

Package ‘causalreg’

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Title Causal Generalized Linear Models

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Description An implementation of methods for causal discovery in a structural causal model where the conditional distribution of the target node is described by a generalized linear model conditional on its causal parents.

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Imports mgcv

NeedsCompilation no

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cgam	<i>Causal generalized additive model</i>
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Description

This function does a search for a causal submodel within the generalized additive model provided.

Usage

```

cgam(
  formula,
  family,
  data,
  alpha = 0.05,
  pval.approx = FALSE,
  B = 100,
  seed = 1,
  search = c("all", "stepwise"),
  ...
)

```

Arguments

formula	A formula object.
family	A distributional family object. Currently supported options are: binomial and poisson.
data	A data frame containing the variables in the model.
alpha	Significance level for statistical test.
pval.approx	If TRUE, chi-squared approximated p-values are calculated. Default is FALSE, in which case p-values are calculated via bootstrap.
B	Number of bootstrap sample when pval.approx=FALSE.
seed	Seed for generating bootstrap samples.
search	If search="stepwise", a greedy forward stepwise search is conducted. Default is search="all", in which case all possible submodels are considered.
...	Further arguments to be passed to the gam function.

Value

A gam object of the selected causal submodel.

Examples

```

#####
#causal Poisson gam#####
n<-1000
set.seed(123)
X1<-rnorm(n,0,1)
Y<-rpois(n,exp(sin(X1)))
X2<-log(Y+1)+rnorm(n,0,0.5)
data<-data.frame(cbind(X1, X2, Y))
cm_all<-cgam(Y ~ s(X1)+s(X2),"poisson",data,pval.approx=TRUE,search="all")
cm_all$model.opt
cm_step<-cgam(Y ~ s(X1)+s(X2),"poisson",data,pval.approx=TRUE,search="stepwise")
cm_step$model.opt

```

```

#bigger simulation with 7 covariates
set.seed(123)
n<-1000
X1<-rnorm(n=n,sd=sqrt(0.04))
X2<-X1+rnorm(n=n,sd=sqrt(0.04))
X3<-X1+X2+rnorm(n=n,sd=sqrt(0.04))
m<-sin(X2*5)+X3^3
Z<-m+rnorm(n=n,sd=sqrt(0.04))
X4<-X2+rnorm(n=n,sd=sqrt(0.04))
X5<-Z+rnorm(n=n,sd=sqrt(0.04))
X6<-Z+rnorm(n=n,sd=sqrt(0.04))
X7<-X6+rnorm(n=n,sd=sqrt(0.04))
Y<-qpois(pnorm(Z, mean = m, sd = sqrt(0.04)), lambda=exp(m))
dat<-data.frame(cbind(X1, X2, X3, X4, X5, X6, X7,Y))
fml<- Y~s(X1)+s(X2)+s(X3)+s(X4)+s(X5)+s(X6)+s(X7)
mod.all <-cgam(fml,"poisson",dat,pval.approx=TRUE,search="all")
mod.all$model.opt
mod.step <-cgam(fml,"poisson",dat,pval.approx=TRUE,search="stepwise")
mod.step$model.opt
#####
#causal logistic gam#####
n<-1000
set.seed(123)
X1<-rnorm(n,0,1)
Y<-rbinom(n,1,exp(X1)/(1+exp(X1)))
flip<-rbinom(n,1,0.1)
X2<-(1-flip)*Y+rnorm(n,0,0.3)
data<-data.frame(cbind(X1, X2, Y))
cm_all<-cgam(Y ~ s(X1)+s(X2),"binomial",data,pval.approx=FALSE,search="all")
cm_all$model.opt
cm_step<-cgam(Y ~ s(X1)+s(X2),"binomial",data,pval.approx=FALSE,search="stepwise")
cm_step$model.opt

```

cglm

Causal generalized linear model

Description

This function does a search for a causal submodel within the generalized linear model provided.

Usage

```

cglm(
  formula,
  family,
  data,
  alpha = 0.05,
  pval.approx = FALSE,
  B = 100,

```

```

    seed = 1,
    search = c("all", "stepwise"),
    ...
  )

```

Arguments

formula	A formula object.
family	A distributional family object. Currently supported options are: binomial and poisson.
data	A data frame containing the variables in the model.
alpha	Significance level for statistical test
pval.approx	If TRUE, chi-squared approximated p-values are calculated. Default is FALSE, in which case p-values are calculated via bootstrap.
B	Number of bootstrap sample when pval.approx=FALSE.
seed	Seed for generating bootstrap samples.
search	If search="stepwise", a greedy forward stepwise search is conducted. Default is search="all", in which case all possible submodels are considered.
...	Further arguments to be passed to the glm function.

Value

A glm object of the selected causal submodel.

Examples

```

#####
#causal Poisson glm#####
n<-1000
set.seed(123)
X1<-rnorm(n,0,1)
Y<-rpois(n,exp(X1))
X2<-log(Y+1)+rnorm(n,0,0.3)
data<-data.frame(cbind(X1, X2, Y))
cm_all<-cglm(Y ~ X1+X2,"poisson",data,pval.approx=TRUE,search="all")
cm_all$model.opt
cm_step<-cglm(Y ~ X1+X2,"poisson",data,pval.approx=TRUE,search="stepwise")
cm_step$model.opt

#####
#causal logistic glm#####
n<-2000
set.seed(123)
X1<-rnorm(n,0,1)
Y<-rbinom(n,1,exp(X1)/(1+exp(X1)))
flip<-rbinom(n,1,0.1)
X2<-(1-flip)*Y+rnorm(n,0,0.3)
data<-data.frame(cbind(X1, X2, Y))
cm_all<-cglm(Y ~ X1+X2,"binomial",data,pval.approx=FALSE,search="all")

```

```
cm_all$model.opt
cm_step<-cglm(Y ~ X1+X2,"binomial",data,pval.approx=FALSE,search="stepwise")
cm_step$model.opt
#bigger simulation with 5 covariates
set.seed(12)
n<-3000
X1<-rnorm(n,0,1)
X2<-rnorm(n,X1,0.5)
X3<-rnorm(n,0,1)
X4<-rnorm(n,X2,.5)
Y<-rbinom(n,1,exp(.8*X2-.9*X3)/(1+exp(.8*X2-.9*X3)))
flip<-rbinom(n,1,0.1)
X5<-(1-flip)*Y+flip*(1-Y)+rnorm(n,0,.3)
dat<-data.frame(cbind(X1, X2, X3, X4, X5,Y))
mod.all <-cglm(Y~X1+X2+X3+X4+X5,"binomial",dat,pval.approx=FALSE,search="all")
mod.all$model.opt
mod.step <-cglm(Y~X1+X2+X3+X4+X5,"binomial",dat,pval.approx=FALSE,search="stepwise")
mod.step$model.opt
```

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