iris %>% mutate(sumVar = rowSums(.[1:4]))

iris %>% mutate(sumVar = rowSums(select(., contains(“Sepal”)))) %>% head

iris %>% mutate(sumVar = select(., contains(“Sepal”)) %>% rowSums()) %>% head

$index  
# A tibble: 3 x 2  
 var1 var2   
 <chr> <chr>   
1 sex.factor sex.factor2  
2 age.factor age.factor2  
3 sex.factor2 age.factor2  
  
$counts  
$counts[[1]]  
# A tibble: 2 x 3  
 sex.factor sex.factor2 n  
 <fct> <fct> <int>  
1 Female M 445  
2 Male F 484  
  
$counts[[2]]  
# A tibble: 3 x 3  
 age.factor age.factor2 n  
 <fct> <fct> <int>  
1 <40 years <60 years 70  
2 40-59 years <60 years 344  
3 60+ years 60+ years 515  
  
$counts[[3]]  
# A tibble: 4 x 3  
 sex.factor2 age.factor2 n  
 <fct> <fct> <int>  
1 M <60 years 204  
2 M 60+ years 241  
3 F <60 years 210  
4 F 60+ years 274

iRenameColumn.R

iSelectColumn.R

<= 22 Low  
>= 23 & <= 41 Average   
>=42 High

# impute

## impute continious

## impute categorical

## impute outlier

# transform

## min -max

## skewness

## log

# binning

## optimal binning

## standardize

# data transformation report

# inspectdf

# Descriptive Statistics

## Table 1

## Categorical Variables

### Split-Group Stats Categorical

### Grouped Categorical

## Continious Variables

### Split-Group Stats Continious

### Grouped Continious

# Cross Tables

# Plots

## Categorical Variables

# Plots

## Continious Variables

# Survival Analysis

# Pairwise comparison

# Multivariate Analysis Survival

# KM plot

explanatory = c(“perfor.factor”) dependent = “Surv(time, status)” colon\_s %>% surv.plot(dependent, explanatory, xlab=“Time (days)”, pval=TRUE, legend=“none”)

Notes

Use Hmisc::label() to assign labels to variables for tables and plots.

label(colon\_s$age.factor) = “Age (years)”

Export dataframe tables directly or to R Markdown using knitr::kable().

Note wrapper summary.missing() can be useful. Wraps mice::md.pattern.

colon\_s %>% summary.missing(dependent, explanatory)

Where a multivariable model contains a subset of the variables specified in the full univariable set, this can be specified.

explanatory = c(“age.factor”, “sex.factor”, “obstruct.factor”, “perfor.factor”) explanatory.multi = c(“age.factor”, “obstruct.factor”) dependent = ‘mort\_5yr’ colon\_s %>% summarizer(dependent, explanatory, explanatory.multi)

Random effects.

e.g. lme4::glmer(dependent ~ explanatory + (1 | random\_effect), family=“binomial”)

explanatory = c(“age.factor”, “sex.factor”, “obstruct.factor”, “perfor.factor”) explanatory.multi = c(“age.factor”, “obstruct.factor”) random.effect = “hospital” dependent = ‘mort\_5yr’ colon\_s %>% summarizer(dependent, explanatory, explanatory.multi, random.effect)

metrics=TRUE provides common model metrics.

colon\_s %>% summarizer(dependent, explanatory, explanatory.multi, metrics=TRUE)

Cox proportional hazards

e.g. survival::coxph(dependent ~ explanatory)

explanatory = c(“age.factor”, “sex.factor”, “obstruct.factor”, “perfor.factor”) dependent = “Surv(time, status)”

colon\_s %>% summarizer(dependent, explanatory)

Rather than going all-in-one, any number of subset models can be manually added on to a summary.factorlist() table using summarizer.merge(). This is particularly useful when models take a long-time to run or are complicated.

Note requirement for glm.id=TRUE. fit2df is a subfunction extracting most common models to a dataframe.

explanatory = c(“age.factor”, “sex.factor”, “obstruct.factor”, “perfor.factor”) explanatory.multi = c(“age.factor”, “obstruct.factor”) random.effect = “hospital” dependent = ‘mort\_5yr’

# Separate tables

colon\_s %>% summary.factorlist(dependent, explanatory, glm.id=TRUE) -> example.summary

colon\_s %>% glmuni(dependent, explanatory) %>% fit2df(estimate.suffix=" (univariable)") -> example.univariable

colon\_s %>% glmmulti(dependent, explanatory) %>% fit2df(estimate.suffix=" (multivariable)") -> example.multivariable

colon\_s %>% glmmixed(dependent, explanatory, random.effect) %>% fit2df(estimate.suffix=" (multilevel") -> example.multilevel

# Pipe together

example.summary %>% summarizer.merge(example.univariable) %>% summarizer.merge(example.multivariable) %>% summarizer.merge(example.multilevel) %>% select(-c(glm.id, index)) -> example.final example.final

Cox Proportional Hazards example with separate tables merged together.

explanatory = c(“age.factor”, “sex.factor”, “obstruct.factor”, “perfor.factor”) explanatory.multi = c(“age.factor”, “obstruct.factor”) dependent = “Surv(time, status)”

# Separate tables

colon\_s %>% summary.factorlist(dependent, explanatory, glm.id=TRUE) -> example2.summary

colon\_s %>% coxphuni(dependent, explanatory) %>% fit2df(estimate.suffix=" (univariable)") -> example2.univariable

colon\_s %>% coxphmulti(dependent, explanatory.multi) %>% fit2df(estimate.suffix=" (multivariable)") -> example2.multivariable

# Pipe together

example2.summary %>% summarizer.merge(example2.univariable) %>% summarizer.merge(example2.multivariable) %>% select(-c(glm.id, index)) -> example2.final example2.final

# OR plot

explanatory = c(“age.factor”, “sex.factor”, “obstruct.factor”, “perfor.factor”) dependent = ‘mort\_5yr’ colon\_s %>% or.plot(dependent, explanatory) # Previously fitted models (glmmulti() or glmmixed()) can be provided directly to glmfit

# HR plot (not fully tested)

explanatory = c(“age.factor”, “sex.factor”, “obstruct.factor”, “perfor.factor”) dependent = “Surv(time, status)” colon\_s %>% hr.plot(dependent, explanatory, dependent\_label = “Survival”) # Previously fitted models (coxphmulti) can be provided directly using coxfit

# ANOVA

# Save Final Data

# Final Data Summary

# Software and Libraries Used

The jamovi project (2019). jamovi. (Version 0.9) [Computer Software]. Retrieved from <https://www.jamovi.org>. R Core Team (2018). R: A Language and envionment for statistical computing. [Computer software]. Retrieved from <https://cran.r-project.org/>. Fox, J., & Weisberg, S. (2018). car: Companion to Applied Regression. [R package]. Retrieved from <https://cran.r-project.org/package=car>.

# Session Info

# Notes

Last update on 2019-11-06 12:28:29

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