Package ‘SurvHiDim’

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Description  High dimensional time to events data analysis with variable selection technique.
Current support LASSO, clustering and Bonferroni's correction.

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R topics documented:

  hdClust ................................................................. 2
  hdNetwork ............................................................ 4
  hidimLasso ............................................................. 6
  hidimSurv ............................................................. 7
  hidimSurvbon .......................................................... 9
hdClust

Description

Creates a network plot of high dimensional variables and lists those variables.

Usage

hdClust(m, n, siglevel, u, ID, OS, Death, PFS, Prog, data)

Arguments

- m: Starting column number from where variables of high dimensional data will be selected.
- n: Ending column number till where variables of high dimensional data will get selected.
- siglevel: Level of significance pre-determined by the user.
- u: Factors of Event column e.g. 0,1 or 2 or Number of clusters to form.
- ID: Column name of subject ID, a string value. i.e. "id"
- OS: Column name of survival duration event, a string value. i.e. "os"
- Death: Column name of survival event, a string value. i.e "death"
- PFS: Column name of progression free survival duration, a string value. i.e "pfs"
- Prog: Column name of progression event, a string value. i.e "prog"
- data: High dimensional data having survival duration, event information, column of time for death cases and observations on various covariates under study.

Details

hdClust function first creates a new column 'Status' in the input data set and assigns values 0, 1, 2 to each rows. It assigns 0 (for progression = 1 & death(event) = 0) is or (when progression = 0 & death(event) = 0. It assigns 1 (for progression = 1 & death = 1, whereas assigns 2 (for progression = 0 and death = 1).
Further, it creates two data sets, one data set named 'deathdata' which includes subjects with status 0 and 1 and applies Cox PH on it. Another data is named as 'compdata' which includes subjects with status 0 and 2, then applies Cox PH after substituting 2 by 1. Then it filters out study variables having P-value < siglevel(significance level taken as input from user) from both subset data. Secondly, it merges the common significant variables from both data and creates a new data frame which contains columns, 'ID', 'OS', 'Death', 'PFS', 'Prog', 'Status' and observations of common significant variables (which are supposed to be leading to death given they leads to progression of cancer as well as accounts for competing risks) Further, it lists the common variables names and correspond in results in .csv format by default in user's current working directory.

hdClust(m,n,siglevel,threshold,data),
1) Subject ID column should be named as 'ID'.
2) OS column must be named as 'OS'.
3) Death status/event column should be named as 'Death'.
4) Progression Press Survival column should be named as 'PFS'.
5) Progression event column should be named as 'Prog'.
deathtdata - A data frame with status column includes only those rows/subjects for which death/event was observed or not, given progression was observed or not.
comdata - A data frame with status column which includes those rows/subjects who died given progression was observed.
data1variables - list of variables/genes from deathdata
data2variables - list of variables/genes from compdata
siginificantpvalueA - A data frame with estimate values, HR, Pvalue, etc. of significant variables from deathdata. significanctpvalueB - A data frame with estimate values, HR, Pvalue, etc. of significant variables from compdata.
commongenes - A data frame consisting observations on common significant study variables.
cvar - List of common significant study variables.
comomdata - A final data out consisting survival information ans observations on common significant study variables.

By default the function stores the output in .csv forms in current directory of user.
Further it creates a cluster plot of variables of similar behavior.

Value
A list containing variable names and the correlation values.

Author(s)
Atanu Bhattacharjee and Akash Pawar

References
See Also

hdNetwork

Examples

```r
#
data(hnscc)
hdClust(7, 105, 0.05, 2, ID="id", OS="os", Death="death", PFS="pfs", Prog="prog", hnscc)
#
```

Description

Creates a network plot of high dimensional variables and lists those variables.

Usage

```r
hdNetwork(m, n, siglevel, threshold, ID, OS, Death, PFS, Prog, data)
```

Arguments

- `m`: Starting column number form where study variables of high dimensional data will get selected.
- `n`: Ending column number till where study variables of high dimensional data will get selected.
- `siglevel`: Level of significance pre-determined by the user.
- `threshold`: Level to categorize the relation among the significant covariates.
- `ID`: Column name of subject ID, a string value. i.e. "id"
- `OS`: Column name of survival duration event, a string value. i.e. "os"
- `Death`: Column name of survival event, a string value. i.e "death"
- `PFS`: Column name of progression free survival duration, a string value. i.e "pfs"
- `Prog`: Column name of progression event, a string value. i.e "prog"
- `data`: High dimensional data containing the survival, progression and genomic observations.

Details

Gives cluster plot and lists the variables showing correlation.

hdNetwork function first creates a new column 'Status' in the input data set and assigns values 0, 1, 2 to each rows. It assigns 0 (for progression = 1 & death(event) = 0) is or (when progression = 0 & death(event) = 0. It assigns 1 (for progression = 1 & death = 1, whereas assigns 2 (for progression = 0 and death = 1).
Further, it creates two data sets, one data set named 'deathdata' which includes subjects with status 0 and 1 and applies Cox PH on it. Another data is named as 'compdata' which includes subjects with status 0 and 2, then applies Cox PH after substituting 2 by 1. Then it filters out study variables having P-value < siglevel (significance level taken as input from user) from both subset data. Secondly, it merges the common significant variables from both data and creates a new data frame which contains columns, 'ID','OS','Death','PFS','Prog','Status' and observations of common significant variables (which are supposed to be leading to death given they leads to progression of cancer as well as accounts for competing risks) Further, it lists the common variables names and correspond in results in .csv format by default in user’s current working directory.

hdNetwork(m,n,siglevel,threshold,data),

1) Subject ID column should be named as 'ID'.
2) OS column must be named as 'OS'.
3) Death status/event column should be named as 'Death'.
4) Progression Fress Survival column should be named as 'PFS'.
5) Progression event column should be named as 'Prog'.

deatdata - A data frame with status column includes only those rows/subjects for which death/event was observed or not, given progression was observed or not.
compdata - A data frame with status column which includes those rows/subjects who died given progression was observed

data1variables - list of variables/genes from deathdata
data2variables - list of variables/genes from compdata
signficantpvalueA - A data frame with estimate values, HR, Pvalue, etc. of significant variables from deathdata. siginificantpvalueB - A data frame with estimate values, HR, Pvalue, etc. of significant variables from compdata.

commongenes - A data frame consisting observations on common significant study variables.
cvar - List of common significant study variables.
commondata - A final data out consisting survival information ans observations on common significant study variables.

By default the function stores the output in .csv forms in current directory of user.

Further it creates a network plot of variables of similar behavior.

Value
A list containing variable names and the correlation values.
A network plot formed by the filtered variables.

Author(s)
Atanu Bhattacharjee and Akash Pawar
hidimLasso

References


See Also

hdClustrr

Examples

```r
##
data(hnscc)
hdNetwork(7,105,0.05,0.2,ID="id",OS="os",Death="death",PFS="pfs",Prog="prog",hnscc)
##
```

hidimLasso

hidimLasso LASSO for high dimensional data

Description

Least Absolute Shrinkage and Selection Operator (LASSO) for High Dimensional Survival data.

Usage

hidimLasso(m, n, OS, Death, data)

Arguments

- `m` Starting column number from where variables of high dimensional data will get
  selected.
- `n` Ending column number till where variables of high dimensional data will get
  selected.
- `OS` Column name of survival duration event, a string value. i.e. "os"
- `Death` Column name of survival event, a string value. i.e "death"
- `data` High dimensional data having survival duration, event and various covariates
  observations

Details

‘HiDimLasso’ allows a user to apply LASSO function on the High Dimensional data and reduce
the study variables to handful number of co-variate which are observed impacting the survival
outcomes.
Column of Overall Survival must be named as ‘OS’ and the column defining the event must be
named as ‘Event’.
By default it stores the outcome data in user’s current directory.
hidimSurv

Value
A list of variables selected by LASSO as predictor variables.

Author(s)
Atanu Bhattacharjee and Akash Pawar

References

See Also
hidimSurvlas hidimSurvbonlas

Examples

```r
##
data(hnscc)
hidimLasso(7,105,OS="os",Death="death",hnscc)
##
```

hidimSurv  

hidimSurv Survival analysis on high dimensional data

Description
Survival analysis using Cox Proportional hazards function on high dimensional data

Usage
hidimSurv(m, n, siglevel, ID, OS, Death, PFS, Prog, data)

Arguments

- `m` Starting column number form where study variables of high dimensional data will get selected.
- `n` Ending column number till where study variables of high dimensional data will get selected.
- `siglevel` Level of significance pre-determined by the user
- `ID` Column name of subject ID, a string value. i.e. "id"
- `OS` Column name of survival duration event, a string value. i.e. "os"
- `Death` Column name of survival event, a string value. i.e "death"
hidimSurv

**PFS**
Column name of progression free survival duration, a string value. i.e "pfs"

**Prog**
Column name of progression event, a string value. i.e "prog"

**data**
High dimensional data containing the survival, progression and genomic observations.

**Details**

hidimSurv function first creates a new column 'Status' in the input data set and assigns values 0, 1, 2 to each rows. It assigns 0 (for progression = 1 & death(event) = 0) is or (when progression = 0 & death(event) = 0. It assigns 1 (for progression = 1 & death = 1, whereas assigns 2 (for progression = 0 and death = 1).

Further, it creates two data sets, one data set named 'deathdata' which includes subjects with status 0 and 1 and applies Cox PH on it. Another data is named as 'compdata' which includes subjects with status 0 and 2, then applies Cox PH after substituting 2 by 1. Then it filters out study variables having P-value < siglevel(significance level taken as input from user) from both subset data. Secondly, it merges the common significant variables from both data and creates a new data frame which contains columns, 'ID','OS','Death','PFS','Prog','Status' and observations of common significant variables (which are supposed to be leading to death given they leads to progression of cancer as well as accounts for competing risks) Further, it lists the common variables names and correspond in results in .csv format by default in user’s current working directory.

hidimSurv(m,n,siglevel,data),

1) Subject ID column should be named as 'ID'.
2) OS column must be named as 'OS'.
3) Death status/event column should be named as 'Death'.
4) Progression Fress Survival column should be named as 'PFS'.
5) Progression event column should be named as 'Prog'.

deathdata - A data frame with status column includes only those rows/subjects for which death/event was observed or not, given progression was observed or not.

compdata - A data frame with status column which includes those rows/subjects who died given progression was observed

data1variables - list of variables/genes from deathdata

data2variables - list of variables/genes from compdata

significantpvalueA - A data frame with estimate values, HR, Pvalue, etc. of significant variables from deathdata. significantpvalueB - A data frame with estimate values, HR, Pvalue, etc. of significant variables from compdata.

commongenes - A data frame consisting observations on common significant study variables.

cvar - List of common significant study variables.

commomdata - A final data out consisting survival information ans observations on common significant study variables.

By default the function stores the output in .csv forms in current directory of user.
hidimSurvbon

Value

List of variables found significant on OS and survival event
List of variables found significant on PFS and progression event
Estimates values for significant variables on OS and survival event
Estimates values for significant variables on PFS and progression event
Estimates data for the DEGs/Variables found common between significant DEGs from data having death due to progression and data showing death without progression
Estimates data for the DEGs/Variables found common between significant DEGs from data having death due to progression and data showing death without progression
List of variable/ DEGs found common between significantDEGs from data having death due to progression and data showing death without progression
Data with Survival outcomes and DEGs/Variable observations on each subject for DEGs found playing crucial role in death due to progression and without

Author(s)

Atanu Bhattacharjee and Akash Pawar

References


See Also

hidimSurvbon hidimSurvbonlas hidimsvc

Examples

```r
##
data(hnscc)
hidimSurv(7,105,0.05,ID="id",OS="os",Death="death",PFS="pfs",Prog="prog",hnscc)
##
```

hidimSurvbon

**hidimSurvbon** Uses bonferroni correction factor in survival analysis

Description

Applies HiDimSurv on high dimensional data using Bonferroni’s correction criteria.
Usage

hidimSurvbon(m, n, boncorr, ID, OS, Death, PFS, Prog, data)

Arguments

m
Starting column number form where study variables of high dimensional data will get selected.

n
Ending column number till where study variables of high dimensional data will get selected.

boncorr
Level of significance on which bonferroni correction will be applied.

ID
Column name of subject ID, a string value. i.e. "id"

OS
Column name of survival duration event, a string value. i.e. "os"

Death
Column name of survival event, a string value. i.e "death"

PFS
Column name of progression free survival duration, a string value. i.e "pfs"

Prog
Column name of progression event, a string value. i.e "prog"

data
High dimensional data containing the survival, progression and genomic observations.

Details

hidimSurvbon function first creates a new column 'Status' in the input data set and assigns values 0, 1, 2 to each rows. It assigns 0 (for progression = 1 & death(event) = 0) is or (when progression = 0 & death(event) = 0. It assigns 1 (for progression = 1 & death = 1, whereas assigns 2 (for progression = 0 and death = 1).

Further, it creates two data sets, one data set named 'deathdata' which includes subjects with status 0 and 1 and applies Cox PH on it. Another data is named as 'compdata' which includes subjects with status 0 and 2, then applies Cox PH after substituting 2 by 1. Then it filters out study variables having P-value < siglevel/no. of columns of high dimensional data(significance level taken as input from user) from both subset data. Secondly, it merges the common significant variables from both data and creates a new data frame which contains columns, 'ID' , 'OS' , 'Death', 'PFS', 'Prog', 'Status' and observations of common significant variables (which are supposed to be leading to death given they leads to progression of cancer as well as accounts for competing risks) Further, it lists the common variables names and correspond in results in .csv format by default in user's current working directory.

hidimSurvbon(m,n,siglevel,data),
1) Subject ID column should be named as 'ID'.
2) OS column must be named as 'OS'.
3) Death status/event column should be named as 'Death'.
4) Progression Fress Survival column should be named as 'PFS'.
5) Progression event column should be named as 'Prog'.

deathtable - A data frame with status column includes only those rows/subjects for which death/event was observed or not, given progression was observed or not.
hidimSurvbon

comdata - A data frame with status column which includes those rows/subjects who died given progression was observed
data1variables - list of variables/genes from deathdata
data2variables - list of variables/genes from compdata
siginificantpvalueA - A data frame with estimate values, HR, Pvalue, etc. of significant variables from deathdata. signinificantpvalueB - A data frame with estimate values, HR, Pvalue, etc. of significant variables from compdata.
commongenes - A data frame consisting observations on common significant study variables.
cvar - List of common significant study variables.
commndata - A final data out consisting survival information ans observations on common significant study variables.

By default the function stores the output in .csv forms in current directory of user.

Value

List of variables found significant on OS and survival event
List of variables found significant on PFS and progression event
Estimates values for significant variables on OS and survival event
Estimates values for significant variables on PFS and progression event
Estimates data for the DEGs/Variables found common between significant DEGs from data having death due to progression and data showing death without progression
Estimates data for the DEGs/Variables found common between significant DEGs from data having death due to progression and data showing death without progression
List of variable/ DEGs found common between significant DEGs from data having death due to progression and data showing death without progression
Data with Survival outcomes and DEGs/Variable observations on each subject for DEGs found playing crucial role in death due to progression and without

Author(s)

Atanu Bhattacharjee and Akash Pawar

References


See Also

hidimSurvbonlas
hidimSurvbonlas

hidimSurvbonlas Two step filteration using bonferroni correction and LASSO

Description

hidimSurvbonlas on high dimensional data using bonferoni’s correction factor and LASSO.

Usage

hidimSurvbonlas(m, n, boncorr, ID, OS, Death, PFS, Prog, data)

Arguments

- **m**: Starting column number form where study variables of high dimensional data will get selected.
- **n**: Ending column number till where study variables of high dimensional data will get selected.
- **boncorr**: Level of significance on which bonferroni correction will be applied.
- **ID**: Column name of subject ID, a string value. i.e. "id"
- **OS**: Column name of survival duration event, a string value. i.e. "os"
- **Death**: Column name of survival event, a string value. i.e "death"
- **PFS**: Column name of progression free survival duration, a string value. i.e "pfs"
- **Prog**: Column name of progression event, a string value. i.e "prog"
- **data**: High dimensional data containing the survival, progression and genomic observations.

Details

hidimSurvbonlas function first creates a new column 'Status' in the input data set and assigns values 0, 1, 2 to each rows. It assigns 0 (for progression = 1 & death(event) = 0) is or (when progression = 0 & death(event) = 0. It assigns 1 (for progression = 1 & death = 1, whereas assigns 2 (for progression = 0 and death = 1).

Further, it creates two data sets, one data set named 'deathdata' which includes subjects with status 0 and 1 and applies Cox PH on it. Another data is named as 'compdata' which includes subjects with status 0 and 2, then applies Cox PH after substituting 2 by 1. Then it filters out study variables using Bonferroni’s correction criteria, i.e. having P-value < siglevel/ no. of study variables(significance level taken as input from user) from both subset data. Secondly, it merges the
common significant variables from both data and creates a new data frame which contains columns, 'ID', 'OS', 'Death', 'PFS', 'Prog', 'Status' and observations of common significant variables (which are supposed to be leading to death given they leads to progression of cancer as well as accounts for competing risks) Further, it lists the common variables names and correspond in results in .csv format by default in user's current working directory.

On obtained commondata it fits LASSO and reduces the dimensions of study variables to handful significant variables.

hidimSurvbonlas(m,n,siglevel,data)

1) Subject ID column should be named as 'ID'.
2) OS column must be named as 'OS'.
3) Death status/event column should be named as 'Death'.
4) Progression Free Survival column should be named as 'PFS'.
5) Progression event column should be named as 'Prog'.

dethdata - A data frame with status column includes only those rows/subjects for which death/event was observed or not, given progression was observed or not.
compdata - A data frame with status column which includes those rows/subjects who died given progression was observed

data1variables - list of variables/genes from dethdata

data2variables - list of variables/genes from compdata

significantpvalueA - A data frame with estimate values, HR, Pvalue, etc. of significant variables from dethdata. significantpvalueB - A data frame with estimate values, HR, Pvalue, etc. of significant variables from compdata.

commongenes - A data frame consisting observations on common significant study variables.
cvar - List of common significant study variables.

commondata - A final data out consisting survival information ans observations on common significant study variables.

By default the function stores the output in .csv forms in current directory of user.

Value

List of significant genes

Author(s)

Atanu Bhattacharjee and Akash Pawar

References


See Also

hidimSurvbon
Examples

```r
##
data(hnscc)
hidimSurvbonlas(6,104,0.05,ID="id",OS="os",Death="death",PFS="pfs",Prog="prog",hnscc)
##
```

Description

Survival analysis on high dimensional data using LASSO technique.

Usage

`hidimSurvbonlas(m, n, siglevel, ID, OS, Death, PFS, Prog, data)`

Arguments

- `m`: Starting column number form where study variables of high dimensional data will get selected.
- `n`: Ending column number till where study variables of high dimensional data will get selected.
- `siglevel`: Level of significance pre-determined by the user.
- `ID`: Column name of subject ID, a string value. i.e. "id"
- `OS`: Column name of survival duration event, a string value. i.e. "os"
- `Death`: Column name of survival event, a string value. i.e "death"
- `PFS`: Column name of progression free survival duration, a string value. i.e "pfs"
- `Prog`: Column name of progression event, a string value. i.e "prog"
- `data`: High dimensional data containing the survival, progression and genomic observations.

Details

`hidimSurvbonlas` function first creates a new column 'Status' in the input data set and assigns values 0, 1, 2 to each rows. It assigns 0 (for progression = 1 & death(event) = 0) or (when progression = 0 & death(event) = 0. It assigns 1 (for progression = 1 & death = 1, whereas assigns 2 (for progression = 0 and death = 1).

Further, it creates two data sets, one data set named 'deathdata' which includes subjects with status 0 and 1 and applies Cox PH on it. Another data is named as 'compdata' which includes subjects with status 0 and 2, then applies Cox PH after substituting 2 by 1. Then it filters out study variables having P-value < siglevel(significance level taken as input from user) from both subset data. Secondly, it merges the common significant variables from both data and creates a new data frame which contains columns, 'ID', 'OS', 'Death', 'PFS', 'Prog', 'Status' and observations of common significant
variables (which are supposed to be leading to death given they leads to progression of cancer as well as accounts for competing risks) Further, it lists the common variables names and correspond in results in .csv format by default in user’s current working directory.

On obtained commondata ‘hidimSurvlas’ fits LASSO and reduces the dimensions of study variables to handful significant variables.

hidimSurvlas(m,n,siglevel,data)

1) Subject ID column should be named as ‘ID’.
2) OS column must be named as ‘OS’.
3) Death status/event column should be named as ‘Death’.
4) Progression Free Survival column should be named as ‘PFS’.
5) Progression event column should be named as ‘Prog’.

deathtdata - A data frame with status column includes only those rows/subjects for which death/event was observed or not, given progression was observed or not.

compdata - A data frame with status column which includes those rows/subjects who died given progression was observed.

data1variables - List of variables/genes from deathdata

data2variables - List of variables/genes from compdata

significantpvalueA - A data frame with estimate values, HR, Pvalue, etc. of significant variables from deathdata.

significantpvalueB - A data frame with estimate values, HR, Pvalue, etc. of significant variables from compdata.

commongenes - A data frame consisting observations on common significant study variables.

cvar - List of common significant study variables.

commondata - A final data out consisting survival information ans observations on common significant study variables.

By default the function stores the output in .csv forms in current directory of user.

Value

List of significant genes

Author(s)

Atanu Bhattacharjee and Akash Pawar

References


hidimsvc

Survival analysis on high dimensional by creating batches of variables

hidimsvc(m, n, batchsize, siglevel, ID, OS, Death, PFS, Prog, data)

- **m**: Starting column number form where study variables of high dimensional data will get selected.
- **n**: Ending column number till where study variables of high dimensional data will get selected.
- **batchsize**: Number of variables to be consider at time while running function (maximum batch size should not be greater than one third of the total number of high dimensional variables)
- **siglevel**: Level of significance pre-determined by the user
- **ID**: Column name of subject ID, a string value. i.e. "id"
- **OS**: Column name of survival duration event, a string value. i.e. "os"
- **Death**: Column name of survival event, a string value. i.e "death"
- **PFS**: Column name of progression free survival duration, a string value. i.e "pfs"
- **Prog**: Column name of progression event, a string value. i.e "prog"
- **data**: High dimensional data containing the survival, progression and genomic observations.

**Details**

hidimsvc function fits Univariate Cox Proportional Hazard models by considering each variables at a time. Then it filters out study variables having P-value < siglevel(significance level taken as input from user). Once by survival and survival event and another by progression and progression events. Secondly, it merges the common significant variables from both OS and PFS analysis and creates a new data frame which contains columns, 'ID', 'OS', 'Death', 'PFS', 'Prog', 'Status' and observations of common significant variables (which are supposed to be leading to death given they leads to
progression of cancer as well as accounts for competing risks. Further, it lists the common variables names and outs corresponding results in .csv format by default in user’s current working directory. It works similary to HiDimSurv unlike it creates batches of decided study variables by user to make the analysis less time consuming.

hidimsvc(m1,m2,batchsize,siglevel,data),
1) Subject ID column should be named as 'ID'.
2) OS column must be named as 'OS'.
3) Death status/event column should be named as 'Death'.
4) Progression Fress Survival column should be named as 'PFS'.
5) Progression event column should be named as 'Prog'.

OSDeathcoeff - A data frame containing HR estimates and p-values for study variables on fitting univariate CoxPh on OS and Survival event. 
PFSProgcoeff - A data frame containing HR estimates and p-values for study variables on fitting univariate CoxPh on PFS and Progression event.
namvect - List of all the study variable names.

significantOSDeathgenes - A data frame containing HR estimates and p-values for significant study variables.

significantPFSProggenes - A data frame containing HR estimates and p-values for significant study variables

commongenes - A data frame containing estimated values of significant study variables found common from significant study variables on fitting CoxPh on survival and progression times and events.

odnames - List of significant variables on fitting CoxPh using survival and survival event.

ppnames - List of significant variables on fitting CoxPh using progression and progression event.
cvar - List of common significant study variables on fitting CoxPh on survival and progression, times and events.

commondata - A data out which contains the clinical observations and observations on common-
genes variables.

Value

Estimate values of significant variables/DEGs on considering Death with Progression
Estimate values of significant variables/DEGs on considering Death without Progression
List of variable/DEGs considering Death with Progression
List of variable/DEGs considering Death without Progression
Estimates data for the DEGs/Variables found common between significant DEGs from data having death due to progression and data showing death without progression
List of variable/DEGs found common between significant DEGs from data having death due to progression and data showing death without progression

Author(s)

Atanu Bhattacharjee and Akash Pawar
References


Examples

##
data(hnscc)
hidimsvc(7,105,5,0.05,ID="id",0S="os",Death="death",PFS="pfs",Prog="prog",hnscc)
##

hnscc High dimensional genomic data on head and neck cancer

Description

High dimensional breast cancer gene expression data

Usage

hnscc

Format

A dataframe with 565 rows and 104 variables

id  ID of subjects
leftcensor Initial censoring time
death Survival event
os Duration of overall survival
pfs Duration of progression free survival
prog Progression event
GJB1,...,HMGCS2 High dimensional covariates

Examples

## Not run:
data(hnscc)
## End(Not run)
multicoxa

Description

Given the dimensions of the variables and survival informations. The function performs multivariate Cox PH by taking 5 variables at a time.

Usage

multicoxa(m, n, OS, event, data)

Arguments

m  Starting number of column from where multivariate variables will get selected.
n  Ending number of column till where multivariate variables will get selected.
OS  "Column/Variable name" consisting duration of survival.
event  "Column/Variable name" consisting survival event.
data  High dimensional data containing survival observations and covariates.

Value

Data set containing the survival estimates and Pvalue.

Examples

##
multicoxa(m=15, n=18, OS="os", event="death", data=hnscc)

multicoxb

Description

Given the dimensions of the variables and survival informations. The function performs multivariate Cox PH by taking 5 variables at a time.
Usage

```
multicoxb(
    C1 = NULL,
    C2 = NULL,
    C3 = NULL,
    C4 = NULL,
    C5 = NULL,
    OS,
    event,
    data
)
```

Arguments

- `C1` Covar1
- `C2` Covar2
- `C3` Covar3
- `C4` Covar4
- `C5` Covar5
- `OS` "Column/Variable name" consisting duration of survival.
- `event` "Column/Variable name" consisting survival event.
- `data` High dimensional data containing survival observations and covariates.

Value

Data set containing the survival estimates and Pvalue.

Examples

```
##
multicoxb(C1="GJB1",C2=NULL,C3="HPN",C4=NULL,C5=NULL,OS="os",event="death",data=hnscc)
```

---

**survdesc**

*High dimensional univariate cox proportional hazard analysis.*

Description

Given the dimension of variables and survival information the function performs uni-variate Cox PH.

Usage

```
survdesc(m, n, survdur, event, aic = TRUE, data)
```
Arguments

m  Starting column number from where study variables of high dimensional data will get selected.

n  Ending column number till where study variables of high dimensional data will get selected.

survdur  Column name of survival duration event, a string value. i.e. "os"

event  Column name of survival event, a string value. i.e "death"

aic  By default aic = FALSE, if aic = TRUE the function returns

data  High dimensional data containing the survival, progression and genomic observations.

Value

A data set containing estimates for variables present in column m to n.

Examples

```
##
data(hnscc)
survdesc(m=10,n=50,survdur="os",event="death",aic=TRUE,data=hnscc)
##
```
Index

* datasets
  hnscc, 18

hdClust, 2
hdNetwork, 4
hidimLasso, 6
hidimSurv, 7
hidimSurvbon, 9
hidimSurvbonlas, 12
hidimSurvlas, 14
hidimsvc, 16
hnscc, 18

multicoxa, 19
multicoxb, 19

survdesc, 20