Package: OneSampleLogRankTest (via r-universe)

September 2, 2024

Title One-Sample Log-Rank Test

Version 0.9.2

Imports magrittr, dplyr, ggplot2, survival, survminer, rlang

Description The log-rank test is performed to assess the survival outcomes between two group. When there is no proper control group or obtaining such data is cumbersome, one sample log-rank test can be applied. This package performs one sample log-rank test as described in Finkelstein et al. (2003)<doi:10.1093/jnci/djt227> and variation of the test for small sample sizes which is detailed in FD Liddell (1984)<doi:10.1136/jech.38.1.85> paper. Visualization function in the package generates Kaplan-Meier Curve comparing survival curve of the general population against that of the population of interest.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Depends R (>= 3.5.0)

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Repository https://dkangeyan.r-universe.dev

RemoteUrl https://github.com/cran/OneSampleLogRankTest

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Contents

`dataPop_1999_2020` *Population data (1999-2020)*

Description

This data set contains mortality rate for various demographic groups by age. all column has overall mortality rate for all groups. Race groups are indicated by the following notation: w - white, b - black, ai - american indian and as - asian. Female and Males are indicated by an additional suffix _f and _m.

Usage

```
dataPop_1999_2020
```

Format

A dataframe with 16 columns and 151 rows.

Source

CDC Wonder Database. Data Colleceted from 1999 - 2020

References

https://wonder.cdc.gov/

`dataPop_2018_2021` *Population data (2018_2021)*

Description

This data set contains mortality rate for various demographic groups by age. all column has overall mortality rate for all groups. Race groups are indicated by the following notation: w - white, b - black, ai - american indian and as - asian, nh - native hawaiian. Female and Males are indicated by an additional suffix _f and _m.

Usage

```
dataPop_2018_2021
```

Format

A dataframe with 19 columns and 151 rows.

Source

CDC Wonder Database. Data Colleceted from 2018_2021

References

https://wonder.cdc.gov/

`dataPop_2018_2021_race_sex_eth` *Population data (2018_2021) by race, sex, ethnicity*

Description

This data set contains mortality rate for various demographic groups by age. all column has overall mortality rate for all groups. Race groups are indicated by the following notation: w - white, b - black, ai - american indian and as - asian, nh - native hawaiian. Female and Males are indicated by an additional suffix _f and _m.

Usage

```
dataPop_2018_2021
```

Format

A dataframe with 16 columns and 151 rows.

Source

CDC Wonder Database. Data Colleceted from 2018_2021

References

https://wonder.cdc.gov/

`dataSurv` *Survival data*

Description

This data set is obtained from Finkelstein et al. paper that contains the following five columns: age, time, event status, sex and race.

Usage

`dataSurv`

Format

A dataframe with 5 columns and 33 rows.

Source

Finkelstein et al. (2003)

References

Finkelstein, D. M., Muzikansky, A., & Schoenfeld, D. A. (2003). Comparing survival of a sample to that of a standard population. Journal of the National Cancer Institute, 95(19), 1434-1439.

`dataSurv_small` *Survival data*

Description

This data set is subset of data obtained from Finkelstein et al. paper that contains the following five columns: age, time, event status, sex and race. In order to apply the exact test 12 patients were randomly selected out of 33 patients.

Usage

`dataSurv`

Format

A dataframe with 5 columns and 12 rows.

Source

Finkelstein et al. (2003)

References

Finkelstein, D. M., Muzikansky, A., & Schoenfeld, D. A. (2003). Comparing survival of a sample to that of a standard population. Journal of the National Cancer Institute, 95(19), 1434-1439.

`findMatchedCumuSurvProb` *Find Matched Cumulative Survival Probability*

Description

Find Matched Cumulative Survival Probability

Usage

```
findMatchedCumuSurvProb(time, ageDiag, sex, race, dataPop, maxFollowUp = NULL)
```

Arguments

`time`	follow up length
`ageDiag`	age at diagnosis
`sex`	sex
`race`	race
`dataPop`	Population level mortality data
`maxFollowUp`	maximum follow-up, if max follow-up not provided then the time would be considered until death or censoring

Value

matched survival probability

Examples

```
# load data
data(dataSurv_small)
data(dataPop_2018_2021)

# Extract info for the first subject
time_vec <- dataSurv_small$time[1]
age_vec <- dataSurv_small$age[1]
sex_vec <- dataSurv_small$sex[1]
race_vec <- dataSurv_small$race[1]

# Generate cumulative survival probability
findMatchedCumuSurvProb(time = time_vec, ageDiag = age_vec, sex = sex_vec,
race = race_vec, dataPop = dataPop_2018_2021)

#If maximum followup is determined to be 20 years
findMatchedCumuSurvProb(time = time_vec, ageDiag = age_vec, sex = sex_vec,
race = race_vec, dataPop = dataPop_2018_2021, maxFollowUp = 20)
```

`oneSampleLogRankTest` *Calculate One-Sample Log-Rank Test*

Description

Calculate One-Sample Log-Rank Test

Usage

```
oneSampleLogRankTest(dataSurv, dataPop, type = c("exact", "approximate"))
```

Arguments

`dataSurv`	Survival data
`dataPop`	Population data
`type`	Type of test

Value

p-value for one-sample log-rank test

Examples

```
# load data
data(dataSurv_small)
data(dataPop_2018_2021)

# Since the dataset is small run an exact test
oneSampleLogRankTest(dataSurv_small, dataPop_2018_2021, type = "exact")
```

`plotKM` *Plot Kaplan-Meier Curve against Population*

Description

Plot Kaplan-Meier Curve against Population

Usage

```
plotKM(dataSurv, dataPop, type = c("exact", "approximate"))
```

Arguments

`dataSurv`	Survival data
`dataPop`	Population data
`type`	Type of test to conduct in order to display p-value

Value

ggplot object

Examples

```
# load data
data(dataSurv_small)
data(dataPop_2018_2021)

plotKM(dataSurv_small, dataPop_2018_2021, type = "exact")
```

`simulated_clinical_data` *Simultaed Clinical data*

Description

This data is simulated data from clinical trial data that contains five columns: race, sex, age, event status and time in years.

Usage

```
simulated_clinical_data
```

Format

A dataframe with 5 columns and 500 rows.

Source

Simulated

References

None

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