

# Package: graper (via r-universe)

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**Type** Package

**Title** Adaptive penalization in high-dimensional regression and classification with external covariates using variational Bayes

**Version** 1.21.0

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**License** GPL (>= 2)

**Description** This package enables regression and classification on high-dimensional data with different relative strengths of penalization for different feature groups, such as different assays or omic types. The optimal relative strengths are chosen adaptively. Optimisation is performed using a variational Bayes approach.

**Depends** R (>= 3.6)

**Encoding** UTF-8

**LazyData** TRUE

**Imports** Matrix, Rcpp, stats, ggplot2, methods, cowplot, matrixStats

**LinkingTo** Rcpp, RcppArmadillo, BH

**biocViews** Regression, Bayesian, Classification

**RoxygenNote** 6.1.1

**Suggests** knitr, rmarkdown, BiocStyle, testthat

**VignetteBuilder** knitr

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/graper>

**RemoteRef** HEAD

**RemoteSha** 7b45fcc7a5f2224a6c9ec8a45755ac316835f73b

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coef.graper	<i>Get estimated coefficients from a graper object</i>
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## Description

Function to obtain estimated coefficients from a fitted graper model.

## Usage

```
## S3 method for class 'graper'
coef(object, include_intercept = TRUE, ...)
```

## Arguments

object	fitted graper model as obtained from <a href="#">graper</a>
include_intercept	whether to include the estimated intercept value in the output
...	other arguments

## Value

1-Column matrix of estimated coefficients.

## Examples

```
# create data
dat <- makeExampleData()
# fit the graper model to the data
fit <- graper(dat$X, dat$y, dat$annot)
# extract the model coefficients
coef(fit)
```

---

`getPIPs`*Get posterior inclusion probabilities per feature*

---

**Description**

Function to obtain estimated posterior inclusion probabilities per feature from a fitted `graper` model.

**Usage**

```
getPIPs(object)
```

**Arguments**

`object` fitted `graper` model as obtained from [graper](#)

**Value**

1-Column matrix of estimated posterior inclusion probabilities.

**Examples**

```
# create data
dat <- makeExampleData()
# fit the graper model to the data
fit <- graper(dat$X, dat$y, dat$annot)
# extract the posterior inclusion probabilities from the fitted model
getPIPs(fit)
```

---

`graper`*Fit a regression model with graper*

---

**Description**

Fit a regression model with `graper` given a matrix of predictors ( $X$ ), a response vector ( $y$ ) and a vector of group memberships for each predictor in  $X$  ( $annot$ ). For each group a different strength of penalization is determined adaptively.

**Usage**

```
graper(X, y, annot, factoriseQ = TRUE, spikeslab = TRUE,
  intercept = TRUE, family = "gaussian", standardize = TRUE,
  n_rep = 1, max_iter = 3000, th = 0.01, d_tau = 0.001,
  r_tau = 0.001, d_gamma = 0.001, r_gamma = 0.001, r_pi = 1,
  d_pi = 1, calcELB = TRUE, verbose = TRUE, freqELB = 1,
  nogamma = FALSE, init_psi = 1)
```

**Arguments**

<code>X</code>	design matrix of size $n$ (samples) $\times$ $p$ (features)
<code>y</code>	response vector of size $n$
<code>annot</code>	factor of length $p$ indicating group membership of each feature (column) in $X$
<code>factoriseQ</code>	if set to <code>TRUE</code> , the variational distribution is assumed to fully factorize across features (faster, default). If <code>FALSE</code> , a multivariate variational distribution is used.
<code>spikeslab</code>	if set to <code>TRUE</code> , a spike and slab prior on the coefficients (default).
<code>intercept</code>	whether to include an intercept into the model
<code>family</code>	Likelihood model for the response, either "gaussian" for linear regression or "binomial" for logistic regression
<code>standardize</code>	whether to standardize the predictors to unit variance
<code>n_rep</code>	number of repetitions with different random initializations to be fit
<code>max_iter</code>	maximum number of iterations
<code>th</code>	convergence threshold for the evidence lower bound (ELB)
<code>d_tau</code>	hyper-parameters for prior of tau (noise precision)
<code>r_tau</code>	hyper-parameters for prior of tau (noise precision)
<code>d_gamma</code>	hyper-parameters for prior of gamma (coefficients' prior precision)
<code>r_gamma</code>	hyper-parameters for prior of gamma (coefficients' prior precision)
<code>r_pi</code>	hyper-parameters for Beta prior of the mixture probabilities in the spike and slab prior
<code>d_pi</code>	hyper-parameters for Beta prior of the mixture probabilities in the spike and slab prior
<code>calcELB</code>	whether to calculate the evidence lower bound (ELB)
<code>verbose</code>	whether to print out intermediate messages during fitting
<code>freqELB</code>	frequency at which the evidence lower bound (ELB) is to be calculated, i.e. each <code>freqELB</code> -th iteration
<code>nogamma</code>	if <code>TRUE</code> , the normal prior will have same variance for all groups (only relevant for <code>spikeslab = TRUE</code> )
<code>init_psi</code>	initial value for the spike variables

**Details**

The function trains the graper model given a matrix of predictors ( $X$ ), a response vector ( $y$ ) and a vector of group memberships for each predictor in  $X$  (`annot`). For each feature group as specified in `annot` a penalty factor and sparsity level is learnt.

By default it uses a Spike-and-Slab prior on the coefficients and uses a fully factorized variational distribution in the inference. This provides a fast way to train the model. Using `spikeslab=FALSE` a ridge regression like model can be fitted using a normal instead of the spike and slab prior. Setting `factoriseQ = FALSE` gives a more exact inference scheme based on a multivariate variational distribution, but can be much slower.

As the optimization is non-convex it can be helpful to use multiple random initializations by setting `n_rep` to a value larger than 1. The returned model is then chosen as the optimal fit with respect to the evidence lower bound (ELB).

Depending on the response vector a linear regression model (`family = "gaussian"`) or a logistic regression model (`family = "binomial"`) is fitted. Note, that the implementation of logistic regression is still experimental.

## Value

A `graper` object containing

**EW\_beta** estimated model coefficients in linear/logistic regression

**EW\_s** estimated posterior-inclusion probabilities for each feature

**intercept** estimated intercept term

**annot** annotation vector of features to the groups as specified when calling `graper`

**EW\_gamma** estimated penalty factor per group

**EW\_pi** estimated sparsity level per group (from 1 (dense) to 0 (sparse))

**EW\_tau** estimated noise precision

**sigma2\_tildebeta\_s1, EW\_tildebeta\_s1, alpha\_gamma, alpha\_tau, beta\_tau, Sigma\_beta, alpha\_pi, beta\_pi** parameters of the variational distributions of beta, gamma, tau and pi

**ELB** final value of the evidence lower bound

**ELB\_trace** values of the evidence lower bound for all iterations

**Options** other options used when calling `graper`

## Examples

```
# create data
dat <- makeExampleData()

# fit a sparse model with spike and slab prior
fit <- graper(dat$X, dat$y, dat$annot)
fit # print fitted object
beta <- coef(fit, include_intercept=FALSE) # model coefficients
pips <- getPIPs(fit) # posterior inclusion probabilities
pf <- fit$EW_gamma # penalty factors per group
sparsities <- fit$EW_pi # sparsity levels per group

# fit a dense model without spike and slab prior
fit <- graper(dat$X, dat$y, dat$annot, spikeslab=FALSE)

# fit a dense model using a multivariate variational distribution
fit <- graper(dat$X, dat$y, dat$annot, factoriseQ=TRUE,
              spikeslab=FALSE)
```

---

makeExampleData      *Simulate example data from the graper model*

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### Description

Simulate data from the graper model with groups of equal size and pre-specified parameters gamma, pi and tau.

### Usage

```
makeExampleData(n = 100, p = 200, g = 4, gammas = c(0.1, 1, 10,
  100), pis = c(0.5, 0.5, 0.5, 0.5), tau = 1, rho = 0,
  response = "gaussian", intercept = 0)
```

### Arguments

n	number of samples
p	number of features
g	number of groups
gammas	vector of length g, specifying the slab precision of the prior on beta per group
pis	vector of length g, specifying the probability of s to be 1 (slab)
tau	noise precision
rho	correlation of design matrix (Toeplitz structure)
response	"gaussian" for continuous response from a linear regression model, "bernoulli" for a binary response from a logistic regression model.
intercept	model intercept (default: 0)

### Value

list containing the design matrix X, the response y, the feature annotation to groups annot as well as the different parameters in the Bayesian model and the correlation strength rho

### Examples

```
dat <- makeExampleData()
```

---

```
makeExampleDataWithUnequalGroups
```

*Simulate example data from the graper model with groups of unequal size*

---

### Description

Simulate data from the graper model with groups of unequal size and pre-specified parameters gamma, pi and tau.

### Usage

```
makeExampleDataWithUnequalGroups(n = 100, pg = c(100, 100, 10, 10),  
  gammas = c(0.1, 10, 0.1, 10), pis = c(0.5, 0.5, 0.5, 0.5), tau = 1,  
  rho = 0, response = "gaussian", intercept = 0)
```

### Arguments

n	number of samples
pg	vector of length g (desired number of groups) with number of features per group
gammas	vector of length g, specifying the slab precision of the prior on beta per group
pis	vector of length g, specifying the probability of s to be 1 (slab)
tau	noise precision (only relevant for gaussian response)
rho	correlation of design matrix (Toeplitz structure)
response	"gaussian" for continuous response from a linear regression model, "bernoulli" for a binary response from a logistic regression model.
intercept	model intercept (default: 0)

### Value

list containin the design matrix X, the response y, the feature annotation to groups annot as well as the different parameters in the Bayesian model and the correlation strength rho

### Examples

```
dat <- makeExampleDataWithUnequalGroups()
```

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plotELBO	<i>Plot evidence lower bound</i>
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**Description**

Function to plot the evidence lower bound (ELBO) over iterations to monitor the convergence of the algorithm.

**Usage**

```
plotELBO(fit)
```

**Arguments**

`fit` fit as produced by [graper](#)

**Value**

a ggplot object

**Examples**

```
dat <- makeExampleData()
fit <- graper(dat$X, dat$y, dat$annot)
plotELBO(fit)
```

---

plotGroupPenalties	<i>Plot group-wise penalties</i>
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---

**Description**

Function to plot the group-wise penalty factors ( $\gamma$ ) and sparsity levels.

**Usage**

```
plotGroupPenalties(fit)
```

**Arguments**

`fit` fit as produced by [graper](#)

**Value**

a ggplot object



**Examples**

```
dat <- makeExampleData()
fit <- graper(dat$X, dat$y, dat$annot)
plotGroupPenalties(fit)
```

---

plotPosterior	<i>Plot posterior distributions</i>
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---

**Description**

Function to plot the posterior of the model parameters obtained by `graper` from the variational inference framework.

**Usage**

```
plotPosterior(fit, param2plot, beta0 = NULL, gamma0 = NULL,
              tau0 = NULL, pi0 = NULL, s0 = NULL, jmax = 2, range = NULL)
```

**Arguments**

<code>fit</code>	fit as produced by <a href="#">graper</a>
<code>param2plot</code>	which parameter of the graper model to plot (gamma, beta, tau or s)
<code>beta0</code>	true beta (if known)
<code>gamma0</code>	true gamma (if known)
<code>tau0</code>	true tau (if known)
<code>pi0</code>	true pi (if known)
<code>s0</code>	true s (if known)
<code>jmax</code>	maximal number of components per group to plot (for beta and s)
<code>range</code>	plotting range (x-axis)

**Value**

a ggplot object

**Examples**

```
# create data
dat <- makeExampleData()
# fit the graper model
fit <- graper(dat$X, dat$y, dat$annot)
# plot posterior distribution of the gamma parameter
plotPosterior(fit, param2plot="gamma")
```

---

predict.graper      *Predict response on new data*

---

## Description

Function to predict the response on a new data set using a fitted graper model.

## Usage

```
## S3 method for class 'graper'
predict(object, newX, type = c("inRange", "response",
  "link"), ...)
```

## Arguments

object	fitted graper model as obtained from <a href="#">graper</a>
newX	Predictor matrix of size n_test (number of new test samples) x p (number of predictors) (same feature structure as used in <a href="#">graper</a> )
type	type of prediction returned, either: <ul style="list-style-type: none"> <li>• <b>response</b>: returns the linear predictions for linear regression and class probabilities for logistic regression</li> <li>• <b>link</b>: returns the linear predictions</li> <li>• <b>inRange</b>: returns linear predictions for linear and class memberships for logistic regression</li> </ul>
...	other arguments

## Value

A vector with predictions.

## Examples

```
# create data
dat <- makeExampleData()
# split data into train and test sets of equal size
ntrain <- dat$n / 2
# fit the model to the train data
fit <- graper(dat$X[seq_len(ntrain), ],
  dat$y[seq_len(ntrain)], dat$annot)
# make predictions on the test data
ypred <- predict(fit, dat$X[seq_len(ntrain) + dat$n / 2, ])

# create data for logistic regression
dat <- makeExampleData(response="bernoulli")
# split data into train and test sets of equal size
ntrain <- dat$n / 2
# fit the graper model for a logistic model
```

```
fit <- graper(dat$X[seq_len(ntrain)], ],
             dat$y[seq_len(ntrain)],
             dat$annot, family="binomial")
# make predictions on the test data
ypred <- predict(fit, dat$X[seq_len(ntrain) + dat$n / 2, ], type = "inRange")
```

---

print.graper                      *Print a graper object*

---

### Description

Function to print a fitted graper model.

### Usage

```
## S3 method for class 'graper'
print(x, ...)
```

### Arguments

x	fitted graper model as obtained from <a href="#">graper</a>
...	additional print arguments

### Value

Print output.

### Examples

```
# create data
dat <- makeExampleData()
# fit the graper model
fit <- graper(dat$X, dat$y, dat$annot)
# print a summary of the fitted model
print(fit)
```

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