

# Package ‘FindIt’

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**Title** Finding Heterogeneous Treatment Effects

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**Depends** R (>= 3.1.0), arm

**Imports** glmnet, lars, Matrix, quadprog, ggplot2, glinternet, igraph, sandwich, lmtest, stats, graphics, utils

**Suggests** testthat

**Description** The heterogeneous treatment effect estimation procedure proposed by Imai and Ratkovic (2013)<DOI: 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 (2016+). It contains a variety of regularization techniques to facilitate analysis of large factorial experiments.

**LazyLoad** yes

**LazyData** yes

**License** GPL (>= 2)

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Carlson *Data from conjoint analysis in Carlson (2015).*

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### 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 (2016+) 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.probab = FALSE, boot = 100, seed = 1234,
  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.
pair.id	(optional). Unique identifiers for each pair of comparison. This option is used when diff=TRUE.
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.
screen	A logical indicating whether select significant factor interactions with glinternet. When users specify interactions using int2.formula or int3.formula, this option is ignored. screen should be used only when users want data-driven selection of factor-interactions. With screen.type, 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 FALSE.
screen.type	Type for screening factor interactions. (1) "fixed" select the fixed number (specified by screen.num.int) 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.
screen.num.int	(optional).The number of factor interactions to select. This option is used when and screen=TRUE and screen.type="fixed". Default is 3.
collapse	A logical indicating whether to collapse insignificant levels within factors. With collapse.type, 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 FALSE.
collapse.type	Type for collapsing levels within factors. (1) "fixed" collapses levels with the fixed cost parameter (specified by collapse.cost). (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.
collapse.cost	(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.
family	A family of outcome variables. "gaussian" when continuous outcomes "binomial" when binary outcomes. Default is "binomial".
cluster	Unique identifies with which cluster standard errors are computed.
maxIter	The number of maximum iteration for glinternet.
eps	A tolerance parameter in the internal optimization algorithm.
fac.level	(optional). A vector containing the number of levels in each factor. The order of fac.level 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 fac.level should be the number of levels in "Education" and "Race", respectively.
ord.fac	(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 levels(). 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.
select.prob	(optional). A logical indicating whether selection probabilities are computed. This option might take time.
boot	The number of bootstrap replicates for select.prob. Default is 50.
seed	Seed for bootstrap.
verbose	Whether it prints the value of a cost parameter used.

## Details

**Regularization:** screen and collapse.

Users can implement regularization in order to reduces false discovery rate and facilitates 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 `glinetnet` (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 estimate the AMEs and AMIEs with `newdata` and provide 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 compute 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.
  - (d) Specify `collapse`. `collapse=TRUE` to implement data-driven collapsing of insignificant levels. `collapse=FALSE` to use the original number of levels.
3. Run `test.CausalANOVA` when `select=TRUE` or `collapse=TRUE`.
4. Run `summary` and `plot` to explore the AMEs and AMIEs.
5. Estimate conditional effects using `ConditionalEffect` function and visualize them using `plot` function.

#### Value

<code>intercept</code>	An intercept of the estimated ANOVA model. If <code>diff=TRUE</code> , this should be close to 0.5.
<code>formula</code>	The formula used in the function.
<code>coefs</code>	A named vector of coefficients of the estimated ANOVA model.
<code>vcov</code>	The variance-covariance matrix for <code>coefs</code> . Only when <code>select=FALSE</code> and <code>collapse=FALSE</code> .
<code>CI.table</code>	The summary of AMEs and AMIEs with confidence intervals. Only when <code>select=FALSE</code> and <code>collapse=FALSE</code> .

AME	The estimated AMEs with the grand-mean as baselines.
AMIE2	The estimated two-way AMIEs with the grand-mean as baselines.
AMIE3	The estimated three-way AMIEs with the grand-mean as baselines.
...	arguments passed to the function or arguments only for the internal use.

**Author(s)**

Naoki Egami and Kosuke Imai.

**References**

Egami, Naoki and Kosuke Imai. 2016+. Causal Interaction in Factorial Experiments: Application to Conjoint Analysis. Working paper. <http://imai.princeton.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**

[cv.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
## #####
##### 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")

```

**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. 2016+. "Causal Interaction in Factorial Experiments: Application to Conjoint Analysis." Working paper. <http://imai.princeton.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

*Cross validation for the CausalANOVA.*


---

## 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.

<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>'CausalANOVA'</code> 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>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) <code>"fixed"</code> select the fixed number (specified by <code>screen.num.int</code> ) of factor interactions. (2) <code>"cv.min"</code> selects factor-interactions with the tuning parameter giving the minimum cross-validation error. (3) <code>"cv.1Std"</code> 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. <code>"gaussian"</code> when continuous outcomes <code>"binomial"</code> when binary outcomes. Default is <code>"binomial"</code> .
<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 <code>"Education"</code> and <code>"Race"</code> , the first and second element of <code>fac.level</code> should be the number of levels in <code>"Education"</code> and <code>"Race"</code> , respectively.

ord.fac	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.
verbose	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. 2016+. "Causal Interaction in Factorial Experiments: Application to Conjoint Analysis." Working paper. <http://imai.princeton.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**

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.

<code>search.lambdas</code>	Whether to search for the tuning parameters for the LASSO constraints. If FALSE, <code>lambdas</code> must be supplied.
<code>lambdas</code>	Tuning parameters to be given to FindIt; 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 FindIt. The default is set to be TRUE.
<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>wts</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> (TRUE) or the regularization path method of LARS (FALSE).
<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 FindIt 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
<code>X.t</code>	A matrix of treatments and treatment-treatment interactions, or treatment-covariate interactions
<code>GCV</code>	GCV statistic at the minimum
<code>ATE</code>	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.princeton.edu/research/files/svm.pdf>
- Egami, Naoki and Kosuke Imai. 2015. "Causal Interaction in High-Dimension." Working paper. <http://imai.princeton.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
phnsrpt	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 phnsrpt and appeal are follows.

phnsrpt: 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.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, ...)
```

### 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>...</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.
```

---

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. 2016+. "Causal Interaction in Factorial Experiments: Application to Conjoint Analysis." Working paper. <http://imai.princeton.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$respcodes), 272, replace=FALSE)
test.ind <- setdiff(unique(Carlson$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")
```

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