# Package 'coxphm'

May 8, 2026

**Type** Package

**Title** Time-to-Event Data Analysis with Missing Survival Times

**Version** 0.2.1

**Date** 2025-07-02

**Description**
Fits a pseudo Cox proprotional hazards model when survival times are missing for control groups.

**License** GPL (>= 2)

**Depends** R (>= 4.2.0), survival, MASS, stats

**NeedsCompilation** no

**Author** Yunro Chung [aut, cre] (ORCID: <https://orcid.org/0000-0001-9125-9277>)

**Maintainer** Yunro Chung <yunro.chung@asu.edu>

**Repository** CRAN

**Date/Publication** 2025-07-22 17:51:25 UTC

## Contents



---

coxphm *Time-to-Event Data Analysis with Missing Survival Times*

---

### Description

Fits a pseudo Cox proprotional hazards model that allow us to analyze time-to-event data when survival times are missing for control groups.

### Usage

```
coxphm(time, status, trt, z, beta0, time0, Atime, Btime, u, s, maxiter, eps)
```

## Arguments

| | |
|---|---|
| time | Right-censored survival time (time is observed if trt=1. time is not observed if trt=0.) |
| status | Event indicator (status=1 if event, status=0 otherwise.) |
| trt | Treatment (or missing) indicator: trt=1 if treatment group (or no missing), trt=0 if control group (missing survival time). |
| z | Predictors (vector or matrix), where z[,1] must be the same as trt. |
| beta0 | Initial value of regression parameters. |
| time0 | Initial value of (pseudo) survival times for trt=0. |
| Atime | Duration from treatment available to time-origin. |
| Btime | Duration from treatment available to survival time. Missing if trt=1. |
| u | A variable to estimate time0. See the below. |
| s | Smoothed parameter. (If s=NULL, s=1/qnorm(exp(-n^(-2)))*0.01 is used, where n is the number of samples.) |
| maxiter | Number of maximim iteration. Default: maxiter=1000. |
| eps | Stopping critiera. Default: eps=0.01. |

## Details

It is not possible to estimate treatment effects under Cox's proportional hazards model when survival times for subjects in the control group are missing. The coxphm function addresses this by regarding the missing survival times as nuisance parameters. A pseudo partial likelihood function is then used to estimate the regression coefficients and nuisance parameters simultaneously with an unspecified baseline hazard function.

In the pseudo partial likelihood function, a smoothed parameter s is used to approximate the risk sets as cumulative normal distributions. Choosing a sufficiently small value of s ensures that the pseudo partial likelihood closely approximates the partial likelihood.

The method is sensitive to the choice of initial values; therefore, it is crucial to choose these values as close as possible to the true values. If this is not feasible, a data-driven approach is used to determine initial values as follows. If beta0=NULL, a logistic regression is used to model the probability of status=1 using z as a predictor, and beta0 is set to the estimated regression coefficient(s). If time0=NULL, a linear regression is used to model Atime using u as a predictor, and time0 is set to Btime minus estimated Atime. Here, u and Btime are observed for all subjects, while Atime is observed only for subjects with trt = 1.

## Value

| | |
|---|---|
| conv | Algorithm convergence: yes or not. |
| beta | Estimated regression parameter: beta: estimated coefficient, se: standard error; lcl: 95% lower confidence limit, ucl: 95% upper confidence limit, statistics: test statistics; pvalue: pvalue. |
| eta | Estimated pseudo survival time. |
| loglik | Log pseudo-partial-likelihood value. |
| iter | Number of iterations. |

## Author(s)

Yunro Chung [aut, cre]

## References

Chung, Y., Murugan, V., Beyene, K, and Chen, D., Pseudo partial likelihood method for proportional hazards models when time origin is missing for control group with applications to SARS-CoV-2 Seroprevalence Study. Journal of Data Science (under review).

## Examples

```
#Mayo's pbc dataset from the survival package.
pbc1=pbc[1:200,] #use the first 200 patients
time=pbc1$time
status=pbc1$status
status[which(status==1)]=0 #transplant
status[which(status==2)]=1 #death
trt=pbc1$trt
trt[which(trt==2)]=0 #0 for placebo, 1 for treatment
age=pbc1$age
z=cbind(trt,age)
colnames(z)=c("trt","age")

#0. Cox model
fit0=coxph(Surv(time,status)~z)

#1. Pseudo-Cox model
#1.1. set (true) initial value
beta0=fit0$coefficients
time0=time[which(trt==0)]

#1.2. fits pseudo-Cox, assuming survival times are missing if trt=0
time[which(trt==0)]=NA
fit1=coxphm(time, status, trt=trt, z=z, beta0=beta0, time0=time0)

#2. Cox vs Pseudo-Cox
print(summary(fit0)$coefficient)
print(fit1$beta)
```

# Index