Package ‘FindIt’

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Title  Finding Heterogeneous Treatment Effects
Author
  Naoki Egami <naoki.egami5@gmail.com>, Marc Ratkovic <ratkovic@princeton.edu>, Ko-
  suke Imai <kimai@princeton.edu>,
Maintainer  Naoki Egami <naoki.egami5@gmail.com>
Depends  R (>= 2.15.0), glmnet, lars, Matrix
Description  The heterogeneous treatment effect estimation procedure
  proposed by Imai and Ratkovic (2013).
  The proposed method is applicable, for example, when selecting a small number of most (or least)
  efficacious treatments from a large number of alternative treatments as well as when identifying subsets of the
  population who benefit (or are harmed by) a treatment of interest. The method adapts the Support Vector Machine
  classifier by placing separate LASSO constraints over the pre-treatment parameters and causal heterogeneity parameters of
  interest. This allows for the qualitative distinction between causal and other parameters, thereby making the variable
  selection suitable for the exploration of causal heterogeneity.
  The package also contains the function, INT, which estimates
  the average marginal treatment effect, the average treatment combination effect, and the average marginal treatment interaction
  effect proposed by Egami and Imai (2015).
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FindIt .......................... FindIt for Estimating Heterogeneous Treatment Effects

Description

FindIt returns a model with the most predictive treatment-treatment interactions or treatment-covariate interactions.

Usage

FindIt(model.treat, model.main, model.int, data = NULL,
      type = "binary", treat.type = "multiple", nway,
      search.lambdas = TRUE, lambdas = NULL,
      make.twoway = TRUE, make.allway = TRUE,
      wts = 1, scale.c = 1, scale.int = 1, fit.glmmnet = TRUE,
      make.reference = TRUE, reference.main = NULL, threshold = 0.999999)

Arguments

model.treat  A formula that specifies outcome and treatment variables.
model.main  An optional formula that specifies pre-treatment covariates to be adjusted.
model.int  A formula specifying pre-treatment covariates to be interacted with treatment assignments when treat.type="single".
data  An optional data frame, list or environment (or object coercible by 'as.data.frame' to a data frame) containing the variables in the model. If not found in 'data', the variables are taken from 'environment(formula)'. typically the environment from which 'FindIt' is called.
type  "binary" for a binary outcome variable, which needs to be integer class; "continuous" for a continuous outcome variable.
treat.type "single" for interactions between a single treatment variable, which needs to be integer class, and multiple pre-treatment covariates specified with model.int; "multiple" is used when treatment-treatment interactions are of interest and treat is a matrix of multiple treatments.

nway An argument passed to makeallway when treat.type="multiple". FindIt generates treatment-treatment interactions up to the order specified with this argument. In general, it is recommended to use the number of factorial treatments. The current version covers up to four way interactions.

search.lambdas Whether to search for the tuning parameters for the LASSO constraints. If FALSE, lambdas must be supplied.

lambdas Tuning parameters to be given to FindIt; only used if search.lambdas=FALSE.

make.twoway If make.twoway=TRUE, all possible two-way interactions for the pre-treatment covariates specified in model.main and model.int are generated within FindIt. The default is set to be TRUE.

make.allway If make.allway=TRUE, all possible treatment-treatment interactions for multiple treatments are generated when treat.type="multiple". Interactions of the order up to the value of nway is computed.

wts An optional set of scaling weights. The default is 1.

scale.c A set of weights for recaling the pre-treatment covariates; only used if make.twoway=FALSE. maketwoway is useful for generating these.

scale.int A set of weights for recaling the covariates to be interacted with treatment variables; only used if make.twoway=FALSE. maketwoway is useful for generating these.

fit.glmnet Whether to fit using the coordinate descent method in glmnet (TRUE) or the regularization path method of LARS (FALSE).

make.reference Whether to make a reference matrix to check which columns are dropped when makeallway=TRUE.

reference.main If make.allway=FALSE and researchers generate a matrix of all possible interactions between factorial treatments, reference from makeallway function is better to be passed to FindIt through this argument.

threshold An argument passed to makeallway when treat.type="multiple". Threshold to drop correlated columns when makeallway is used.

Details

Implements the alternating line search algorithm for estimating the tuning parameters, as described in Imai and Ratkovic (2013).

Value

coefs A named vector of scaled coefficients
coefs.orig A vector of coefficients on the original scale, if scale.c and scale.t was used
fit Fitted values on an SVM scale
names.out Names of the coefficients
y is A vector of observed outcomes
X.c is A matrix of pre-treatment covariates to be adjusted
X.t is A matrix of treatments and treatment-treatment interactions, or treatment-covariate interactions
GCV is GCV statistic at the minimum
ATE is ATE. When treat.type="single", the estimated ATE. When treat.type="multiple", the estimated treatment effect of each unique treatment combination
lambdas is Tuning parameters used for the fit
reference is Reference shows which columns are kept and dropped.

Author(s)
Naoki Egami, Marc Ratkovic and Kosuke Imai.

References

Examples

```
# Example 1: Treatment-Covariate Interaction
# The model includes a treatment variable,
# nine covariates to be interacted with the treatment variable,
# and the same nine covariates to be adjusted.

# Not run:

# Run to find the LASSO parameters
F1 <- findIt(model.treat= outcome ~ treat,
              model.main= ~ age+educ+black+hisp+white+
                          marr+nodegr+log.re75+u75,
              model.int= ~ age+educ+black+hisp+white+
                          marr+nodegr+log.re75+u75,
              data = LaLonde,
              type="binary",
              treat.type="single")
```

```
# Example 1: Treatment-Main Effects

```r
findit(model.treat = outcome ~ treat, 
  model.main = ~ age+educ+black+hisp+white+
                 marr+nodegr+log.re75+u75, 
  model.int = ~ age+educ+black+hisp+white+
              marr+nodegr+log.re75+u75, 
  data = Lalonde, 
  type="binary", 
  treat.type="single", 
  search.lambdas=FALSE, 
  lambdas = c(-3.8760,-4.0025) )
```

summary(F1)

# Returns all the estimated treatment effects.
```r
pred1 <- predict(F1)
```

# Visualize all the estimated treatment effects.
```r
plot(pred1)
```

# Example 2: Treatment-Treatment Interaction

```r
data(GerberGreen)
```

# The model includes four factorial treatments and
# all two, three, four-way interactions between them.
# Four pre-treatment covariates are adjusted.

# Run to search for lambdas.
```r
f2 <- findit(model.treat = voted98 ~ persngrp+phnscript+mailings+appeal, 
              nway=4, 
              model.main = ~ age+majorpty+vot96.1+vot96.0, 
              data = GerberGreen, 
              type="binary", 
              treat.type="multiple")
```

# Fit, given selected lambdas.
```r
f2 <- findit(model.treat = voted98 ~ persngrp+phnscript+mailings+appeal, 
              nway=4, 
              model.main = ~ age+majorpty+vot96.1+vot96.0, 
              data = GerberGreen, 
              type="binary", 
```
# Returns coefficient estimates.
summary(f2)

# Returns predicted values for unique treatment combinations.
pred2 <- predict(f2, unique=TRUE)
# Top 10
head(pred2$data, n=10)
# Bottom 10
tail(pred2$data, n=10)

## Visualize predicted values for each treatment combination.
plot(pred2)

## End (Not run)

# Example 3: Conjoint Analysis. Causal Interaction.

# The SVM classifier with a lasso constraint is estimated.
# The model includes all three-way and two-way interactions as well as main effects of five factorial treatments.

## Run to search for lambdas.
F.conjoint <- findIt(model = outcome ~ Education + Gender + Origin + Experience + Plans, nway=3, data = Immigration, type = "binary", treat.type = "multiple")

## Make the full factorial design matrix as the target population.
full <- full.FindIt(F.conjoint)

## Compute the predicted potential outcomes for the target population.
Unifdata <- predict(F.conjoint, newdata=full, sort=FALSE)$data

## End (Not run)
## Load pre-computed F.conjoint and Unifdata
data(F.conjoint)
data(Unifdata)

## Compute AMTEs, ATCEs, and AMTIEs

## Range of each factor interaction.
## The range of the AMTEs for all factors
full.FindIt

Generating the full factorial design matrix for a FindIt output

Description

full.FindIt takes an output object from FindIt and returns the full factorial design matrix for factorial treatments in the data used to fit the model.

Usage

full.FindIt(object)

Arguments

object An output object from FindIt.

Value

full A full factorial design matrix for factorial treatments in the data used to fit the model.
**Author(s)**

Naoki Egami, Marc Ratkovic and Kosuke Imai.

**Examples**

```
## See the help page for findIt() for an example.
```

---

**GerberGreen**

*Data from the 1998 New Haven Get-Out-the-Vote Experiment*

**Description**

This data set contains the most recent corrected data from the field experiment analyzed in Gerber and Green (2000).

**Usage**

data

**Format**

A data frame consisting of 9 columns and 29,380 observations.

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Description</th>
<th>Levels</th>
</tr>
</thead>
<tbody>
<tr>
<td>voted98</td>
<td>integer</td>
<td>voted in 1998</td>
<td>0,1</td>
</tr>
<tr>
<td>persngrp</td>
<td>factor</td>
<td>personal contact attempted</td>
<td>0,1</td>
</tr>
<tr>
<td>phnscrpt</td>
<td>factor</td>
<td>script read to phone respondents</td>
<td>7 levels</td>
</tr>
<tr>
<td>mailings</td>
<td>factor</td>
<td>number of mailings sent</td>
<td>0 - 3</td>
</tr>
<tr>
<td>appeal</td>
<td>factor</td>
<td>content of message</td>
<td>3 levels</td>
</tr>
<tr>
<td>age</td>
<td>integer</td>
<td>age of respondent</td>
<td></td>
</tr>
<tr>
<td>majorpty</td>
<td>factor</td>
<td>Democratic or Republican</td>
<td></td>
</tr>
<tr>
<td>voted96.1</td>
<td>factor</td>
<td>voted in 1996</td>
<td>0,1</td>
</tr>
<tr>
<td>voted96.0</td>
<td>factor</td>
<td>abstained in 1996</td>
<td>0,1</td>
</tr>
</tbody>
</table>

Note: The levels of phnscrpt and appeal are follows.

- phnscrpt: Script read to phone respondents
  - 0: No phone
  - 1: Civic-Blood
  - 2: Civic
  - 3: Civic or Blood-Civic
  - 4: Neighbor
  - 5: Neighbor or Civic-Neighbor
  - 6: Close
appeal: Content of message

1. Civic Duty
2. Neighborhood Solidarity
3. Close Election

References


Description

This data set gives the outcomes as well as treatment assignments the conjoint analysis in Hainmueller and Hopkins (2014) and Hainmueller, Hopkins and Yamamoto (2014).

Usage
data

Format

A data frame consisting of 6 columns and 6980 observations (5 profiles for each 1396 respondents).

<table>
<thead>
<tr>
<th>outcome</th>
<th>integer</th>
<th>whether a profile is chosen</th>
<th>0,1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Education</td>
<td>factor</td>
<td>education</td>
<td>7 levels</td>
</tr>
<tr>
<td>Gender</td>
<td>factor</td>
<td>gender</td>
<td>male or female</td>
</tr>
<tr>
<td>Origin</td>
<td>factor</td>
<td>origin</td>
<td>10 levels</td>
</tr>
<tr>
<td>Experience</td>
<td>factor</td>
<td>job experience</td>
<td>4 levels</td>
</tr>
<tr>
<td>Plans</td>
<td>factor</td>
<td>job plans</td>
<td>4 levels</td>
</tr>
</tbody>
</table>

Source

Data from the conjoint analysis in Hainmueller and Hopkins (2014) and Hainmueller, Hopkins and Yamamoto (2014). Because of pairings, we randomly select one profile within each pair and define a binary outcome variable for that pair, which is equal to 1 if this profile is chosen and to 0 if the other profile is selected. Columns contain 5 factors from the original conjoint analysis. The details of levels of each factor are described in Hainmueller and Hopkins (2014) and Egami and Imai (2015).
References


Examples

```r
# Conjoint Analysis: Causal Interaction.

data(immigration)

# The SVM classifier with a lasso constraint is estimated.
# The model includes all three-way and two-way interactions as
# well as main effects of five factorial treatments.

# Run to search for lambdas.
F.conjoint <- findit(model.treat = outcome ~
                      Education + Gender + Origin + Experience + Plans,
                      nway = 3,
                      data = immigration,
                      type = "binary",
                      treat.type = "multiple")

# Make the full factorial design matrix as the target population.
full <- fullFindit(F.conjoint)

# Compute the predicted potential outcomes for the target population.
Unifdata <- predict(F.conjoint, newdata = full, sort = FALSE)$data

# Compute AMTEs, ATCEs, and AMTEs

# Range of each factor interaction.
# The range of the AMTEs for all factors
compare1 <- int(F.conjoint, target.data = Unifdata, compare = TRUE, order = 1)
```

Estimating the AMTE, the ATCE and the AMTIE

### Description
Estimating the average marginal treatment effect (AMTE), the average treatment combination effect (ATCE) and the average marginal treatment interaction effect (AMTIE) under the assumption of independently randomized factorial treatments. Researchers need to change the baseline condition by relevel the target.data.

### Usage
```r
INT(object, target.data, column, dist = "target", base, 
    sort = TRUE, compare = FALSE, order = 2)
```

### Arguments
- **object**: An output object from FindIt.
- **target.data**: If dist= "target", this data is used to compute the AMTEs, ATCEs and AMTIEs. This data should represent the target population in terms of the treatment distribution and samples. The first column contains outcome variables and the other columns should be factorial treatments of interest.
column Researchers can explore the AMTIEs within any factor interactions by specifying the names of factors through this argument.

dist If dist="target", INT computes the AMTEs, ATCEs and AMTIEs for the target population specified by target.data. If dist="sample", it computes them for the data used to fit the model. If dist="unique", it computes them for the unique samples in the data used to fit the model.

base An optional argument that specifies the baseline condition. This argument can be used only when column is used, and the order of base should follow the order of column.

sort If sort=TRUE, the AMTE, the ATCE and the AMTIE are sorted in descending order.

compare If compare=TRUE, INT computes the range of all factor interactions of the order specified with order. Researchers can identify the most important factor interaction for the specified order.

order INT computes the ATCEs and AMTIEs of this order. Can be 2 or 3.

Details

INT estimates the AMTEs, ATCEs and AMTIEs under the assumption of independently randomized factorial treatments.

Value

<table>
<thead>
<tr>
<th>Key</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Range of AMTIE</td>
<td>The range of the estimated AMTIEs</td>
</tr>
<tr>
<td>AMTIE</td>
<td>Estimated AMTIEs for treatment combinations</td>
</tr>
<tr>
<td>ATCE</td>
<td>Estimated ATCEs and AMTIEs for treatment combina-</td>
</tr>
<tr>
<td>Sum of AMTEs</td>
<td>Sum of the estimated AMTEs of each factor and AMTIEs for treatment combinations</td>
</tr>
</tbody>
</table>

Author(s)

Naoki Egami, Marc Ratkovic and Kosuke Imai.

References


Examples

```
# Conjoint Analysis: Causal Interaction.

data(Immigration)
```
## Not run:
## The SVM classifier with a lasso constraint is estimated.
## The model includes all three-way and two-way interactions as
## well as main effects of five factorial treatments.

## Run to search for lambdas.
F.conjoint <- findit(model.treat = outcome ~
                     Education + Gender + Origin + Experience + Plans,
                     nway = 3,
                     data = Immigration,
                     type = "binary",
                     treat.type = "multiple")

## Make the full factorial design matrix as the target population.
full <- full.findit(F.conjoint)

## Compute the predicted potential outcomes for the target population.
Unifdata <- predict(F.conjoint, newdata = full, sort = FALSE)$data

## End(Not run)
## load pre-computed F.conjoint and Unifdata
data(F.conjoint)
data(Unifdata)

## Compute AMTEs, ATCEs, and AMTIEs

## Range of each factor interaction.
## The range of the AMTEs for all factors
compare1 <- INT(F.conjoint, target.data = Unifdata, compare = TRUE, order = 1)

## The range of the two-way AMTIEs for all two-way factor interactions
compare2 <- INT(F.conjoint, target.data = Unifdata, compare = TRUE, order = 2)

## Not run:
## The range of the three-way AMTIEs for all three-way factor interactions
compare3 <- INT(F.conjoint, target.data = Unifdata, compare = TRUE, order = 3)

## End(Not run)

## Compute AMTIEs within factor interactions.
## Origin x Experience
out.OP <- INT(F.conjoint, target.data = Unifdata,
              column = c("Origin", "Experience"),
              base = c("India", "No. job"), order = 2)
out.OP

## Not run:
## Education x Gender x Origin
out.EGO <- INT(F.conjoint, target.data = Unifdata,
Description

This data set gives the outcomes as well as treatment assignments and covariates for the National Supported Work Study, as analyzed in LaLonde (1986).

Usage

data

Format

A data frame consisting of 12 columns (including a treatment assignment vector) and 2787 observations.

<table>
<thead>
<tr>
<th>Name</th>
<th>Role</th>
<th>Description</th>
<th>0,1</th>
</tr>
</thead>
<tbody>
<tr>
<td>outcome</td>
<td>integer</td>
<td>whether earnings in 1978 are larger than in 1975</td>
<td></td>
</tr>
<tr>
<td>treat</td>
<td>integer</td>
<td>whether the individual received the treatment</td>
<td></td>
</tr>
<tr>
<td>age</td>
<td>numeric</td>
<td>age in years</td>
<td></td>
</tr>
<tr>
<td>educ</td>
<td>numeric</td>
<td>education in years</td>
<td></td>
</tr>
<tr>
<td>black</td>
<td>factor</td>
<td>black or not</td>
<td></td>
</tr>
<tr>
<td>hisp</td>
<td>factor</td>
<td>hispanic or not</td>
<td></td>
</tr>
<tr>
<td>white</td>
<td>factor</td>
<td>white or not</td>
<td></td>
</tr>
<tr>
<td>marr</td>
<td>factor</td>
<td>married or not</td>
<td></td>
</tr>
<tr>
<td>nodegr</td>
<td>factor</td>
<td>an indicator for no high school degree</td>
<td></td>
</tr>
<tr>
<td>log.re75</td>
<td>numeric</td>
<td>log of earnings in 1975</td>
<td></td>
</tr>
<tr>
<td>u75</td>
<td>factor</td>
<td>unemployed in 1975</td>
<td></td>
</tr>
<tr>
<td>wts.extrap</td>
<td>numeric</td>
<td>extrapolation weights to the 1978 Panel Study for Income Dynamics dataset</td>
<td></td>
</tr>
</tbody>
</table>

Source

Data from the National Supported Work Study. A benchmark matching dataset. 1975 earnings are pre-treatment.

References

makellway

Description

makellway takes a data frame of factors, each denoting a treatment level, and returns a matrix of 0’s and 1’s for all possible interactions. The current version can produce up to four way interactions.

Usage

makellway(X, threshold = 0.999999, deletion = TRUE, make.reference = TRUE, sparse.use = FALSE, nway)

Arguments

- **X**: A matrix of data frame of treatments, each column interpreted as a factor.
- **threshold**: Threshold to drop correlated columns.
- **deletion**: Whether to automatically drop pairwise linearly dependent columns and columns of all 0’s or 1’s.
- **make.reference**: Whether to make a reference matrix to check which columns are dropped when makeallway = TRUE.
- **sparse.use**: Whether to use a sparse matrix or not.
- **nway**: The order of interaction terms. All possible interactions up to this value are computed.

Details

Useful for constructing a matrix for FindIt with type = "multiple". Takes a data frame of factors and returns a design matrix with all possible interactions. A named matrix of 0’s and 1’s, for every possible interaction, is returned. Pairwise linearly dependent columns and columns of all 0’s or 1’s are eliminated.

Value

- **FinalData**: A named matrix of 0’s and 1’s.
- **reference**: A matrix that keeps track of all columns and shows which columns are dropped.

Author(s)

Naoki Egami, Marc Ratkovic and Kosuke Imai.

Examples

#See the help page for FindIt() for an example.
maketwoway

**Constructing a named matrix of all two-way interactions.**

**Description**

`maketwoway` takes a set of pre-treatment covariates and returns all sensible two-way interactions.

**Usage**

```r
maketwoway(X, wts = 1, center = TRUE, deletion = TRUE, threshold = 0.99999, frame.meanPre, predict = FALSE)
```

**Arguments**

- `X` A matrix of pre-treatment covariates.
- `wts` An optional set of extrapolation weights.
- `center` Whether the columns should be centered before interacting.
- `deletion` Whether to automatically drop pairwise linearly dependent columns and columns of all 0’s or 1’s.
- `threshold` Threshold to drop correlated columns.
- `frame.meanPre` An argument to use when `maketwoway` is called within `predict.FindIt`.
- `predict` An argument to use when `maketwoway` is called within `predict.FindIt`.

**Details**

Useful for constructing a matrix for `FindIt`. Takes a matrix and returns a matrix of two-way interactions. A named matrix with an intercept, all two-way interactions and square terms are returned. If `center=TRUE`, interactions are formed by (1) centering, (2) scaling to sd 1, and (3) interacting. Non-sensible interactions, such as interacting dummy variables for male and female, as well as squared terms for dummy variables, are not returned. A rescaling vector is returned, so that the columns of the standardized matrix can be returned to their original scale.

**Value**

- `X` A matrix with all linear terms, squared terms, and two-way interactions from the original matrix.
- `scale.X` A vector of weights for reutrning X to its original scale.

**Author(s)**

Naoki Egami, Marc Ratkovic and Kosuke Imai.

**Examples**

```
#See the help page for FindIt() for an example.
```
plot.PredictFindIt

Plot estimated treatment effects or predicted outcomes for each treatment combination.

Description

Plot estimated treatment effects when treat.type="single" and predicted outcomes for each treatment combination when treat.type="multiple".

Usage

```r
## S3 method for class 'PredictFindIt'
plot(x, main, xlab, ylab, ...)
```

Arguments

- `x`: output from predict.FindIt.
- `main`: the argument specifying the main title of the plot.
- `xlab`: the argument specifying the name of x axis.
- `ylab`: the argument specifying the name of y axis.
- `...`: further arguments passed to or from other methods.

Details

Plot estimated treatment effects when treat.type="single" and predicted outcomes for each treatment combination when treat.type="multiple".

Value

- `plot`: Plot estimated treatment effects when treat.type="single" and predicted outcomes for each treatment combination when treat.type="multiple".

Author(s)

Naoki Egami, Marc Ratkovic and Kosuke Imai.

Examples

```r
## See the help page for FindIt() for an example.
```
predict.FindIt  

Computing predicted values for each sample in the data.

Description

predict.FindIt takes an output from FindIt and returns estimated treatment effects when `treat.type="single"` and predicted outcomes for each treatment combination when `treat.type="multiple"`.

Usage

```r
## S3 method for class 'FindIt'
predict(object, newdata, sort = TRUE, decreasing = TRUE,
        wts = 1, unique = FALSE, ...)
```

Arguments

- **object**: An output object from FindIt.
- **newdata**: An optional data frame in which to look for variables with which to predict. If omitted, the data used in FindIt is used.
- **sort**: Whether to sort samples according to estimated treatment effects.
- **decreasing**: When sort=TRUE, whether to sort the output in descending order or not.
- **wts**: Weights.
- **unique**: If unique=TRUE, predict returns estimated treatment effects or predicted outcomes for unique samples.
- **...**: further arguments passed to or from other methods.

Details

Useful for computing estimated treatment effects or predicted outcomes for each treatment combination. By using newdata, researchers can compute them for any samples.

Value

- **data**: A matrix of estimated treatment effects when `treat.type="single"` and predicted outcomes for each treatment combination when `treat.type="multiple"`.

Author(s)

Naoki Egami, Marc Ratkovic and Kosuke Imai.

Examples

```r
## See the help page for FindIt() for an example.
```
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