Package: highMLR (via r-universe)

Title Feature Selection for High Dimensional Survival Data

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Depends R (>= 3.5.0)

Imports mlr3, mlr3learners, survival, gtools, tibble, dplyr, utils, coxme, missForest, R6

LazyData Yes

LazyDataCompression xz

ByteCompile Yes

Description Perform high dimensional Feature Selection in the presence of survival outcome. Based on Feature Selection method and different survival analysis, it will obtain the best markers with optimal threshold levels according to their effect on disease progression and produce the most consistent level according to those threshold values. The functions' methodology is based on by Sonabend et al (2021) <doi:10.1093/bioinformatics/btab039> and Bhattacharjee et al (2021) <arXiv:2012.02102>.

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Encoding UTF-8

NeedsCompilation no

Maintainer Atanu Bhattacharjee <atanustat@gmail.com>

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Author Atanu Bhattacharjee [aut, cre, ctb], Gajendra K. Vishwakarma [aut, ctb], Souvik Banerjee [aut, ctb]

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Contents

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hnscc	*High dimensional head and neck cancer survival and gene expression data*

Description

High dimensional head and neck cancer gene expression data

Usage

```
hnscc
```

Format

A dataframe with 565 rows and 104 variables

ID "Column/Variable name" consisting id of subjects

Death "Column/Variable name" consisting survival event

OS "Column/Variable name" consisting duration of overall survival

PFS "Column/Variable name" consisting duration of progression free survival

Prog "Column/Variable name" consisting progression event

GJB1,...,HMGCS2 High dimensional covariates

Examples

```
data(hnscc)
```

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mlclassCox	*Applications of machine learning in survival analysis by prognostic classification of genes by CoxPH model.*

Description

Applications of machine learning in survival analysis by prognostic classification of genes by CoxPH model.

Usage

```
mlclassCox(m, n, idSurv, idEvent, Time, s_ID, per = 20, fold = 3, data)
```

Arguments

m	Starting column number from where high dimensional variates to be selected.
n	Ending column number till where high dimensional variates to be selected.
idSurv	"Column/Variable name" consisting duration of survival.
idEvent	"Column/Variable name" consisting survival event.
Time	"Column/Variable name" consisting Times of repeated observations.
s_ID	"Column/Variable name" consisting unique identification for each subject.
per	Percentage value for ordering, default=20.
fold	Number of folds for re-sampling, default=3.
data	High dimensional data containing survival observations with multiple covariates.

Value

A list of genes as per their classifications

GeneClassification List of genes classified using Cox proportional hazard model

GeneClassification$Positive_Gene Sublist of genes classified as positive genes

GeneClassification$Negative_Gene Sublist of genes classified as negative genes

GeneClassification$Volatile_Gene Sublist of genes classified as volatile genes

Result A dataframe consisting threshold values with corresponding coefficients and p-values.

Examples

```
## Not run:
data(srdata)
mlclassCox(m=50,n=59,idSurv="OS",idEvent="event",Time="Visit",s_ID="ID",per=20,fold=3,data=srdata)

## End(Not run)
```

mlclassKap	*Applications of machine learning in survival analysis by prognostic classification of genes by Kaplan-Meier estimator.*

Description

Applications of machine learning in survival analysis by prognostic classification of genes by Kaplan-Meier estimator.

Usage

```
mlclassKap(m, n, idSurv, idEvent, Time, s_ID, per = 20, fold = 3, data)
```

Arguments

m	Starting column number from where high dimensional variates to be selected.
n	Ending column number till where high dimensional variates to be selected.
idSurv	"Column/Variable name" consisting duration of survival.
idEvent	"Column/Variable name" consisting survival event.
Time	"Column/Variable name" consisting timepoints of repeated observations.
s_ID	"Column/Variable name" consisting unique identification for each subject.
per	Percentage value for ordering, default=20.
fold	Number of fold for resampling, default=3.
data	High dimensional data containing survival observations and high dimensional covariates.

Value

A list of genes as per their classifications

GeneClassification List of genes classified using Cox proportional hazard model

GeneClassification$Positive_Gene Sublist of genes classified as positive genes

GeneClassification$Negative_Gene Sublist of genes classified as negative genes

GeneClassification$Volatile_Gene Sublist of genes classified as volatile genes

Result A dataframe consisting threshold values with corresponding coefficients and p-values.

Examples

```
 ## Not run:
##
mlclassKap(m=50,n=59,idSurv="OS",idEvent="event",Time="Visit",s_ID="ID",per=20,fold=3,data=srdata)
##

## End(Not run)
```

---

mlhighCox   *mlhighCox*

Description

This function extracts desired number of features based on minimum log-Loss function using Cox proportional hazard model as learner method on a high dimensional survival data.

Usage

```
mlhighCox(cols, idSurv, idEvent, per = 20, fold = 3, data)
```

Arguments

cols	A numeric vector of column numbers indicating the features for which the log Loss functions are to be computed
idSurv	The name of the survival time variable
idEvent	The name of the survival event variable
per	Percentage of total features to be selected, default value 20
fold	An integer denoting number of folds in cross validation, default value 3
data	A data frame that contains the survival and covariate information for the subjects

Details

Performs feature Selection using Cox PH on high-dimensional data

Using the Cox proportional hazard model on the given survival data, this function selects the most significant feature based on a performance measure. The performance measure is considered as logarithmic loss function. It is defined as,

$$L(f, t) = -log(f(t))$$

. The features with minimum log-loss function are extracted.

Value

A dataframe containing desired number of features and the corresponding log Loss function.

Author(s)

Atanu Bhattacharjee, Gajendra K. Vishwakarma & Souvik Banerjee

References

Sonabend, R., Király, F. J., Bender, A., Bernd Bischl B. and Lang M. mlr3proba: An R Package for Machine Learning in Survival Analysis, 2021, Bioinformatics, <https://doi.org/10.1093/bioinformatics/btab039>

See Also

mlhighKap, mlhighFrail

Examples

```
## Not run:
data(hnscc)
mlhighCox(cols=c(6:15), idSurv="OS", idEvent="Death", per=20, fold = 3, data=hnscc)

## End(Not run)
```

---

mlhighFrail   *mlhighFrail*

Description

This function extracts features based on minimum log-Loss function using Cox proportional hazard model as learner method on a high dimensional survival data. For those genes, we obtain frailty variances using CoxPH.

Usage

```
mlhighFrail(
  cols,
  idSurv,
  idEvent,
  idFrail,
  dist = "gaussian",
  per = 20,
  fold = 3,
  data
)
```

Arguments

cols	A numeric vector of column numbers indicating the features for which the log Loss functions are to be computed
idSurv	The name of the survival time variable
idEvent	The name of the survival event variable
idFrail	The name of the frailty variable
dist	The name of the frailty distribution. Options are "gamma", "gaussian" or "t", default is "gaussian"
per	Percentage of features to be selected, default value 20
fold	An integer denoting number of folds in cross validation, default value 3
data	A data frame that contains the survival and covariate information for the subjects

Details

Performs CoxPH frailty on high doimensional survival data

Using the Cox proportional hazard model on the given survival data, this function selects the most significant feature based on minimum logarithmic loss function. The logarithmic loss function is defined as,

$$L(f, t) = -log(f(t))$$

After selcting the most significant features, a Cox proportional hazard frailty model is fitted on the selected features. The CoxPH frailty model is defined as,

$$\lambda(t) = \lambda 0(t)\nu exp X'\beta$$

where ν is called the frailty component. The variance of the frailty term is considered as the heterogeneity among the subjects or patients. The distribution of frailty component is considered as either Gaussian, Gamma or t distribution.

Value

A dataframe containing desired number of features with corresponding frailty variances.

Author(s)

Atanu Bhattacharjee, Gajendra K. Vishwakarma & Souvik Banerjee

References

Sonabend, R., Kiraly, F. J., Bender, A., Bernd Bischl B. and Lang M. mlr3proba: An R Package for Machine Learning in Survival Analysis, 2021, Bioinformatics, <https://doi.org/10.1093/bioinformatics/btab039>

See Also

mlhighHet, mlhighCox

Examples

```
## Not run:
data(hnscc)
mlhighFrail(cols=c(10:20), idSurv="OS", idEvent="Death", idFrail="ID", dist="gaussian",
per=20, fold = 3, data=hnscc)

## End(Not run)
```

---

mlhighHet	*mlhighHet*

Description

This function extracts features based on ML method, finds optimal cut-off values of features using sequencial Cox PH model and obtain the most consistent level according to the cut-offs.

Usage

```
mlhighHet(cols, idSurv, idEvent, idFrail, num, fold = 3, data)
```

Arguments

cols	A numeric vector of column numbers indicating the features for which the log Loss functions are to be computed
idSurv	The name of the survival time variable
idEvent	The name of the survival event variable
idFrail	The name of the frailty variable
num	Number of features to be selected
fold	An integer denoting number of folds in cross validation, default value 3
data	A data frame that contains the survival and covariate information for the subjects

Details

Performs heterogeneity analysis in gene expression

This function extracts features based on minimum log-Loss function using Cox proportional hazard model as learner method on a high dimensional survival data. For those selected genes, we obtain optimal cutoff values using minimum p-value in a Cox PH model. The Cox PH model is used sequencially for each combination of genes and all possible gene combinations are tested to obtain best possible combination with minimum BIC value. The subjects are classified according to different levels of those genes. Using a Cox PH frailty model, we obtain the most consistent level for which the frailty variance is minimum. The data is splited using cross validation technique. The performance measure is considered as logarithmic loss function. It is defined as,

$$L(f, t) = -log(f(t))$$

The CoxPH frailty model is defined as,

$$\lambda(t) = \lambda 0(t)\nu exp X'\beta$$

where ν is called the frailty. The variance of the frailty term is considered as the heterogeneity among the subjects or patients. Gaussian distribution with mean 0 is considered for the distribution of frailty component.

Value

dataframes containing optimal gene cutoff values and most consistent level according to those cut-offs with frailty variance.

Author(s)

Atanu Bhattacharjee, Gajendra K. Vishwakarma & Souvik Banerjee

References

Sonabend, R., Király, F. J., Bender, A., Bernd Bischl B. and Lang M. mlr3proba: An R Package for Machine Learning in Survival Analysis, 2021, Bioinformatics, <https://doi.org/10.1093/bioinformatics/btab039>

Bhattacharjee, A. Vishwakarma, G.K. and Banerjee, S. A modified risk detection approach of biomarkers by frailty effect on multiple time to event data, 2020, <arXiv:2012.02102>.

See Also

mlhighCox, mlhighFrail

Examples

```
## Not run:
data(hnscc)
mlhighHet(cols=c(27:32), idSurv="OS", idEvent="Death", idFrail="ID", num=2, fold = 3, data=hnscc)

## End(Not run)
```

---

mlhighKap *mlhighKap*

Description

This function extracts desired number of features based on minimum log-Loss function using Kaplan Meier model as learner method on a high dimensional survival data.

Usage

```
mlhighKap(cols, idSurv, idEvent, per = 20, fold = 3, data)
```

Arguments

cols	A numeric vector of column numbers indicating the features for which the log Loss functions are to be computed
idSurv	The name of the survival time variable
idEvent	The name of the survival event variable
per	Percentage of features to be selected, default value 20
fold	An integer denoting number of folds in cross validation, default value 3
data	A data frame that contains the survival and covariate information for the subjects

Details

Performs feature selection using Kaplan Meier method

Using the Kaplan Meier method on the given survival data, this function selects the most significant feature based on a performance measure. The performance measure is considered as logarithmic loss function. It is defined as,

$$L(f, t) = -log(f(t))$$

. The features with minimum log-loss function are extracted.

Value

A dataframe containing desired number of features based on minimum log Loss function

Author(s)

Atanu Bhattacharjee, Gajendra K. Vishwakarma & Souvik Banerjee

References

Sonabend, R., Kiraly, F. J., Bender, A., Bernd Bischl B. and Lang M. mlr3proba: An R Package for Machine Learning in Survival Analysis, 2021, Bioinformatics

See Also

mlhighCox

Examples

```
## Not run:
data(hnscc)
mlhighKap(cols=c(6:15), idSurv="OS", idEvent="Death", per=20, fold = 3, data=hnscc)

## End(Not run)
```

---

srdata   *High dimensional protein gene expression data*

Description

High dimensional protein gene expression data

Usage

srdata

Format

A dataframe with 288 rows and 250 variables

ID "Column/Variable name" consisting id of subjects

Visit "Column/Variable name" consisting number of times observations recorded

event "Column/Variable name" consisting survival event

OS "Column/Variable name" consisting duration of overall survival

C6kine,.....,GFRalpha4 High dimensional covariates

Examples

```
data(srdata)
```

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