Package 'mpersonalized'

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Type Package

Title What the Package Does (Title Case)

Version 0.1.0

Author Who wrote it

Maintainer The package maintainer <yourself@somewhere.net>

Description More about what it does (maybe more than one line)
    Use four spaces when indenting paragraphs within the Description.

License What license is it under?

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Imports glmnet, SGL, Rcpp, ggplot2, gridExtra

Suggests knitr, rmarkdown

VignetteBuilder knitr

LinkingTo Rcpp

R topics documented:

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admm_optim   *ADMM Algorithm for Meta-analysis/Multiple Outcomes Personalized Medicine*

Usage

```
admm_optim(x, y, p, q, lambda1, lambda2, lambda3, rho, abs.tol = 1e-05,
  rel.tol = 1e-05, maxit = 500L)
```

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mpersonalized   *Meta-analysis/Multiple Outcomes for Personalized Medicine*

Usage

```
mpersonalized(problem = c("meta-analysis", "multiple outcomes"), X, Trt, P,
  Xlist, Ylist, Trtlist, Plist, typelist = NULL, penalty = c("none",
  "lasso", "GL", "SGL", "fused", "lasso+fused", "GL+fused", "SGL+fused"),
  lambda1 = NULL, lambda2 = NULL, unique_rule_lambda = NULL,
  alpha = NULL, unique_rule = FALSE)
```

Arguments

problem	a character specifiy whether you want to solve "meta-analysis" or "multiple outcomes" problem. For "meta-analysis" problem, the user should supply `Xlist`, `Ylist`, `Trtlist` and `Plist`. For "multiple outcomes" problem, the user should supply `X`, `Ylist`, `Trt` and `P`.
X	the covariate matrix that should be supplied when the problem is "multiple outcomes" with rows indicating subjects and columns indicating covariates.
Trt	the treatment vector that should be supplied when the problem is "multiple outcomes". It should be coded as 0 or 1.
P	the propensity score vector when the problem is "multiple outcomes".
Xlist	a list object with kth element denoting the covariate matrix of study k. This should be supplied when the problem is "meta-analysis".
Ylist	When the problem is "meta-analysis", `Ylist` should be a list object with kth element denoting the response vector of study k. When the problem is "multiple outcomes", `Ylist` should be a list object with kth element denoting the kth outcome.
Trtlist	a list object with kth element denoting the treatment vector of study k (coded as 0 or 1). This should be supplied when the problem is "meta-analysis".
Plist	a list object with $k$the element denoting the propensity score vector of study k.
penalty	For different rules, the penalty could be "none", "lasso", "GL", "SGL", "fused", "lasso+fused", "GL+fused", "SGL+fused". For unique rule, the penalty could be "none" or "lasso".
lambda1	lambda1 supplied in the framework when different rules are used.
lambda2	lambda2 supplied in the framework when different rules are used.
unique_rule_lambda	
	λ when unique rule is used.
alpha	alpha in the framework when different rules are used.
unique_rule	a logical value, whether a unique treatment rule is required
typelist	a list object with kth element denoting the type of response corresponding to the kth element in the list `Ylist`. Each element should be "continuous" or "binary".

Details

Assume the total number of studies is K. This function is aimed to solve meta-analysis/multiple outcomes problems for personalized medicine based on the following framework:

$$\min_{g_1,\ldots,g_K} \frac{1}{2} \sum_{k=1}^{K} \sum_{i=1}^{n_k} \frac{|\hat{C}_k(X_i)|}{\sum_{i=1}^{n_k} |\hat{C}_k(X_i)|} \left[1\{\hat{C}_k(X_i) > 0\} - g_k(X_i) \right]^2 + h(g_1,\ldots,g_K)$$

Here the regularization function h is of the form of a sum of sparse group lasso and fused lasso penalty

$$h = (1-\alpha)\lambda_1 \sqrt{q} \sum_{j=1}^{p} \|\boldsymbol{\beta_j}\|_2 + \alpha\lambda_1 \sum_{j=1}^{p} \|\boldsymbol{\beta_j}\|_1 + \lambda_2 \sum_{j=1}^{p} \sum_{1 \le a < b \le K} |\beta_{ja} - \beta_{jb}|$$

where $\boldsymbol{\beta_j} = (\beta_{j1},\ldots,\beta_{jK})$

If we would like a unique rule to be obtained, we let $g_1 = \ldots = g_K$ and solve the following question instead

$$\min_{g} \frac{1}{2} \sum_{k=1}^{K} \sum_{i=1}^{n_k} \frac{|\hat{C}_k(X_i)|}{\sum_{i=1}^{n_k} |\hat{C}_k(X_i)|} \left[1\{\hat{C}_k(X_i) > 0\} - g(X_i) \right]^2 + h(g_1,\ldots,g_K) + \lambda_{uni}\|\beta\|_1$$

If we want different rules, by setting $\lambda_1, \lambda_2, \alpha$ differently, different penalties can be obtained.

- If $\lambda_1, \lambda_2 \neq 0$ and $\alpha \neq 0$ or 1, the penalty is "SGL+fused".
- If $\lambda_1, \lambda_2 \neq 0$ and $\alpha = 0$, the penalty is "GL+fused".
- If $\lambda_1, \lambda_2 \neq 0$ and $\alpha = 1$, the penalty is "lasso+fused".
- If $\lambda_1 = 0, \lambda_2 \neq 0$, the penalty is "fused".
- If $\lambda_1 \neq 0, \lambda_2 = 0$ and $\alpha \neq 0$ or 1, the penalty is "SGL".
- If $\lambda_1 \neq 0, \lambda_2 = 0$ and $\alpha = 0$, the penalty is "GL".
- If $\lambda_1 \neq 0, \lambda_2 = 0$ and $\alpha = 1$, the penalty is "lasso".
- If $\lambda_1, \lambda_2 = 0$, there is no penalty.

If we want unique rule,

- If $\lambda \neq 0$, the penalty is "lasso".
- If $\lambda = 0$, there is no penalty.

Value

an S3 object of class "mp", which contains the information of the fitted model. It could be supplied to the predict function

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mpersonalized_cv	*Meta-analysis/Multiple Outcomes for Personalized Medicine with Cross Validation*

Usage

```
mpersonalized_cv(problem = c("meta-analysis", "multiple outcomes"), X, Trt, P,
   Xlist, Ylist, Trtlist, Plist, typelist = NULL, penalty = c("lasso", "GL",
   "SGL", "fused", "lasso+fused", "GL+fused", "SGL+fused"), lambda1 = NULL,
   lambda2 = NULL, unique_rule_lambda = NULL, alpha = NULL,
   unique_rule = FALSE, cv_folds = 5)
```

Arguments

problem	a character specifiy whether you want to solve "meta-analysis" or "multiple outcomes" problem. For "meta-analysis" problem, the user should supply Xlist, Ylist, Trtlist and Plist. For "multiple outcomes" problem, the user should supply X, Ylist, Trt and P.
X	the covariate matrix that should be supplied when the problem is "multiple outcomes" with rows indicating subjects and columns indicating covariates.
Trt	the treatment vector that should be supplied when the problem is "multiple outcomes". It should be coded as 0 or 1.
P	the propensity score vector when the problem is "multiple outcomes".
Xlist	a list object with kth element denoting the covariate matrix of study k. This should be supplied when the problem is "meta-analysis".
Ylist	When the problem is "meta-analysis", Ylist should be a list object with kth element denoting the response vector of study k. When the problem is "multiple outcomes", Ylist should be a list object with kth element denoting the kth outcome.
Trtlist	a list object with kth element denoting the treatment vector of study k (coded as 0 or 1). This should be supplied when the problem is "meta-analysis".
Plist	a list object with $k$the element denoting the propensity score vector of study k.
penalty	For different rules, the penalty could be "none", "lasso", "GL", "SGL", "fused", "lasso+fused", "GL+fused", "SGL+fused". For unique rule, the penalty could be "none" or "lasso".
lambda1	lambda1 supplied in the framework when different rules are used.
lambda2	lambda2 supplied in the framework when different rules are used.
unique_rule_lambda	
	λ when unique rule is used.
alpha	alpha in the framework when different rules are used.
unique_rule	a logical value, whether a unique treatment rule is required
cv_folds	number of folds needed for cross-validation, default is 5
typelist	a list object with kth element denoting the type of response corresponding to the kth element in the list Ylist. Each element should be "continuous" or "binary".

Details

This function implments basically implements `mpersonalized` but use cross validatation for the tuning of penalty parameter. The optimal penalty parameter is selected by minimizing

$$\sum_{i=1}^{n_k} \frac{|\hat{C}_k(X_i)|}{\sum_{i=1}^{n_k} |\hat{C}_k(X_i)|} \big[1\{\hat{C}_k(X_i) > 0\} - g_k(X_i)\big]^2$$

where $\hat{C}_k(X_i)$ in the leave-out fold is separately estimated from the training set.

Value

an S3 object of class "mp_cv", which contains the information of the model with the best fitted lambda. It can be supplied to the predict function.

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plot.mp   *Plot for a 'mp' Class Object.*

Usage

```
## S3 method for class 'mp'
plot(mp, ind1, ind2, unique_ind)
```

Arguments

mp	the 'mp' class object returned by `mpersonalzied` function
ind1	the index of the lambda1 if different rules are used
ind2	the index of the lambda2 if different rules are used
unique_ind	the index of the unique_rule_lambda if an unique rule is used

Details

This function plots the results for estimated treatment effects. Depending on the received treatment and recommended treatment, the group means of the outcome are computed and the relations between them are plotted. This plot provides a sanity check of the treatment recommendation rule. By specifiying the index of the penalty parameters, we can obtain the plots of the corresponding treatment recommendation rule.

Value

a list object with kth element denoting the plot of study k

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plot.mp_cv   *Plot for a 'mp' Class Object.*

Usage

```
## S3 method for class 'mp_cv'
plot(mp_cv)
```

Arguments

mp_cv   the 'mp_cv' class object returned by `mpersonalzied_cv` function

Details

This function plots the results for estimated treatment effects by using the estimated optimal treatment recommendation rule obtained from corss validation.

Value

a list object with kth element denoting the plot of study k

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predict.mp   *Predict for "mp" object*

Description

This function predict the benefit scores and optimal treatment for new patients

Usage

```
## S3 method for class 'mp'
predict(mp, newx = NULL, weight = NULL, overall_rec = TRUE)
```

Arguments

mp   the fitted "mp" object returned by "mpersonalized"

newx   the covariate matrix of the new patients. If newx = NULL, then the prediction is made for each data set based on the rule of that study/outcome.

weight   a weight vector for the overall recommendation. If leave as NULL, a equally weighted recommendation will be made.

overall_rec   a logical value. If TRUE, an overall recommendation will be made weighted by the "weight" parameter.

Value

a list of results with each element in the list corresponding to the prediciton by using each penalty parameter. Each element in this list contains:

treatment recommended treatment for each patient for each study/outcome. If `overall_rec = TRUE`, the weighted overall recommended treatment will be computed as well. If the overall recommened treatment is equal to 0.5, it means the sum of weight is equal for 0 and 1.

benefit_score the benefit score computed from $g_1, \ldots, g_K$

---

predict.mp_cv   *Predict for "mp_cv" object*

Description

This function predict the benefit scores and optimal treatment for new patients

Usage

```
## S3 method for class 'mp_cv'
predict(mp_cv, newx = NULL, weight = NULL,
  overall_rec = TRUE)
```

Arguments

mp_cv the fitted "mp_cv" object returned from "mpersonalized_cv" function

newx the covariate matrix of the new patients. If newx = NULL, then the prediction is made for each data set based on the rule of that study/outcome.

weight a weight vector for the overall recommendation. If leave as `NULL`, a equally weighted recommendation will be made.

overall_rec a logical value. If `TRUE`, an overall recommendation will be made weighted by the "weight" parameter.

Value

the prediciton by using the optimal penalty parameter selected by cross validation. It contains:

treatment recommended treatment for each patient for each study/outcome. If `overall_rec = TRUE`, the weighted overall recommended treatment will be computed as well. If the overall recommened treatment is equal to 0.5, it means the sum of weight is equal for 0 and 1.

benefit_score the benefit score computed from $g_1, \ldots, g_K$

simulated_dataset	*Simulated Dataset Generator*

Description

This function could generate a simulated dataset for the test and usage of this package.

Usage

```
simulated_dataset(n, sim_seed)
```

Arguments

n	sample size
sim_seed	the seed supplied to the generation

Value

A simulated dataset.

Xlist	a list object with kth element denoting the covariate matrix of study k
Ylist	a list object with kth element denoting the response vector of study k
Trtlist	a list object with kth element denoting the treatment vector of study k (coded as 0 or 1)

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