

Package ‘FindIt’

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Title Finding Heterogeneous Treatment Effects

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lmtest, stats, graphics, utils, limSolve

Description The heterogeneous treatment effect estimation procedure proposed by Imai and Ratkovic (2013)<[DOI:10.1214/12-AOAS593](https://doi.org/10.1214/12-AOAS593)>. 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 a class of functions, CausalANOVA, which estimates the average marginal interaction effects (AMIEs) by a regularized ANOVA as proposed by Egami and Imai (2019)<[DOI:10.1080/01621459.2018.1476246](https://doi.org/10.1080/01621459.2018.1476246)>. It contains a variety of regularization techniques to facilitate analysis of large factorial experiments.

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LazyData yes

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FindIt-package

FindIt: Finding Heterogeneous Treatment Effects

Description

Package: factorEx
 Type: Package
 Version: 1.1.5
 Date: 2019-11-19

Author(s)

Naoki Egami, Marc Ratkovic and Kosuke Imai.

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References

Imai, Kosuke and Marc Ratkovic. 2013. “Estimating Treatment Effect Heterogeneity in Randomized Program Evaluation.” *Annals of Applied Statistics*, Vol.7, No.1(March), pp. 443-470. <http://imai.fas.harvard.edu/research/files/svm.pdf>

Egami, Naoki and Kosuke Imai. 2019. Causal Interaction in Factorial Experiments: Application to Conjoint Analysis. *Journal of the American Statistical Association*, Vol.114, No.526 (June), pp. 529–540. <http://imai.fas.harvard.edu/research/files/int.pdf>

Carlson

Data from conjoint analysis in Carlson (2015).

Description

This data set gives the outcomes as well as treatment assignments of the conjoint analysis in Carlson (2015). Please Carlson (2015) and Egami and Imai (2019) for more details.

Format

A data frame consisting of 7 columns (including a treatment assignment vector) and 3232 observations.

outcome	integer	whether a profile is chosen	0,1
newRecordF	factor	record as a politician	7 levels
promise	factor	platform	3 levels (job, clinic, education)
coeth_voting	factor	whether a profile is coethnic to a respondent	Yes, No
Degree	factor	job whether a profile has relevant degrees	4 Yes, No

Source

Data from Carlson (2015).

References

Carlson, E. 2015. “Ethnic voting and accountability in africa: A choice experiment in uganda.” *World Politics* 67, 02, 353–385.

Description

CausalANOVA estimates coefficients of the specified ANOVA with regularization. By taking differences in coefficients, the function recovers the AMEs and AMIEs.

Usage

```
CausalANOVA(
  formula,
  int2.formula = NULL,
  int3.formula = NULL,
  data,
  nway = 1,
  pair.id = NULL,
  diff = FALSE,
  screen = FALSE,
  screen.type = "fixed",
  screen.num.int = 3,
  collapse = FALSE,
  collapse.type = "fixed",
  collapse.cost = 0.3,
  family = "binomial",
  cluster = NULL,
  maxIter = 50,
  eps = 1e-05,
  fac.level = NULL,
  ord.fac = NULL,
  select.prob = FALSE,
  boot = 100,
  seed = 1234,
  verbose = TRUE
)
```

Arguments

<code>formula</code>	A formula that specifies outcome and treatment variables.
<code>int2.formula</code>	(optional). A formula that specifies two-way interactions.
<code>int3.formula</code>	(optional). A formula that specifies three-way interactions.
<code>data</code>	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 'CausalANOVA' is called.

<code>nway</code>	With <code>nway=1</code> , the function estimates the Average Marginal Effects (AMEs) only. With <code>nway=2</code> , the function estimates the AMEs and the two-way Average Marginal Interaction Effects (AMIEs). With <code>nway=3</code> , the function estimates the AMEs, the two-way and three-way AMIEs. Default is 1.
<code>pair.id</code>	(optional). Unique identifiers for each pair of comparison. This option is used when <code>diff=TRUE</code> .
<code>diff</code>	A logical indicating whether the outcome is the choice between a pair. If <code>diff=TRUE</code> , <code>pair.id</code> should specify a pair of comparison. Default is <code>FALSE</code> .
<code>screen</code>	A logical indicating whether select significant factor interactions with <code>glinternet</code> . When users specify interactions using <code>int2.formula</code> or <code>int3.formula</code> , this option is ignored. <code>screen</code> should be used only when users want data-driven selection of factor-interactions. With <code>screen.type</code> , users can specify how to screen factor interactions. We recommend to use this option when the number of factors is large, e.g., more than 6. Default is <code>FALSE</code> .
<code>screen.type</code>	Type for screening factor interactions. (1) "fixed" select the fixed number (specified by <code>screen.num.int</code>) of factor interactions. (2) "cv.min" selects factor-interactions with the tuning parameter giving the minimum cross-validation error. (3) "cv.1Std" selects factor-interactions with the tuning parameter giving a cross-validation error that is within 1 standard deviation of the minimum cv error.
<code>screen.num.int</code>	(optional). The number of factor interactions to select. This option is used when and <code>screen=TRUE</code> and <code>screen.type="fixed"</code> . Default is 3.
<code>collapse</code>	A logical indicating whether to collapse insignificant levels within factors. With <code>collapse.type</code> , users can specify how to collapse levels within factors. We recommend to use this option when the number of levels is large, e.g., more than 6. Default is <code>FALSE</code> .
<code>collapse.type</code>	Type for collapsing levels within factors. (1) "fixed" collapses levels with the fixed cost parameter (specified by <code>collapse.cost</code>). (2) "cv.min" collapses levels with the cost parameter giving the minimum cross-validation error. This option might take time. (3) "cv.1Std" collapses with the cost parameter giving a cross-validation error that is within 1 standard deviation of the minimum cv error. This option might take time.
<code>collapse.cost</code>	(optional). A cost parameter ranging from 0 to 1. 1 corresponds to no collapsing. The closer to 0, the stronger regularization. Default is 0.3.
<code>family</code>	A family of outcome variables. "gaussian" when continuous outcomes "binomial" when binary outcomes. Default is "binomial".
<code>cluster</code>	Unique identifies with which cluster standard errors are computed.
<code>maxIter</code>	The number of maximum iteration for <code>glinternet</code> .
<code>eps</code>	A tolerance parameter in the internal optimization algorithm.
<code>fac.level</code>	(optional). A vector containing the number of levels in each factor. The order of <code>fac.level</code> should match to the order of columns in the data. For example, when the first and second columns of the design matrix is "Education" and "Race", the first and second element of <code>fac.level</code> should be the number of levels in "Education" and "Race", respectively.

<code>ord.fac</code>	(optional). Logical vectors indicating whether each factor has ordered (TRUE) or unordered (FALSE) levels. When levels are ordered, the function uses the order given by function <code>levels()</code> . If levels are ordered, the function places penalties on the differences between adjacent levels. If levels are unordered, the function places penalties on the differences based on every pairwise comparison.
<code>select.prob</code>	(optional). A logical indicating whether selection probabilities are computed. This option might take time.
<code>boot</code>	The number of bootstrap replicates for <code>select.prob</code> . Default is 50.
<code>seed</code>	Seed for bootstrap.
<code>verbose</code>	Whether it prints the value of a cost parameter used.

Details

Regularization: screen and collapse.

Users can implement regularization in order to reduce false discovery rate and facilitate interpretation. This is particularly useful when analyzing factorial experiments with a large number of factors, each having many levels.

- When `screen=TRUE`, the function selects significant factor interactions with `glinternet` (Lim and Hastie 2015) before estimating the AMEs and AMIEs. This option is recommended when there are many factors, e.g., more than 6 factors. Alternatively, users can pre-specify interactions of interest using `int2.formula` and `int3.formula`.
- When `collapse=TRUE`, the function collapses insignificant levels within each factor by `GashANOVA` (Post and Bondell 2013) before estimating the AMEs and AMIEs. This option is recommended when there are many levels within some factors, e.g., more than 6 levels.

Inference after Regularization:

- When `screen=TRUE` or `collapse=TRUE`, in order to make valid inference after regularization, we recommend to use `test.CausalANOVA` function. It takes the output from `CausalANOVA` function and estimates the AMEs and AMIEs with `newdata` and provides confidence intervals. Ideally, users should split samples into two; use a half for regularization with `CausalANOVA` function and use the other half for inference with `test.CausalANOVA`.
- If users do not need regularization, specify `screen=FALSE` and `collapse=FALSE`. The function estimates the AMEs and AMIEs and computes confidence intervals with the full sample.

Suggested Workflow: (See Examples below as well)

1. Specify the order of levels within each factor using `levels()`. When `collapse=TRUE`, the function places penalties on the differences between adjacent levels when levels are ordered, it is crucial to specify the order of levels within each factor carefully.
2. Run `CausalANOVA`.
 - (a) Specify `formula` to indicate outcomes and treatment variables and `nway` to indicate the order of interactions.
 - (b) Specify `diff=TRUE` and `pair.id` if the outcome is the choice between a pair.
 - (c) Specify `screen`. `screen=TRUE` to implement data-driven selection of factor interactions. `screen=FALSE` to specify interactions through `int2.formula` and `int3.formula` by hand.


```

Carlson$promise <- factor(Carlson$promise,ordered=TRUE,levels=c("jobs","clinic","education"))
Carlson$coeth_voting <- factor(Carlson$coeth_voting,ordered=FALSE,levels=c("0","1"))
Carlson$relevantdegree <- factor(Carlson$relevantdegree,ordered=FALSE,levels=c("0","1"))

## #####
## Without Screening and Collapsing
## #####
##### only AMEs #####
fit1 <- CausalANOVA(formula=won ~ newRecordF + promise + coeth_voting + relevantdegree,
                    data=Carlson, pair.id=Carlson$contestresp, diff=TRUE,
                    cluster=Carlson$respcodes, nway=1)

summary(fit1)
plot(fit1)

##### AMEs and two-way AMIEs #####
fit2 <- CausalANOVA(formula=won ~ newRecordF + promise + coeth_voting + relevantdegree,
                    int2.formula = ~ newRecordF:coeth_voting,
                    data=Carlson, pair.id=Carlson$contestresp,diff=TRUE,
                    cluster=Carlson$respcodes, nway=2)

summary(fit2)
plot(fit2, type="ConditionalEffect", fac.name=c("newRecordF","coeth_voting"))
ConditionalEffect(fit2, treat.fac="newRecordF", cond.fac="coeth_voting")

## Not run:
##### AMEs and two-way and three-way AMIEs #####
## Note: All pairs within thee-way interactions should show up in int2.formula (Strong Hierarchy).
fit3 <- CausalANOVA(formula=won ~ newRecordF + promise + coeth_voting + relevantdegree,
                    int2.formula = ~ newRecordF:promise + newRecordF:coeth_voting
                    + promise:coeth_voting,
                    int3.formula = ~ newRecordF:promise:coeth_voting,
                    data=Carlson, pair.id=Carlson$contestresp,diff=TRUE,
                    cluster=Carlson$respcodes, nway=3)

summary(fit3)
plot(fit3, type="AMIE", fac.name=c("newRecordF","promise","coeth_voting"),space=25,adj.p=2.2)

## End(Not run)

## #####
## With Screening and Collapsing
## #####
## Sample Splitting
train.ind <- sample(unique(Carlson$respcodes), 272, replace=FALSE)
test.ind <- setdiff(unique(Carlson$respcodes), train.ind)
Carlson.train <- Carlson[is.element(Carlson$respcodes,train.ind), ]
Carlson.test <- Carlson[is.element(Carlson$respcodes,test.ind), ]

##### AMEs and two-way AMIEs #####
fit.r2 <- CausalANOVA(formula=won ~ newRecordF + promise + coeth_voting + relevantdegree,
                    data=Carlson.train, pair.id=Carlson.train$contestresp,diff=TRUE,
                    screen=TRUE, collapse=TRUE,
                    cluster=Carlson.train$respcodes, nway=2)

summary(fit.r2)

```



```
## refit with test.CausalANOVA
fit.r2.new <- test.CausalANOVA(fit.r2, newdata=Carlson.test, diff=TRUE,
                              pair.id=Carlson.test$contestresp, cluster=Carlson.test$respcodes)

summary(fit.r2.new)
plot(fit.r2.new)
plot(fit.r2.new, type="ConditionalEffect", fac.name=c("newRecordF","coeth_voting"))
ConditionalEffect(fit.r2.new, treat.fac="newRecordF", cond.fac="coeth_voting")
```

ConditionalEffect *Estimating the Conditional Effects with the CausalANOVA.*

Description

ConditionalEffect estimates a variety of conditional effects using the output from CausalANOVA.

Usage

```
ConditionalEffect(
  object,
  treat.fac = NULL,
  cond.fac = NULL,
  base.ind = 1,
  round = 3,
  inference = NULL,
  verbose = TRUE
)
```

Arguments

object	The output from CausalANOVA function.
treat.fac	The name of factor acting as the main treatment variable.
cond.fac	The name of factor acting as the conditioning (moderating) variable.
base.ind	An indicator for the baseline of the treatment factor. Default is 1.
round	Digits to round estimates. Default is 3.
inference	(optional). This argument is mainly for internal use. It indicates whether CausalANOVA has done inference or not.
verbose	Whether it prints the progress.

Details

See Details in CausalANOVA.

Value

ConditionalEffects
 The summary of estimated conditional effects.
 ... Arguments for the internal use.

Author(s)

Naoki Egami and Kosuke Imai.

References

Egami, Naoki and Kosuke Imai. 2019. Causal Interaction in Factorial Experiments: Application to Conjoint Analysis, Journal of the American Statistical Association. <http://imai.fas.harvard.edu/research/files/int.pdf>

Lim, M. and Hastie, T. 2015. Learning interactions via hierarchical group-lasso regularization. Journal of Computational and Graphical Statistics 24, 3, 627–654.

Post, J. B. and Bondell, H. D. 2013. “Factor selection and structural identification in the interaction anova model.” Biometrics 69, 1, 70–79.

See Also

[CausalANOVA](#).

Examples

```
data(Carlson)
## Specify the order of each factor
Carlson$newRecordF<- factor(Carlson$newRecordF,ordered=TRUE,
                           levels=c("YesLC", "YesDis", "YesMP",
                                     "noLC", "noDis", "noMP", "noBusi"))
Carlson$promise <- factor(Carlson$promise,ordered=TRUE,levels=c("jobs", "clinic", "education"))
Carlson$coeth_voting <- factor(Carlson$coeth_voting,ordered=FALSE,levels=c("0", "1"))
Carlson$relevantdegree <- factor(Carlson$relevantdegree,ordered=FALSE,levels=c("0", "1"))

## #####
## Without Screening and Collapsing
## #####
##### AMEs and two-way AMIEs #####
fit2 <- CausalANOVA(formula=won ~ newRecordF + promise + coeth_voting + relevantdegree,
                    int2.formula = ~ newRecordF:coeth_voting,
                    data=Carlson, pair.id=Carlson$contestresp,diff=TRUE,
                    cluster=Carlson$respcodeS, nway=2)

summary(fit2)
plot(fit2, type="ConditionalEffect", fac.name=c("newRecordF", "coeth_voting"))
ConditionalEffect(fit2, treat.fac="newRecordF", cond.fac="coeth_voting")
```

cv.CausalANOVA	<i>Cross validation for the CausalANOVA.</i>
----------------	--

Description

cv.CausalANOVA implements cross-validation for CausalANOVA to select the collapse.cost parameter. CausalANOVA runs this function internally when defaults when collapse.type=cv.min or collapse.type=cv.1Std.

Usage

```
cv.CausalANOVA(
  formula,
  int2.formula = NULL,
  int3.formula = NULL,
  data,
  nway = 1,
  pair.id = NULL,
  diff = FALSE,
  cv.collapse.cost = c(0.1, 0.3, 0.7),
  nfolds = 5,
  screen = FALSE,
  screen.type = "fixed",
  screen.num.int = 3,
  family = "binomial",
  cluster = NULL,
  maxIter = 50,
  eps = 1e-05,
  seed = 1234,
  fac.level = NULL,
  ord.fac = NULL,
  verbose = TRUE
)
```

Arguments

formula	a formula that specifies outcome and treatment variables.
int2.formula	(optional). A formula that specifies two-way interactions.
int3.formula	(optional). A formula that specifies three-way interactions.
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 'CausalANOVA' is called.
nway	With nway=1, the function estimates the Average Marginal Effects (AMEs) only. With nway=2, the function estimates the AMEs and the two-way Average Marginal Interaction Effects (AMIEs). With nway=3, the function estimates the AMEs, the two-way and three-way AMIEs. Default is 1.

<code>pair.id</code>	(optional). Unique identifiers for each pair of comparison. This option is used when <code>diff=TRUE</code> .
<code>diff</code>	A logical indicating whether the outcome is the choice between a pair. If <code>diff=TRUE</code> , <code>pair.id</code> should specify a pair of comparison. Default is <code>FALSE</code> .
<code>cv.collapse.cost</code>	A vector containing candidates for a cost parameter ranging from 0 to 1. 1 corresponds to no regularization and the smaller value corresponds to the stronger regularization. Default is <code>c(0.1, 0.3, 0.7)</code> .
<code>nfolds</code>	number of folds - default is 5. Although <code>nfolds</code> can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets.
<code>screen</code>	A logical indicating whether select significant factor interactions with <code>glinetnet</code> . When users specify interactions using <code>int2.formula</code> or <code>int3.formula</code> , this option is ignored. <code>screen</code> should be used only when users want data-driven selection of factor-interactions. With <code>screen.type</code> , users can specify how to screen factor interactions. We recommend to use this option when the number of factors is large, e.g., more than 6. Default is <code>FALSE</code> .
<code>screen.type</code>	Type for screening factor interactions. (1) "fixed" select the fixed number (specified by <code>screen.num.int</code>) of factor interactions. (2) "cv.min" selects factor-interactions with the tuning parameter giving the minimum cross-validation error. (3) "cv.1Std" selects factor-interactions with the tuning parameter giving a cross-validation error that is within 1 standard deviation of the minimum cv error.
<code>screen.num.int</code>	(optional). The number of factor interactions to select. This option is used when and <code>screen=TRUE</code> and <code>screen.type="fixed"</code> . Default is 3.
<code>family</code>	A family of outcome variables. "gaussian" when continuous outcomes "binomial" when binary outcomes. Default is "binomial".
<code>cluster</code>	Unique identifies with which cluster standard errors are computed.
<code>maxIter</code>	The number of maximum iteration for <code>glinetnet</code> .
<code>eps</code>	A tolerance parameter in the internal optimization algorithm.
<code>seed</code>	an argument for <code>set.seed()</code> .
<code>fac.level</code>	optional. A vector containing the number of levels in each factor. The order of <code>fac.level</code> should match to the order of columns in the data. For example, when the first and second columns of the design matrix is "Education" and "Race", the first and second element of <code>fac.level</code> should be the number of levels in "Education" and "Race", respectively.
<code>ord.fac</code>	optional. logical vectors indicating whether each factor has ordered (<code>TRUE</code>) or unordered (<code>FALSE</code>) levels. When levels are ordered, the function uses the order given by function <code>levels()</code> . If levels are ordered, the function places penalties on the differences between adjacent levels. If levels are unordered, the function places penalties on the differences based on every pairwise comparison.
<code>verbose</code>	whether it prints the value of a cost parameter used.

Details

See Details in `CausalANOVA`.

Value

cv.error	The mean cross-validated error - a vector of length <code>length(cv.t)</code> .
cv.min	A value of <code>t</code> that gives minimum <code>cv.missclass</code> .
cv.1Std	The largest value of <code>t</code> such that error is within 1 standard error of the minimum.
cv.each.mat	A matrix containing cross-validation errors for each fold and cost parameter.
cv.cost	The <code>cv.collapse.cost</code> used in the function.

Author(s)

Naoki Egami and Kosuke Imai.

References

Post, J. B. and Bondell, H. D. 2013. "Factor selection and structural identification in the interaction anova model." *Biometrics* 69, 1, 70–79.

Egami, Naoki and Kosuke Imai. 2019. Causal Interaction in Factorial Experiments: Application to Conjoint Analysis, *Journal of the American Statistical Association*. <http://imai.fas.harvard.edu/research/files/int.pdf>

See Also

[CausalANOVA](#).

Examples

```
data(Carlson)
## Specify the order of each factor
Carlson$newRecordF<- factor(Carlson$newRecordF,ordered=TRUE,
                           levels=c("YesLC", "YesDis", "YesMP",
                                     "noLC", "noDis", "noMP", "noBusi"))
Carlson$promise <- factor(Carlson$promise,ordered=TRUE,levels=c("jobs", "clinic", "education"))
Carlson$coeth_voting <- factor(Carlson$coeth_voting,ordered=FALSE,levels=c("0", "1"))
Carlson$relevantdegree <- factor(Carlson$relevantdegree,ordered=FALSE,levels=c("0", "1"))

## #####
## Collapsing Without Screening
## #####
##### AMEs and two-way AMIEs #####
## We show a very small example for illustration.
## Recommended to use cv.collapse.cost=c(0.1,0.3,0.5) and nfolds=10 in practice.
fit.cv <- cv.CausalANOVA(formula=won ~ newRecordF + promise + coeth_voting + relevantdegree,
                          int2.formula = ~ newRecordF:coeth_voting,
                          data=Carlson, pair.id=Carlson$contestresp,diff=TRUE,
                          cv.collapse.cost=c(0.1,0.3), nfolds=2,
                          cluster=Carlson$respcodeS, nway=2)

fit.cv
```

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.glmnet = TRUE,
  make.reference = TRUE,
  reference.main = NULL,
  threshold = 0.999999
)
```

Arguments

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

	"multiple" is used when treatment-treatment interactions are of interest and <code>treat</code> is a matrix of multiple treatments.
<code>nway</code>	An argument passed to <code>makeallway</code> when <code>treat.type="multiple"</code> . <code>FindIt</code> 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.
<code>search.lambdas</code>	Whether to search for the tuning parameters for the LASSO constraints. If <code>FALSE</code> , <code>lambdas</code> must be supplied.
<code>lambdas</code>	Tuning parameters to be given to <code>FindIt</code> ; only used if <code>search.lambdas=FALSE</code> .
<code>make.twoway</code>	If <code>make.twoway=TRUE</code> , all possible two-way interactions for the pre-treatment covariates specified in <code>model.main</code> and <code>model.int</code> are generated within <code>FindIt</code> . The default is set to be <code>TRUE</code> .
<code>make.allway</code>	If <code>make.allway=TRUE</code> , all possible treatment-treatment interactions for multiple treatments are generated when <code>treat.type="multiple"</code> . Interactions of the order up to the value of <code>nway</code> is computed.
<code>wt</code>	An optional set of scaling weights. The default is 1.
<code>scale.c</code>	A set of weights for recalcing the pre-treatment covariates; only used if <code>make.twoway=FALSE</code> . <code>maketwoway</code> is useful for generating these.
<code>scale.int</code>	A set of weights for recalcing the covariates to be interacted with treatment variables ; only used if <code>make.twoway=FALSE</code> . <code>maketwoway</code> is useful for generating these.
<code>fit.glmnet</code>	Whether to fit using the coordinate descent method in <code>glmnet</code> (<code>TRUE</code>) or the regularization path method of <code>LARS</code> (<code>FALSE</code>).
<code>make.reference</code>	Whether to make a reference matrix to check which columns are dropped when <code>makeallway=TRUE</code> .
<code>reference.main</code>	If <code>make.allway=FALSE</code> and researchers generate a matrix of all possible interactions between factorial treatments, reference from <code>makeallway</code> function is better to be passed to <code>FindIt</code> through this argument.
<code>threshold</code>	An argument passed to <code>makeallway</code> when <code>treat.type="multiple"</code> . Threshold to drop correlated columns when <code>makeallway</code> is used.

Details

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

Value

<code>coefs</code>	A named vector of scaled coefficients
<code>coefs.orig</code>	A vector of coefficients on the original scale, if <code>scale.c</code> and <code>scale.t</code> was used
<code>fit</code>	Fitted values on an SVM scale
<code>names.out</code>	Names of the coefficients
<code>y</code>	A vector of observed outcomes
<code>X.c</code>	A matrix of pre-treatment covariates to be adjusted

X.t	A matrix of treatments and treatment-treatment interactions, or treatment-covariate interactions
GCV	GCV statistic at the minimum
ATE	When <code>treat.type="single"</code> , the estimated ATE. When <code>treat.type="multiple"</code> , the estimated treatment effect of each unique treatment combination
lambdas	Tuning parameters used for the fit
reference	When <code>treat.type="multiple"</code> , after making all interaction terms, columns with no variation or columns perfectly correlated with one of other columns are automatically dropped. <code>reference</code> shows which columns are kept and dropped.

Author(s)

Naoki Egami, Marc Ratkovic and Kosuke Imai.

References

- Imai, Kosuke and Marc Ratkovic. 2013. "Estimating Treatment Effect Heterogeneity in Randomized Program Evaluation." *Annals of Applied Statistics*, Vol.7, No.1(March), pp. 443-470. <http://imai.fas.harvard.edu/research/files/svm.pdf>
- Egami, Naoki and Kosuke Imai. 2019. Causal Interaction in Factorial Experiments: Application to Conjoint Analysis, *Journal of the American Statistical Association*. <http://imai.fas.harvard.edu/research/files/int.pdf>

Examples

```
#####
## Example 1: Treatment-Covariate Interaction
#####
data(LaLonde)

## 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+hispanic+white+
            marr+nodegr+log.re75+u75,
            model.int= ~ age+educ+black+hispanic+white+
            marr+nodegr+log.re75+u75,
            data = LaLonde,
            type="binary",
            treat.type="single")

## End(Not run)

## Fit with uncovered lambda parameters.
```



```

F1 <-FindIt(model.treat= outcome ~ treat,
            model.main= ~ age+educ+black+hispanic+white+
            marr+nodegr+log.re75+u75,
            model.int= ~ age+educ+black+hispanic+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.
pred1 <- predict(F1)
## Top10
head(pred1$data, n=10)
## Bottom 10
tail(pred1$data ,n=10)

## Visualize all the estimated treatment effects.
## Not run:
plot(pred1)

## End(Not run)

#####
## Example 2: Treatment-Treatment Interaction
#####

## Not run:
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.
F2<- FindIt(model.treat= voted98 ~ persngrp+phnscrip+mailings+appeal,
            nway=4,
            model.main= ~ age+majorpty+vote96.1+vote96.0,
            data = GerberGreen,
            type="binary",
            treat.type="multiple")

## Fit, given selected lambdas.
F2<- FindIt(model.treat= voted98 ~ persngrp+phnscrip+mailings+appeal,
            nway=4,
            model.main= ~ age+majorpty+vote96.1+vote96.0,
            data = GerberGreen,
            type="binary",
            treat.type="multiple",
            search.lambdas=FALSE,

```

```

        lambdas=c(-15.000,-6.237))

## 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)

```

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).

Format

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

voted98	integer	voted in 1998	0,1
persngrp	factor	personal contact attempted	0,1
phnscrpt	factor	script read to phone respondents	7 levels
mailings	factor	number of mailings sent	0 - 3
appeal	factor	content of message	3 levels
age	integer	age of respondent	
majorpty	factor	Democratic or Republican	
voted96.1	factor	voted in 1996	0,1
voted96.0	factor	abstained in 1996	0,1

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

- Gerber, A. S. and Green, D. P. 2000 . "The effects of canvassing, telephone calls, and direct mail on voter turnout: A field experiment." *American Political Science Review*, Vol.94, No.3, pp. 653-663.
- Imai, K. 2005 . "Do get-out-the-vote calls reduce turnout?: The importance of statistical methods for field experiments." *American Political Science Review*, Vol.99, No.2, pp. 283-300.

LaLonde

National Supported Work Study Experimental Data

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).

Format

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

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

Source

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

References

LaLonde, R.J. 1986. "Evaluating the econometric evaluations of training programs with experimental data." American Economic Review, Vol.76, No.4, pp. 604-620.

plot.CausalANOVA *Plotting CausalANOVA*

Description

Plotting CausalANOVA

Usage

```
## S3 method for class 'CausalANOVA'
plot(
  x,
  fac.name,
  treat.ind = 1,
  type = "ConditionalEffect",
  space = 15,
  xlim,
  ...
)
```

Arguments

x	An output from CausalANOVA
fac.name	Factor names to plot. Length should be 2.
treat.ind	Which factor serves as the main treatment. Should be 1 (the first element of fac.name) or 2 (the second element of fac.name).
type	What types of effects to plot. Should be one of AME, AMIE and ConditionalEffect.
space	Space on the left side of the plot.
xlim	Range for the x-axis
...	Other graphical parameters

plot.PredictFindIt	<i>Plot estimated treatment effects or predicted outcomes for each treatment combination.</i>
--------------------	---

Description

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

Usage

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

Arguments

<code>x</code>	output from <code>predict.FindIt</code> .
<code>main</code>	the argument specifying the main title of the plot.
<code>xlab</code>	the argument specifying the name of x axis.
<code>ylab</code>	the argument specifying the name of y axis.
<code>interactive</code>	whether to make a plot interactive; default is <code>FALSE</code> .
<code>...</code>	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

<code>plot</code>	Plot estimated treatment effects when <code>treat.type="single"</code> and predicted outcomes for each treatment combination when <code>treat.type="multiple"</code> .
-------------------	--

Author(s)

Naoki Egami, Marc Ratkovic and Kosuke Imai.

Examples

```
## 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

```
## 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 <code>treat.type="single"</code> and predicted outcomes for each treatment combination when <code>treat.type="multiple"</code> .
------	---

Author(s)

Naoki Egami, Marc Ratkovic and Kosuke Imai.

Examples

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

```
summary.CausalANOVA    Summarizing CausalANOVA output
```

Description

Summarizing CausalANOVA output

Usage

```
## S3 method for class 'CausalANOVA'
summary(object, digit = 4, verbose = TRUE, verbose.full = TRUE, ...)
```

Arguments

object	An object from CausalANOVA
digit	the number of digits
verbose	report additional summary results
verbose.full	report full summary results
...	Other parameters

```
summary.FindIt    Summarizing FindIt output
```

Description

Summarizing FindIt output

Usage

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

Arguments

object	An object from FindIt
...	Other parameters

test.CausalANOVA	<i>Estimating the AMEs and AMIEs after Regularization with the CausalANOVA.</i>
------------------	---

Description

test.CausalANOVA estimates the AMEs and AMIEs with confidence intervals after regularization with CausalANOVAfunction.

Usage

```
test.CausalANOVA(
  fit,
  newdata,
  collapse.level = TRUE,
  diff = FALSE,
  pair.id = NULL,
  cluster = NULL
)
```

Arguments

fit	The output from CausalANOVA function.
newdata	A data frame to use for re-estimating the AMEs and AMIEs with confidence intervals.
collapse.level	A logical indicating whether to collapse insignificant levels within factors as suggested by the CausalANOVA output users provide.
diff	A logical indicating whether the outcome is the choice between a pair. If diff=TRUE, pair.id should specify a pair of comparison. Default is FALSE.
pair.id	(optional).Unique identifiers for each pair of comparison. This option is used when diff=TRUE.
cluster	Unique identifies with which cluster standard errors are computed.

Details

See Details in CausalANOVA.

Value

fit	The output of class CausalANOVA.
-----	----------------------------------

Author(s)

Naoki Egami and Kosuke Imai.

References

- Egami, Naoki and Kosuke Imai. 2019. Causal Interaction in Factorial Experiments: Application to Conjoint Analysis, Journal of the American Statistical Association. <http://imai.fas.harvard.edu/research/files/int.pdf>
- Lim, M. and Hastie, T. 2015. Learning interactions via hierarchical group-lasso regularization. Journal of Computational and Graphical Statistics 24, 3, 627–654.
- Post, J. B. and Bondell, H. D. 2013. “Factor selection and structural identification in the interaction anova model.” Biometrics 69, 1, 70–79.

See Also

[CausalANOVA](#).

Examples

```
## #####
## With Screening and Collapsing
## #####
data(Carlson)
## Specify the order of each factor
Carlson$newRecordF<- factor(Carlson$newRecordF,ordered=TRUE,
                           levels=c("YesLC", "YesDis", "YesMP",
                                     "noLC", "noDis", "noMP", "noBusi"))
Carlson$promise <- factor(Carlson$promise,ordered=TRUE,levels=c("jobs", "clinic", "education"))
Carlson$coeth_voting <- factor(Carlson$coeth_voting,ordered=FALSE,levels=c("0", "1"))
Carlson$relevantdegree <- factor(Carlson$relevantdegree,ordered=FALSE,levels=c("0", "1"))

## Sample Splitting
train.ind <- sample(unique(Carlson$respcodesS), 272, replace=FALSE)
test.ind <- setdiff(unique(Carlson$respcodesS), train.ind)
Carlson.train <- Carlson[is.element(Carlson$respcodesS,train.ind), ]
Carlson.test <- Carlson[is.element(Carlson$respcodesS,test.ind), ]

##### AMEs and two-way AMIEs #####
fit.r2 <- CausalANOVA(formula=won ~ newRecordF + promise + coeth_voting + relevantdegree,
                     data=Carlson.train, pair.id=Carlson.train$contestresp,diff=TRUE,
                     screen=TRUE, collapse=TRUE,
                     cluster=Carlson.train$respcodesS, nway=2)

summary(fit.r2)

## refit with test.CausalANOVA
fit.r2.new <- test.CausalANOVA(fit.r2, newdata=Carlson.test, diff=TRUE,
                              pair.id=Carlson.test$contestresp, cluster=Carlson.test$respcodesS)

summary(fit.r2.new)
plot(fit.r2.new)
plot(fit.r2.new, type="ConditionalEffect", fac.name=c("newRecordF", "coeth_voting"))
ConditionalEffect(fit.r2.new, treat.fac="newRecordF", cond.fac="coeth_voting")
```

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