

# Package: copcor (via r-universe)

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**LazyLoad** yes

**Version** 2024.7-31

**Title** Correlates of Protection and Correlates of Risk Functions

**Depends** R (>= 3.6), kyotil

**Imports** methods

**Suggests** RUnit, R.rsp, survival

**Description** Correlates of protection (CoP) and correlates of risk (CoR) study the immune biomarkers associated with an infectious disease outcome, e.g. COVID or HIV-1 infection. This package contains shared functions for analyzing CoP and CoR, including bootstrapping procedures, competing risk estimation, and bootstrapping marginalized risks.

**VignetteBuilder** R.rsp

**License** GPL (>= 2)

**NeedsCompilation** no

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copcor	<i>copcor</i>
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**Description**

Functions used in the study of correlates of protection and correlates of risk.

See the [Index](#) link below for a list of available functions.

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cove.boost.collapse.strata	<i>Collapse sample strata for COVE boost correlates study</i>
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**Description**

Collapse sample strata for COVE boost correlates study

**Usage**

```
cove.boost.collapse.strata (dat.b, n.demo)
```

**Arguments**

dat.b	data frame
n.demo	number of demographics strata, e.g. 6 for COVE correlates

**Details**

This function is used by both `correlates_processing` repo and `correlates_reporting3` repo

**Value**

dat.b, whose Wstratum has been updated

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plotting

*Plotting Helper Functions*


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**Description**

Functions for plotting.

**Usage**

```
draw.x.axis.cor(xlim, llox, llox.label, for.ggplot=FALSE)
get.xlim(dat, marker, lloxs)
```

**Arguments**

xlim	xlim
llox	lower limit
llox.label	label for lower limit
for.ggplot	Boolean
dat	data frame
marker	name of the biomarker variable
lloxs	list of lloxs

**Details**

draw.x.axis.cor is used by both cor\_coxph and cor\_threshold

**Value**

real

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predictCompetingRisk *Cumulative Incidence Function (CIF) Under Competing Risk*


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**Description**

Offers two approaches (Approach 2 is recommended, pcr2 is just an alias for predictCompetingRisk2). Weights are allowed in the optional arguments.

**Usage**

```
predictCompetingRisk2(formula.list, data, t0, newdata = data, ...)
pcr2(formula.list, data, t0, newdata=data, ...)
```

```
predictCompetingRisk(formula, formula.all, data, t0, newdata=data, stype=2, ctype=2, ...)
pcr(formula, formula.all, data, t0, newdata=data, stype=2, ctype=2, ...)
```

**Arguments**

<code>formula.list</code>	list of formulae for cause-specific failures. Assume the first cause to be the cause of interest
<code>formula</code>	formula for the cause-specific failure
<code>formula.all</code>	formula for all-cause failure
<code>data</code>	data frame
<code>t0</code>	the time till which cumulative incidence function is computed
<code>newdata</code>	new data for making prediction, default to the data for fitting the models
<code>stype</code>	computation of the survival curve, 1=direct, 2= exponential of the cumulative hazard. Default 2, which is the default of <code>basehaz</code> and <code>predict.coxph</code>
<code>ctype</code>	whether the cumulative hazard computation should have a correction for ties, 1=no, 2=yes. Default 2, which is the default of <code>basehaz</code> and <code>predict.coxph</code>
<code>...</code>	optional arguments that are passed to <code>coxph</code> , the most import of which is <code>weights</code>

**Details**

Approach 2, `predictCompetingRisk2`, fits cause-specific Cox models to each cause to compute cumulative incidence function for the cause of interest under competing risk.

When there is only one cause, CIF is conceptually 1 - survival prob. (<https://www.publichealth.columbia.edu/research/population-health-methods/competing-risk-analysis>)

The function is implemented in R with matrix operation. Because looping through time points and subjects is vectorized, it is quite fast (faster than `riskRegression` in limited testing, which implements in C, but `pcr` uses more memory.)

One way to check the implementation of this function is to compare its results with the results of `predict.coxph` when there is only one cause. The tests in the examples code below show that when the risk is small (e.g. shorter followup time), the CIF computed by this function and the 1-survival estimated via  $1 - \exp(-H)$  by `predict.coxph`, where  $H$  is cumulative hazard, are close to each other. But when the risk is high, the difference between the two are more noticeable. These results make sense because, e.g.,

If  $t_0$  = the first time failure point,  $CIF = h_1 = H_1 \sim 1 - \exp(-H_1)$  If  $t_0$  = the second time point,

$$CIF = H_1 + \exp(-H_1) * h_2 \text{ (by def)}$$

$$\sim H_1 + \exp(-H_1)(1 - \exp(-h_2))$$

$$= H_1 + \exp(-H_1) - \exp(-H_2)$$

$$\sim 1 - \exp(-H_2)$$

Approach 1, `predictCompetingRisk`, fits a cause-specific Cox model and a all-cause Cox model to compute cumulative incidence function for the cause of interest under competing risk.

The difference between `predictCompetingRisk` and `predictCompetingRisk2` is that instead of fitting a model to the overall failure, a model is fit for each cause, including the cause of interest. The overall survival is computed by adding together the cumulative hazard from individual causes.

The second approach is recommended because it is more stable.

**Value**

A vector of real numbers as the risk till  $t_0$  for each subject in newdata

**References**

riskRegression: Predicting the Risk of an Event using Cox Regression Models by Brice Ozenne, Anne Lyngholm Sorensen, Thomas Scheike, Christian Torp-Pedersen, Thomas Alexander Gerds <https://journal.r-project.org/archive/2017/RJ-2017-062/RJ-2017-062.pdf> Thanks to Professor Gerds for helpful discussion.

Competing Risk Analysis Columbia Public Health <https://www.publichealth.columbia.edu/research/population-health-methods/competing-risk-analysis>

Introduction to the Analysis of Survival Data in the Presence of Competing Risks Peter C Austin, Douglas S Lee, Jason P Fine <https://www.ahajournals.org/doi/full/10.1161/CIRCULATIONAHA.115.017719>

**See Also**

[predictCompetingRisk](#).

**Examples**

```
library(survival)

# prepare a dataset with competing risk
lung1=lung[order(lung$time),]
lung1$status=lung1$status-1
lung1$status[1:50]=2
with(lung1, table(status))
lung1$status.1=ifelse(lung1$status==1,1,0)
lung1$status.2=ifelse(lung1$status==2,1,0)
lung1$status.a=ifelse(lung1$status==0,0,1)
lung1$wt=rep(1, nrow(lung1))

#####
# predictCompetingRisk2

t0=1000
formula.list=list(
  Surv(time, status.1) ~ age,
  Surv(time, status.2) ~ age
)

cif.2=pcr2(formula.list, lung1, t0)

fit=coxph(formula.list[[1]], lung1)
newdata=lung1
newdata$time=t0
coxpred = 1 - exp(-predict(fit, newdata=newdata, type="expected"))
```

```

plot(cif.2, coxpred)

# dealing with weights
lung1$wt=c(rep(2,50), rep(1, nrow(lung1)-50))
cif=predictCompetingRisk2(formula.list, lung1, t0, weights=lung1$wt)

#####
# predictCompetingRisk

t0=1000
form =Surv(time, status.1) ~ age
form.a=Surv(time, status.a) ~ age
cif=predictCompetingRisk(form, form.a, lung1, t0, newdata=lung1, weights=lung1$wt, stype=2, ctype=2)

# more validation code

# when there is no covariate and one cause, CIF = 1 - KM estimate of survival prob

lung1=lung[order(lung$time),]
lung1$status=lung1$status-1
with(lung1, table(status))
lung1$status.1=ifelse(lung1$status==1,1,0)
lung1$status.a=ifelse(lung1$status==0,0,1)
lung1$wt=rep(1, nrow(lung1))

# stype=2 is surv=prod limit
fitKM <- survfit(Surv(time, status.1) ~ 1, data=lung1, stype=1, ctype=2)
cbind(summary(fitKM)$cumhaz, exp(-summary(fitKM)$cumhaz), summary(fitKM)$surv)[1:2,]
#[1,] 0.004385965 0.9956236 0.9956140
#[2,] 0.017660474 0.9824946 0.9824561
cif=predictCompetingRisk(Surv(time, status.1) ~ 1, Surv(time, status.1) ~ 1, lung1, t0=11,
  newdata=lung1[1,,drop=FALSE], weights=lung1$wt, stype=1, ctype=2)
cif # 0.01754386
1-cif # 0.9824561 = summary(fitKM)$surv at t=11

# when there are covariates and one cause, CIF and 1-exp(-H) are close to each other
# when H is small but not close when H is large
form =Surv(time, status.1) ~ age
form.a=Surv(time, status.a) ~ age

oldpar <- par(mfrow = c(1,2))
for (t0 in c(12,1000)) {
  fit=coxph(form, lung1, weights=lung1$wt)
  lung2=lung1; lung2$time=t0
  r=predict(fit, type="expected", newdata=lung2)
  message(head(basehaz(fit, centered=TRUE)))
  cif=predictCompetingRisk(form, form.a, lung1, t0, newdata=lung1, weights=lung1$wt, stype=2,
    ctype=2)
  plot(cif, 1-exp(-r), xlab="Cumulative incidence function",
    ylab="Expected number of events from predict.coxph", main=paste0("t0: ", t0))
}

```

```
      abline(0,1)
      message(head(cbind(cif, "1-exp(-r)"=1-exp(-r))))
    }
  par(oldpar)
```

---

utils

*Utility Functions*

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### **Description**

Helpful functions.

### **Usage**

```
marker.name.to.assay (a)
```

### **Arguments**

a                    assay name

### **Details**

This function ...

### **Value**

string

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