

Package ‘gausscov’

July 9, 2025

Version 1.1.8

Date 2025-7-4

Title The Gaussian Covariate Method for Variable Selection

Author Laurie Davies [aut, cre]

Maintainer Laurie Davies <pldavies44@cantab.net>

Description The standard linear regression theory whether frequentist or Bayesian is based on an 'assumed (revealed?) truth' (John Tukey) attitude to models. This is reflected in the language of statistical inference which involves a concept of truth, for example confidence intervals, hypothesis testing and consistency. The motivation behind this package was to remove the word true from the theory and practice of linear regression and to replace it by approximation. The approximations considered are the least squares approximations. An approximation is called valid if it contains no irrelevant covariates. This is operationalized using the concept of a Gaussian P-value which is the probability that pure Gaussian noise is better in term of least squares than the covariate. The precise definition given in the paper ``An Approximation Based Theory of Linear Regression''. Only four simple equations are required. Moreover the Gaussian P-values can be simply derived from standard F P-values. Furthermore they are exact and valid whatever the data in contrast F P-values are only valid for specially designed simulations. A valid approximation is one where all the Gaussian P-values are less than a threshold p_0 specified by the statistician, in this package with the default value 0.01. This approximations approach is not only much simpler it is overwhelmingly better than the standard model based approach. The will be demonstrated using high dimensional regression and vector autoregression real data sets. The goal is to find valid approximations. The search function is `f1st` which is a greedy forward selection procedure which results in either just one or no approximations which may however not be valid. If the size is less than than a threshold with default value 21 then an all subset procedure is called which returns the best valid subset. A good default start is `f1st(y,x,kmn=15)` The best function for returning multiple approximations is `f3st` which repeatedly calls `f1st`. For more information see the papers: L. Davies and L. Duembgen, ``Covariate Selection Based on a Model-free Approach to Linear Regression with Exact Probabilities'', <doi:10.48550/arXiv.2202.01553>, L. Davies, ``An Approximation Based Theory of Linear Regression'', 2024, <doi:10.48550/arXiv.2402.09858>.

LazyData true

License GPL-3

Depends R (>= 3.5.0), stats

Encoding UTF-8

RoxygenNote 6.1.1

NeedsCompilation yes

Repository CRAN

Date/Publication 2025-07-09 13:00:02 UTC

Contents

abcq	2
boston	3
decode	4
f1bsf	4
f1st	5
f2st	6
f3st	7
f3sti	8
fasb	9
fdecode	9
fgenbsf	10
fgeninter	11
fgentrig	11
fgr1st	12
flag	13
fpval	13
fselect	14
fundr	15
leukeia	15
lymphoma	16
m15005m	16
mel-temp	17
redwine	17
snspt	18
vardata	18
Index	19

abcq

American Business Cycle

Description

The 22 variables are quarterly data from 1919-1941 and 1947-1983 of the variables GNP72, CPRATE, CORPYIELD, M1, M2, BASE, C STOCK, WRICE67, PRODUR72, NONRES72, IRES72, DBUSI72, CDUR72, CNDUR72, XPT72, MPT72, GOVPUR72, NCS PDE72, NCSBS72, NCSCON72, CC-SPDE72 and CCSBS72.

Usage

abcq

Format

A matrix of size 240 x 22

Source<http://data.nber.org/data/abc/>

boston

Boston data

Description

This data set is part of the MASS package. The 14 columns are:

crim per capita crime rate by town

zn proportion of residential land zoned for lots over 25,000 sq.ft.

indus proportion of non-residential business acres per town

chas Charles River dummy variable (=1 if tract bounds river; 0 otherwise)

nox nitrogen oxides concentration (parts per 10 million)

rm average number of rooms per dwelling

age proportion of owner-occupied units built prior to 1940

dis weighted mean of distances to five Boston employment centres

rad index of accessibility to radial highways

tax full-value property-tax rate per \$10,000

pttration pupil-teacher ration by town

black $100(Bk-0.63)^2$ where Bk is the proportion of blacks by town

lstat lower status of the population (percent)

medv median value of owner occupies homes in \$1000s.

Usage

boston

Format

A 506 x 14 matrix.

SourceR package MASS https://cran.r-project.org/web/packages/available_packages_by_name.html

References

MASS Support Functions and Datasets for Venables and Ripley's MASS

decode	<i>Decodes the number of a subset selected by fasb.R to give the covariates</i>
--------	---

Description

Decodes the number of a subset selected by fasb.R to give the covariates

Usage

```
decode(ns, k)
```

Arguments

ns	The number of the subset
k	The number of covariates

Value

ind The list of covariates
 set A binary vector giving the covariates

Examples

```
a<- decode(19,8)
```

f1bsf	<i>Stepwise selection of interval covariates in non-paametric regression</i>
-------	--

Description

Stepwise selection of interval covariates in non-paametric regression

Usage

```
f1bsf(y, k, lam, pr=0.5, mm=20, p0=0.01)
```

Arguments

y	Dependent variable
k	Length of smallest interval
lam	Factor for increasing size of intervals
pr	Proportional increase in size of sample to reduce edge effects
mm	Parameter of fgentrig for the number of trigonometric functions
p0	Gaussian P-value threshold

Value

pv ff The approximation
 res The residuals

Examples

```
data(vardata)
a<-f1bsf(vardata[,70],4,1.1,pr=0,mm=10)
```

f1st *Stepwise selection of covariates*

Description

Stepwise selection of covariates

Usage

```
f1st(y,x,p0=0.01,kmn=0,kmx=0,kex=0,mx=21,sub=T,inr=T,xinr=F,qq=-1)
```

Arguments

y	Dependent variable
x	Covariates
p0	The P-value cut-off
kmn	The minimum number of included covariates irrespective of cut-off P-value
kmx	The maximum number of included covariates irrespective of cut-off P-value.
kex	The excluded covariates
mx	The maximum number covariates for an all subset search
sub	Logical if TRUE best subset selected
inr	Logical if TRUE include intercept if not present
xinr	Logical if TRUE intercept already present
qq	The number of covariates to choose from. If qq=-1 the number of covariates of x is used.

Value

pv In order the included covariates, the regression coefficient values, the Gaussian P-values, the standard P-values.
 res The residuals

Examples

```
data(boston)
bostint<-fgeninter(boston[,1:13],2)[[1]]
a<-f1st(boston[,14],bostint,kmn=10,sub=TRUE)
```

f2st

*Repeated stepwise selection of covariates***Description**

Repeated stepwise selection of covariates

Usage

```
f2st(y,x,p0=0.01,kmn=0,kmx=0,kex=0,mx=21,lm=9^9,sub=T,inr=T,xinr=F,qq=-1)
```

Arguments

y	Dependent variable
x	Covariates
p0	The P-value cut-off
kmn	The minimum number of included covariates irrespective of cut-off P-value
kmx	The maximum number of included covariates irrespective of cut-off P-value.
kex	The excluded covariates
mx	The maximum number of covariates for an all subset search
lm	The maximum number of linear approximations
sub	Logical if TRUE select the best subset
inr	Logical if TRUE include an intercept
xinr	Logical if TRUE intercept already included
qq	The number of covariates to choose from. If qq=-1 the number of covariates of x is used.

Value

pv In order the linear approximation, the included covariates, the Gaussian P-values.

Examples

```
data(boston)
bostint<-fgeninter(boston[,1:13],2)[[1]]
a<-f2st(boston[,14],bostint,lm=3,sub=FALSE)
```

f3st

*Stepwise selection of covariates***Description**

Stepwise selection of covariates

Usage

```
f3st(y, x, m, p0=0.01, kmn=0, kmx=0, kex=0, mx=21, sub=T, inr=T, xinr=F, qq=-1, kexmx=100)
```

Arguments

y	Dependent variable
x	Covariates
m	The number of iterations
p0	The P-value cut-off
kmn	The minimum number of included covariates irrespective of cut-off P-value
kmx	The maximum number of included covariates irrespective of cut-off P-value.
kex	The excluded covariates
mx	The maximum number covariates for an all subset search
sub	Logical if TRUE best subset selected
inr	Logical if TRUE include intercept if not present
xinr	Logical if TRUE intercept already present
qq	The number of covariates to choose from. If qq=-1 the number of covariates of x is used.
kexmx	The maximum number of covariates in an approximation.

Value

covch The sum of squared residuals and the selected covariates ordered in increasing size of sum of squared residuals.

lai The number of rows of covch

Examples

```
data(leukemia)
a<-f3st(leukemia[[1]],leukemia[[2]],m=2,kmn=5,sub=TRUE,kexmx=10)
```

f3sti

*Selection of covariates with given excluded covariates***Description**

Selection of covariates with given excluded covariates

Usage

```
f3sti(y,x,covch,ind,m,p0=0.01,kmn=0,kmx=0, kex=0,mx=21,sub=T,inr=F,xinr=F,qq=-1,kexmx=100)
```

Arguments

y	Dependent variable
x	Covariates
covch	Sum of squared residuals and selected covariates
ind	The excluded covariates
m	Number of iterations
p0	The P-value cut-off
kmn	The minimum number of included covariates irrespective of cut-off P-value
kmx	The maximum number of included covariates irrespective of cut-off P-value.
kex	The excluded covariates
mx	The maximum number covariates for an all subset search
sub	Logical if TRUE best subset selected
inr	Logical if TRUE include intercept if not present
xinr	Logical if TRUE intercept already present
qq	The number of covariates to choose from. If qq=-1 the number of covariates of x is used.
kexmx	The maximum number of covariates in an approximation.

Value

ind1 The excluded covariates

covch The sum of squared residuals and the selected covariates ordered in increasing size of sum of squared residuals

Examples

```
data(leukemia)
covch=c(2.023725,1182,1219,2888,0)
covch<-matrix(covch,nrow=1,ncol=5)
ind<-c(1182,1219,2888)
ind<-matrix(ind,nrow=3,ncol=1)
m<-1
a<-f3sti(leukemia[[1]],leukemia[[2]],covch,ind,m,kexmx=5)
```

fasb	<i>Calculates all subsets where each included covariate is significant.</i>
------	---

Description

The subset are ordered according to the sum of squared residuals. Subsets can be decoded with `decode.R`.

Usage

```
fasb(y, x, p0=0.01, ind=0, inr=T, xinr=F, qq=-1)
```

Arguments

y	The dependent variable
x	The covariates
p0	Cut-off p-value for significance
ind	The indices of a subset of covariates for which all subsets are to be considered
inr	If TRUE to include intercept
xinr	If TRUE intercept already included
qq	The number of covariates from which to choose. Equals number of covariates minus length of ind if qq=-1.

Value

nv Coded List of subsets with number of covariates and sum of squared residuals

Examples

```
data(redwine)
nvv<-fasb(redwine[,12],redwine[,1:11])
```

fdecode	<i>Decodes the number of a subset selected by fasb.R to give the covariates</i>
---------	---

Description

Decodes the number of a subset selected by `fasb.R` to give the covariates

Usage

```
fdecode(ns, k)
```

Arguments

ns The number of the subset
 k The number of covariates

Value

ind The list of covariates
 set A binary vector giving the covariates

Examples

```
a<- fdecode(19,8)
```

fgenbsf *Generates basis functions on disjoint intervals*

Description

Generation of basic functions on intervals

Usage

```
fgenbsf(n,k,lam)
```

Arguments

n Sample size
 k Size of smallest interval
 lam Proportionality factor for increasing size of intervals

Value

x the matrix of the intervals

Examples

```
a<-fgenbsf(100,4,1.2)
```

fgeninter *Generation of interactions*

Description

Generates all interactions of degree at most ord

Usage

```
fgeninter(x,ord)
```

Arguments

x	Covariates
ord	Order of interactions

Value

xx All interactions of order at most ord.
intx Decomposes a given interaction covariate of xx

Examples

```
data(boston)  
bostint<-fgeninter(boston[,1:13],2)[[1]]
```

fgentrig *Generation of sine and cosine functions*

Description

Generates $\sin(\pi*j*(1:n)/n)$ (odd) and $\cos(\pi*j*(1:n)/n)$ (even) for $j=1,\dots,m$ for a given sample size n .

Usage

```
fgentrig(n,m)
```

Arguments

n	Sample size
m	Maximum order of sine and cosine functions

Value

x The functions $\sin(\pi*j*(1:n)/n)$ (odd) and $\cos(\pi*j*(1:n)/n)$ (even) for $j=1,\dots,m$.

Examples

```
trig<-fgentrig(36,36)
```

fgr1st

Calculates a dependence graph using Gaussian stepwise selection

Description

Calculates an independence graph using Gaussian stepwise selection

Usage

```
fgr1st(x,p0=0.01,ind=0,kmn=0,kmx=0,mx=21,nedge=10^5,inr=T,xinr=F,qq=-1)
```

Arguments

x	The matrix of covariates
p0	Cut-off P-value
ind	Restricts the dependent nodes to this subset
kmn	The minimum number selected variables for each node irrespective of cut-off P-value
kmx	The maximum number selected variables for each node irrespective of cut-off P-value
mx	Maximum number of selected covariates for each node for all subset search
nedge	Maximum number of edges
inr	Logical, if TRUE include an intercept
xinr	Logical, if TRUE intercept already included
qq	The number of covariates to choose from. If qq=-1 the number of covariates of x is used

Value

ned Number of edges

edg List of edges together with P-values for each edge and proportional reduction of sum of squared residuals.

Examples

```
data(boston)
a<-fgr1st(boston[,1:13],ind=3:6)
```

flag *Calculation of lagged covariates*

Description

Calculation of lagged covariates

Usage

```
flag(x, n, i, lag)
```

Arguments

x	The covariates
n	The sample size
i	The dependent variable
lag	The maximum lag

Value

y The ith covariate of x without a lag, the dependent variable.
 x1 The covariates with lags from 1 :lag starting with the first covariate.

Examples

```
data(abcq)
abcq1<-flag(abcq, 240, 1, 16)
a<-f1st(abcq1[[1]], abcq1[[2]])
```

fpval *Calculates the regression coefficients, the P-values and the standard P-values for the chosen subset ind*

Description

Calculates the regression coefficients, the P-values and the standard P-values for the chosen subset ind.

Usage

```
fpval(y, x, ind, inr=T, xinr=F, qq=-1)
```

Arguments

y	The dependent variable
x	The covariates
ind	The indices of the subset of the covariates whose P-values are required
inr	Logical If TRUE intercept to be included
xinr	If TRUE intercept already included
qq	The total number of covariates from which ind was chosen. If qq=-1 the number of covariates of x minus length ind plus 1 is taken.

Value

apv In order the subset ind, the regression coefficients, the Gaussian P-values, the standard P-values and the proportion of sum of squares explained.

res The residuals

Examples

```
data(boston)
a<-fpval(boston[,14],boston[,1:13],c(1,2,4:6,8:13))
```

fselect

Selects the subsets specified by fasb.R and frasb.R.

Description

All subsets which are a subset of a specified subset are removed. The remaining subsets are ordered by the sum of squares of the residuals (fasb.R) or the scale (frasb.R)

Usage

```
fselect(nv, k)
```

Arguments

nv	The subsets specified by fasb.R or frasb.R
k	The variables

Value

ind The selected subsets.

Examples

```
b<-fasb(redwine[,12],redwine[,1:5 ])[[1]]
a<-fselect(b,11)[[1]]
b[a,]
```

fundr	<i>Converts directed into an undirected graph</i>
-------	---

Description

Conversion of a directed graph into an undirected graph

Usage

```
fundr(gr)
```

Arguments

`gr` A directed graph

Value

`gr` The undirected graph

Examples

```
data(boston)
grb<-fgr1st(boston[,1:13])
grbu<-fundr(grb[[2]][,1:2])
```

leukeia	<i>Leukemia data set</i>
---------	--------------------------

Description

Dataset of $n = 72$ persons indicating presence or absence of leukemia (variable 3572) and $q = 3571$ gene expressions of the 72 persons (variables 1 to 3571)

Usage

```
data(leukemia)
```

Format

y 0-1 data of individuals with and without leukemia.
x covariates of the level of 3571 genes.

Source

<http://stat.ethz.ch/~dettling/bagboost.html>

References

Boosting for tumor classification with gene expression data. Dettling, M. and Buehlmann, P. Bioinformatics, 2003,19(9):1061–1069.

 lymphoma

Lymphoma data set

Description

Dataset of $n = 62$ persons with one of three different forms of lymphoma and $q = 4026$ gene expressions of the 62 persons

Usage

`data(leukemia)`

Format

y 0-1-2 data of individuals with lymphoma.
x covariates of the level of 4062 genes.

Source

R Package ‘spls’

References

Sparse partial least squares classification for high dimensional data. Dongjun Chung and Sunduz Keles. Stat. Appl. Genet. Mol. Biol., (2010;9)

 m15005m

m15005m data

Description

Angle and photon counts in thin film x-ray refraction.

Usage

`m15005m`

Format

A matrix of size 7001 x 2, first component angle, second photon count

Source

The data were provided by Professor Dieter Mergel, Faculty of Physics, University of Duisburg-Essen, Essen, Germany

mel-temp	<i>Melbourne minimum temperature</i>
----------	--------------------------------------

Description

The daily minimum temperature in Melbourne for the years 1981-1990.

Usage

mel_temp

Format

A vector of length 3650

Source

<https://www.kaggle.com/paulbrabban/daily-minimum-temperatures-in-melbourne>

redwine	<i>Redwine data</i>
---------	---------------------

Description

The subjective quality of wine on an integer scale from 1-10 (variable 12) together with 11 physicochemical properties

Usage

redwine

Format

A matrix of size 1599 x 12

Source

<https://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/>

References

Modeling wine preferences by data mining from physicochemical properties, Cortez, P., Cerdeira, A., Almeida, F., Matos, T., and Reis, J., Decision Support Systems, Elsevier, 2009,47(4):547–553.

snspt	<i>Sunspot data</i>
-------	---------------------

Description

The average number of sunspots each month from January 1749 to January 2020

Usage

snspt

Format

A vector of size 3253

Source

WDC-SILSO, Royal Observatory of Belgium, Brussels

vardata	<i>USA economics data</i>
---------	---------------------------

Description

United States economic data taken from the FRED-MD macroeconomic database with the NAs removed. 182 indices each of length 256

Usage

vardata

Format

A matrix of size 256 X 182

Source

<https://research.stlouisfed.org/econ/mccracken/fred-databases>

Index

* datasets

- abcq, [2](#)
 - boston, [3](#)
 - leukeia, [15](#)
 - lymphoma, [16](#)
 - m15005m, [16](#)
 - mel-temp, [17](#)
 - redwine, [17](#)
 - snspt, [18](#)
 - vardata, [18](#)
-
- abcq, [2](#)
 - boston, [3](#)
 - decode, [4](#)
 - f1bsf, [4](#)
 - f1st, [5](#)
 - f2st, [6](#)
 - f3st, [7](#)
 - f3sti, [8](#)
 - fasb, [9](#)
 - fdecode, [9](#)
 - fgenbsf, [10](#)
 - fgeninter, [11](#)
 - fgentrig, [11](#)
 - fgr1st, [12](#)
 - flag, [13](#)
 - fpval, [13](#)
 - fselect, [14](#)
 - fundr, [15](#)
 - leukeia, [15](#)
 - leukemia (leukeia), [15](#)
 - lymphoma, [16](#)
 - m15005m, [16](#)
 - mel-temp, [17](#)
 - mel_temp (mel-temp), [17](#)