R-Helper-Functions

Marcus Vollmer

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Contents

Data import and R in-build summary

```
library(survival)
cdg = get("cgd")
summary(cgd)
```

```
##        id                            center       random
##  Min.   :  1.00   NIH                  :41   Min.   :1989-06-07
##  1st Qu.: 24.50   Scripps Institute    :36   1st Qu.:1989-08-19
##  Median : 54.00   Amsterdam            :28   Median :1989-09-15
##  Mean   : 58.09   Univ. of Zurich      :21   Mean   :1989-09-22
##  3rd Qu.: 89.50   Mott Children's Hosp:20   3rd Qu.:1989-11-03
##  Max.   :135.00   L.A. Children's Hosp:13   Max.   :1989-12-29
##                   (Other)              :44
##      treat          sex           age           height
##  placebo:120   male  :168   Min.   : 1.0   Min.   : 76.3
##  rIFN-g : 83   female: 35   1st Qu.: 6.0   1st Qu.:114.5
##                             Median :12.0   Median :140.0
##                             Mean   :13.7   Mean   :138.1
##                             3rd Qu.:20.0   3rd Qu.:169.2
##                             Max.   :44.0   Max.   :189.0
##
##      weight            inherit       steroids          propylac
##  Min.   : 10.40   X-linked :131   Min.   :0.00000   Min.   :0.0000
##  1st Qu.: 20.25   autosomal: 72   1st Qu.:0.00000   1st Qu.:1.0000
##  Median : 33.40                   Median :0.00000   Median :1.0000
##  Mean   : 39.34                   Mean   :0.03448   Mean   :0.8473
##  3rd Qu.: 58.70                   3rd Qu.:0.00000   3rd Qu.:1.0000
##  Max.   :101.50                   Max.   :1.00000   Max.   :1.0000
##
##              hos.cat        tstart           enum           tstop
##  US:NIH          : 41   Min.   :  0.0   Min.   :1.000   Min.   :  4.0
##  US:other        :108   1st Qu.:  0.0   1st Qu.:1.000   1st Qu.:204.5
##  Europe:Amsterdam: 28   Median :  0.0   Median :1.000   Median :273.0
##  Europe:other    : 26   Mean   : 69.5   Mean   :1.665   Mean   :254.1
##                         3rd Qu.:121.0   3rd Qu.:2.000   3rd Qu.:320.0
##                         Max.   :373.0   Max.   :8.000   Max.   :439.0
##
##      status
##  Min.   :0.0000
##  1st Qu.:0.0000
##  Median :0.0000
##  Mean   :0.3744
##  3rd Qu.:1.0000
##  Max.   :1.0000
##
```

Required libraries and own functions for summary

```
  library(stargazer)
```

```
##
## Please cite as:
```

```
## Hlavac, Marek (2015). stargazer: Well-Formatted Regression and Summary Statistics Tables.
```

```
##  R package version 5.2. http://CRAN.R-project.org/package=stargazer
```

```
  library(stringr)
  source("stargazer_long.R")
  source("strtable.R")

# generate summary table
  s = strtable(cdg[,-1], n=10, width=300)

# for LaTeX output as longtable use:
  stargazer_long(s[,1:4], summary=FALSE, rownames=FALSE, output="cccp{9cm}")
```

variable	NAs	class	stats
center	0	Factor w/ 13 levels	"Harvard Medical Sch" (4), "Scripps Institute" (36), "Copenhagen" (5), "NIH" (41), "L.A. Children's Hosp" (13), "Mott Children's Hosp" (20), "Univ. of Utah" (5), "Univ. of Washington" (4), "Univ. of Minnesota" (10), "Univ. of Zurich" (21), ...
random	0	Date	
treat	0	Factor w/ 2 levels	"placebo" (120), "rIFN-g" (83)
sex	0	Factor w/ 2 levels	"male" (168), "female" (35)
age	0	integer	m=13.70, sd=9.34, q=[1.00, 6.00, 12.00, 20.00, 44.00]
height	0	numeric	m=138.12, sd=31.41, q=[76.30, 114.50, 140.00, 169.50, 189.00]
weight	0	numeric	m=39.34, sd=21.83, q=[10.40, 20.10, 33.40, 59.00, 101.50]
inherit	0	Factor w/ 2 levels	"X-linked" (131), "autosomal" (72)
steroids	0	numeric	m=0.03, sd=0.18, q=[0.00, 0.00, 0.00, 0.00, 1.00]
propylac	0	numeric	m=0.85, sd=0.36, q=[0.00, 1.00, 1.00, 1.00, 1.00]
hos.cat	0	Factor w/ 4 levels	"US:NIH" (41), "US:other" (108), "Europe:Amsterdam" (28), "Europe:other" (26)
tstart	0	integer	m=69.50, sd=111.62, q=[0.00, 0.00, 0.00, 121.00, 373.00]
enum	0	integer	m=1.67, sd=1.16, q=[1.00, 1.00, 1.00, 2.00, 8.00]
tstop	0	integer	m=254.11, sd=96.38, q=[4.00, 203.00, 273.00, 322.00, 439.00]
status	0	integer	m=0.37, sd=0.49, q=[0.00, 0.00, 0.00, 1.00, 1.00]

Create stratified table with characteristics and statistical significance

```
source("characteristics_table.R")
 s = characteristics_table(-1, "treat", cdg[,-c(1:2)], "col", prec="%.1f%%")

 library(xtable)
 # Longtable LaTeX output
   out = capture.output(xtable(s, align="rp{1.5cm}p{4cm}rrrr"))
   out = out[6:NROW(out)-1]
   out = sub("\\{tabular\\}", "\\{longtable\\}", out)
   cat(out)
```

	Variable	Level	placebo	rIFN-g	P	NAs
1	sex	male	100 (83.3%)	68 (81.9%)	0.8510	0
2		female	20 (16.7%)	15 (18.1%)		
3	inherit	X-linked	74 (61.7%)	57 (68.7%)	0.3709	0
4		autosomal	46 (38.3%)	26 (31.3%)		
5	hos.cat	US:NIH	20 (16.7%)	21 (25.3%)	0.4469	0
6		US:other	67 (55.8%)	41 (49.4%)		
7		Europe:Amsterdam	16 (13.3%)	12 (14.5%)		
8		Europe:other	17 (14.2%)	9 (10.8%)		