

Package: nnt (via r-universe)

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Type Package

Title The Number Needed to Treat (NNT) for Survival Endpoint

Version 0.1.4

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Description Estimate the NNT using the proposed method in Yang and Yin's paper (2019) <[doi:10.1371/journal.pone.0223301](https://doi.org/10.1371/journal.pone.0223301)>, in which the NNT-RMST (number needed to treat based on the restricted mean survival time) is defined as the RMST (restricted mean survival time) in the control group divided by the difference in RMSTs between the treatment and control groups up to a chosen time t .

Depends R ($\geq 3.2.0$)

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Imports stats, survival, survRM2

License GPL-3

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LazyData true

RoxygenNote 7.0.2

NeedsCompilation no

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Repository <https://yangzhao98.r-universe.dev>

RemoteUrl <https://github.com/cran/nnt>

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| | |
|--------|--|
| KM2NNT | <i>Calculate the NNT based on the Kaplan-Meier estimated survival rates between the treatment and control groups</i> |
|--------|--|

Description

For survival endpoints, the NNT-KM is computed as the reciprocal of the absolute risk reduction (ARR), which is the difference in Kaplan-Meier estimated survival rates or the difference in cumulative incidences at a time point of clinical interest between the treatment and control groups.

Usage

```
KM2NNT(time, status, arm, tau = NULL, confint = 0.95, digits = 3)
```

Arguments

| | |
|---------|--|
| time | The time to event or censor. |
| status | The indicator of the event or censor at the end of the follow-up. |
| arm | The variable indicates the treatment (arm = 1) and control (arm = 0) groups. |
| tau | The chosen time point of clinical interest. |
| confint | The percentile of confidence interval. The default value is confint = 0.95. |
| digits | The decimal of the results. The default value is digits = 3. |

Value

A matrix contains the KM-NNT and its confidence interval.

References

1. Altman DG, Andersen PK: Calculating the number needed to treat for trials where the outcome is time to an event. *BMJ* 319:1492-5, 1999
2. Altman DG: Confidence intervals for the number needed to treat. *BMJ* 317:1309-12, 1998

Examples

```
library(survival)
dat <- pbc[!is.na(pbc$trt),]
time <- dat$time/365.25
status <- (dat$status == 2) + 0
arm <- (dat$trt == 2) + 0
KM2NNT(time, status, arm, tau = NULL, confint = 0.95, digits = 3)
```

| | |
|--------|---|
| RM2NNT | <i>Calculate the NNT based on the restricted mean survival times between the treatment and control groups</i> |
|--------|---|

Description

For survival endpoints, the NNT-RMST is defined as the RMST in the control group divided by the difference in RMSTs between the treatment and control groups up to a chosen time t .

Usage

```
RM2NNT(time, status, arm, tau = NULL, confint = 0.95, digits = 3)
```

Arguments

| | |
|----------------------|--|
| <code>time</code> | The time to event or censor. |
| <code>status</code> | The indicator of the event or censor at the end of the follow-up. |
| <code>arm</code> | The variable indicates the treatment ($arm = 1$) and control ($arm = 0$) groups. |
| <code>tau</code> | The chosen time point of clinical interest. |
| <code>confint</code> | The percentile of confidence interval. The default value is $confint = 0.95$. |
| <code>digits</code> | The decimal of the results. The default value is $digits = 3$. |

Value

A matrix contains the RMST-NNT and its confidence interval.

References

1. An alternative approach for estimating the number needed to treat for survival endpoints. PLoS One. 2019 Oct 18;14(10):e0223301. doi: 10.1371/journal.pone.0223301.

Examples

```
library(survival)
dat <- pbc[!is.na(pbc$trt),]
time <- dat$time/365.25
status <- (dat$status == 2) + 0
arm <- (dat$trt == 2) + 0
RM2NNT(time, status, arm, tau = NULL, confint = 0.95, digits = 3)
```

| | |
|--------|--|
| RMvsKM | <i>Compare the performance between the NNT-RMST and NNT-KM through the average life gain per patient</i> |
|--------|--|

Description

For the NNT-RMST, the average life gain per patient is the area between the survival curves, which is the intrinsic treatment benefit in survival time during the t-period follow-up. For the NNT-KM, the average life gain per patient is defined as the ratio between the average survival time of one death in patients and the NNT-KM up to t.

Usage

```
RMvsKM(time, status, arm, tau = NULL, confint = 0.95, digits = 3)
```

Arguments

| | |
|---------|--|
| time | The time to event or censor. |
| status | The indicator of the event or censor at the end of the follow-up. |
| arm | The variable indicates the treatment (arm = 1) and control (arm = 0) groups. |
| tau | The chosen time point of clinical interest. |
| confint | The percentile of confidence interval. The default value is confint = 0.95. |
| digits | The decimal of the results. The default value is digits = 3. |

Value

A list contains:

| | |
|----------|---|
| RMSTNNT | The RMST-NNT and its confidence interval. |
| KMNNT | The KM-NNT and its confidence interval. |
| LifeGain | The average life gain per patient based on the RMST-NNT and KM-NNT. |

References

1. An alternative approach for estimating the number needed to treat for survival endpoints. PLoS One. 2019 Oct 18;14(10):e0223301. doi: 10.1371/journal.pone.0223301.

Examples

```
library(survival)
dat <- pbc[!is.na(pbc$trt),]
time <- dat$time/365.25
status <- (dat$status == 2) + 0
arm <- (dat$trt == 2) + 0
RMvsKM(time, status, arm, tau = NULL, confint = 0.95, digits = 3)
```

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