

Reciprocal Chimera Cox Proportional Hazard Model

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2020-07-02

```
if (!require("pacman")) install.packages("pacman")

## Loading required package: pacman
pacman::p_load("tidyverse", "survival", "survminer", "readr")

library(tidyverse)
library(survival)
library(survminer)
library(readr)

urlfile <- "https://raw.githubusercontent.com/wht10/Chimera_Survival/master/Recip_Chimera.csv"
dat <- read_csv(url(urlfile))

## Parsed with column specification:
## cols(
##   days_pi = col_double(),
##   censored = col_double(),
##   donor_genotype = col_character(),
##   recip_genotype = col_character(),
##   rep = col_double()
## )

dat <- dat %>% mutate(donor_genotype = as.factor(donor_genotype)) %>%
  mutate(recip_genotype = as.factor(recip_genotype)) %>%
  mutate(rep = as.factor(rep))

res.cox <- coxph(Surv(days_pi, censored) ~ donor_genotype*recip_genotype + donor_genotype*rep + recip_genotype*rep +
  donor_genotype:recip_genotype*rep, data = dat)
summary(res.cox)

## Call:
## coxph(formula = Surv(days_pi, censored) ~ donor_genotype * recip_genotype +
##   donor_genotype * rep + recip_genotype * rep + donor_genotype:recip_genotype *
##   rep, data = dat)
##
## n= 59, number of events= 58
##
##               coef exp(coef) se(coef)      z Pr(>|z|)
## donor_genotypeWT    0.35005   1.41915  0.54486  0.642  0.52057
## recip_genotypeWT    1.55272   4.72429  0.55715  2.787  0.00532 **
## rep2              -0.10806   0.89758  0.51941 -0.208  0.83520
## donor_genotypeWT:recip_genotypeWT  0.03238   1.03291  0.74473  0.043  0.96532
## donor_genotypeWT:rep2    0.90340   2.46798  0.78206  1.155  0.24802
```

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## recip_genowT:rep2          0.68820   1.99013   0.75193   0.915   0.36006
## donor_genowT:recip_genowT:rep2 -0.97394   0.37759   1.08094  -0.901   0.36758
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##               exp(coef) exp(-coef) lower .95 upper .95
## donor_genowT      1.4191    0.7046   0.48780    4.129
## recip_genowT      4.7243    0.2117   1.58523   14.079
## rep2              0.8976    1.1141   0.32430    2.484
## donor_genowT:recip_genowT  1.0329    0.9681   0.23996    4.446
## donor_genowT:rep2    2.4680    0.4052   0.53291   11.430
## recip_genowT:rep2    1.9901    0.5025   0.45587    8.688
## donor_genowT:recip_genowT:rep2  0.3776    2.6484   0.04539    3.141
##
## Concordance= 0.762 (se = 0.035 )
## Likelihood ratio test= 32.56 on 7 df,  p=3e-05
## Wald test              = 28.81 on 7 df,  p=2e-04
## Score (logrank) test = 35.72 on 7 df,  p=8e-06

```

Sources: 1. [<http://www.sthda.com/english/wiki/cox-proportional-hazards-model>] 2. [<http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.459.4496&rep=rep1&type=pdf>]