

Package ‘IVGC’

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Type Package

Title Two-step Estimation Using IV Regression and Graph-constrained
Regularization Method

Version 1.0.1

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Depends R (>= 3.1.0)

Imports glmnet

Description Efficient two-step procedure to achieve variable selection and estimation under an IV regression framework by incorporating gene network information. The method is applicable in both low and high dimensional situations and the cyclical coordinate descent algorithm is used to solve them.

License GPL-2

LazyData true

NeedsCompilation yes

Repository github

URL <https://github.com/xliusufe/IVGC>

Encoding UTF-8

Archs i386, x64

R topics documented:

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| | |
|--------------|--|
| IVGC-package | <i>Two-step Estimation Using IV Regression and Graph-constrained Regularization Method</i> |
|--------------|--|

Description

Efficient two-step procedure to achieve variable selection and estimation under an IV regression framework by incorporating gene network information. The method is applicable in both low and high dimensional situations and the cyclical coordinate descent algorithm is used to solve them.

Details

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References

Gao, B., Liu, X., Li, H. and Cui, Y. (2019). Integrative Analysis of Genetical Genomics Data Incorporating Network Structures. Manuscript.

| | |
|------|---|
| main | <i>Fit an IV regression model with lasso and graph-constrained regularization</i> |
|------|---|

Description

This function is a two-step procedure to achieve variable selection and estimation under an IV regression framework by incorporating gene regulatory network structures. Because of high correlations between coefficients, in the first step, the LASSO-type regression is applied to estimate the coefficient matrix. And in the second step, two penalties (LASSO and graph-constrained penalties) are applied to encourage the shrinking coefficients of a pair of connected variable in a network, thus achieving a grouping effect.

Usage

```
main(y, x, S, G, is.graph="IVGC", nlambdas=50, nalpha=50, nfold=5, epsilon=1e-6)
```

Arguments

| | |
|---|--|
| y | The response, a vector of size n |
| x | The expression data dimension $n \times p$ |
| S | The SNP variable with dimension $n \times q$ |

| | |
|----------|---|
| G | The graph structure of X with dimension $p \times p$ |
| is.graph | The method including "IVGC", "IV", "both". "IVGC" denotes IV regression incorporating network structures (Gao et al. 2019); "IV" denotes IV regression without network structures; "both" outputs the results by "IVGC" and "IV". Default is "IVGC". |
| nlambda | The length of tuning parameter λ which is selected automatically. Default is 50. |
| nalpha | The length of tuning parameter α which is selected automatically. Default is 50. |
| nfold | The number of folds for the tuning selection by CV. Default is 5. |
| epsilon | The perturbation when the proposed algorithm is used. Default is epsilon=1e-6. |

Details

The simulated data set is saved in simulatedData.RData, which is list with four values Y, X, gene (S) and graph (G).

Value

| | |
|-----------|---|
| beta_ivgc | the beta estimator by the proposed method |
| beta_iv | the beta estimator by IV method without graph structure |
| Gamma_hat | the Gamma estimator by grouped lasso |

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References

Gao, B., Liu, X., Li, H. and Cui, Y. (2019+) Integrative Analysis of Genetical Genomics Data Incorporating Network Structures. Manuscript.

Examples

```
data(simulatedData)
y <- simulatedData$Y
x <- simulatedData$X
S <- simulatedData$gene
G <- simulatedData$graph
fit <- main(y, x, S, G)
```

simulatedData

Genetical Genomics Data Incorporating Network Structures

Description

This is a simulated data on gene expression. Certain correlation structures on genes are also imposed to show the impact of network structures on variable selection and estimation.

Usage

```
data("simulatedData")
```

Details

We simulated a total of p variables of gene expression and considered three group structures on coefficients with five variables in each group. Within each group, the variables are correlated. The strength of the correlation was controlled by the number of effective SNPs they had in common.

Y: the response, a vector of size 200

X: the expression data dimension 200×100

gene: the SNP variable with dimension 200×100

graph: the graph structure of X with dimension 100×100

References

Gao, B., Liu, X., Li, H. and Cui, Y. (2019+) Integrative Analysis of Genetical Genomics Data Incorporating Network Structures. Manuscript.

Examples

```
data(simulatedData)
y <- simulatedData$Y
x <- simulatedData$X
S <- simulatedData$gene
G <- simulatedData$graph
```

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