameters. See [the parameter documentation](#) for more information. A few key parameters:
- `learning_rate`: The learning rate, also called shrinkage or damping parameter (default = 0.1). An important tuning parameter for boosting. Lower values usually lead to higher predictive accuracy but more boosting iterations are needed
  - `num_leaves`: Number of leaves in a tree. Tuning parameter for tree-boosting (default = 31)
  - `max_depth`: Maximal depth of a tree. Tuning parameter for tree-boosting (default = no limit)
  - `min_data_in_leaf`: Minimal number of samples per leaf. Tuning parameter for tree-boosting (default = 20)
  - `lambda_l2`: L2 regularization (default = 0)
  - `lambda_l1`: L1 regularization (default = 0)
  - `max_bin`: Maximal number of bins that feature values will be bucketed in (default = 255)
  - `line_search_step_length` (default = FALSE): If TRUE, a line search is done to find the optimal step length for every boosting update (see, e.g., Friedman 2001). This is then multiplied by the learning rate
  - `train_gp_model_cov_pars` (default = TRUE): If TRUE, the covariance parameters of the Gaussian process are estimated in every boosting iterations, otherwise the `gp_model` parameters are not estimated. In the latter case, you need to either estimate them beforehand or provide values via the `'init_cov_pars'` parameter when creating the `gp_model`

- `use_gp_model_for_validation` (default = TRUE): If TRUE, the Gaussian process is also used (in addition to the tree model) for calculating predictions on the validation data
- `leaves_newton_update` (default = FALSE): Set this to TRUE to do a Newton update step for the tree leaves after the gradient step. Applies only to Gaussian process boosting (GPBoost algorithm)
- `num_threads`: Number of threads. For the best speed, set this to the number of real CPU cores (`parallel::detectCores(logical = FALSE)`), not the number of threads (most CPU using hyper-threading to generate 2 threads per CPU core).

<code>data</code>	a <code>gpb.Dataset</code> object, used for training. Some functions, such as <code>gpb.cv</code> , may allow you to pass other types of data like <code>matrix</code> and then separately supply label as a keyword argument.
<code>gp_model</code>	A <code>GPMoel</code> object that contains the random effects (Gaussian process and / or grouped random effects) model
<code>nrounds</code>	number of boosting iterations (= number of trees). This is the most important tuning parameter for boosting
<code>early_stopping_rounds</code>	int. Activates early stopping. Requires at least one validation data and one metric. When this parameter is non-null, training will stop if the evaluation of any metric on any validation set fails to improve for <code>early_stopping_rounds</code> consecutive boosting rounds. If training stops early, the returned model will have attribute <code>best_iter</code> set to the iteration number of the best iteration.
<code>folds</code>	list provides a possibility to use a list of pre-defined CV folds (each element must be a vector of test fold's indices). When folds are supplied, the <code>nfold</code> and <code>stratified</code> parameters are ignored.
<code>nfold</code>	the original dataset is randomly partitioned into <code>nfold</code> equal size subsamples.
<code>metric</code>	Evaluation metric to be monitored when doing CV and parameter tuning. Can be a character string or vector of character strings. If not NULL, the metric in <code>params</code> will be overridden. Non-exhaustive list of supported metrics: "test_neg_log_likelihood", "mse", "rmse", "mae", "auc", "average_precision", "binary_logloss", "binary_error". See the " <a href="#">metric</a> " section of the <a href="#">parameter documentation</a> for a complete list of valid metrics.
<code>verbose</code>	verbosity for output, if $\leq 0$ , also will disable the print of evaluation during training
<code>use_gp_model_for_validation</code>	Boolean. If TRUE, the <code>gp_model</code> (Gaussian process and/or random effects) is also used (in addition to the tree model) for calculating predictions on the validation data. If FALSE, the <code>gp_model</code> (random effects part) is ignored for making predictions and only the tree ensemble is used for making predictions for calculating the validation / test error.
<code>fit_GP_cov_pars_00S</code>	Boolean (default = FALSE). If TRUE, the covariance parameters of the <code>gp_model</code> model are estimated using the out-of-sample (OOS) predictions on the validation data using the optimal number of iterations (after performing the CV). This corresponds to the GPBoostOOS algorithm.

train_gp_model_cov_pars	Boolean. If TRUE, the covariance parameters of the gp_model (Gaussian process and/or random effects) are estimated in every boosting iterations, otherwise the gp_model parameters are not estimated. In the latter case, you need to either estimate them beforehand or provide the values via the init_cov_pars parameter when creating the gp_model
label	Vector of labels, used if data is not an <a href="#">gpb.Dataset</a>
weight	vector of response values. If not NULL, will set to dataset
obj	(character) The distribution of the response variable (=label) conditional on fixed and random effects. This only needs to be set when doing independent boosting without random effects / Gaussian processes.
eval	Evaluation metric to be monitored when doing CV and parameter tuning. This can be a string, function, or list with a mixture of strings and functions. <ul style="list-style-type: none"> <li>• <b>a. character vector:</b> Non-exhaustive list of supported metrics: "test_neg_log_likelihood", "mse", "rmse", "mae", "auc", "average_precision", "binary_logloss", "binary_error" See <a href="#">the "metric" section of the parameter documentation</a> for a complete list of valid metrics.</li> <li>• <b>b. function:</b> You can provide a custom evaluation function. This should accept the keyword arguments preds and dtrain and should return a named list with three elements: <ul style="list-style-type: none"> <li>– name: A string with the name of the metric, used for printing and storing results.</li> <li>– value: A single number indicating the value of the metric for the given predictions and true values</li> <li>– higher_better: A boolean indicating whether higher values indicate a better fit. For example, this would be FALSE for metrics like MAE or RMSE.</li> </ul> </li> <li>• <b>c. list:</b> If a list is given, it should only contain character vectors and functions. These should follow the requirements from the descriptions above.</li> </ul>
record	Boolean, TRUE will record iteration message to booster\$record_evals
eval_freq	evaluation output frequency, only effect when verbose > 0
showsd	boolean, whether to show standard deviation of cross validation. This parameter defaults to TRUE.
stratified	a boolean indicating whether sampling of folds should be stratified by the values of outcome labels.
init_model	path of model file of gpb. Booster object, will continue training from this model
colnames	feature names, if not null, will use this to overwrite the names in dataset
categorical_feature	categorical features. This can either be a character vector of feature names or an integer vector with the indices of the features (e.g. c(1L, 10L) to say "the first and tenth columns").
callbacks	List of callback functions that are applied at each iteration.
reset_data	Boolean, setting it to TRUE (not the default value) will transform the booster model into a predictor model which frees up memory and the original datasets



```

delete_boosters_folds
    Boolean, setting it to TRUE (not the default value) will delete the boosters of
    the individual folds
...
    other parameters, see Parameters.rst for more information.

```

**Value**

a trained model `gpb.CVBooster`.

**Early Stopping**

"early stopping" refers to stopping the training process if the model's performance on a given validation set does not improve for several consecutive iterations.

If multiple arguments are given to `eval`, their order will be preserved. If you enable early stopping by setting `early_stopping_rounds` in `params`, by default all metrics will be considered for early stopping.

If you want to only consider the first metric for early stopping, pass `first_metric_only = TRUE` in `params`. Note that if you also specify `metric` in `params`, that metric will be considered the "first" one. If you omit `metric`, a default metric will be used based on your choice for the parameter `obj` (keyword argument) or `objective` (passed into `params`).

**Author(s)**

Authors of the LightGBM R package, Fabio Sigrüst

**Examples**

# See <https://github.com/fabsig/GPBoost/tree/master/R-package> for more examples

```

library(gpboost)
data(GPBoost_data, package = "gpboost")

# Create random effects model and dataset
gp_model <- GPModel(group_data = group_data[,1], likelihood="gaussian")
dtrain <- gpb.Dataset(X, label = y)
params <- list(learning_rate = 0.05,
              max_depth = 6,
              min_data_in_leaf = 5)

# Run CV
cvbst <- gpb.cv(params = params,
               data = dtrain,
               gp_model = gp_model,
               nrounds = 100,
               nfold = 4,
               eval = "l2",
               early_stopping_rounds = 5,
               use_gp_model_for_validation = TRUE)
print(paste0("Optimal number of iterations: ", cvbst$best_iter,
            ", best test error: ", cvbst$best_score))

```

---

gpb.Dataset                      *Construct gpb.Dataset object*

---

### Description

Construct gpb.Dataset object from dense matrix, sparse matrix or local file (that was created previously by saving an gpb.Dataset).

### Usage

```
gpb.Dataset(data, params = list(), reference = NULL, colnames = NULL,
            categorical_feature = NULL, free_raw_data = FALSE, info = list(), ...)
```

### Arguments

data	a matrix object, a dgCMatix object or a character representing a filename
params	a list of parameters. See the <a href="#">"Dataset Parameters" section of the parameter documentation</a> for a list of parameters and valid values.
reference	reference dataset. When GPBoost creates a Dataset, it does some preprocessing like binning continuous features into histograms. If you want to apply the same bin boundaries from an existing dataset to new data, pass that existing Dataset to this argument.
colnames	names of columns
categorical_feature	categorical features. This can either be a character vector of feature names or an integer vector with the indices of the features (e.g. c(1L, 10L) to say "the first and tenth columns").
free_raw_data	GPBoost constructs its data format, called a "Dataset", from tabular data. By default, this Dataset object on the R side does keep a copy of the raw data. If you set free_raw_data = TRUE, no copy of the raw data is kept (this reduces memory usage)
info	a list of information of the gpb.Dataset object
...	other information to pass to info or parameters pass to params

### Value

constructed dataset

### Examples

```
data(agaricus.train, package = "gboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
data_file <- tempfile(fileext = ".data")
gpb.Dataset.save(dtrain, data_file)
dtrain <- gpb.Dataset(data_file)
```

```
gpb.Dataset.construct(dtrain)
```

---

```
gpb.Dataset.construct Construct Dataset explicitly
```

---

**Description**

Construct Dataset explicitly

**Usage**

```
gpb.Dataset.construct(dataset)
```

**Arguments**

dataset            Object of class gpb.Dataset

**Value**

constructed dataset

**Examples**

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
gpb.Dataset.construct(dtrain)
```

---

```
gpb.Dataset.create.valid
                          Construct validation data
```

---

**Description**

Construct validation data according to training data

**Usage**

```
gpb.Dataset.create.valid(dataset, data, info = list(), ...)
```

**Arguments**

dataset            gpb.Dataset object, training data  
data                a matrix object, a dgCMatix object or a character representing a filename  
info                a list of information of the gpb.Dataset object  
...                 other information to pass to info.

**Value**

constructed dataset

**Examples**

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
data(agaricus.test, package = "gpboost")
test <- agaricus.test
dtest <- gpb.Dataset.create.valid(dtrain, test$data, label = test$label)
```

---

gpb.Dataset.save	<i>Save gpb.Dataset to a binary file</i>
------------------	--

---

**Description**

Please note that `init_score` is not saved in binary file. If you need it, please set it again after loading Dataset.

**Usage**

```
gpb.Dataset.save(dataset, fname)
```

**Arguments**

dataset	object of class <code>gpb.Dataset</code>
fname	object filename of output file

**Value**

the dataset you passed in

**Examples**

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
gpb.Dataset.save(dtrain, tempfile(fileext = ".bin"))
```

---

`gpb.Dataset.set.categorical`  
*Set categorical feature of gpb.Dataset*

---

**Description**

Set the categorical features of an `gpb.Dataset` object. Use this function to tell GPBoost which features should be treated as categorical.

**Usage**

```
gpb.Dataset.set.categorical(dataset, categorical_feature)
```

**Arguments**

`dataset`            object of class `gpb.Dataset`  
`categorical_feature`  
                    categorical features. This can either be a character vector of feature names or an integer vector with the indices of the features (e.g. `c(1L, 10L)` to say "the first and tenth columns").

**Value**

the dataset you passed in

**Examples**

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
data_file <- tempfile(fileext = ".data")
gpb.Dataset.save(dtrain, data_file)
dtrain <- gpb.Dataset(data_file)
gpb.Dataset.set.categorical(dtrain, 1L:2L)
```

---

`gpb.Dataset.set.reference`  
*Set reference of gpb.Dataset*

---

**Description**

If you want to use validation data, you should set reference to training data

**Usage**

```
gpb.Dataset.set.reference(dataset, reference)
```

**Arguments**

dataset            object of class gpb.Dataset  
reference         object of class gpb.Dataset

**Value**

the dataset you passed in

**Examples**

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
data(agaricus.test, package = "gpboost")
test <- agaricus.test
dtest <- gpb.Dataset(test$data, test = train$label)
gpb.Dataset.set.reference(dtest, dtrain)
```

---

gpb.dump

*Dump GPBoost model to json*

---

**Description**

Dump GPBoost model to json

**Usage**

```
gpb.dump(booster, num_iteration = NULL)
```

**Arguments**

booster            Object of class gpb.Booster  
num\_iteration     number of iteration want to predict with, NULL or <= 0 means use best iteration

**Value**

json format of model

**Examples**

```
library(gpboost)
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
data(agaricus.test, package = "gpboost")
test <- agaricus.test
dtest <- gpb.Dataset.create.valid(dtrain, test$data, label = test$label)
```

```

params <- list(objective = "regression", metric = "l2")
valids <- list(test = dtest)
model <- gpb.train(
  params = params
  , data = dtrain
  , nrounds = 10L
  , valids = valids
  , min_data = 1L
  , learning_rate = 1.0
  , early_stopping_rounds = 5L
)
json_model <- gpb.dump(model)

```

---

`gpb.get.eval.result`     *Get record evaluation result from booster*

---

## Description

Given a `gpb.Booster`, return evaluation results for a particular metric on a particular dataset.

## Usage

```

gpb.get.eval.result(booster, data_name, eval_name, iters = NULL,
  is_err = FALSE)

```

## Arguments

<code>booster</code>	Object of class <code>gpb.Booster</code>
<code>data_name</code>	Name of the dataset to return evaluation results for.
<code>eval_name</code>	Name of the evaluation metric to return results for.
<code>iters</code>	An integer vector of iterations you want to get evaluation results for. If <code>NULL</code> (the default), evaluation results for all iterations will be returned.
<code>is_err</code>	<code>TRUE</code> will return evaluation error instead

## Value

numeric vector of evaluation result

## Examples

```

# train a regression model
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
data(agaricus.test, package = "gpboost")
test <- agaricus.test
dtest <- gpb.Dataset.create.valid(dtrain, test$data, label = test$label)

```

```

params <- list(objective = "regression", metric = "l2")
valids <- list(test = dtest)
model <- gpb.train(
  params = params
  , data = dtrain
  , nrounds = 5L
  , valids = valids
  , min_data = 1L
  , learning_rate = 1.0
)

# Examine valid data_name values
print(setdiff(names(model$record_evals), "start_iter"))

# Examine valid eval_name values for dataset "test"
print(names(model$record_evals[["test"]]))

# Get L2 values for "test" dataset
gpb.get.eval.result(model, "test", "l2")

```

---

gpb.grid.search.tune.parameters

*Function for choosing tuning parameters*

---

## Description

Function that allows for choosing tuning parameters from a grid in a deterministic or random way using cross validation or validation data sets.

## Usage

```

gpb.grid.search.tune.parameters(param_grid, num_try_random = NULL, data,
  gp_model = NULL, params = list(), nrounds = 1000L,
  early_stopping_rounds = NULL, folds = NULL, nfold = 5L, metric = NULL,
  verbose_eval = 1L, cv_seed = NULL, use_gp_model_for_validation = TRUE,
  train_gp_model_cov_pars = TRUE, label = NULL, weight = NULL,
  obj = NULL, eval = NULL, stratified = TRUE, init_model = NULL,
  colnames = NULL, categorical_feature = NULL, callbacks = list(),
  return_all_combinations = FALSE, ...)

```

## Arguments

param_grid	list with candidate parameters defining the grid over which a search is done
num_try_random	integer with number of random trial on parameter grid. If NULL, a deterministic search is done
data	a gpb.Dataset object, used for training. Some functions, such as <a href="#">gpb.cv</a> , may allow you to pass other types of data like matrix and then separately supply label as a keyword argument.



gp_model	A GPMoDel object that contains the random effects (Gaussian process and / or grouped random effects) model
params	list with other parameters not included in param_grid
nrounds	number of boosting iterations (= number of trees). This is the most important tuning parameter for boosting
early_stopping_rounds	int. Activates early stopping. Requires at least one validation data and one metric. When this parameter is non-null, training will stop if the evaluation of any metric on any validation set fails to improve for early_stopping_rounds consecutive boosting rounds. If training stops early, the returned model will have attribute best_iter set to the iteration number of the best iteration.
folds	list provides a possibility to use a list of pre-defined CV folds (each element must be a vector of test fold's indices). When folds are supplied, the nfold and stratified parameters are ignored.
nfold	the original dataset is randomly partitioned into nfold equal size subsamples.
metric	Evaluation metric to be monitored when doing CV and parameter tuning. Can be a character string or vector of character strings. If not NULL, the metric in params will be overridden. Non-exhaustive list of supported metrics: "test_neg_log_likelihood", "mse", "rmse", "mae", "auc", "average_precision", "binary_logloss", "binary_error". See <a href="#">the "metric" section of the parameter documentation</a> for a complete list of valid metrics.
verbose_eval	integer. Whether to display information on the progress of tuning parameter choice. If None or 0, verbose is of. If = 1, summary progress information is displayed for every parameter combination. If >= 2, detailed progress is displayed at every boosting stage for every parameter combination.
cv_seed	Seed for generating folds when doing nfold CV
use_gp_model_for_validation	Boolean. If TRUE, the gp_model (Gaussian process and/or random effects) is also used (in addition to the tree model) for calculating predictions on the validation data. If FALSE, the gp_model (random effects part) is ignored for making predictions and only the tree ensemble is used for making predictions for calculating the validation / test error.
train_gp_model_cov_pars	Boolean. If TRUE, the covariance parameters of the gp_model (Gaussian process and/or random effects) are estimated in every boosting iterations, otherwise the gp_model parameters are not estimated. In the latter case, you need to either estimate them beforehand or provide the values via the init_cov_pars parameter when creating the gp_model
label	Vector of labels, used if data is not an <a href="#">gpb.Dataset</a>
weight	vector of response values. If not NULL, will set to dataset
obj	(character) The distribution of the response variable (=label) conditional on fixed and random effects. This only needs to be set when doing independent boosting without random effects / Gaussian processes.
eval	Evaluation metric to be monitored when doing CV and parameter tuning. This can be a string, function, or list with a mixture of strings and functions.

- **a. character vector:** Non-exhaustive list of supported metrics: "test\_neg\_log\_likelihood", "mse", "rmse", "mae", "auc", "average\_precision", "binary\_logloss", "binary\_error" See [the "metric" section of the parameter documentation](#) for a complete list of valid metrics.
- **b. function:** You can provide a custom evaluation function. This should accept the keyword arguments `preds` and `dtrain` and should return a named list with three elements:
  - `name`: A string with the name of the metric, used for printing and storing results.
  - `value`: A single number indicating the value of the metric for the given predictions and true values
  - `higher_better`: A boolean indicating whether higher values indicate a better fit. For example, this would be `FALSE` for metrics like MAE or RMSE.
- **c. list:** If a list is given, it should only contain character vectors and functions. These should follow the requirements from the descriptions above.

<code>stratified</code>	a boolean indicating whether sampling of folds should be stratified by the values of outcome labels.
<code>init_model</code>	path of model file of <code>gpb.Booster</code> object, will continue training from this model
<code>colnames</code>	feature names, if not null, will use this to overwrite the names in dataset
<code>categorical_feature</code>	categorical features. This can either be a character vector of feature names or an integer vector with the indices of the features (e.g. <code>c(1L, 10L)</code> to say "the first and tenth columns").
<code>callbacks</code>	List of callback functions that are applied at each iteration.
<code>return_all_combinations</code>	a boolean indicating whether all tried parameter combinations are returned
<code>...</code>	other parameters, see <code>Parameters.rst</code> for more information.

## Value

A list with the best parameter combination and score The list has the following format: `list("best_params" = best_params, "best_iter" = best_iter, "best_score" = best_score)` If `return_all_combinations` is `TRUE`, then the list contains an additional entry `'all_combinations'`

## Early Stopping

"early stopping" refers to stopping the training process if the model's performance on a given validation set does not improve for several consecutive iterations.

If multiple arguments are given to `eval`, their order will be preserved. If you enable early stopping by setting `early_stopping_rounds` in `params`, by default all metrics will be considered for early stopping.

If you want to only consider the first metric for early stopping, pass `first_metric_only = TRUE` in `params`. Note that if you also specify `metric` in `params`, that metric will be considered the "first" one. If you omit `metric`, a default metric will be used based on your choice for the parameter `obj` (keyword argument) or `objective` (passed into `params`).

**Author(s)**

Fabio Sigrist

**Examples**

```
# See https://github.com/fabsig/GPBoost/tree/master/R-package for more examples

library(gpboost)
data(GPBoost_data, package = "gpboost")

n <- length(y)
param_grid <- list("learning_rate" = c(0.001, 0.01, 0.1, 1, 10),
                  "min_data_in_leaf" = c(1, 10, 100, 1000),
                  "max_depth" = c(-1),
                  "num_leaves" = 2^(1:10),
                  "lambda_l2" = c(0, 1, 10, 100),
                  "max_bin" = c(250, 500, 1000, min(n,10000)),
                  "line_search_step_length" = c(TRUE, FALSE))
# Note: "max_depth" = c(-1) means no depth limit as we tune 'num_leaves'.
# Can also additionally tune 'max_depth', e.g., "max_depth" = c(-1, 1, 2, 3, 5, 10)
metric = "mse" # Define metric
# Note: can also use metric = "test_neg_log_likelihood".
# See https://github.com/fabsig/GPBoost/blob/master/docs/Parameters.rst#metric-parameters
gp_model <- GPModel(group_data = group_data[,1], likelihood="gaussian")
data_train <- gpb.Dataset(data = X, label = y)
set.seed(1)
opt_params <- gpb.grid.search.tune.parameters(param_grid = param_grid,
                                             data = data_train, gp_model = gp_model,
                                             num_try_random = 100, nfold = 5,
                                             nrounds = 1000, early_stopping_rounds = 20,
                                             verbose_eval = 1, metric = metric, cv_seed = 4)

print(paste0("Best parameters: ",
            paste0(unlist(lapply(seq_along(opt_params$best_params),
                                function(y, n, i) { paste0(n[[i]],": ", y[[i]] )},
                                y=opt_params$best_params,
                                n=names(opt_params$best_params))), collapse=", "))

print(paste0("Best number of iterations: ", opt_params$best_iter))
print(paste0("Best score: ", round(opt_params$best_score, digits=3)))
# Alternatively and faster: using manually defined validation data instead of cross-validation
# use 20% of the data as validation data
valid_tune_idx <- sample.int(length(y), as.integer(0.2*length(y)))
folds <- list(valid_tune_idx)
opt_params <- gpb.grid.search.tune.parameters(param_grid = param_grid,
                                             data = data_train, gp_model = gp_model,
                                             num_try_random = 100, folds = folds,
                                             nrounds = 1000, early_stopping_rounds = 20,
                                             verbose_eval = 1, metric = metric, cv_seed = 4)
```

---

gpb.importance	<i>Compute feature importance in a model</i>
----------------	--

---

**Description**

Creates a data.table of feature importances in a model.

**Usage**

```
gpb.importance(model, percentage = TRUE)
```

**Arguments**

model	object of class gpb.Booster.
percentage	whether to show importance in relative percentage.

**Value**

For a tree model, a data.table with the following columns:

- Feature: Feature names in the model.
- Gain: The total gain of this feature's splits.
- Cover: The number of observation related to this feature.
- Frequency: The number of times a feature splitted in trees.

**Examples**

```
data(agaricus.train, package = "gboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)

params <- list(
  objective = "binary"
  , learning_rate = 0.1
  , max_depth = -1L
  , min_data_in_leaf = 1L
  , min_sum_hessian_in_leaf = 1.0
)
model <- gpb.train(
  params = params
  , data = dtrain
  , nrounds = 5L
)

tree_imp1 <- gpb.importance(model, percentage = TRUE)
tree_imp2 <- gpb.importance(model, percentage = FALSE)
```

---

gpb.interprete	<i>Compute feature contribution of prediction</i>
----------------	---

---

### Description

Computes feature contribution components of rawscore prediction.

### Usage

```
gpb.interprete(model, data, idxset, num_iteration = NULL)
```

### Arguments

model	object of class <code>gpb.Booster</code> .
data	a matrix object or a <code>dgCMatrix</code> object.
idxset	an integer vector of indices of rows needed.
num_iteration	number of iteration want to predict with, NULL or $\leq 0$ means use best iteration.

### Value

For regression, binary classification and lambdarank model, a list of `data.table` with the following columns:

- Feature: Feature names in the model.
- Contribution: The total contribution of this feature's splits.

For multiclass classification, a list of `data.table` with the Feature column and Contribution columns to each class.

### Examples

```
Logit <- function(x) log(x / (1.0 - x))
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
setinfo(dtrain, "init_score", rep(Logit(mean(train$label)), length(train$label)))
data(agaricus.test, package = "gpboost")
test <- agaricus.test

params <- list(
  objective = "binary"
  , learning_rate = 0.1
  , max_depth = -1L
  , min_data_in_leaf = 1L
  , min_sum_hessian_in_leaf = 1.0
)
model <- gpb.train(
  params = params
```

```

      , data = dtrain
      , nrounds = 3L
    )

    tree_interpretation <- gpb.interprete(model, test$data, 1L:5L)

```

---

gpb.load

*Load GPBoost model*

---

### Description

Load GPBoost takes in either a file path or model string. If both are provided, Load will default to loading from file Boosters with `gp_models` can only be loaded from file.

### Usage

```
gpb.load(filename = NULL, model_str = NULL)
```

### Arguments

filename	path of model file
model_str	a str containing the model

### Value

gpb.Booster

### Author(s)

Fabio Sigrist, authors of the LightGBM R package

### Examples

```

library(gpboost)
data(GPBoost_data, package = "gpboost")

# Train model and make prediction
gp_model <- GPMModel(group_data = group_data[,1], likelihood = "gaussian")
bst <- gpboost(data = X, label = y, gp_model = gp_model, nrounds = 16,
              learning_rate = 0.05, max_depth = 6, min_data_in_leaf = 5,
              verbose = 0)
pred <- predict(bst, data = X_test, group_data_pred = group_data_test[,1],
              predict_var= TRUE, pred_latent = TRUE)

# Save model to file
filename <- tempfile(fileext = ".json")
gpb.save(bst,filename = filename)
# Load from file and make predictions again
bst_loaded <- gpb.load(filename = filename)

```

```

pred_loaded <- predict(bst_loaded, data = X_test, group_data_pred = group_data_test[,1],
                      predict_var= TRUE, pred_latent = TRUE)
# Check equality
pred$fixed_effect - pred_loaded$fixed_effect
pred$random_effect_mean - pred_loaded$random_effect_mean
pred$random_effect_cov - pred_loaded$random_effect_cov

```

---

`gpb.model.dt.tree`      *Parse a GPBoost model json dump*

---

## Description

Parse a GPBoost model json dump into a `data.table` structure.

## Usage

```
gpb.model.dt.tree(model, num_iteration = NULL)
```

## Arguments

<code>model</code>	object of class <code>gpb.Booster</code>
<code>num_iteration</code>	number of iterations you want to predict with. <code>NULL</code> or <code>&lt;= 0</code> means use best iteration

## Value

A `data.table` with detailed information about model trees' nodes and leaves.

The columns of the `data.table` are:

- `tree_index`: ID of a tree in a model (integer)
- `split_index`: ID of a node in a tree (integer)
- `split_feature`: for a node, it's a feature name (character); for a leaf, it simply labels it as "NA"
- `node_parent`: ID of the parent node for current node (integer)
- `leaf_index`: ID of a leaf in a tree (integer)
- `leaf_parent`: ID of the parent node for current leaf (integer)
- `split_gain`: Split gain of a node
- `threshold`: Splitting threshold value of a node
- `decision_type`: Decision type of a node
- `default_left`: Determine how to handle NA value, `TRUE` -> Left, `FALSE` -> Right
- `internal_value`: Node value
- `internal_count`: The number of observation collected by a node
- `leaf_value`: Leaf value
- `leaf_count`: The number of observation collected by a leaf

**Examples**

```

data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)

params <- list(
  objective = "binary"
  , learning_rate = 0.01
  , num_leaves = 63L
  , max_depth = -1L
  , min_data_in_leaf = 1L
  , min_sum_hessian_in_leaf = 1.0
)
model <- gpb.train(params, dtrain, 10L)

tree_dt <- gpb.model.dt.tree(model)

```

---

`gpb.plot.importance`     *Plot feature importance as a bar graph*

---

**Description**

Plot previously calculated feature importance: Gain, Cover and Frequency, as a bar graph.

**Usage**

```

gpb.plot.importance(tree_imp, top_n = 10L, measure = "Gain",
  left_margin = 10L, cex = NULL, ...)

```

**Arguments**

<code>tree_imp</code>	a data.table returned by <a href="#">gpb.importance</a> .
<code>top_n</code>	maximal number of top features to include into the plot.
<code>measure</code>	the name of importance measure to plot, can be "Gain", "Cover" or "Frequency".
<code>left_margin</code>	(base R barplot) allows to adjust the left margin size to fit feature names.
<code>cex</code>	(base R barplot) passed as <code>cex.names</code> parameter to <a href="#">barplot</a> . Set a number smaller than 1.0 to make the bar labels smaller than R's default and values greater than 1.0 to make them larger.
<code>...</code>	other parameters passed to <code>graphics::barplot</code>

**Details**

The graph represents each feature as a horizontal bar of length proportional to the defined importance of a feature. Features are shown ranked in a decreasing importance order.



**Value**

The `gpb.plot.importance` function creates a barplot and silently returns a processed `data.table` with `top_n` features sorted by defined importance.

**Examples**

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)

params <- list(
  objective = "binary"
  , learning_rate = 0.1
  , min_data_in_leaf = 1L
  , min_sum_hessian_in_leaf = 1.0
)

model <- gpb.train(
  params = params
  , data = dtrain
  , nrounds = 5L
)

tree_imp <- gpb.importance(model, percentage = TRUE)
gpb.plot.importance(tree_imp, top_n = 5L, measure = "Gain")
```

---

`gpb.plot.interpretation`

*Plot feature contribution as a bar graph*

---

**Description**

Plot previously calculated feature contribution as a bar graph.

**Usage**

```
gpb.plot.interpretation(tree_interpretation_dt, top_n = 10L, cols = 1L,
  left_margin = 10L, cex = NULL)
```

**Arguments**

<code>tree_interpretation_dt</code>	a <code>data.table</code> returned by <a href="#">gpb.interprete</a> .
<code>top_n</code>	maximal number of top features to include into the plot.
<code>cols</code>	the column numbers of layout, will be used only for multiclass classification feature contribution.
<code>left_margin</code>	(base R barplot) allows to adjust the left margin size to fit feature names.
<code>cex</code>	(base R barplot) passed as <code>cex.names</code> parameter to <code>barplot</code> .

## Details

The graph represents each feature as a horizontal bar of length proportional to the defined contribution of a feature. Features are shown ranked in a decreasing contribution order.

## Value

The `gpb.plot.interpretation` function creates a barplot.

## Examples

```
Logit <- function(x) {
  log(x / (1.0 - x))
}
data(agaricus.train, package = "gpboost")
labels <- agaricus.train$label
dtrain <- gpb.Dataset(
  agaricus.train$data
  , label = labels
)
setinfo(dtrain, "init_score", rep(Logit(mean(labels)), length(labels)))

data(agaricus.test, package = "gpboost")

params <- list(
  objective = "binary"
  , learning_rate = 0.1
  , max_depth = -1L
  , min_data_in_leaf = 1L
  , min_sum_hessian_in_leaf = 1.0
)
model <- gpb.train(
  params = params
  , data = dtrain
  , nrounds = 5L
)

tree_interpretation <- gpb.interprete(
  model = model
  , data = agaricus.test$data
  , idxset = 1L:5L
)
gpb.plot.interpretation(
  tree_interpretation_dt = tree_interpretation[[1L]]
  , top_n = 3L
)
```

---

gpb.plot.part.dep.interact

*Plot interaction partial dependence plots*


---

## Description

Plot interaction partial dependence plots

## Usage

```
gpb.plot.part.dep.interact(model, data, variables, n.pt.per.var = 20,
  subsample = pmin(1, n.pt.per.var^2 * 100/nrow(data)),
  discrete.variables = c(FALSE, FALSE), which.class = NULL,
  type = "filled.contour", nlevels = 20, xlab = variables[1],
  ylab = variables[2], zlab = "", main = "", return_plot_data = FALSE,
  ...)
```

## Arguments

model	A gpb.Booster model object
data	A matrix with data for creating partial dependence plots
variables	A vector of length two of type string with names of the columns or integer with indices of the columns in data for which an interaction dependence plot is created
n.pt.per.var	Number of grid points per variable (used only if a variable is not discrete) For continuous variables, the two-dimensional grid for the interaction plot has dimension $c(n.pt.per.var, n.pt.per.var)$
subsample	Fraction of random samples in data to be used for calculating the partial dependence plot
discrete.variables	A vector of length two of type boolean. If an entry is TRUE, the evaluation grid of the corresponding variable is set to the unique values of the variable
which.class	An integer indicating the class in multi-class classification (value from 0 to num_class - 1)
type	A character string indicating the type of the plot. Supported values: "filled.contour" and "contour"
nlevels	Parameter passed to the filled.contour or contour function
xlab	Parameter passed to the filled.contour or contour function
ylab	Parameter passed to the filled.contour or contour function
zlab	Parameter passed to the filled.contour or contour function
main	Parameter passed to the filled.contour or contour function
return_plot_data	A boolean. If TRUE, the data for creating the partial dependence plot is returned
...	Additional parameters passed to the filled.contour or contour function

**Value**

A list with three entries for creating the partial dependence plot: the first two entries are vectors with x and y coordinates. The third is a two-dimensional matrix of dimension  $c(\text{length}(x), \text{length}(y))$  with z-coordinates. This is only returned if `return_plot_data==TRUE`

**Author(s)**

Fabio Sigrist

**Examples**

```
library(gpboost)
data(GPBoost_data, package = "gpboost")
gp_model <- GPModel(group_data = group_data[,1], likelihood = "gaussian")
gpboost_model <- gpboost(data = X,
                          label = y,
                          gp_model = gp_model,
                          nrounds = 16,
                          learning_rate = 0.05,
                          max_depth = 6,
                          min_data_in_leaf = 5,
                          verbose = 0)
gpb.plot.part.dep.interact(gpboost_model, X, variables = c(1,2))
```

---

`gpb.plot.partial.dependence`

*Plot partial dependence plots*

---

**Description**

Plot partial dependence plots

**Usage**

```
gpb.plot.partial.dependence(model, data, variable, n.pt = 100,
                             subsample = pmin(1, n.pt * 100/nrow(data)), discrete.x = FALSE,
                             which.class = NULL, xlab = deparse(substitute(variable)), ylab = "",
                             type = if (discrete.x) "p" else "b", main = "",
                             return_plot_data = FALSE, ...)
```

**Arguments**

<code>model</code>	A <code>gpb.Booster</code> model object
<code>data</code>	A matrix with data for creating partial dependence plots
<code>variable</code>	A string with a name of the column or an integer with an index of the column in data for which a dependence plot is created

n.pt	Evaluation grid size (used only if x is not discrete)
subsample	Fraction of random samples in data to be used for calculating the partial dependence plot
discrete.x	A boolean. If TRUE, the evaluation grid is set to the unique values of x
which.class	An integer indicating the class in multi-class classification (value from 0 to num_class - 1)
xlab	Parameter passed to plot
ylab	Parameter passed to plot
type	Parameter passed to plot
main	Parameter passed to plot
return_plot_data	A boolean. If TRUE, the data for creating the partial dependence plot is returned
...	Additional parameters passed to plot

**Value**

A two-dimensional matrix with data for creating the partial dependence plot. This is only returned if return\_plot\_data==TRUE

**Author(s)**

Fabio Sigrist (adapted from a version by Michael Mayer)

**Examples**

```
library(gpboost)
data(GPBoost_data, package = "gpboost")

gp_model <- GPModel(group_data = group_data[,1], likelihood = "gaussian")
gpboost_model <- gpboost(data = X,
  label = y,
  gp_model = gp_model,
  nrounds = 16,
  learning_rate = 0.05,
  max_depth = 6,
  min_data_in_leaf = 5,
  verbose = 0)
gpb.plot.partial.dependence(gpboost_model, X, variable = 1)
```

---

gpb.save                      *Save GPBoost model*

---

### Description

Save GPBoost model

### Usage

```
gpb.save(booster, filename, start_iteration = NULL, num_iteration = NULL,
         save_raw_data = FALSE, ...)
```

### Arguments

booster	Object of class <code>gpb.Booster</code>
filename	saved filename
start_iteration	int or NULL, optional (default=NULL) Start index of the iteration to predict. If NULL or $\leq 0$ , starts from the first iteration.
num_iteration	int or NULL, optional (default=NULL) Limit number of iterations in the prediction. If NULL, if the best iteration exists and <code>start_iteration</code> is NULL or $\leq 0$ , the best iteration is used; otherwise, all iterations from <code>start_iteration</code> are used. If $\leq 0$ , all iterations from <code>start_iteration</code> are used (no limits).
save_raw_data	If TRUE, the raw data (predictor / covariate data) for the <code>Booster</code> is also saved. Enable this option if you want to change <code>start_iteration</code> or <code>num_iteration</code> at prediction time after loading.
...	Additional named arguments passed to the <code>predict()</code> method of the <code>gpb.Booster</code> object passed to <code>object</code> . This is only used when there is a <code>gp_model</code> and when <code>save_raw_data=FALSE</code>

### Value

`gpb.Booster`

### Author(s)

Fabio Sigrist, authors of the LightGBM R package

### Examples

```
library(gpboost)
data(GPBoost_data, package = "gpboost")

# Train model and make prediction
gp_model <- GPModel(group_data = group_data[,1], likelihood = "gaussian")
bst <- gpboost(data = X, label = y, gp_model = gp_model, nrounds = 16,
              learning_rate = 0.05, max_depth = 6, min_data_in_leaf = 5,
```

```

        verbose = 0)
pred <- predict(bst, data = X_test, group_data_pred = group_data_test[,1],
               predict_var= TRUE, pred_latent = TRUE)
# Save model to file
filename <- tempfile(fileext = ".json")
gpb.save(bst,filename = filename)
# Load from file and make predictions again
bst_loaded <- gpb.load(filename = filename)
pred_loaded <- predict(bst_loaded, data = X_test, group_data_pred = group_data_test[,1],
                      predict_var= TRUE, pred_latent = TRUE)
# Check equality
pred$fixed_effect - pred_loaded$fixed_effect
pred$random_effect_mean - pred_loaded$random_effect_mean
pred$random_effect_cov - pred_loaded$random_effect_cov

```

---

gpb.train

*Main training logic for GBPoost*


---

## Description

Logic to train with GBPoost

## Usage

```

gpb.train(params = list(), data, nrounds = 100L, gp_model = NULL,
          use_gp_model_for_validation = TRUE, train_gp_model_cov_pars = TRUE,
          valids = list(), obj = NULL, eval = NULL, verbose = 1L,
          record = TRUE, eval_freq = 1L, init_model = NULL, colnames = NULL,
          categorical_feature = NULL, early_stopping_rounds = NULL,
          callbacks = list(), reset_data = FALSE, ...)

```

## Arguments

- |        |   |
|--------|---|
| params | <p>list of "tuning" parameters. See <a href="#">the parameter documentation</a> for more information. A few key parameters:</p> <ul style="list-style-type: none"> <li>• <code>learning_rate</code>: The learning rate, also called shrinkage or damping parameter (default = 0.1). An important tuning parameter for boosting. Lower values usually lead to higher predictive accuracy but more boosting iterations are needed</li> <li>• <code>num_leaves</code>: Number of leaves in a tree. Tuning parameter for tree-boosting (default = 31)</li> <li>• <code>max_depth</code>: Maximal depth of a tree. Tuning parameter for tree-boosting (default = no limit)</li> <li>• <code>min_data_in_leaf</code>: Minimal number of samples per leaf. Tuning parameter for tree-boosting (default = 20)</li> <li>• <code>lambda_l2</code>: L2 regularization (default = 0)</li> </ul> |
|--------|---|

- `lambda_l1`: L1 regularization (default = 0)
- `max_bin`: Maximal number of bins that feature values will be bucketed in (default = 255)
- `line_search_step_length` (default = FALSE): If TRUE, a line search is done to find the optimal step length for every boosting update (see, e.g., Friedman 2001). This is then multiplied by the learning rate
- `train_gp_model_cov_pars` (default = TRUE): If TRUE, the covariance parameters of the Gaussian process are estimated in every boosting iterations, otherwise the `gp_model` parameters are not estimated. In the latter case, you need to either estimate them beforehand or provide values via the `'init_cov_pars'` parameter when creating the `gp_model`
- `use_gp_model_for_validation` (default = TRUE): If TRUE, the Gaussian process is also used (in addition to the tree model) for calculating predictions on the validation data
- `leaves_newton_update` (default = FALSE): Set this to TRUE to do a Newton update step for the tree leaves after the gradient step. Applies only to Gaussian process boosting (GPBoost algorithm)
- `num_threads`: Number of threads. For the best speed, set this to the number of real CPU cores (`parallel::detectCores(logical = FALSE)`), not the number of threads (most CPU using hyper-threading to generate 2 threads per CPU core).

<code>data</code>	a <code>gpb.Dataset</code> object, used for training. Some functions, such as <code>gpb.cv</code> , may allow you to pass other types of data like <code>matrix</code> and then separately supply <code>label</code> as a keyword argument.
<code>nrounds</code>	number of boosting iterations (= number of trees). This is the most important tuning parameter for boosting
<code>gp_model</code>	A <code>GPMoDel</code> object that contains the random effects (Gaussian process and / or grouped random effects) model
<code>use_gp_model_for_validation</code>	Boolean. If TRUE, the <code>gp_model</code> (Gaussian process and/or random effects) is also used (in addition to the tree model) for calculating predictions on the validation data. If FALSE, the <code>gp_model</code> (random effects part) is ignored for making predictions and only the tree ensemble is used for making predictions for calculating the validation / test error.
<code>train_gp_model_cov_pars</code>	Boolean. If TRUE, the covariance parameters of the <code>gp_model</code> (Gaussian process and/or random effects) are estimated in every boosting iterations, otherwise the <code>gp_model</code> parameters are not estimated. In the latter case, you need to either estimate them beforehand or provide the values via the <code>init_cov_pars</code> parameter when creating the <code>gp_model</code>
<code>valids</code>	a list of <code>gpb.Dataset</code> objects, used for validation
<code>obj</code>	(character) The distribution of the response variable (=label) conditional on fixed and random effects. This only needs to be set when doing independent boosting without random effects / Gaussian processes.
<code>eval</code>	Evaluation metric to be monitored when doing CV and parameter tuning. This can be a string, function, or list with a mixture of strings and functions.



- **a. character vector:** Non-exhaustive list of supported metrics: "test\_neg\_log\_likelihood", "mse", "rmse", "mae", "auc", "average\_precision", "binary\_logloss", "binary\_error" See [the "metric" section of the parameter documentation](#) for a complete list of valid metrics.
- **b. function:** You can provide a custom evaluation function. This should accept the keyword arguments preds and dtrain and should return a named list with three elements:
  - name: A string with the name of the metric, used for printing and storing results.
  - value: A single number indicating the value of the metric for the given predictions and true values
  - higher\_better: A boolean indicating whether higher values indicate a better fit. For example, this would be FALSE for metrics like MAE or RMSE.
- **c. list:** If a list is given, it should only contain character vectors and functions. These should follow the requirements from the descriptions above.

verbose	verbosity for output, if $\leq 0$ , also will disable the print of evaluation during training
record	Boolean, TRUE will record iteration message to booster\$record_evals
eval_freq	evaluation output frequency, only effect when verbose $> 0$
init_model	path of model file of gpb.Booster object, will continue training from this model
colnames	feature names, if not null, will use this to overwrite the names in dataset
categorical_feature	categorical features. This can either be a character vector of feature names or an integer vector with the indices of the features (e.g. c(1L, 10L) to say "the first and tenth columns").
early_stopping_rounds	int. Activates early stopping. Requires at least one validation data and one metric. When this parameter is non-null, training will stop if the evaluation of any metric on any validation set fails to improve for early_stopping_rounds consecutive boosting rounds. If training stops early, the returned model will have attribute best_iter set to the iteration number of the best iteration.
callbacks	List of callback functions that are applied at each iteration.
reset_data	Boolean, setting it to TRUE (not the default value) will transform the booster model into a predictor model which frees up memory and the original datasets
...	other parameters, see <a href="#">the parameter documentation</a> for more information.

### Value

a trained booster model gpb.Booster.

### Early Stopping

"early stopping" refers to stopping the training process if the model's performance on a given validation set does not improve for several consecutive iterations.

If multiple arguments are given to `eval`, their order will be preserved. If you enable early stopping by setting `early_stopping_rounds` in `params`, by default all metrics will be considered for early stopping.

If you want to only consider the first metric for early stopping, pass `first_metric_only = TRUE` in `params`. Note that if you also specify `metric` in `params`, that metric will be considered the "first" one. If you omit `metric`, a default metric will be used based on your choice for the parameter `obj` (keyword argument) or `objective` (passed into `params`).

### Author(s)

Fabio Sigrist, authors of the LightGBM R package

### Examples

# See <https://github.com/fabsig/GPBoost/tree/master/R-package> for more examples

```
library(gpboost)
data(GPBoost_data, package = "gpboost")

#-----Combine tree-boosting and grouped random effects model-----
# Create random effects model
gp_model <- GPModel(group_data = group_data[,1], likelihood = "gaussian")
# The default optimizer for covariance parameters (hyperparameters) is
# Nesterov-accelerated gradient descent.
# This can be changed to, e.g., Nelder-Mead as follows:
# re_params <- list(optimizer_cov = "nelder_mead")
# gp_model$set_optim_params(params=re_params)
# Use trace = TRUE to monitor convergence:
# re_params <- list(trace = TRUE)
# gp_model$set_optim_params(params=re_params)
dtrain <- gpb.Dataset(data = X, label = y)
# Train model
bst <- gpb.train(data = dtrain, gp_model = gp_model, nrounds = 16,
                 learning_rate = 0.05, max_depth = 6, min_data_in_leaf = 5,
                 verbose = 0)
# Estimated random effects model
summary(gp_model)
# Make predictions
pred <- predict(bst, data = X_test, group_data_pred = group_data_test[,1],
               predict_var= TRUE)
pred$random_effect_mean # Predicted mean
pred$random_effect_cov # Predicted variances
pred$fixed_effect # Predicted fixed effect from tree ensemble
# Sum them up to obtain a single prediction
pred$random_effect_mean + pred$fixed_effect

#-----Combine tree-boosting and Gaussian process model-----
# Create Gaussian process model
gp_model <- GPModel(gp_coords = coords, cov_function = "exponential",
                   likelihood = "gaussian")
# Train model
```

```

dtrain <- gpb.Dataset(data = X, label = y)
bst <- gpb.train(data = dtrain, gp_model = gp_model, nrounds = 16,
               learning_rate = 0.05, max_depth = 6, min_data_in_leaf = 5,
               verbose = 0)
# Estimated random effects model
summary(gp_model)
# Make predictions
pred <- predict(bst, data = X_test, gp_coords_pred = coords_test,
               predict_cov_mat = TRUE)
pred$random_effect_mean # Predicted (posterior) mean of GP
pred$random_effect_cov # Predicted (posterior) covariance matrix of GP
pred$fixed_effect # Predicted fixed effect from tree ensemble
# Sum them up to obtain a single prediction
pred$random_effect_mean + pred$fixed_effect

#-----Using validation data-----
set.seed(1)
train_ind <- sample.int(length(y),size=250)
dtrain <- gpb.Dataset(data = X[train_ind,], label = y[train_ind])
dtest <- gpb.Dataset.create.valid(dtrain, data = X[-train_ind,], label = y[-train_ind])
valids <- list(test = dtest)
gp_model <- GPModel(group_data = group_data[train_ind,1], likelihood="gaussian")
# Need to set prediction data for gp_model
gp_model$set_prediction_data(group_data_pred = group_data[-train_ind,1])
# Training with validation data and use_gp_model_for_validation = TRUE
bst <- gpb.train(data = dtrain, gp_model = gp_model, nrounds = 100,
               learning_rate = 0.05, max_depth = 6, min_data_in_leaf = 5,
               verbose = 1, valids = valids,
               early_stopping_rounds = 10, use_gp_model_for_validation = TRUE)
print(paste0("Optimal number of iterations: ", bst$best_iter,
            ", best test error: ", bst$best_score))
# Plot validation error
val_error <- unlist(bst$record_evals$test$l2$eval)
plot(1:length(val_error), val_error, type="l", lwd=2, col="blue",
     xlab="iteration", ylab="Validation error", main="Validation error vs. boosting iteration")

#-----Do Newton updates for tree leaves-----
# Note: run the above examples first
bst <- gpb.train(data = dtrain, gp_model = gp_model, nrounds = 100,
               learning_rate = 0.05, max_depth = 6, min_data_in_leaf = 5,
               verbose = 1, valids = valids,
               early_stopping_rounds = 5, use_gp_model_for_validation = FALSE,
               leaves_newton_update = TRUE)
print(paste0("Optimal number of iterations: ", bst$best_iter,
            ", best test error: ", bst$best_score))
# Plot validation error
val_error <- unlist(bst$record_evals$test$l2$eval)
plot(1:length(val_error), val_error, type="l", lwd=2, col="blue",
     xlab="iteration", ylab="Validation error", main="Validation error vs. boosting iteration")

```

```

#-----GPBoostOOS algorithm: GP parameters estimated out-of-sample-----
# Create random effects model and dataset
gp_model <- GPModel(group_data = group_data[,1], likelihood="gaussian")
dtrain <- gpb.Dataset(X, label = y)
params <- list(learning_rate = 0.05,
              max_depth = 6,
              min_data_in_leaf = 5)
# Stage 1: run cross-validation to (i) determine to optimal number of iterations
#           and (ii) to estimate the GPModel on the out-of-sample data
cvbst <- gpb.cv(params = params,
               data = dtrain,
               gp_model = gp_model,
               nrounds = 100,
               nfold = 4,
               eval = "l2",
               early_stopping_rounds = 5,
               use_gp_model_for_validation = TRUE,
               fit_GP_cov_pars_OOS = TRUE)
print(paste0("Optimal number of iterations: ", cvbst$best_iter))
# Estimated random effects model
# Note: ideally, one would have to find the optimal combination of
#       other tuning parameters such as the learning rate, tree depth, etc.)
summary(gp_model)
# Stage 2: Train tree-boosting model while holding the GPModel fix
bst <- gpb.train(data = dtrain,
                 gp_model = gp_model,
                 nrounds = cvbst$best_iter,
                 learning_rate = 0.05,
                 max_depth = 6,
                 min_data_in_leaf = 5,
                 verbose = 0,
                 train_gp_model_cov_pars = FALSE)
# The GPModel has not changed:
summary(gp_model)

```

---

gpboost

*Train a GPBoost model*


---

## Description

Simple interface for training a GPBoost model.

## Usage

```

gpboost(data, label = NULL, weight = NULL, params = list(),
        nrounds = 100L, gp_model = NULL, use_gp_model_for_validation = TRUE,
        train_gp_model_cov_pars = TRUE, valids = list(), obj = NULL,
        eval = NULL, verbose = 1L, record = TRUE, eval_freq = 1L,
        early_stopping_rounds = NULL, init_model = NULL, colnames = NULL,
        categorical_feature = NULL, callbacks = list(), ...)

```

**Arguments**

data	a <code>gpb.Dataset</code> object, used for training. Some functions, such as <code>gpb.cv</code> , may allow you to pass other types of data like <code>matrix</code> and then separately supply <code>label</code> as a keyword argument.
label	Vector of response values / labels, used if data is not an <code>gpb.Dataset</code>
weight	Vector of weights. The GPBoost algorithm currently does not support weights
params	list of "tuning" parameters. See <a href="#">the parameter documentation</a> for more information. A few key parameters: <ul style="list-style-type: none"> <li>• <code>learning_rate</code>: The learning rate, also called shrinkage or damping parameter (default = 0.1). An important tuning parameter for boosting. Lower values usually lead to higher predictive accuracy but more boosting iterations are needed</li> <li>• <code>num_leaves</code>: Number of leaves in a tree. Tuning parameter for tree-boosting (default = 31)</li> <li>• <code>max_depth</code>: Maximal depth of a tree. Tuning parameter for tree-boosting (default = no limit)</li> <li>• <code>min_data_in_leaf</code>: Minimal number of samples per leaf. Tuning parameter for tree-boosting (default = 20)</li> <li>• <code>lambda_l2</code>: L2 regularization (default = 0)</li> <li>• <code>lambda_l1</code>: L1 regularization (default = 0)</li> <li>• <code>max_bin</code>: Maximal number of bins that feature values will be bucketed in (default = 255)</li> <li>• <code>line_search_step_length</code> (default = FALSE): If TRUE, a line search is done to find the optimal step length for every boosting update (see, e.g., Friedman 2001). This is then multiplied by the learning rate</li> <li>• <code>train_gp_model_cov_pars</code> (default = TRUE): If TRUE, the covariance parameters of the Gaussian process are estimated in every boosting iterations, otherwise the <code>gp_model</code> parameters are not estimated. In the latter case, you need to either estimate them beforehand or provide values via the <code>'init_cov_pars'</code> parameter when creating the <code>gp_model</code></li> <li>• <code>use_gp_model_for_validation</code> (default = TRUE): If TRUE, the Gaussian process is also used (in addition to the tree model) for calculating predictions on the validation data</li> <li>• <code>leaves_newton_update</code> (default = FALSE): Set this to TRUE to do a Newton update step for the tree leaves after the gradient step. Applies only to Gaussian process boosting (GPBoost algorithm)</li> <li>• <code>num_threads</code>: Number of threads. For the best speed, set this to the number of real CPU cores (<code>parallel::detectCores(logical = FALSE)</code>), not the number of threads (most CPU using hyper-threading to generate 2 threads per CPU core).</li> </ul>
nrounds	number of boosting iterations (= number of trees). This is the most important tuning parameter for boosting
gp_model	A <code>GPMoDel</code> object that contains the random effects (Gaussian process and / or grouped random effects) model

<code>use_gp_model_for_validation</code>	Boolean. If TRUE, the <code>gp_model</code> (Gaussian process and/or random effects) is also used (in addition to the tree model) for calculating predictions on the validation data. If FALSE, the <code>gp_model</code> (random effects part) is ignored for making predictions and only the tree ensemble is used for making predictions for calculating the validation / test error.
<code>train_gp_model_cov_pars</code>	Boolean. If TRUE, the covariance parameters of the <code>gp_model</code> (Gaussian process and/or random effects) are estimated in every boosting iterations, otherwise the <code>gp_model</code> parameters are not estimated. In the latter case, you need to either estimate them beforehand or provide the values via the <code>init_cov_pars</code> parameter when creating the <code>gp_model</code>
<code>valids</code>	a list of <code>gpb.Dataset</code> objects, used for validation
<code>obj</code>	(character) The distribution of the response variable (=label) conditional on fixed and random effects. This only needs to be set when doing independent boosting without random effects / Gaussian processes.
<code>eval</code>	Evaluation metric to be monitored when doing CV and parameter tuning. This can be a string, function, or list with a mixture of strings and functions. <ul style="list-style-type: none"> <li>• <b>a. character vector:</b> Non-exhaustive list of supported metrics: "test_neg_log_likelihood", "mse", "rmse", "mae", "auc", "average_precision", "binary_logloss", "binary_error" See <a href="#">the "metric" section of the parameter documentation</a> for a complete list of valid metrics.</li> <li>• <b>b. function:</b> You can provide a custom evaluation function. This should accept the keyword arguments <code>preds</code> and <code>dtrain</code> and should return a named list with three elements: <ul style="list-style-type: none"> <li>– <code>name</code>: A string with the name of the metric, used for printing and storing results.</li> <li>– <code>value</code>: A single number indicating the value of the metric for the given predictions and true values</li> <li>– <code>higher_better</code>: A boolean indicating whether higher values indicate a better fit. For example, this would be FALSE for metrics like MAE or RMSE.</li> </ul> </li> <li>• <b>c. list:</b> If a list is given, it should only contain character vectors and functions. These should follow the requirements from the descriptions above.</li> </ul>
<code>verbose</code>	verbosity for output, if $\leq 0$ , also will disable the print of evaluation during training
<code>record</code>	Boolean, TRUE will record iteration message to <code>booster\$record_evals</code>
<code>eval_freq</code>	evaluation output frequency, only effect when <code>verbose &gt; 0</code>
<code>early_stopping_rounds</code>	int. Activates early stopping. Requires at least one validation data and one metric. When this parameter is non-null, training will stop if the evaluation of any metric on any validation set fails to improve for <code>early_stopping_rounds</code> consecutive boosting rounds. If training stops early, the returned model will have attribute <code>best_iter</code> set to the iteration number of the best iteration.
<code>init_model</code>	path of model file of <code>gpb.Booster</code> object, will continue training from this model

<code>colnames</code>	feature names, if not null, will use this to overwrite the names in dataset
<code>categorical_feature</code>	categorical features. This can either be a character vector of feature names or an integer vector with the indices of the features (e.g. <code>c(1L, 10L)</code> to say "the first and tenth columns").
<code>callbacks</code>	List of callback functions that are applied at each iteration.
<code>...</code>	Additional arguments passed to <code>gpb.train</code> . For example <ul style="list-style-type: none"> <li>• <code>valids</code>: a list of <code>gpb.Dataset</code> objects, used for validation</li> <li>• <code>eval</code>: evaluation function, can be (a list of) character or custom eval function</li> <li>• <code>record</code>: Boolean, TRUE will record iteration message to <code>booster\$record_evals</code></li> <li>• <code>colnames</code>: feature names, if not null, will use this to overwrite the names in dataset</li> <li>• <code>categorical_feature</code>: categorical features. This can either be a character vector of feature names or an integer vector with the indices of the features (e.g. <code>c(1L, 10L)</code> to say "the first and tenth columns").</li> <li>• <code>reset_data</code>: Boolean, setting it to TRUE (not the default value) will transform the booster model into a predictor model which frees up memory and the original datasets</li> </ul>

**Value**

a trained `gpb.Booster`

**Early Stopping**

"early stopping" refers to stopping the training process if the model's performance on a given validation set does not improve for several consecutive iterations.

If multiple arguments are given to `eval`, their order will be preserved. If you enable early stopping by setting `early_stopping_rounds` in `params`, by default all metrics will be considered for early stopping.

If you want to only consider the first metric for early stopping, pass `first_metric_only = TRUE` in `params`. Note that if you also specify `metric` in `params`, that metric will be considered the "first" one. If you omit `metric`, a default metric will be used based on your choice for the parameter `obj` (keyword argument) or `objective` (passed into `params`).

**Author(s)**

Fabio Sigrist, authors of the LightGBM R package

**Examples**

```
# See https://github.com/fabsig/GPBoost/tree/master/R-package for more examples
```

```
library(gpboost)
data(GPBoost_data, package = "gpboost")
```

```

#-----Combine tree-boosting and grouped random effects model-----
# Create random effects model
gp_model <- GPModel(group_data = group_data[,1], likelihood = "gaussian")
# The default optimizer for covariance parameters (hyperparameters) is
# Nesterov-accelerated gradient descent.
# This can be changed to, e.g., Nelder-Mead as follows:
# re_params <- list(optimizer_cov = "nelder_mead")
# gp_model$set_optim_params(params=re_params)
# Use trace = TRUE to monitor convergence:
# re_params <- list(trace = TRUE)
# gp_model$set_optim_params(params=re_params)

# Train model
bst <- gpboost(data = X, label = y, gp_model = gp_model, nrounds = 16,
              learning_rate = 0.05, max_depth = 6, min_data_in_leaf = 5,
              verbose = 0)
# Estimated random effects model
summary(gp_model)

# Make predictions
# Predict latent variables
pred <- predict(bst, data = X_test, group_data_pred = group_data_test[,1],
              predict_var = TRUE, pred_latent = TRUE)
pred$random_effect_mean # Predicted latent random effects mean
pred$random_effect_cov # Predicted random effects variances
pred$fixed_effect # Predicted fixed effects from tree ensemble
# Predict response variable
pred_resp <- predict(bst, data = X_test, group_data_pred = group_data_test[,1],
                  predict_var = TRUE, pred_latent = FALSE)
pred_resp$response_mean # Predicted response mean
# For Gaussian data: pred$random_effect_mean + pred$fixed_effect = pred_resp$response_mean
pred$random_effect_mean + pred$fixed_effect - pred_resp$response_mean

#-----Combine tree-boosting and Gaussian process model-----
# Create Gaussian process model
gp_model <- GPModel(gp_coords = coords, cov_function = "exponential",
                  likelihood = "gaussian")
# Train model
bst <- gpboost(data = X, label = y, gp_model = gp_model, nrounds = 8,
              learning_rate = 0.1, max_depth = 6, min_data_in_leaf = 5,
              verbose = 0)
# Estimated random effects model
summary(gp_model)
# Make predictions
pred <- predict(bst, data = X_test, gp_coords_pred = coords_test,
              predict_var = TRUE, pred_latent = TRUE)
pred$random_effect_mean # Predicted latent random effects mean
pred$random_effect_cov # Predicted random effects variances
pred$fixed_effect # Predicted fixed effects from tree ensemble
# Predict response variable
pred_resp <- predict(bst, data = X_test, gp_coords_pred = coords_test,
                  predict_var = TRUE, pred_latent = FALSE)

```



```
pred_resp$response_mean # Predicted response mean
```

---

GPBoost\_data                      *Example data for the GPBoost package*

---

### Description

Simulated example data for the GPBoost package This data set includes the following fields:

- y: response variable
- X: a matrix with covariate information
- group\_data: a matrix with categorical grouping variables
- coords: a matrix with spatial coordinates
- X\_test: a matrix with covariate information for predictions
- group\_data\_test: a matrix with categorical grouping variables for predictions
- coords\_test: a matrix with spatial coordinates for predictions

### Usage

```
data(GPBoost_data)
```

---

GPMoDel                              *Create a GPMoDel object*

---

### Description

Create a GPMoDel which contains a Gaussian process and / or mixed effects model with grouped random effects

### Usage

```
GPMoDel(likelihood = "gaussian", group_data = NULL,
        group_rand_coef_data = NULL, ind_effect_group_rand_coef = NULL,
        drop_intercept_group_rand_effect = NULL, gp_coords = NULL,
        gp_rand_coef_data = NULL, cov_function = "matern", cov_fct_shape = 1.5,
        gp_approx = "none", num_parallel_threads = NULL,
        cov_fct_taper_range = 1, cov_fct_taper_shape = 1, num_neighbors = 20L,
        vecchia_ordering = "random", ind_points_selection = "kmeans++",
        num_ind_points = 500L, cover_tree_radius = 1,
        matrix_inversion_method = "cholesky", seed = 0L, cluster_ids = NULL,
        likelihood_additional_param = NULL, free_raw_data = FALSE,
        vecchia_approx = NULL, vecchia_pred_type = NULL,
        num_neighbors_pred = NULL)
```

**Arguments**

likelihood	<p>A string specifying the likelihood function (distribution) of the response variable. Available options:</p> <ul style="list-style-type: none"> <li>• "gaussian"</li> <li>• "bernoulli_probit": binary data with Bernoulli likelihood and a probit link function</li> <li>• "bernoulli_logit": binary data with Bernoulli likelihood and a logit link function</li> <li>• "gamma": gamma distribution with a with log link function</li> <li>• "poisson": Poisson distribution with a with log link function</li> <li>• "negative_binomial": negative binomial distribution with a with log link function</li> <li>• "t": t-distribution (e.g., for robust regression)</li> <li>• "t_fix_df": t-distribution with the degrees-of-freedom (df) held fixed and not estimated. The df can be set via the <code>likelihood_additional_param</code> parameter</li> <li>• Note: other likelihoods could be implemented upon request</li> </ul>
group_data	<p>A vector or matrix whose columns are categorical grouping variables. The elements being group levels defining grouped random effects. The elements of 'group_data' can be integer, double, or character. The number of columns corresponds to the number of grouped (intercept) random effects</p>
group_rand_coef_data	<p>A vector or matrix with numeric covariate data for grouped random coefficients</p>
ind_effect_group_rand_coef	<p>A vector with integer indices that indicate the corresponding categorical grouping variable (=columns) in 'group_data' for every covariate in 'group_rand_coef_data'. Counting starts at 1. The length of this index vector must equal the number of covariates in 'group_rand_coef_data'. For instance, <code>c(1,1,2)</code> means that the first two covariates (=first two columns) in 'group_rand_coef_data' have random coefficients corresponding to the first categorical grouping variable (=first column) in 'group_data', and the third covariate (=third column) in 'group_rand_coef_data' has a random coefficient corresponding to the second grouping variable (=second column) in 'group_data'</p>
drop_intercept_group_rand_effect	<p>A vector of type logical (boolean). Indicates whether intercept random effects are dropped (only for random coefficients). If <code>drop_intercept_group_rand_effect[k]</code> is TRUE, the intercept random effect number k is dropped / not included. Only random effects with random slopes can be dropped.</p>
gp_coords	<p>A matrix with numeric coordinates (= inputs / features) for defining Gaussian processes</p>
gp_rand_coef_data	<p>A vector or matrix with numeric covariate data for Gaussian process random coefficients</p>

cov_function	<p>A string specifying the covariance function for the Gaussian process. Available options:</p> <ul style="list-style-type: none"> <li>• "exponential": Exponential covariance function (using the parametrization of Diggle and Ribeiro, 2007)</li> <li>• "gaussian": Gaussian, aka squared exponential, covariance function (using the parametrization of Diggle and Ribeiro, 2007)</li> <li>• "matern": Matern covariance function with the smoothness specified by the cov_fct_shape parameter (using the parametrization of Rasmussen and Williams, 2006)</li> <li>• "powered_exponential": powered exponential covariance function with the exponent specified by the cov_fct_shape parameter (using the parametrization of Diggle and Ribeiro, 2007)</li> <li>• "wendland": Compactly supported Wendland covariance function (using the parametrization of Bevilacqua et al., 2019, AOS)</li> <li>• "matern_space_time": Spatio-temporal Matern covariance function with different range parameters for space and time. Note that the first column in gp_coords must correspond to the time dimension</li> <li>• "matern_ard": anisotropic Matern covariance function with Automatic Relevance Determination (ARD), i.e., with a different range parameter for every coordinate dimension / column of gp_coords</li> <li>• "gaussian_ard": anisotropic Gaussian, aka squared exponential, covariance function with Automatic Relevance Determination (ARD), i.e., with a different range parameter for every coordinate dimension / column of gp_coords</li> </ul>
cov_fct_shape	<p>A numeric specifying the shape parameter of the covariance function (=smoothness parameter for Matern covariance) This parameter is irrelevant for some covariance functions such as the exponential or Gaussian</p>
gp_approx	<p>A string specifying the large data approximation for Gaussian processes. Available options:</p> <ul style="list-style-type: none"> <li>• "none": No approximation</li> <li>• "vecchia": A Vecchia approximation; see Sigrist (2022, JMLR) for more details</li> <li>• "tapering": The covariance function is multiplied by a compactly supported Wendland correlation function</li> <li>• "fitc": Fully Independent Training Conditional approximation aka modified predictive process approximation; see Gyger, Furrer, and Sigrist (2024) for more details</li> <li>• "full_scale_tapering": A full scale approximation combining an inducing point / predictive process approximation with tapering on the residual process; see Gyger, Furrer, and Sigrist (2024) for more details</li> <li>• "vecchia_latent": similar as "vecchia" but a Vecchia approximation is applied to the latent Gaussian process for likelihood == "gaussian". For likelihood != "gaussian", "vecchia" and "vecchia_latent" are equivalent</li> </ul>
num_parallel_threads	<p>An integer specifying the number of parallel threads for OMP. If num_parallel_threads = NULL, all available threads are used</p>

<code>cov_fct_taper_range</code>	A numeric specifying the range parameter of the Wendland covariance function and Wendland correlation taper function. We follow the notation of Bevilacqua et al. (2019, AOS)
<code>cov_fct_taper_shape</code>	A numeric specifying the shape (=smoothness) parameter of the Wendland covariance function and Wendland correlation taper function. We follow the notation of Bevilacqua et al. (2019, AOS)
<code>num_neighbors</code>	An integer specifying the number of neighbors for the Vecchia approximation. Note: for prediction, the number of neighbors can be set through the <code>'num_neighbors_pred'</code> parameter in the <code>'set_prediction_data'</code> function. By default, <code>num_neighbors_pred = 2 * num_neighbors</code> . Further, the type of Vecchia approximation used for making predictions is set through the <code>'vecchia_pred_type'</code> parameter in the <code>'set_prediction_data'</code> function
<code>vecchia_ordering</code>	A string specifying the ordering used in the Vecchia approximation. Available options: <ul style="list-style-type: none"> <li>• "none": the default ordering in the data is used</li> <li>• "random": a random ordering</li> <li>• "time": ordering according to time (only for space-time models)</li> <li>• "time_random_space": ordering according to time and randomly for all spatial points with the same time points (only for space-time models)</li> </ul>
<code>ind_points_selection</code>	A string specifying the method for choosing inducing points Available options: <ul style="list-style-type: none"> <li>• "kmeans++": the k-means++ algorithm</li> <li>• "cover_tree": the cover tree algorithm</li> <li>• "random": random selection from data points</li> </ul>
<code>num_ind_points</code>	An integer specifying the number of inducing points / knots for, e.g., a predictive process approximation
<code>cover_tree_radius</code>	A numeric specifying the radius (= "spatial resolution") for the cover tree algorithm
<code>matrix_inversion_method</code>	A string specifying the method used for inverting covariance matrices. Available options: <ul style="list-style-type: none"> <li>• "cholesky": Cholesky factorization</li> <li>• "iterative": iterative methods. A combination of conjugate gradient, Lanczos algorithm, and other methods.</li> </ul> This is currently only supported for the following cases: <ul style="list-style-type: none"> <li>– likelihood != "gaussian" and <code>gp_approx == "vecchia"</code> (non-Gaussian likelihoods with a Vecchia-Laplace approximation)</li> <li>– likelihood == "gaussian" and <code>gp_approx == "full_scale_tapering"</code> (Gaussian likelihood with a full-scale tapering approximation)</li> </ul>
<code>seed</code>	An integer specifying the seed used for model creation (e.g., random ordering in Vecchia approximation)

- `cluster_ids` A vector with elements indicating independent realizations of random effects / Gaussian processes (same values = same process realization). The elements of 'cluster\_ids' can be integer, double, or character.
- `likelihood_additional_param` A numeric specifying an additional parameter for the likelihood which cannot be estimated for this likelihood (e.g., degrees of freedom for likelihood = "t\_fix\_df"). This is not to be confused with any auxiliary parameters that can be estimated and accessed through the function `get_aux_pars` after estimation. Note that this `likelihood_additional_param` parameter is irrelevant for many likelihoods. If `likelihood_additional_param = NULL`, the following internal default values are used:
- `df = 2` for likelihood = "t\_fix\_df"
- `free_raw_data` A boolean. If TRUE, the data (groups, coordinates, covariate data for random coefficients) is freed in R after initialization
- `vecchia_approx` Discontinued. Use the argument `gp_approx` instead
- `vecchia_pred_type` A string specifying the type of Vecchia approximation used for making predictions. This is discontinued here. Use the function 'set\_prediction\_data' to specify this
- `num_neighbors_pred` an integer specifying the number of neighbors for making predictions. This is discontinued here. Use the function 'set\_prediction\_data' to specify this

**Value**

A GPMoDel containing contains a Gaussian process and / or mixed effects model with grouped random effects

**Author(s)**

Fabio Sigrist

**Examples**

```
# See https://github.com/fabsig/GPBoost/tree/master/R-package for more examples

data(GPBoost_data, package = "gpboost")

#-----Grouped random effects model: single-level random effect-----
gp_model <- GPMoDel(group_data = group_data[,1], likelihood="gaussian")

#-----Gaussian process model-----
gp_model <- GPMoDel(gp_coords = coords, cov_function = "matern", cov_fct_shape = 1.5,
  likelihood="gaussian")

#-----Combine Gaussian process with grouped random effects-----
gp_model <- GPMoDel(group_data = group_data,
  gp_coords = coords, cov_function = "matern", cov_fct_shape = 1.5,
  likelihood="gaussian")
```

---

GPModel\_shared\_params *Documentation for parameters shared by GPModel, gpb.cv, and gpboost*

---

## Description

Documentation for parameters shared by GPModel, gpb.cv, and gpboost

## Arguments

- likelihood** A string specifying the likelihood function (distribution) of the response variable. Available options:
- "gaussian"
  - "bernoulli\_probit": binary data with Bernoulli likelihood and a probit link function
  - "bernoulli\_logit": binary data with Bernoulli likelihood and a logit link function
  - "gamma": gamma distribution with a with log link function
  - "poisson": Poisson distribution with a with log link function
  - "negative\_binomial": negative binomial distribution with a with log link function
  - "t": t-distribution (e.g., for robust regression)
  - "t\_fix\_df": t-distribution with the degrees-of-freedom (df) held fixed and not estimated. The df can be set via the likelihood\_additional\_param parameter
  - Note: other likelihoods could be implemented upon request
- likelihood\_additional\_param** A numeric specifying an additional parameter for the likelihood which cannot be estimated for this likelihood (e.g., degrees of freedom for likelihood = "t\_fix\_df"). This is not to be confused with any auxiliary parameters that can be estimated and accessed through the function `get_aux_pars` after estimation. Note that this `likelihood_additional_param` parameter is irrelevant for many likelihoods. If `likelihood_additional_param = NULL`, the following internal default values are used:
- `df = 2` for likelihood = "t\_fix\_df"
- group\_data** A vector or matrix whose columns are categorical grouping variables. The elements being group levels defining grouped random effects. The elements of 'group\_data' can be integer, double, or character. The number of columns corresponds to the number of grouped (intercept) random effects
- group\_rand\_coef\_data** A vector or matrix with numeric covariate data for grouped random coefficients

<code>ind_effect_group_rand_coef</code>	A vector with integer indices that indicate the corresponding categorical grouping variable (=columns) in 'group_data' for every covariate in 'group_rand_coef_data'. Counting starts at 1. The length of this index vector must equal the number of covariates in 'group_rand_coef_data'. For instance, c(1,1,2) means that the first two covariates (=first two columns) in 'group_rand_coef_data' have random coefficients corresponding to the first categorical grouping variable (=first column) in 'group_data', and the third covariate (=third column) in 'group_rand_coef_data' has a random coefficient corresponding to the second grouping variable (=second column) in 'group_data'
<code>drop_intercept_group_rand_effect</code>	A vector of type logical (boolean). Indicates whether intercept random effects are dropped (only for random coefficients). If <code>drop_intercept_group_rand_effect[k]</code> is TRUE, the intercept random effect number k is dropped / not included. Only random effects with random slopes can be dropped.
<code>gp_coords</code>	A matrix with numeric coordinates (= inputs / features) for defining Gaussian processes
<code>gp_rand_coef_data</code>	A vector or matrix with numeric covariate data for Gaussian process random coefficients
<code>cov_function</code>	A string specifying the covariance function for the Gaussian process. Available options: <ul style="list-style-type: none"> <li>"exponential": Exponential covariance function (using the parametrization of Diggle and Ribeiro, 2007)</li> <li>"gaussian": Gaussian, aka squared exponential, covariance function (using the parametrization of Diggle and Ribeiro, 2007)</li> <li>"matern": Matern covariance function with the smoothness specified by the <code>cov_fct_shape</code> parameter (using the parametrization of Rasmussen and Williams, 2006)</li> <li>"powered_exponential": powered exponential covariance function with the exponent specified by the <code>cov_fct_shape</code> parameter (using the parametrization of Diggle and Ribeiro, 2007)</li> <li>"wendland": Compactly supported Wendland covariance function (using the parametrization of Bevilacqua et al., 2019, AOS)</li> <li>"matern_space_time": Spatio-temporal Matern covariance function with different range parameters for space and time. Note that the first column in <code>gp_coords</code> must correspond to the time dimension</li> <li>"matern_ard": anisotropic Matern covariance function with Automatic Relevance Determination (ARD), i.e., with a different range parameter for every coordinate dimension / column of <code>gp_coords</code></li> <li>"gaussian_ard": anisotropic Gaussian, aka squared exponential, covariance function with Automatic Relevance Determination (ARD), i.e., with a different range parameter for every coordinate dimension / column of <code>gp_coords</code></li> </ul>
<code>cov_fct_shape</code>	A numeric specifying the shape parameter of the covariance function (=smoothness parameter for Matern covariance) This parameter is irrelevant for some covariance functions such as the exponential or Gaussian

gp_approx	<p>A string specifying the large data approximation for Gaussian processes. Available options:</p> <ul style="list-style-type: none"> <li>• "none": No approximation</li> <li>• "vecchia": A Vecchia approximation; see Sigrist (2022, JMLR) for more details</li> <li>• "tapering": The covariance function is multiplied by a compactly supported Wendland correlation function</li> <li>• "fitc": Fully Independent Training Conditional approximation aka modified predictive process approximation; see Gyger, Furrer, and Sigrist (2024) for more details</li> <li>• "full_scale_tapering": A full scale approximation combining an inducing point / predictive process approximation with tapering on the residual process; see Gyger, Furrer, and Sigrist (2024) for more details</li> <li>• "vecchia_latent": similar as "vecchia" but a Vecchia approximation is applied to the latent Gaussian process for likelihood == "gaussian". For likelihood != "gaussian", "vecchia" and "vecchia_latent" are equivalent</li> </ul>
num_parallel_threads	<p>An integer specifying the number of parallel threads for OMP. If num_parallel_threads = NULL, all available threads are used</p>
cov_fct_taper_range	<p>A numeric specifying the range parameter of the Wendland covariance function and Wendland correlation taper function. We follow the notation of Bevilacqua et al. (2019, AOS)</p>
cov_fct_taper_shape	<p>A numeric specifying the shape (=smoothness) parameter of the Wendland covariance function and Wendland correlation taper function. We follow the notation of Bevilacqua et al. (2019, AOS)</p>
num_neighbors	<p>An integer specifying the number of neighbors for the Vecchia approximation. Note: for prediction, the number of neighbors can be set through the 'num_neighbors_pred' parameter in the 'set_prediction_data' function. By default, num_neighbors_pred = 2 * num_neighbors. Further, the type of Vecchia approximation used for making predictions is set through the 'vecchia_pred_type' parameter in the 'set_prediction_data' function</p>
vecchia_ordering	<p>A string specifying the ordering used in the Vecchia approximation. Available options:</p> <ul style="list-style-type: none"> <li>• "none": the default ordering in the data is used</li> <li>• "random": a random ordering</li> <li>• "time": ordering according to time (only for space-time models)</li> <li>• "time_random_space": ordering according to time and randomly for all spatial points with the same time points (only for space-time models)</li> </ul>
ind_points_selection	<p>A string specifying the method for choosing inducing points Available options:</p> <ul style="list-style-type: none"> <li>• "kmeans++": the k-means++ algorithm</li> <li>• "cover_tree": the cover tree algorithm</li> </ul>



	<ul style="list-style-type: none"> <li>• "random": random selection from data points</li> </ul>
num_ind_points	An integer specifying the number of inducing points / knots for, e.g., a predictive process approximation
cover_tree_radius	A numeric specifying the radius (= "spatial resolution") for the cover tree algorithm
matrix_inversion_method	A string specifying the method used for inverting covariance matrices. Available options: <ul style="list-style-type: none"> <li>• "cholesky": Cholesky factorization</li> <li>• "iterative": iterative methods. A combination of conjugate gradient, Lanczos algorithm, and other methods.</li> </ul> This is currently only supported for the following cases: <ul style="list-style-type: none"> <li>– likelihood != "gaussian" and gp_approx == "vecchia" (non-Gaussian likelihoods with a Vecchia-Laplace approximation)</li> <li>– likelihood == "gaussian" and gp_approx == "full_scale_tapering" (Gaussian likelihood with a full-scale tapering approximation)</li> </ul>
seed	An integer specifying the seed used for model creation (e.g., random ordering in Vecchia approximation)
vecchia_pred_type	A string specifying the type of Vecchia approximation used for making predictions. Default value if vecchia_pred_type = NULL: "order_obs_first_cond_obs_only". Available options: <ul style="list-style-type: none"> <li>• "order_obs_first_cond_obs_only": Vecchia approximation for the observable process and observed training data is ordered first and the neighbors are only observed training data points</li> <li>• "order_obs_first_cond_all": Vecchia approximation for the observable process and observed training data is ordered first and the neighbors are selected among all points (training + prediction)</li> <li>• "latent_order_obs_first_cond_obs_only": Vecchia approximation for the latent process and observed data is ordered first and neighbors are only observed points</li> <li>• "latent_order_obs_first_cond_all": Vecchia approximation for the latent process and observed data is ordered first and neighbors are selected among all points</li> <li>• "order_pred_first": Vecchia approximation for the observable process and prediction data is ordered first for making predictions. This option is only available for Gaussian likelihoods</li> </ul>
num_neighbors_pred	an integer specifying the number of neighbors for the Vecchia approximation for making predictions. Default value if NULL: num_neighbors_pred = 2 * num_neighbors
cg_delta_conv_pred	a numeric specifying the tolerance level for L2 norm of residuals for checking convergence in conjugate gradient algorithms when being used for prediction. Default value if NULL: 1e-3

<code>nsim_var_pred</code>	an integer specifying the number of samples when simulation is used for calculating predictive variances Default value if NULL: 1000
<code>rank_pred_approx_matrix_lanczos</code>	an integer specifying the rank of the matrix for approximating predictive covariances obtained using the Lanczos algorithm Default value if NULL: 1000
<code>cluster_ids</code>	A vector with elements indicating independent realizations of random effects / Gaussian processes (same values = same process realization). The elements of 'cluster_ids' can be integer, double, or character.
<code>free_raw_data</code>	A boolean. If TRUE, the data (groups, coordinates, covariate data for random coefficients) is freed in R after initialization
<code>y</code>	A vector with response variable data
<code>X</code>	A matrix with numeric covariate data for the fixed effects linear regression term (if there is one)
<code>params</code>	A list with parameters for the estimation / optimization <ul style="list-style-type: none"> <li>• <code>optimizer_cov</code>: string (default = "lbfgs"). Optimizer used for estimating covariance parameters. Options: "gradient_descent", "lbfgs", "fisher_scoring", "newton", "nelder_mead". If there are additional auxiliary parameters for non-Gaussian likelihoods, 'optimizer_cov' is also used for those</li> <li>• <code>optimizer_coef</code>: string (default = "wls" for Gaussian likelihoods and "lbfgs" for other likelihoods). Optimizer used for estimating linear regression coefficients, if there are any (for the GPBoost algorithm there are usually none). Options: "gradient_descent", "lbfgs", "wls", "nelder_mead". Gradient descent steps are done simultaneously with gradient descent steps for the covariance parameters. "wls" refers to doing coordinate descent for the regression coefficients using weighted least squares. If 'optimizer_cov' is set to "nelder_mead" or "lbfgs", 'optimizer_coef' is automatically also set to the same value.</li> <li>• <code>maxit</code>: integer (default = 1000). Maximal number of iterations for optimization algorithm</li> <li>• <code>delta_rel_conv</code>: numeric (default = 1E-6 except for "nelder_mead" for which the default is 1E-8). Convergence tolerance. The algorithm stops if the relative change in either the (approximate) log-likelihood or the parameters is below this value. If &lt; 0, internal default values are used</li> <li>• <code>convergence_criterion</code>: string (default = "relative_change_in_log_likelihood"). The convergence criterion used for terminating the optimization algorithm. Options: "relative_change_in_log_likelihood" or "relative_change_in_parameters"</li> <li>• <code>init_coef</code>: vector with numeric elements (default = NULL). Initial values for the regression coefficients (if there are any, can be NULL)</li> <li>• <code>init_cov_pars</code>: vector with numeric elements (default = NULL). Initial values for covariance parameters of Gaussian process and random effects (can be NULL). The order is the same as the order of the parameters in the summary function: first is the error variance (only for "gaussian" likelihood), next follow the variances of the grouped random effects (if there are any, in the order provided in 'group_data'), and then follow the marginal variance and the range of the Gaussian process. If there are multiple Gaussian processes, then the variances and ranges follow alternately. If 'init_cov_pars</li> </ul>

= NULL', an internal choice is used that depends on the likelihood and the random effects type and covariance function. If you select the option 'trace = TRUE' in the 'params' argument, you will see the first initial covariance parameters in iteration 0.

- lr\_coef: numeric (default = 0.1). Learning rate for fixed effect regression coefficients if gradient descent is used
- lr\_cov: numeric (default = 0.1 for "gradient\_descent" and 1. otherwise). Initial learning rate for covariance parameters if a gradient-based optimization method is used
  - If lr\_cov < 0, internal default values are used (0.1 for "gradient\_descent" and 1. otherwise)
  - If there are additional auxiliary parameters for non-Gaussian likelihoods, 'lr\_cov' is also used for those
  - For "lbfgs", this is divided by the norm of the gradient in the first iteration
- use\_nesterov\_acc: boolean (default = TRUE). If TRUE Nesterov acceleration is used. This is used only for gradient descent
- acc\_rate\_coef: numeric (default = 0.5). Acceleration rate for regression coefficients (if there are any) for Nesterov acceleration
- acc\_rate\_cov: numeric (default = 0.5). Acceleration rate for covariance parameters for Nesterov acceleration
- momentum\_offset: integer (Default = 2). Number of iterations for which no momentum is applied in the beginning.
- trace: boolean (default = FALSE). If TRUE, information on the progress of the parameter optimization is printed
- std\_dev: boolean (default = TRUE). If TRUE, approximate standard deviations are calculated for the covariance and linear regression parameters (= square root of diagonal of the inverse Fisher information for Gaussian likelihoods and square root of diagonal of a numerically approximated inverse Hessian for non-Gaussian likelihoods)
- init\_aux\_pars: vector with numeric elements (default = NULL). Initial values for additional parameters for non-Gaussian likelihoods (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- estimate\_aux\_pars: boolean (default = TRUE). If TRUE, additional parameters for non-Gaussian likelihoods are also estimated (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- cg\_max\_num\_it: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithms
- cg\_max\_num\_it\_tridiag: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithm when being run as Lanczos algorithm for tridiagonalization
- cg\_delta\_conv: numeric (default = 1E-2). Tolerance level for L2 norm of residuals for checking convergence in conjugate gradient algorithm when being used for parameter estimation
- num\_rand\_vec\_trace: integer (default = 50). Number of random vectors (e.g., Rademacher) for stochastic approximation of the trace of a matrix

- reuse\_rand\_vec\_trace: boolean (default = TRUE). If true, random vectors (e.g., Rademacher) for stochastic approximations of the trace of a matrix are sampled only once at the beginning of the parameter estimation and reused in later trace approximations. Otherwise they are sampled every time a trace is calculated
  - seed\_rand\_vec\_trace: integer (default = 1). Seed number to generate random vectors (e.g., Rademacher)
  - piv\_chol\_rank: integer (default = 50). Rank of the pivoted Cholesky decomposition used as preconditioner in conjugate gradient algorithms
  - cg\_preconditioner\_type: string. Type of preconditioner used for conjugate gradient algorithms.
    - Options for likelihood != "gaussian" and gp\_approx == "vecchia" or likelihood == "gaussian" and gp\_approx == "vecchia\_latent":
      - \* "vadu" (= default):  $(B^T * (D^{-1} + W) * B)$  as preconditioner for inverting  $(B^T * D^{-1} * B + W)$ , where  $B^T * D^{-1} * B \approx \Sigma^{-1}$
      - \* "fitc": modified predictive process preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$
      - \* "pivoted\_cholesky":  $(Lk * Lk^T + W^{-1})$  as preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$ , where  $Lk$  is a low-rank pivoted Cholesky approximation for  $\Sigma$  and  $B^{-1} * D * B^{-T} \approx \Sigma$
      - \* "incomplete\_cholesky": zero fill-in incomplete (reverse) Cholesky factorization of  $(B^T * D^{-1} * B + W)$  using the sparsity pattern of  $B^T * D^{-1} * B \approx \Sigma^{-1}$
    - Options for likelihood == "gaussian" and gp\_approx == "full\_scale\_tapering":
      - \* "fitc" (= default): modified predictive process preconditioner
      - \* "none": no preconditioner
- offset      A numeric vector with additional fixed effects contributions that are added to the linear predictor (= offset). The length of this vector needs to equal the number of training data points.
- fixed\_effects      This is discontinued. Use the renamed equivalent argument offset instead
- group\_data\_pred      A vector or matrix with elements being group levels for which predictions are made (if there are grouped random effects in the GPModel)
- group\_rand\_coef\_data\_pred      A vector or matrix with covariate data for grouped random coefficients (if there are some in the GPModel)
- gp\_coords\_pred      A matrix with prediction coordinates (=features) for Gaussian process (if there is a GP in the GPModel)
- gp\_rand\_coef\_data\_pred      A vector or matrix with covariate data for Gaussian process random coefficients (if there are some in the GPModel)
- cluster\_ids\_pred      A vector with elements indicating the realizations of random effects / Gaussian processes for which predictions are made (set to NULL if you have not specified this when creating the GPModel)

X_pred	A matrix with prediction covariate data for the fixed effects linear regression term (if there is one in the GPModel)
predict_cov_mat	A boolean. If TRUE, the (posterior) predictive covariance is calculated in addition to the (posterior) predictive mean
predict_var	A boolean. If TRUE, the (posterior) predictive variances are calculated
vecchia_approx	Discontinued. Use the argument gp_approx instead

---

group_data	<i>Example data for the GPBoost package</i>
------------	---

---

**Description**

A matrix with categorical grouping variables for the example data of the GPBoost package

**Usage**

```
data(GPBoost_data)
```

---

group_data_test	<i>Example data for the GPBoost package</i>
-----------------	---

---

**Description**

A matrix with categorical grouping variables for predictions for the example data of the GPBoost package

**Usage**

```
data(GPBoost_data)
```

---

loadGPModel	<i>Load a GPModel from a file</i>
-------------	-----------------------------------

---

**Description**

Load a GPModel from a file

**Usage**

```
loadGPModel(filename)
```

**Arguments**

filename            filename for loading

**Value**

A GPModel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
# Add intercept column
X1 <- cbind(rep(1,dim(X)[1]),X)
X_test1 <- cbind(rep(1,dim(X_test)[1]),X_test)

gp_model <- fitGPModel(group_data = group_data[,1], y = y, X = X1, likelihood="gaussian")
pred <- predict(gp_model, group_data_pred = group_data_test[,1],
               X_pred = X_test1, predict_var = TRUE)

# Save model to file
filename <- tempfile(fileext = ".json")
saveGPModel(gp_model,filename = filename)
# Load from file and make predictions again
gp_model_loaded <- loadGPModel(filename = filename)
pred_loaded <- predict(gp_model_loaded, group_data_pred = group_data_test[,1],
                     X_pred = X_test1, predict_var = TRUE)

# Check equality
pred$mu - pred_loaded$mu
pred$var - pred_loaded$var
```

---

neg\_log\_likelihood      *Evaluate the negative log-likelihood*

---

### Description

Evaluate the negative log-likelihood. If there is a linear fixed effects predictor term, this needs to be calculated "manually" prior to calling this function (see example below)

### Usage

```
neg_log_likelihood(gp_model, cov_pars, y, fixed_effects = NULL,  
  aux_pars = NULL)
```

### Arguments

gp_model	A GPModel
cov_pars	A vector with numeric elements. Covariance parameters of Gaussian process and random effects
y	A vector with response variable data
fixed_effects	A numeric vector with fixed effects, e.g., containing a linear predictor. The length of this vector needs to equal the number of training data points.
aux_pars	A vector with numeric elements. Additional parameters for non-Gaussian likelihoods (e.g., shape parameter of a gamma or negative_binomial likelihood)

### Author(s)

Fabio Sigrist

### Examples

```
data(GPBoost_data, package = "gpboost")  
gp_model <- GPModel(group_data = group_data, likelihood="gaussian")  
X1 <- cbind(rep(1,dim(X)[1]), X)  
coef <- c(0.1, 0.1, 0.1)  
fixed_effects <- as.numeric(X1 %*% coef)  
neg_log_likelihood(gp_model, y = y, cov_pars = c(0.1,1,1),  
  fixed_effects = fixed_effects)
```

---

`neg_log_likelihood.GPModel`*Evaluate the negative log-likelihood*

---

**Description**

Evaluate the negative log-likelihood. If there is a linear fixed effects predictor term, this needs to be calculated "manually" prior to calling this function (see example below)

**Usage**

```
## S3 method for class 'GPModel'  
neg_log_likelihood(gp_model, cov_pars, y,  
  fixed_effects = NULL, aux_pars = NULL)
```

**Arguments**

<code>gp_model</code>	A GPModel
<code>cov_pars</code>	A vector with numeric elements. Covariance parameters of Gaussian process and random effects
<code>y</code>	A vector with response variable data
<code>fixed_effects</code>	A numeric vector with fixed effects, e.g., containing a linear predictor. The length of this vector needs to equal the number of training data points.
<code>aux_pars</code>	A vector with numeric elements. Additional parameters for non-Gaussian likelihoods (e.g., shape parameter of a gamma or negative_binomial likelihood)

**Value**

A GPModel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")  
gp_model <- GPModel(group_data = group_data, likelihood="gaussian")  
X1 <- cbind(rep(1,dim(X)[1]), X)  
coef <- c(0.1, 0.1, 0.1)  
fixed_effects <- as.numeric(X1 %*% coef)  
neg_log_likelihood(gp_model, y = y, cov_pars = c(0.1,1,1),  
  fixed_effects = fixed_effects)
```



---

predict.gpb.Booster      *Prediction function for gpb.Booster objects*

---

## Description

Prediction function for gpb.Booster objects

## Usage

```
## S3 method for class 'gpb.Booster'
predict(object, data, start_iteration = NULL,
        num_iteration = NULL, pred_latent = FALSE, predleaf = FALSE,
        predcontrib = FALSE, header = FALSE, reshape = FALSE,
        group_data_pred = NULL, group_rand_coef_data_pred = NULL,
        gp_coords_pred = NULL, gp_rand_coef_data_pred = NULL,
        cluster_ids_pred = NULL, predict_cov_mat = FALSE, predict_var = FALSE,
        cov_pars = NULL, ignore_gp_model = FALSE, rawscore = NULL,
        vecchia_pred_type = NULL, num_neighbors_pred = NULL, ...)
```

## Arguments

object	Object of class gpb.Booster
data	a matrix object, a dgCMatrix object or a character representing a filename
start_iteration	int or NULL, optional (default=NULL) Start index of the iteration to predict. If NULL or <= 0, starts from the first iteration.
num_iteration	int or NULL, optional (default=NULL) Limit number of iterations in the prediction. If NULL, if the best iteration exists and start_iteration is NULL or <= 0, the best iteration is used; otherwise, all iterations from start_iteration are used. If <= 0, all iterations from start_iteration are used (no limits).
pred_latent	If TRUE latent variables, both fixed effects (tree-ensemble) and random effects (gp_model) are predicted. Otherwise, the response variable (label) is predicted. Depending on how the argument 'pred_latent' is set, different values are returned from this function; see the 'Value' section for more details. If there is no gp_model, this argument corresponds to 'raw_score' in LightGBM.
predleaf	whether predict leaf index instead.
predcontrib	return per-feature contributions for each record.
header	only used for prediction for text file. True if text file has header
reshape	whether to reshape the vector of predictions to a matrix form when there are several prediction outputs per case.
group_data_pred	A vector or matrix with elements being group levels for which predictions are made (if there are grouped random effects in the GPModel)

group_rand_coef_data_pred	A vector or matrix with covariate data for grouped random coefficients (if there are some in the GPModel)
gp_coords_pred	A matrix with prediction coordinates (=features) for Gaussian process (if there is a GP in the GPModel)
gp_rand_coef_data_pred	A vector or matrix with covariate data for Gaussian process random coefficients (if there are some in the GPModel)
cluster_ids_pred	A vector with elements indicating the realizations of random effects / Gaussian processes for which predictions are made (set to NULL if you have not specified this when creating the GPModel)
predict_cov_mat	A boolean. If TRUE, the (posterior) predictive covariance is calculated in addition to the (posterior) predictive mean
predict_var	A boolean. If TRUE, the (posterior) predictive variances are calculated
cov_pars	A vector containing covariance parameters which are used if the gp_model has not been trained or if predictions should be made for other parameters than the trained ones
ignore_gp_model	A boolean. If TRUE, predictions are only made for the tree ensemble part and the gp_model is ignored
rawscore	This is discontinued. Use the renamed equivalent argument pred_latent instead
vecchia_pred_type	A string specifying the type of Vecchia approximation used for making predictions. This is discontinued here. Use the function 'set_prediction_data' to specify this
num_neighbors_pred	an integer specifying the number of neighbors for making predictions. This is discontinued here. Use the function 'set_prediction_data' to specify this
...	Additional named arguments passed to the predict() method of the gpb.Booster object passed to object.

### Value

either a list with vectors or a single vector / matrix depending on whether there is a gp\_model or not. If there is a gp\_model, the result dict contains the following entries. 1. If pred\_latent is TRUE, the dict contains the following 3 entries: - result["fixed\_effect"] are the predictions from the tree-ensemble. - result["random\_effect\_mean"] are the predicted means of the gp\_model. - result["random\_effect\_cov"] are the predicted covariances or variances of the gp\_model (only if 'predict\_var' or 'predict\_cov' is TRUE). 2. If pred\_latent is FALSE, the dict contains the following 2 entries: - result["response\_mean"] are the predicted means of the response variable (Label) taking into account both the fixed effects (tree-ensemble) and the random effects (gp\_model) - result["response\_var"] are the predicted covariances or variances of the response variable (only if 'predict\_var' or 'predict\_cov' is TRUE) If there is no gp\_model or pred\_contrib or ignore\_gp\_model are TRUE, the result contains predictions from the tree-boosted only.

**Author(s)**

Fabio Sigrist, authors of the LightGBM R package

**Examples**

# See <https://github.com/fabsig/GPBoost/tree/master/R-package> for more examples

```
library(gpboost)
data(GPBoost_data, package = "gpboost")

#-----Combine tree-boosting and grouped random effects model-----
# Create random effects model
gp_model <- GPModel(group_data = group_data[,1], likelihood = "gaussian")
# The default optimizer for covariance parameters (hyperparameters) is
# Nesterov-accelerated gradient descent.
# This can be changed to, e.g., Nelder-Mead as follows:
# re_params <- list(optimizer_cov = "nelder_mead")
# gp_model$set_optim_params(params=re_params)
# Use trace = TRUE to monitor convergence:
# re_params <- list(trace = TRUE)
# gp_model$set_optim_params(params=re_params)

# Train model
bst <- gpboost(data = X, label = y, gp_model = gp_model, nrounds = 16,
               learning_rate = 0.05, max_depth = 6, min_data_in_leaf = 5,
               verbose = 0)
# Estimated random effects model
summary(gp_model)

# Make predictions
# Predict latent variables
pred <- predict(bst, data = X_test, group_data_pred = group_data_test[,1],
               predict_var = TRUE, pred_latent = TRUE)
pred$random_effect_mean # Predicted latent random effects mean
pred$random_effect_cov # Predicted random effects variances
pred$fixed_effect # Predicted fixed effects from tree ensemble
# Predict response variable
pred_resp <- predict(bst, data = X_test, group_data_pred = group_data_test[,1],
                    predict_var = TRUE, pred_latent = FALSE)
pred_resp$response_mean # Predicted response mean
# For Gaussian data: pred$random_effect_mean + pred$fixed_effect = pred_resp$response_mean
pred$random_effect_mean + pred$fixed_effect - pred_resp$response_mean

#-----Combine tree-boosting and Gaussian process model-----
# Create Gaussian process model
gp_model <- GPModel(gp_coords = coords, cov_function = "exponential",
                    likelihood = "gaussian")

# Train model
bst <- gpboost(data = X, label = y, gp_model = gp_model, nrounds = 8,
               learning_rate = 0.1, max_depth = 6, min_data_in_leaf = 5,
               verbose = 0)
```

```

# Estimated random effects model
summary(gp_model)
# Make predictions
pred <- predict(bst, data = X_test, gp_coords_pred = coords_test,
               predict_var = TRUE, pred_latent = TRUE)
pred$random_effect_mean # Predicted latent random effects mean
pred$random_effect_cov # Predicted random effects variances
pred$fixed_effect # Predicted fixed effects from tree ensemble
# Predict response variable
pred_resp <- predict(bst, data = X_test, gp_coords_pred = coords_test,
                    predict_var = TRUE, pred_latent = FALSE)
pred_resp$response_mean # Predicted response mean

```

---

predict.GPModel      *Make predictions for a GPModel*

---

## Description

Make predictions for a GPModel

## Usage

```

## S3 method for class 'GPModel'
predict(object, predict_response = TRUE,
        predict_var = FALSE, predict_cov_mat = FALSE, y = NULL,
        cov_pars = NULL, group_data_pred = NULL,
        group_rand_coef_data_pred = NULL, gp_coords_pred = NULL,
        gp_rand_coef_data_pred = NULL, cluster_ids_pred = NULL, X_pred = NULL,
        use_saved_data = FALSE, offset = NULL, offset_pred = NULL,
        fixed_effects = NULL, fixed_effects_pred = NULL,
        vecchia_pred_type = NULL, num_neighbors_pred = NULL, ...)

```

## Arguments

object	a GPModel
predict_response	A boolean. If TRUE, the response variable (label) is predicted, otherwise the latent random effects
predict_var	A boolean. If TRUE, the (posterior) predictive variances are calculated
predict_cov_mat	A boolean. If TRUE, the (posterior) predictive covariance is calculated in addition to the (posterior) predictive mean
y	Observed data (can be NULL, e.g. when the model has been estimated already and the same data is used for making predictions)
cov_pars	A vector containing covariance parameters which are used if the GPModel has not been trained or if predictions should be made for other parameters than the trained ones

group_data_pred	A vector or matrix with elements being group levels for which predictions are made (if there are grouped random effects in the GPModel)
group_rand_coef_data_pred	A vector or matrix with covariate data for grouped random coefficients (if there are some in the GPModel)
gp_coords_pred	A matrix with prediction coordinates (=features) for Gaussian process (if there is a GP in the GPModel)
gp_rand_coef_data_pred	A vector or matrix with covariate data for Gaussian process random coefficients (if there are some in the GPModel)
cluster_ids_pred	A vector with elements indicating the realizations of random effects / Gaussian processes for which predictions are made (set to NULL if you have not specified this when creating the GPModel)
X_pred	A matrix with prediction covariate data for the fixed effects linear regression term (if there is one in the GPModel)
use_saved_data	A boolean. If TRUE, predictions are done using a priory set data via the function '\$set_prediction_data' (this option is not used by users directly)
offset	A numeric vector with additional fixed effects contributions that are added to the linear predictor (= offset). The length of this vector needs to equal the number of training data points.
offset_pred	A numeric vector with additional fixed effects contributions that are added to the linear predictor for the prediction points (= offset). The length of this vector needs to equal the number of prediction points.
fixed_effects	This is discontinued. Use the renamed equivalent argument offset instead
fixed_effects_pred	This is discontinued. Use the renamed equivalent argument offset_pred instead
vecchia_pred_type	A string specifying the type of Vecchia approximation used for making predictions. This is discontinued here. Use the function 'set_prediction_data' to specify this
num_neighbors_pred	an integer specifying the number of neighbors for making predictions. This is discontinued here. Use the function 'set_prediction_data' to specify this
...	(not used, ignore this, simply here that there is no CRAN warning)

## Value

Predictions from a GPModel. A list with three entries is returned:

- "mu" (first entry): predictive (=posterior) mean. For (generalized) linear mixed effects models, i.e., models with a linear regression term, this consists of the sum of fixed effects and random effects predictions
- "cov" (second entry): predictive (=posterior) covariance matrix. This is NULL if 'predict\_cov\_mat=FALSE'
- "var" (third entry) : predictive (=posterior) variances. This is NULL if 'predict\_var=FALSE'

**Author(s)**

Fabio Sigrist

**Examples**

```
# See https://github.com/fabsig/GPBoost/tree/master/R-package for more examples

data(GPBoost_data, package = "gpboost")
# Add intercept column
X1 <- cbind(rep(1,dim(X)[1]),X)
X_test1 <- cbind(rep(1,dim(X_test)[1]),X_test)

#-----Grouped random effects model: single-level random effect-----
gp_model <- fitGPModel(group_data = group_data[,1], y = y, X = X1,
                      likelihood="gaussian", params = list(std_dev = TRUE))
summary(gp_model)
# Make predictions
pred <- predict(gp_model, group_data_pred = group_data_test[,1],
               X_pred = X_test1, predict_var = TRUE)
pred$mu # Predicted mean
pred$var # Predicted variances
# Also predict covariance matrix
pred <- predict(gp_model, group_data_pred = group_data_test[,1],
               X_pred = X_test1, predict_cov_mat = TRUE)
pred$mu # Predicted mean
pred$cov # Predicted covariance

#-----Gaussian process model-----
gp_model <- fitGPModel(gp_coords = coords, cov_function = "matern", cov_fct_shape = 1.5,
                      likelihood="gaussian", y = y, X = X1, params = list(std_dev = TRUE))
summary(gp_model)
# Make predictions
pred <- predict(gp_model, gp_coords_pred = coords_test,
               X_pred = X_test1, predict_cov_mat = TRUE)
pred$mu # Predicted (posterior) mean of GP
pred$cov # Predicted (posterior) covariance matrix of GP
```

---

predict\_training\_data\_random\_effects

*Predict ("estimate") training data random effects for a GPModel*

---

**Description**

Predict ("estimate") training data random effects for a GPModel

**Usage**

```
predict_training_data_random_effects(gp_model, predict_var = FALSE)
```

**Arguments**

```
gp_model      A GPModel
predict_var    A boolean. If TRUE, the (posterior) predictive variances are calculated
```

**Value**

A GPModel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
# Add intercept column
X1 <- cbind(rep(1,dim(X)[1]),X)
X_test1 <- cbind(rep(1,dim(X_test)[1]),X_test)

gp_model <- fitGPModel(group_data = group_data[,1], y = y, X = X1, likelihood="gaussian")
all_training_data_random_effects <- predict_training_data_random_effects(gp_model)
first_occurrences <- match(unique(group_data[,1]), group_data[,1])
unique_training_data_random_effects <- all_training_data_random_effects[first_occurrences]
head(unique_training_data_random_effects)
```

---

```
predict_training_data_random_effects.GPModel
      Predict ("estimate") training data random effects for a GPModel
```

---

**Description**

Predict ("estimate") training data random effects for a GPModel

**Usage**

```
## S3 method for class 'GPModel'
predict_training_data_random_effects(gp_model,
  predict_var = FALSE)
```

**Arguments**

```
gp_model      A GPModel
predict_var    A boolean. If TRUE, the (posterior) predictive variances are calculated
```

**Value**

A GPMoel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
# Add intercept column
X1 <- cbind(rep(1,dim(X)[1]),X)
X_test1 <- cbind(rep(1,dim(X_test)[1]),X_test)

gp_model <- fitGPMoel(group_data = group_data[,1], y = y, X = X1, likelihood="gaussian")
all_training_data_random_effects <- predict_training_data_random_effects(gp_model)
first_occurences <- match(unique(group_data[,1]), group_data[,1])
unique_training_data_random_effects <- all_training_data_random_effects[first_occurences]
head(unique_training_data_random_effects)
```

---

readRDS.gpb.Booster    *readRDS for gpb.Booster models*

---

**Description**

Attempts to load a model stored in a .rds file, using [readRDS](#)

**Usage**

```
readRDS.gpb.Booster(file, refhook = NULL)
```

**Arguments**

file                    a connection or the name of the file where the R object is saved to or read from.  
refhook                a hook function for handling reference objects.

**Value**

gpb.Booster



## Examples

```
library(gpboost)
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
data(agaricus.test, package = "gpboost")
test <- agaricus.test
dtest <- gpb.Dataset.create.valid(dtrain, test$data, label = test$label)
params <- list(objective = "regression", metric = "l2")
valids <- list(test = dtest)
model <- gpb.train(
  params = params
  , data = dtrain
  , nrounds = 10L
  , valids = valids
  , min_data = 1L
  , learning_rate = 1.0
  , early_stopping_rounds = 5L
)
model_file <- tempfile(fileext = ".rds")
saveRDS.gpb.Booster(model, model_file)
new_model <- readRDS.gpb.Booster(model_file)
```

---

saveGPMoDel

*Save a GPMoDel*

---

## Description

Save a GPMoDel

## Usage

```
saveGPMoDel(gp_model, filename)
```

## Arguments

gp_model	a GPMoDel
filename	filename for saving

## Value

A GPMoDel

## Author(s)

Fabio Sigris

**Examples**

```

data(GPBoost_data, package = "gpboost")
# Add intercept column
X1 <- cbind(rep(1,dim(X)[1]),X)
X_test1 <- cbind(rep(1,dim(X_test)[1]),X_test)

gp_model <- fitGPModel(group_data = group_data[,1], y = y, X = X1, likelihood="gaussian")
pred <- predict(gp_model, group_data_pred = group_data_test[,1],
               X_pred = X_test1, predict_var = TRUE)

# Save model to file
filename <- tempfile(fileext = ".json")
saveGPModel(gp_model,filename = filename)
# Load from file and make predictions again
gp_model_loaded <- loadGPModel(filename = filename)
pred_loaded <- predict(gp_model_loaded, group_data_pred = group_data_test[,1],
                      X_pred = X_test1, predict_var = TRUE)

# Check equality
pred$mu - pred_loaded$mu
pred$var - pred_loaded$var

```

---

saveRDS.gpb.Booster     *saveRDS for gpb.Booster models*

---

**Description**

Attempts to save a model using RDS. Has an additional parameter (*raw*) which decides whether to save the raw model or not.

**Usage**

```

saveRDS.gpb.Booster(object, file, ascii = FALSE, version = NULL,
                    compress = TRUE, refhook = NULL, raw = TRUE)

```

**Arguments**

<code>object</code>	R object to serialize.
<code>file</code>	a connection or the name of the file where the R object is saved to or read from.
<code>ascii</code>	a logical. If TRUE or NA, an ASCII representation is written; otherwise (default), a binary one is used. See the comments in the help for save.
<code>version</code>	the workspace format version to use. NULL specifies the current default version (2). Versions prior to 2 are not supported, so this will only be relevant when there are later versions.
<code>compress</code>	a logical specifying whether saving to a named file is to use "gzip" compression, or one of "gzip", "bzip2" or "xz" to indicate the type of compression to be used. Ignored if file is a connection.
<code>refhook</code>	a hook function for handling reference objects.

raw                    whether to save the model in a raw variable or not, recommended to leave it to TRUE.

### Value

NULL invisibly.

### Examples

```
library(gpboost)
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
data(agaricus.test, package = "gpboost")
test <- agaricus.test
dtest <- gpb.Dataset.create.valid(dtrain, test$data, label = test$label)
params <- list(objective = "regression", metric = "l2")
valids <- list(test = dtest)
model <- gpb.train(
  params = params
  , data = dtrain
  , nrounds = 10L
  , valids = valids
  , min_data = 1L
  , learning_rate = 1.0
  , early_stopping_rounds = 5L
)
model_file <- tempfile(fileext = ".rds")
saveRDS.gpb.Booster(model, model_file)
```

---

setinfo                    *Set information of an gpb.Dataset object*

---

### Description

Set one attribute of a gpb.Dataset

### Usage

```
setinfo(dataset, ...)
```

```
## S3 method for class 'gpb.Dataset'
setinfo(dataset, name, info, ...)
```

**Arguments**

dataset	Object of class <code>gpb.Dataset</code>
...	other parameters
name	the name of the field to get
info	the specific field of information to set

**Details**

The name field can be one of the following:

- `label`: vector of labels to use as the target variable
- `weight`: to do a weight rescale
- `init_score`: initial score is the base prediction `gpboost` will boost from
- `group`: used for learning-to-rank tasks. An integer vector describing how to group rows together as ordered results from the same set of candidate results to be ranked. For example, if you have a 100-document dataset with `group = c(10, 20, 40, 10, 10, 10)`, that means that you have 6 groups, where the first 10 records are in the first group, records 11-30 are in the second group, etc.

**Value**

the dataset you passed in

the dataset you passed in

**Examples**

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)
gpb.Dataset.construct(dtrain)
```

```
labels <- gpboost::getinfo(dtrain, "label")
gpboost::setinfo(dtrain, "label", 1 - labels)
```

```
labels2 <- gpboost::getinfo(dtrain, "label")
stopifnot(all.equal(labels2, 1 - labels))
```

---

set\_optim\_params

*Set parameters for estimation of the covariance parameters*

---

**Description**

Set parameters for optimization of the covariance parameters of a `GPMoDel`

**Usage**

```
set_optim_params(gp_model, params = list())
```

**Arguments**

gp\_model            A GPModel

params             A list with parameters for the estimation / optimization

- optimizer\_cov: string (default = "lbfgs"). Optimizer used for estimating covariance parameters. Options: "gradient\_descent", "lbfgs", "fisher\_scoring", "newton", "nelder\_mead". If there are additional auxiliary parameters for non-Gaussian likelihoods, 'optimizer\_cov' is also used for those
- optimizer\_coef: string (default = "wls" for Gaussian likelihoods and "lbfgs" for other likelihoods). Optimizer used for estimating linear regression coefficients, if there are any (for the GPBoost algorithm there are usually none). Options: "gradient\_descent", "lbfgs", "wls", "nelder\_mead". Gradient descent steps are done simultaneously with gradient descent steps for the covariance parameters. "wls" refers to doing coordinate descent for the regression coefficients using weighted least squares. If 'optimizer\_cov' is set to "nelder\_mead" or "lbfgs", 'optimizer\_coef' is automatically also set to the same value.
- maxit: integer (default = 1000). Maximal number of iterations for optimization algorithm
- delta\_rel\_conv: numeric (default = 1E-6 except for "nelder\_mead" for which the default is 1E-8). Convergence tolerance. The algorithm stops if the relative change in either the (approximate) log-likelihood or the parameters is below this value. If < 0, internal default values are used
- convergence\_criterion: string (default = "relative\_change\_in\_log\_likelihood"). The convergence criterion used for terminating the optimization algorithm. Options: "relative\_change\_in\_log\_likelihood" or "relative\_change\_in\_parameters"
- init\_coef: vector with numeric elements (default = NULL). Initial values for the regression coefficients (if there are any, can be NULL)
- init\_cov\_pars: vector with numeric elements (default = NULL). Initial values for covariance parameters of Gaussian process and random effects (can be NULL). The order is the same as the order of the parameters in the summary function: first is the error variance (only for "gaussian" likelihood), next follow the variances of the grouped random effects (if there are any, in the order provided in 'group\_data'), and then follow the marginal variance and the range of the Gaussian process. If there are multiple Gaussian processes, then the variances and ranges follow alternately. If 'init\_cov\_pars = NULL', an internal choice is used that depends on the likelihood and the random effects type and covariance function. If you select the option 'trace = TRUE' in the 'params' argument, you will see the first initial covariance parameters in iteration 0.
- lr\_coef: numeric (default = 0.1). Learning rate for fixed effect regression coefficients if gradient descent is used

- lr\_cov: numeric (default = 0.1 for "gradient\_descent" and 1. otherwise). Initial learning rate for covariance parameters if a gradient-based optimization method is used
  - If lr\_cov < 0, internal default values are used (0.1 for "gradient\_descent" and 1. otherwise)
  - If there are additional auxiliary parameters for non-Gaussian likelihoods, 'lr\_cov' is also used for those
  - For "lbfgs", this is divided by the norm of the gradient in the first iteration
- use\_nesterov\_acc: boolean (default = TRUE). If TRUE Nesterov acceleration is used. This is used only for gradient descent
- acc\_rate\_coef: numeric (default = 0.5). Acceleration rate for regression coefficients (if there are any) for Nesterov acceleration
- acc\_rate\_cov: numeric (default = 0.5). Acceleration rate for covariance parameters for Nesterov acceleration
- momentum\_offset: integer (Default = 2). Number of iterations for which no momentum is applied in the beginning.
- trace: boolean (default = FALSE). If TRUE, information on the progress of the parameter optimization is printed
- std\_dev: boolean (default = TRUE). If TRUE, approximate standard deviations are calculated for the covariance and linear regression parameters (= square root of diagonal of the inverse Fisher information for Gaussian likelihoods and square root of diagonal of a numerically approximated inverse Hessian for non-Gaussian likelihoods)
- init\_aux\_pars: vector with numeric elements (default = NULL). Initial values for additional parameters for non-Gaussian likelihoods (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- estimate\_aux\_pars: boolean (default = TRUE). If TRUE, additional parameters for non-Gaussian likelihoods are also estimated (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- cg\_max\_num\_it: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithms
- cg\_max\_num\_it\_tridiag: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithm when being run as Lanczos algorithm for tridiagonalization
- cg\_delta\_conv: numeric (default = 1E-2). Tolerance level for L2 norm of residuals for checking convergence in conjugate gradient algorithm when being used for parameter estimation
- num\_rand\_vec\_trace: integer (default = 50). Number of random vectors (e.g., Rademacher) for stochastic approximation of the trace of a matrix
- reuse\_rand\_vec\_trace: boolean (default = TRUE). If true, random vectors (e.g., Rademacher) for stochastic approximations of the trace of a matrix are sampled only once at the beginning of the parameter estimation and reused in later trace approximations. Otherwise they are sampled every time a trace is calculated
- seed\_rand\_vec\_trace: integer (default = 1). Seed number to generate random vectors (e.g., Rademacher)

- piv\_chol\_rank: integer (default = 50). Rank of the pivoted Cholesky decomposition used as preconditioner in conjugate gradient algorithms
- cg\_preconditioner\_type: string. Type of preconditioner used for conjugate gradient algorithms.
  - Options for likelihood != "gaussian" and gp\_approx == "vecchia" or likelihood == "gaussian" and gp\_approx == "vecchia\_latent":
    - \* "vadu" (= default):  $(B^T * (D^{-1} + W) * B)$  as preconditioner for inverting  $(B^T * D^{-1} * B + W)$ , where  $B^T * D^{-1} * B \approx \Sigma^{-1}$
    - \* "fitc": modified predictive process preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$
    - \* "pivoted\_cholesky":  $(Lk * Lk^T + W^{-1})$  as preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$ , where Lk is a low-rank pivoted Cholesky approximation for Sigma and  $B^{-1} * D * B^{-T} \approx \Sigma$
    - \* "incomplete\_cholesky": zero fill-in incomplete (reverse) Cholesky factorization of  $(B^T * D^{-1} * B + W)$  using the sparsity pattern of  $B^T * D^{-1} * B \approx \Sigma^{-1}$
  - Options for likelihood == "gaussian" and gp\_approx == "full\_scale\_tapering":
    - \* "fitc" (= default): modified predictive process preconditioner
    - \* "none": no preconditioner

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
gp_model <- GPModel(group_data = group_data, likelihood="gaussian")
set_optim_params(gp_model, params=list(optimizer_cov="nelder_mead"))
```

---

```
set_optim_params.GPModel
```

*Set parameters for estimation of the covariance parameters*

---

**Description**

Set parameters for optimization of the covariance parameters of a GPModel

**Usage**

```
## S3 method for class 'GPModel'
set_optim_params(gp_model, params = list())
```

**Arguments**

gp_model	A GPModel
params	<p>A list with parameters for the estimation / optimization</p> <ul style="list-style-type: none"> <li>• optimizer_cov: string (default = "lbfgs"). Optimizer used for estimating covariance parameters. Options: "gradient_descent", "lbfgs", "fisher_scoring", "newton", "nelder_mead". If there are additional auxiliary parameters for non-Gaussian likelihoods, 'optimizer_cov' is also used for those</li> <li>• optimizer_coef: string (default = "wls" for Gaussian likelihoods and "lbfgs" for other likelihoods). Optimizer used for estimating linear regression coefficients, if there are any (for the GPBoost algorithm there are usually none). Options: "gradient_descent", "lbfgs", "wls", "nelder_mead". Gradient descent steps are done simultaneously with gradient descent steps for the covariance parameters. "wls" refers to doing coordinate descent for the regression coefficients using weighted least squares. If 'optimizer_cov' is set to "nelder_mead" or "lbfgs", 'optimizer_coef' is automatically also set to the same value.</li> <li>• maxit: integer (default = 1000). Maximal number of iterations for optimization algorithm</li> <li>• delta_rel_conv: numeric (default = 1E-6 except for "nelder_mead" for which the default is 1E-8). Convergence tolerance. The algorithm stops if the relative change in either the (approximate) log-likelihood or the parameters is below this value. If &lt; 0, internal default values are used</li> <li>• convergence_criterion: string (default = "relative_change_in_log_likelihood"). The convergence criterion used for terminating the optimization algorithm. Options: "relative_change_in_log_likelihood" or "relative_change_in_parameters"</li> <li>• init_coef: vector with numeric elements (default = NULL). Initial values for the regression coefficients (if there are any, can be NULL)</li> <li>• init_cov_pars: vector with numeric elements (default = NULL). Initial values for covariance parameters of Gaussian process and random effects (can be NULL). The order is the same as the order of the parameters in the summary function: first is the error variance (only for "gaussian" likelihood), next follow the variances of the grouped random effects (if there are any, in the order provided in 'group_data'), and then follow the marginal variance and the range of the Gaussian process. If there are multiple Gaussian processes, then the variances and ranges follow alternately. If 'init_cov_pars = NULL', an internal choice is used that depends on the likelihood and the random effects type and covariance function. If you select the option 'trace = TRUE' in the 'params' argument, you will see the first initial covariance parameters in iteration 0.</li> <li>• lr_coef: numeric (default = 0.1). Learning rate for fixed effect regression coefficients if gradient descent is used</li> <li>• lr_cov: numeric (default = 0.1 for "gradient_descent" and 1. otherwise). Initial learning rate for covariance parameters if a gradient-based optimization method is used <ul style="list-style-type: none"> <li>– If lr_cov &lt; 0, internal default values are used (0.1 for "gradient_descent" and 1. otherwise)</li> </ul> </li> </ul>



- If there are additional auxiliary parameters for non-Gaussian likelihoods, 'lr\_cov' is also used for those
- For "lbfgs", this is divided by the norm of the gradient in the first iteration
- use\_nesterov\_acc: boolean (default = TRUE). If TRUE Nesterov acceleration is used. This is used only for gradient descent
- acc\_rate\_coef: numeric (default = 0.5). Acceleration rate for regression coefficients (if there are any) for Nesterov acceleration
- acc\_rate\_cov: numeric (default = 0.5). Acceleration rate for covariance parameters for Nesterov acceleration
- momentum\_offset: integer (Default = 2). Number of iterations for which no momentum is applied in the beginning.
- trace: boolean (default = FALSE). If TRUE, information on the progress of the parameter optimization is printed
- std\_dev: boolean (default = TRUE). If TRUE, approximate standard deviations are calculated for the covariance and linear regression parameters (= square root of diagonal of the inverse Fisher information for Gaussian likelihoods and square root of diagonal of a numerically approximated inverse Hessian for non-Gaussian likelihoods)
- init\_aux\_pars: vector with numeric elements (default = NULL). Initial values for additional parameters for non-Gaussian likelihoods (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- estimate\_aux\_pars: boolean (default = TRUE). If TRUE, additional parameters for non-Gaussian likelihoods are also estimated (e.g., shape parameter of a gamma or negative\_binomial likelihood)
- cg\_max\_num\_it: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithms
- cg\_max\_num\_it\_tridiag: integer (default = 1000). Maximal number of iterations for conjugate gradient algorithm when being run as Lanczos algorithm for tridiagonalization
- cg\_delta\_conv: numeric (default = 1E-2). Tolerance level for L2 norm of residuals for checking convergence in conjugate gradient algorithm when being used for parameter estimation
- num\_rand\_vec\_trace: integer (default = 50). Number of random vectors (e.g., Rademacher) for stochastic approximation of the trace of a matrix
- reuse\_rand\_vec\_trace: boolean (default = TRUE). If true, random vectors (e.g., Rademacher) for stochastic approximations of the trace of a matrix are sampled only once at the beginning of the parameter estimation and reused in later trace approximations. Otherwise they are sampled every time a trace is calculated
- seed\_rand\_vec\_trace: integer (default = 1). Seed number to generate random vectors (e.g., Rademacher)
- piv\_chol\_rank: integer (default = 50). Rank of the pivoted Cholesky decomposition used as preconditioner in conjugate gradient algorithms
- cg\_preconditioner\_type: string. Type of preconditioner used for conjugate gradient algorithms.

- Options for likelihood != "gaussian" and gp\_approx == "vecchia" or likelihood == "gaussian" and gp\_approx == "vecchia\_latent":
  - \* "vadu" (= default):  $(B^T * (D^{-1} + W) * B)$  as preconditioner for inverting  $(B^T * D^{-1} * B + W)$ , where  $B^T * D^{-1} * B \approx \text{Sigma}^{-1}$
  - \* "fitc": modified predictive process preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$
  - \* "pivoted\_cholesky":  $(Lk * Lk^T + W^{-1})$  as preconditioner for inverting  $(B^{-1} * D * B^{-T} + W^{-1})$ , where Lk is a low-rank pivoted Cholesky approximation for Sigma and  $B^{-1} * D * B^{-T} \approx \text{Sigma}$
  - \* "incomplete\_cholesky": zero fill-in incomplete (reverse) Cholesky factorization of  $(B^T * D^{-1} * B + W)$  using the sparsity pattern of  $B^T * D^{-1} * B \approx \text{Sigma}^{-1}$
- Options for likelihood == "gaussian" and gp\_approx == "full\_scale\_tapering":
  - \* "fitc" (= default): modified predictive process preconditioner
  - \* "none": no preconditioner

**Value**

A GPMoel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
gp_model <- GPMoel(group_data = group_data, likelihood="gaussian")
set_optim_params(gp_model, params=list(optimizer_cov="nelder_mead"))
```

---

set\_prediction\_data    *Set prediction data for a GPMoel*

---

**Description**

Set the data required for making predictions with a GPMoel

**Usage**

```
set_prediction_data(gp_model, vecchia_pred_type = NULL,
  num_neighbors_pred = NULL, cg_delta_conv_pred = NULL,
  nsim_var_pred = NULL, rank_pred_approx_matrix_lanczos = NULL,
  group_data_pred = NULL, group_rand_coef_data_pred = NULL,
  gp_coords_pred = NULL, gp_rand_coef_data_pred = NULL,
  cluster_ids_pred = NULL, X_pred = NULL)
```

**Arguments**

- `gp_model` A `GPMoDel`
- `vecchia_pred_type` A string specifying the type of Vecchia approximation used for making predictions. Default value if `vecchia_pred_type = NULL`: "order\_obs\_first\_cond\_obs\_only". Available options:
- "order\_obs\_first\_cond\_obs\_only": Vecchia approximation for the observable process and observed training data is ordered first and the neighbors are only observed training data points
  - "order\_obs\_first\_cond\_all": Vecchia approximation for the observable process and observed training data is ordered first and the neighbors are selected among all points (training + prediction)
  - "latent\_order\_obs\_first\_cond\_obs\_only": Vecchia approximation for the latent process and observed data is ordered first and neighbors are only observed points
  - "latent\_order\_obs\_first\_cond\_all": Vecchia approximation for the latent process and observed data is ordered first and neighbors are selected among all points
  - "order\_pred\_first": Vecchia approximation for the observable process and prediction data is ordered first for making predictions. This option is only available for Gaussian likelihoods
- `num_neighbors_pred` an integer specifying the number of neighbors for the Vecchia approximation for making predictions. Default value if `NULL`: `num_neighbors_pred = 2 * num_neighbors`
- `cg_delta_conv_pred` a numeric specifying the tolerance level for L2 norm of residuals for checking convergence in conjugate gradient algorithms when being used for prediction Default value if `NULL`: `1e-3`
- `nsim_var_pred` an integer specifying the number of samples when simulation is used for calculating predictive variances Default value if `NULL`: `1000`
- `rank_pred_approx_matrix_lanczos` an integer specifying the rank of the matrix for approximating predictive covariances obtained using the Lanczos algorithm Default value if `NULL`: `1000`
- `group_data_pred` A vector or matrix with elements being group levels for which predictions are made (if there are grouped random effects in the `GPMoDel`)
- `group_rand_coef_data_pred` A vector or matrix with covariate data for grouped random coefficients (if there are some in the `GPMoDel`)
- `gp_coords_pred` A matrix with prediction coordinates (=features) for Gaussian process (if there is a GP in the `GPMoDel`)
- `gp_rand_coef_data_pred` A vector or matrix with covariate data for Gaussian process random coefficients (if there are some in the `GPMoDel`)

cluster_ids_pred	A vector with elements indicating the realizations of random effects / Gaussian processes for which predictions are made (set to NULL if you have not specified this when creating the GPModel)
X_pred	A matrix with prediction covariate data for the fixed effects linear regression term (if there is one in the GPModel)

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
set.seed(1)
train_ind <- sample.int(length(y), size=250)
gp_model <- GPModel(group_data = group_data[train_ind,1], likelihood="gaussian")
set_prediction_data(gp_model, group_data_pred = group_data[-train_ind,1])
```

---

```
set_prediction_data.GPModel
  Set prediction data for a GPModel
```

---

**Description**

Set the data required for making predictions with a GPModel

**Usage**

```
## S3 method for class 'GPModel'
set_prediction_data(gp_model, vecchia_pred_type = NULL,
  num_neighbors_pred = NULL, cg_delta_conv_pred = NULL,
  nsim_var_pred = NULL, rank_pred_approx_matrix_lanczos = NULL,
  group_data_pred = NULL, group_rand_coef_data_pred = NULL,
  gp_coords_pred = NULL, gp_rand_coef_data_pred = NULL,
  cluster_ids_pred = NULL, X_pred = NULL)
```

**Arguments**

gp_model	A GPModel
vecchia_pred_type	A string specifying the type of Vecchia approximation used for making predictions. Default value if vecchia_pred_type = NULL: "order_obs_first_cond_obs_only". Available options:

- "order\_obs\_first\_cond\_obs\_only": Vecchia approximation for the observable process and observed training data is ordered first and the neighbors are only observed training data points
- "order\_obs\_first\_cond\_all": Vecchia approximation for the observable process and observed training data is ordered first and the neighbors are selected among all points (training + prediction)
- "latent\_order\_obs\_first\_cond\_obs\_only": Vecchia approximation for the latent process and observed data is ordered first and neighbors are only observed points
- "latent\_order\_obs\_first\_cond\_all": Vecchia approximation for the latent process and observed data is ordered first and neighbors are selected among all points
- "order\_pred\_first": Vecchia approximation for the observable process and prediction data is ordered first for making predictions. This option is only available for Gaussian likelihoods

num_neighbors_pred	an integer specifying the number of neighbors for the Vecchia approximation for making predictions. Default value if NULL: $\text{num\_neighbors\_pred} = 2 * \text{num\_neighbors}$
cg_delta_conv_pred	a numeric specifying the tolerance level for L2 norm of residuals for checking convergence in conjugate gradient algorithms when being used for prediction Default value if NULL: 1e-3
nsim_var_pred	an integer specifying the number of samples when simulation is used for calculating predictive variances Default value if NULL: 1000
rank_pred_approx_matrix_lanczos	an integer specifying the rank of the matrix for approximating predictive covariances obtained using the Lanczos algorithm Default value if NULL: 1000
group_data_pred	A vector or matrix with elements being group levels for which predictions are made (if there are grouped random effects in the GPModel)
group_rand_coef_data_pred	A vector or matrix with covariate data for grouped random coefficients (if there are some in the GPModel)
gp_coords_pred	A matrix with prediction coordinates (=features) for Gaussian process (if there is a GP in the GPModel)
gp_rand_coef_data_pred	A vector or matrix with covariate data for Gaussian process random coefficients (if there are some in the GPModel)
cluster_ids_pred	A vector with elements indicating the realizations of random effects / Gaussian processes for which predictions are made (set to NULL if you have not specified this when creating the GPModel)
X_pred	A matrix with prediction covariate data for the fixed effects linear regression term (if there is one in the GPModel)

**Value**

A GPMoel

**Author(s)**

Fabio Sigrist

**Examples**

```
data(GPBoost_data, package = "gpboost")
set.seed(1)
train_ind <- sample.int(length(y),size=250)
gp_model <- GPMoel(group_data = group_data[train_ind,1], likelihood="gaussian")
set_prediction_data(gp_model, group_data_pred = group_data[-train_ind,1])
```

---

slice

*Slice a dataset*

---

**Description**

Get a new `gpb.Dataset` containing the specified rows of original `gpb.Dataset` object

**Usage**

```
slice(dataset, ...)

## S3 method for class 'gpb.Dataset'
slice(dataset, idxset, ...)
```

**Arguments**

dataset	Object of class <code>gpb.Dataset</code>
...	other parameters (currently not used)
idxset	an integer vector of indices of rows needed

**Value**

constructed sub dataset

**Examples**

```
data(agaricus.train, package = "gpboost")
train <- agaricus.train
dtrain <- gpb.Dataset(train$data, label = train$label)

dsub <- gpboost::slice(dtrain, seq_len(42L))
gpb.Dataset.construct(dsub)
labels <- gpboost::getinfo(dsub, "label")
```

---

summary.GPModel	<i>Summary for a GPModel</i>
-----------------	------------------------------

---

**Description**

Summary for a GPModel

**Usage**

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

**Arguments**

```
object      a GPModel
...         (not used, ignore this, simply here that there is no CRAN warning)
```

**Value**

Summary of a (fitted) GPModel

**Author(s)**

Fabio Sigrist

**Examples**

```
# See https://github.com/fabsig/GPBoost/tree/master/R-package for more examples

data(GPBoost_data, package = "gpboost")
# Add intercept column
X1 <- cbind(rep(1,dim(X)[1]),X)
X_test1 <- cbind(rep(1,dim(X_test)[1]),X_test)

#-----Grouped random effects model: single-level random effect-----
gp_model <- fitGPModel(group_data = group_data[,1], y = y, X = X1,
                      likelihood="gaussian", params = list(std_dev = TRUE))
summary(gp_model)

#-----Gaussian process model-----
gp_model <- fitGPModel(gp_coords = coords, cov_function = "matern", cov_fct_shape = 1.5,
                      likelihood="gaussian", y = y, X = X1, params = list(std_dev = TRUE))
summary(gp_model)
```

---

x	<i>Example data for the GPBoost package</i>
---	---

---

**Description**

A matrix with covariate data for the example data of the GPBoost package

**Usage**

```
data(GPBoost_data)
```

---

x_test	<i>Example data for the GPBoost package</i>
--------	---

---

**Description**

A matrix with covariate information for the predictions for the example data of the GPBoost package

**Usage**

```
data(GPBoost_data)
```

---

y	<i>Example data for the GPBoost package</i>
---	---

---

**Description**

Response variable for the example data of the GPBoost package

**Usage**

```
data(GPBoost_data)
```



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