Package ‘remss’

October 14, 2022

Title Refining Evaluation Methodology on Stage System

Version 1.0.1

Description
T (extent of the primary tumor), N (absence or presence and extent of regional lymph node metastasis) and M (absence or presence of distant metastasis) are three components to describe the anatomical tumor extent. TNM stage is important in treatment decision-making and outcome predicting. The existing oropharyngeal Cancer (OPC) TNM stages have not made distinction of the two sub sites of Human papillomavirus positive (HPV+) and Human papillomavirus negative (HPV-) diseases. We developed novel criteria to assess performance of the TNM stage grouping schemes based on parametric modeling adjusting on important clinical factors. These criteria evaluate the TNM stage grouping scheme in five different measures: hazard consistency, hazard discrimination, explained variation, likelihood difference, and balance. The methods are described in Xu, W., et al. (2015) <`https://www.austinpublishinggroup.com/biometrics/fulltext/biometrics-v2-id1014.php`>.

Depends R (>= 3.5.0)

License GPL-2

Encoding UTF-8

LazyData true

Imports survival

RoxygenNote 6.1.1

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

`balance_measure` *Balance measurement.*

Description

`balance_measure` returns balance measurement for the grouping scheme.

Usage

```
balance_measure(OS_ind, stage_list, data)
```

Arguments

`OS_ind`	OS_ind is the survival indicator variable.
`stage_list`	stage_list original of each scheme.
`data`	Data set.

Value

Ranking of balance measurement and its standardized score.

References

Xu, W., et al. 'Refining evaluation methodology on TNM stage system: assessment on HPV-related oropharyngeal cancer.' Austin Biometrics and Biostatistics 2 (2015): 1014.

`explain_var_measure` *Explained variation measurement.*

Description

`explain_var_measure` returns explained variation measurement for the grouping scheme.

Usage

```
explain_var_measure(main_list, stage_list, stage_list_2, covar_list, data)
```

Arguments

`main_list`	main_list includes survival indicator variable, Duration time of survival variable and basic group variable.
`stage_list`	stage_list original of each scheme.
`stage_list_2`	stage_list_2 is numerical form of each scheme by using other of stages information.
`covar_list`	Covariate variables taking into consideration.
`data`	Data set.

Value

Ranking of explained variation measurement and its standardized score.

References

Xu, W., et al. 'Refining evaluation methodology on TNM stage system: assessment on HPV-related oropharyngeal cancer.' Austin Biometrics and Biostatistics 2 (2015): 1014.

`hz_cons_measure` *Hazard consistency measurement.*

Description

`hz_cons_measure` returns Hazard consistency for the grouping scheme.

Usage

```
hz_cons_measure(main_list, stage_list, covar_list, data)
```

Arguments

`main_list`	main_list includes survival indicator variable, Duration time of survival variable and basic group variable.
`stage_list`	stage_list is numerical form of each scheme by using other of stages information.
`covar_list`	Covariate variables taking into consideration.
`data`	Data set.

Value

Ranking of hazard consistency measurement and standardized score.

References

Xu, W., et al. 'Refining evaluation methodology on TNM stage system: assessment on HPV-related oropharyngeal cancer.' Austin Biometrics and Biostatistics 2 (2015): 1014.

`hz_dis_measure` *Hazard discrimination measurement.*

Description

`hz_dis_measure` returns hazard discrimination for the grouping scheme.

Usage

```
hz_dis_measure(main_list, stage_list, stage_list2, covar_list, data)
```

Arguments

`main_list`	main_list includes survival indicator variable, Duration time of survival variable and basic group variable.
`stage_list`	stage_list original of each scheme.
`stage_list2`	stage_list2 is numerical form of each scheme by using other of stages information.
`covar_list`	Covariate variables taking into consideration.
`data`	Data set.

Value

Ranking of hazard discrimination measurement and its standardized score.

References

Xu, W., et al. 'Refining evaluation methodology on TNM stage system: assessment on HPV-related oropharyngeal cancer.' Austin Biometrics and Biostatistics 2 (2015): 1014.

`lik_diff_measure` *Likelihood difference measurement.*

Description

`lik_diff_measure` returns likelihood difference for the grouping scheme.

Usage

```
lik_diff_measure(main_list, stage_list, covar_list, data)
```

Arguments

`main_list`	main_list includes survival indicator variable, Duration time of survival variable and basic group variable.
`stage_list`	stage_list is numerical form of each scheme by using other of stages information.
`covar_list`	Covariate variables taking into consideration.
`data`	Data set.

Value

Ranking of likelihood difference measurement and its standardized score.

References

Xu, W., et al. 'Refining evaluation methodology on TNM stage system: assessment on HPV-related oropharyngeal cancer.'Austin Biometrics and Biostatistics 2 (2015): 1014.

`overall_rank` *Overall Ranking.*

Description

`overall_rank` returns overall ranking for the grouping scheme.

Usage

```
overall_rank(HCM, HDM, LDM, EVM, BM, weight)
```

Arguments

`HCM`	HCM is the hazard consistency measurement results.
`HDM`	HDM is the hazard discrimination measurement results.
`LDM`	LDM is the likelihood difference measurement results.
`EVM`	EVM is the explained variance measurement results.
`BM`	BM is the balance measurement results.
`weight`	weight vector of five measurements.

Value

Overall score and overall ranking.

References

Xu, W., et al. 'Refining evaluation methodology on TNM stage system: assessment on HPV-related oropharyngeal cancer.' Austin Biometrics and Biostatistics 2 (2015): 1014.

`rank` *Refining evaluation methodology on stage system.*

Description

`rank` returns five measurements for the grouping scheme and its overall rank.

Usage

```
rank(os, ostime, groupvar, scheme, order, covariate, weight, data)
```

Arguments

`os`	Survival indicator, 1 for death, 0 for censoring.
`ostime`	Duration time of survival.
`groupvar`	Basic group variable having the most number of stages.
`scheme`	Different grouping scheme, which has less stages than the basic group variable.
`order`	The other of stages in each grouping, from
`covariate`	Covariate variables taking into consideration.
`weight`	Weight on five measurements of grouping scheme.
`data`	Data set.

Value

Ranking of five measurements, which are Hazard consistency, Hazard discrimination, Explained variation, Likelihood difference and Balance. By standardized each measurement score, we provides overall ranking of schemes.

References

Xu, W., et al. 'Refining evaluation methodology on TNM stage system: assessment on HPV-related oropharyngeal cancer.' Austin Biom Biostat 2 (2015): 1014.

Examples

```
data(Rdata)
Scheme=c('Scheme.1','Scheme.2','Scheme.3')
Covar=c('Age','Treatment')
weight=c(1,1,0.5,0.5,1)
Order=list(c('I','II','III'),c('I','II','III','IV'),c('I','II','III','IV'))
rank(os='OS',ostime='survmonth',groupvar='Basic_group', scheme=Scheme, order=Order,
     covariate=Covar,weight=weight,data=Rdata)
```

`Rdata` *Simulation data for Genetic association models for X-chromosome SNPS*

Description

A simulated dataset containing 504 observations. The variables list as follows:

Usage

`data(Rdata)`

Format

A data frame with 504 rows and 10 variables.

Details

- Id Identification number.
- Gender 1 for male, 0 for female.
- Age Age variable.
- OS Survival indicator, 1 for death, 0 for censoring.
- survmonth Duration time of survival.
- Treatment Treatment variable.
- Basic_group Basic group variable having the most number of stages.
- Scheme.1 Grouping scheme 1.
- Scheme.2 Grouping scheme 2.
- Scheme.3 Grouping scheme 3.

`remss` *remss: A package for refining evaluation methodology on stage system.*

Description

TNM stage is important in treatment decision-making and outcome predicting. The existing oropharyngeal Cancer (OPC) TNM stages have not made distinction of the two sub sites of HPV+ and HPV- diseases.We developed novel criteria to assess performance of the TNM stage grouping schemes based on parametric modeling adjusting on important clinical factors. These criteria evaluate the TNM stage grouping scheme in five different measures: hazard consistency, hazard discrimination, explained variation, likelihood difference, and balance.

remss functions

rank

References

Xu, W., et al. 'Refining evaluation methodology on TNM stage system: assessment on HPV-related oropharyngeal cancer.' Austin Biom Biostat 2 (2015): 1014.

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