Package 'gesso'

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Type Package Title Hierarchical GxE Interactions in a Regularized Regression Model Version 1.0.2 Date 2021-11-28 Author Natalia Zemlianskaia Maintainer Natalia Zemlianskaia <natasha.zemlianskaia@gmail.com> **Description** The method focuses on a single environmental exposure and induces a main-effect-before-interaction hierarchical structure for the joint selection of interaction terms in a regularized regression model. For details see Zemlianskaia et al. (2021) arxiv.2103.13510>. License MIT + file LICENSE Imports Rcpp (>= 1.0.3), Matrix, bigmemory, methods **Depends** dplyr, R (\geq 3.5) Suggests glmnet, testthat, knitr, rmarkdown, ggplot2 LinkingTo Rcpp, RcppEigen, RcppThread, BH, bigmemory VignetteBuilder knitr NeedsCompilation yes **Repository** CRAN Date/Publication 2021-11-30 07:30:02 UTC

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gesso-package

Description

The method focuses on a single environmental exposure and induces a main-effect-before-interaction hierarchical structure for the joint selection of interaction terms in a regularized regression model. For details see Zemlianskaia et al. (2021) arxiv.com (2021) arxiv.com (2021) <a href="https://www.arxiv.com (2021) <a href="https://www.arxiv.com (202

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References

"A Scalable Hierarchical Lasso for Gene-Environment Interactions", Natalia Zemlianskaia, W.James Gauderman, Juan Pablo Lewinger https://arxiv.org/abs/2103.13510

data.gen

Data Generation

Description

Generates genotypes data matrix G (sample_size by p), vector of environmental measurments E, and an outcome vector Y of size sample_size. Simulates training, validation, and test datasets.

Usage

```
data.gen(sample_size = 100, p = 20, n_g_non_zero = 15, n_gxe_non_zero = 10,
    family = "gaussian", mode = "strong_hierarchical",
    normalize = FALSE, normalize_response = FALSE,
    seed = 1, pG = 0.2, pE = 0.3,
    n_confounders = NULL)
```

Arguments

<pre>sample_size</pre>	sample size of the data
р	total number of main effects
n_g_non_zero	number of non-zero main effects to generate
n_gxe_non_zero	number of non-zero interaction effects to generate
family	"gaussian" for continous outcome Y and "binomial" for binary 0/1 outcome

data.gen

mode	either "strong_hierarchical", "hierarchical", or "anti_hierarchical". In the <i>strong hierarchical</i> mode the hierarchical structure is maintained (beta_g = 0 then beta_gxe = 0) and also lbeta_gl >= lbeta_gxel. In the <i>hierarchical</i> mode the hierarchical structure is maintained, but lbeta_Gl < lbeta_gxel. In the <i>anti_hierarchical</i> mode the hierarchical structure is violated (beta_g = 0 then beta_gxe != 0).
normalize normalize_resp	TRUE to normalize matrix G and vector E onse
	TRUE to normalize vector Y
pG	genotypes prevalence, value from 0 to 1
рЕ	environment prevalence, value from 0 to 1
seed	random seed
n_confounders	number of confounders to generate, either NULL or >1

Value

A list of simulated datasets and generating coefficients

G_train, G_valid, G_test					
generated genotypes matrices					
E_train, E_vali	d,E_test				
	generated vectors of environmental values				
Y_train, Y_vali					
	generated outcome vectors				
C_train, C_vali					
	generated confounders matrices				
GxE_train, GxE_					
	generated GxE matrix				
Beta_G	main effect coefficients vector				
Beta_GxE	interaction coefficients vector				
beta_0	intercept coefficient value				
beta_E	environment coefficient value				
Beta_C	confounders coefficient values				
index_beta_non_	_zero, index_beta_gxe_non_zero, index_beta_zero, index_beta_gxe_zero				
	inner data generation variables				
n_g_non_zero	number of non-zero main effects generated				
n_gxe_non_zero	number of non-zero interactions generated				
n_total_non_zer					
	total number of non-zero variables				
SNR_g	signal-to-noise ratio for the main effects				
SNR_gxe	signal-to-noise ratio for the interactions				
family, p, sampl	.e_size, mode, seed				
	input simulation parameters				

Examples

```
data = data.gen(sample_size=100, p=100)
G = data$G_train; GxE = data$GxE_train
E = data$E_train; Y = data$Y_train
```

gesso.coef

Get model coefficients

Description

A function to obtain coefficients from the model fit object corresponding to the desired pair of tuning parameters lambda = (lambda_1, lambda_2).

Usage

gesso.coef(fit, lambda)

Arguments

fit	model fit object obtained either by using function gesso.fit or gesso.cv
lambda	a pair of tuning parameters organized in a tibble (ex: lambda = tibble(lambda_1=grid[1], lambda_2=g

Value

A list of model coefficients corresponding to lambda values of tuning parameters

beta_0	estimated intercept value
beta_e	estimated environmental coefficient value
beta_g	a vector of estimated main effect coefficients
beta_c	a vector of estimated confounders coefficients
beta_gxe	a vector of estimated interaction coefficients

Examples

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gesso.coefnum

Description

A function to obtain coefficients with target_b_gxe_non_zero specified to control the desired sparsity of interactions in the model.

Usage

gesso.coefnum(cv_model, target_b_gxe_non_zero, less_than = TRUE)

Arguments

cv_model	cross-validated model fit object obtained by using function gesso.cv						
target_b_gxe_non_zero							
	number of non-zero interactions we want to inlcude in the model						
less_than	TRUE if we want to control a number of at most non-zero interactions, FALSE if						
	we want to control a number of at least non-zero interactions						

Value

A list of model coefficients corresponding to the best model that contains at most or at least target_b_gxe_non_zero non-zero interaction terms.

The target model is selected based on the averaged cross-validation (cv) results: for each pair of parameters lambda=(lambda_1, lambda_2) in the grid and each cv fold we obtain a number of non-zero estimated interaction terms, then average cv results by lambda and choose the tuning parameters corresponding to the minimum average cv loss that have *at most* or *at least* target_b_gxe_non_zero non-zero interaction terms. Returned coefficients are obtained by fitting the model on the full data with the selected tuning parameters.

Note that the number of estimated non-zero interactions will only approximately reflect the numbers obtained on cv datasets.

beta_0	estimated intercept value
beta_e	estimated environmental coefficient value
beta_g	a vector of estimated main effect coefficients
beta_gxe	a vector of estimated interaction coefficients
beta_c	a vector of estimated confounders coefficients

Examples

```
data = data.gen()
model = gesso.cv(data$G_train, data$E_train, data$Y_train)
model_coefficients = gesso.coefnum(model, 5)
gxe_coefficients = model_coefficients$beta_gxe; sum(gxe_coefficients!=0)
```

gesso.cv

Description

Performs nfolds-fold cross-validation to tune hyperparmeters lambda_1 and lambda_2 for the gesso model.

Usage

```
gesso.cv(G, E, Y, C = NULL, normalize = TRUE, normalize_response = FALSE, grid = NULL,
    grid_size = 20, grid_min_ratio = NULL, alpha = NULL, family = "gaussian",
    type_measure = "loss", fold_ids = NULL, nfolds = 4,
    parallel = TRUE, seed = 42, tolerance = 1e-3, max_iterations = 5000,
    min_working_set_size = 100, verbose = TRUE)
```

Arguments

G	matrix of main effects of size n x p, variables organized by columns
E	vector of environmental measurments
Υ	outcome vector. Set family="gaussian" for the continuous outcome and family="binomial" for the binary outcome with 0/1 levels
С	matrix of confounders of size n x m, variables organized by columns
normalize normalize_respo	TRUE to normalize matrix G and vector E
	TRUE to normalize vector Y (for family="gaussian")
grid	grid sequence for tuning hyperparameters, we use the same grid for lambda_1 and lambda_2
grid_size	specify grid_size to generate grid automatically. Grid is generated by cal- culating max_lambda from the data (smallest lambda such that all the coeffi- cients are zero). min_lambda is calculated as a product of max_lambda and grid_min_ratio. The program then generates grid_size values equidistant on the log10 scale from min_lambda to max_lambda
grid_min_ratio	parameter to determine min_lambda (smallest value for the grid of lambdas), default is 0.1 for $p > n$, 0.01 otherwise
alpha	if NULL independent 2D grid is used for (lambda_1, lambda_2), else 1D grid is used where lambda_2 = alpha * lambda_1, i.e. (lambda_1, alpha * lambda_1)
family	"gaussian" for continuous outcome and "binomial" for binary
type_measure	loss to use for cross-validation. Specity type_measure="loss" for neative log likelihood or type_measure="auc" for AUC (for family="binomial" only)
fold_ids	option to input custom folds assignments
tolerance	tolerance for the dual gap convergence criterion
<pre>max_iterations</pre>	maximum number of iterations

gesso.fit

<pre>min_working_set_size</pre>					
	minimum size of the working set				
nfolds	number of cross-validation splits				
parallel	TRUE to enable parallel cross-validation				
seed	set random seed to control random folds assignments				
verbose	TRUE to print messages				

Value

A list of objects

cv_result	a tibble with cross-validation results: averaged across folds loss and the number of non-zero coefficients for each value of (lambda_1, lambda_2) path. Could be used for custom parameters tuning (ex: select (lambda_1, lambda_2) with a sertain number of non-zero main effects and/or a sertain number of interactions).
	 mean_loss averaged across folds loss value, vector of size lambda_1*lambda_2
	 mean_beta_g_nonzero averaged across folds number of non-zero main effects, vector of size lambda_1*lambda_2
	 mean_beta_gxe_nonzero averaged across folds number of non-zero inter- actions, vector of size lambda_1*lambda_2
	 lambda_1 lambda_1 pass, decreasing
	 lambda_2 lambda_2 pass, oscillating
lambda_min	a tibble of optimal (lambda_1, lambda_2) values, tuning parameter values that give minimum cross-validation loss (mean_loss)
fit	list, return of the function gesso.fit on the full data
grid	vector of values used for hyperparameters tuning
full_cv_result	inner variables

Examples

gesso.fit gesso fit

Description

Fits gesso model over the two dimentional grid of hyperparameters lambda_1 and lambda_2, returns estimated coefficients for each pair of hyperparameters.

Usage

```
gesso.fit(G, E, Y, C = NULL, normalize = TRUE, normalize_response = FALSE,
  grid = NULL, grid_size = 20, grid_min_ratio = NULL,
  alpha = NULL, family = "gaussian", weights = NULL,
  tolerance = 1e-3, max_iterations = 5000,
  min_working_set_size = 100,
  verbose = FALSE)
```

Arguments

G	matrix of main effects of size n x p, variables organized by columns						
E	vector of environmental measurments						
Y	outcome vector. Set family="gaussian" for the continuous outcome and family="binomial" for the binary outcome with 0/1 levels						
С	matrix of confounders of size n x m, variables organized by columns						
normalize normalize_respo	TRUE to normalize matrix G and vector E						
	TRUE to normalize vector Y						
grid	grid sequence for tuning hyperparameters, we use the same grid for lambda_1 and lambda_2						
grid_size	specify grid_size to generate grid automatically. Grid is generated by cal- culating max_lambda from the data (smallest lambda such that all the coeffi- cients are zero). min_lambda is calculated as a product of max_lambda and grid_min_ratio. The program then generates grid_size values equidistant on the log10 scale from min_lambda to max_lambda						
grid_min_ratio	parameter to determine min_lambda (smallest value for the grid of lambdas), default is 0.1 for $p > n$, 0.01 otherwise						
alpha	if NULL independent 2D grid is used for (lambda_1, lambda_2), else 1D grid is used where lambda_2 = alpha * lambda_1, i.e. (lambda_1, alpha * lambda_1)						
family	"gaussian" for continuous outcome and "binomial" for binary						
tolerance	tolerance for the dual gap convergence criterion						
	<pre>max_iterations maximum number of iterations min_working_set_size</pre>						
	minimum size of the working set						
weights	inner fitting parameter						
verbose	TRUE to print messages						

Value

A list of estimated coefficients and other model fit metrics for each pair of hyperparameters (lambda_1, lambda_2)

beta_0	vector of estimated intercept values of size lambda_1*lambda_2
beta_e	vector of estimated environment coefficients of size lambda_1*lambda_2

gesso.predict

beta_g	matrix of estimated main effects coefficients organized by rows, size (lambda_1*lambda_2) by p	
beta_gxe	matrix of estimated interactions coefficients organized by rows, size (lambda_1*lambda_2) by p	
beta_c	matrix of estimated confounders coefficients organized by rows, size (lambda_1*lambda_2) by m, where m is the number of confounders	
num_iterations	number of iterations until convergence for each fit	
working_set_size		
	maximum number of variables in the working set for each fit	
has_converged	1 if the model converged within given max_iterations, 0 otherwise	
objective_value		
	objective function (loss) value for each fit	
beta_g_nonzero	number of estimated non-zero main effects for each fit	
beta_gxe_nonzero		
	number of estimated non-zero interactions for each fit	
lambda_1	lambda_1 path values, decreasing	
lambda_2	lambda_2 path values, oscillating	
grid	vector of values used for hyperparameters tuning	

Examples

```
data = data.gen()
fit = gesso.fit(G=data$G_train, E=data$E_train, Y=data$Y_train, normalize=TRUE)
plot(fit$beta_g_nonzero, pch=19, cex=0.4,
    ylab="num of non-zero features", xlab="lambdas path")
points(fit$beta_gxe_nonzero, pch=19, cex=0.4, col="red")
```

gesso.predict *Predict new outcome vector*

Description

Predict new outcome vector based on the new data and estimated model coefficients.

Usage

Arguments

beta_0	estimated intercept value
beta_e	estimated environmental coefficient value
beta_g	a vector of estimated main effect coefficients
beta_gxe	a vector of estimated interaction coefficients
new_G	matrix of main effects, variables organized by columns
new_E	vector of environmental measurments
beta_c	a vector of estimated confounders coefficients
new_C	matrix of confounders, variables organized by columns
family	set family="gaussian" for the continuous outcome and family="binomial" for the binary outcome with 0/1 levels

Value

Returns a vector of predicted values

Examples

```
data = data.gen()
tune_model = gesso.cv(data$G_train, data$E_train, data$Y_train)
coefficients = gesso.coef(tune_model$fit, tune_model$lambda_min)
beta_0 = coefficients$beta_0; beta_e = coefficients$beta_e
beta_g = coefficients$beta_g; beta_gxe = coefficients$beta_gxe
new_G = data$G_test; new_E = data$E_test
new_Y = gesso.predict(beta_0, beta_e, beta_g, beta_gxe, new_G, new_E)
cor(new_Y, data$Y_test)^2
```

selection.metrics Selection metrics

Description

Calculates principal selection metrics for the binary zero/non-zero classification problem (sensitivity, specificity, precision, auc).

Usage

```
selection.metrics(true_b_g, true_b_gxe, estimated_b_g, estimated_b_gxe)
```

Arguments

true_b_g	vector of true main effect coefficients
true_b_gxe	vector of true interaction coefficients
estimated_b_g	vector of estimated main effect coefficients
estimated_b_gxe	
	vector of estimated interaction coefficients

vector of estimated interaction coefficients

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selection.metrics

Value

A list of principal selection metrics

b_g_non_zero	number of non-zero main effects	
<pre>b_gxe_non_zero</pre>	number of non-zero interactions	
mse_b_g	mean squared error for estimation of main effects effect sizes	
mse_b_gxe	mean squared error for estimation of interactions effect sizes	
<pre>sensitivity_g</pre>	recall of the non-zero main effects	
<pre>specificity_g</pre>	recall of the zero main effects	
precision_g	precision with respect to non-zero main effects	
sensitivity_gxe		
	recall of the non-zero interactions	
specificity_gxe		
	recall of the zero interactions	
precision_gxe	precision with respect to non-zero interactions	
auc_g	area under the curve for zero/non-zero binary classification problem for main effects	
auc_gxe	area under the curve for zero/non-zero binary classification problem for interac- tions	

Examples

```
data = data.gen()
model = gesso.cv(data$G_train, data$E_train, data$Y_train)
gxe_coefficients = gesso.coef(model$fit, model$lambda_min)$beta_gxe
g_coefficients = gesso.coef(model$fit, model$lambda_min)$beta_g
selection.metrics(data$Beta_G, data$Beta_GXE, g_coefficients, gxe_coefficients)
```

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