

Package ‘OneSampleLogRankTest’

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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](https://doi.org/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](https://doi.org/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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| | |
|-------------------|------------------------------------|
| dataPop_1999_2020 | <i>Population data (1999-2020)</i> |
|-------------------|------------------------------------|

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 Collected from 1999 - 2020

References

<https://wonder.cdc.gov/>

| | |
|-------------------|------------------------------------|
| dataPop_2018_2021 | <i>Population data (2018_2021)</i> |
|-------------------|------------------------------------|

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 Collected 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 Collected 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.

findMatchedCumSurvProb

Find Matched Cumulative Survival Probability

Description

Find Matched Cumulative Survival Probability

Usage

```
findMatchedCumSurvProb(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
findMatchedCumSurvProb(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

| | |
|-----------------------|---|
| <code>dataSurv</code> | Survival data |
| <code>dataPop</code> | Population data |
| <code>type</code> | 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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