

```
knitrSet()
require(Hmisc)
```

```
require(tables)
```

```
table_latexdefs() # defines \blfootnotef, \keytrio, \keytrionsd
```

```
n <- 400
set.seed(1)
d <- data.frame(country=factor(sample(c('US', 'Canada', 'Mexico'), n, TRUE)),
                sex=factor(sample(c('Female', 'Male'), n, TRUE)),
                age=rnorm(n, 50, 10),
                sbp=rnorm(n, 120, 8))
d <- upData(d,
            preghx=ifelse(sex=='Female', sample(c('No', 'Yes'), n, TRUE), NA),
            labels=c(sbp='Systolic BP', age='Age', preghx='Pregnancy History'),
            units=c(sbp='mmHg', age='years'))
```

```
Input object size: 11592 bytes; 4 variables
Added variable    preghx
New object size:  16728 bytes; 5 variables
```

```
with(d, table(country, sex))
```

country	sex	
	Female	Male
Canada	69	74
Mexico	62	61
US	63	71

```
g <- function(x) {
  x <- x[!is.na(x)]
  if(length(x) == 0) return('')
  if(!useLatex)
    paste(nFm(mean(x), 3, 1), ' (', length(x), ')', sep='')
  else
    paste(latexNumeric(nFm(mean(x), 3, 1)),
          ' \\hfill{\\smaller[2]}(', length(x), ')', sep='')
}
```

```
useLatex <- TRUE
invisible(booktabs())
z <- tabulr((age + Heading('Females'))*(sex == 'Female')*sbp) *
        Heading()*g + (age + sbp)*Heading()*trio ~
        Heading()*country*Heading()*sex, data=d, nofill = ~ sbp)
cat('\\begin{landscape}\\n')
```

```
cat('\begin{minipage}{\textwidth}\n')
```

```
cat('\keytrio\n')
```

```
latex(z)
```

		Canada			Mexico			US											
		Female		Male	Female		Male	Female		Male									
Females	Age	51.3	(69)	47.4	(74)	48.9	(62)	50.4	(61)	47.8	(63)	50.0	(71)						
	Systolic BP	119.7	(69)			119.3	(62)			120.0	(63)								
	Age	43.4	52.1	58.5	39.8	47.0	54.6	41.0	48.0	56.2	44.1	50.1	57.0	39.0	47.8	56.4	42.3	48.6	59.1
	Systolic BP	113.5	120.1	126.5	113.3	119.0	123.8	114.6	119.8	123.9	113.8	119.7	123.9	114.1	120.6	126.0	115.3	120.6	126.1

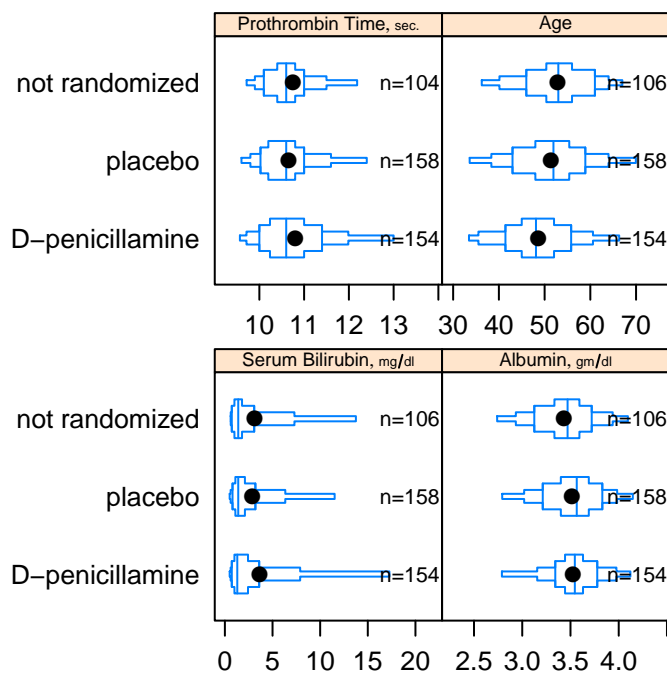
```
cat('\end{minipage}\end{landscape}\n')
```

Numbers in parentheses are the number of non-missing values. *a*, *bc* represents the first quartile *a*, the median *b*, and the third quartile *c*.

```
getHdata(pbc)
pbc ← upData(pbc, moveUnits=TRUE)
```

```
Input object size:      76592 bytes;    19 variables
Label for bili changed from Serum Bilirubin (mg/dl) to Serum Bilirubin
  units set to mg/dl
Label for albumin changed from Albumin (gm/dl) to Albumin
  units set to gm/dl
Label for protime changed from Prothrombin Time (sec.) to Prothrombin Time
  units set to sec.
Label for alk.phos changed from Alkaline Phosphatase (U/liter) to Alkaline Phosphatase
  units set to U/liter
Label for sgot changed from SGOT (U/ml) to SGOT
  units set to U/ml
Label for chol changed from Cholesterol (mg/dl) to Cholesterol
  units set to mg/dl
Label for trig changed from Triglycerides (mg/dl) to Triglycerides
  units set to mg/dl
Label for platelet changed from Platelets (per cm^3/1000) to Platelets
  units set to per cm^3/1000
Label for copper changed from Urine Copper (ug/day) to Urine Copper
  units set to ug/day
New object size:      78376 bytes;    19 variables
```

```
bpplotM(drug ~ bili + albumin + protime + age ~ drug, data=pbc,
  par.strip.text=list(cex=.6))
```



```
# Convert to character to prevent tabular from stratifying
for(x in c('sex', 'stage', 'spiders')) {
  pbc[[x]] ← as.character(pbc[[x]])
  label(pbc[[x]]) ← paste(toupper(substring(x, 1, 1)), substring(x, 2), sep='')
}
table_options(pn=TRUE, showfreq='all', pnwhen='ifna')
## puts (n=) after trios if any NAs, show all frequencies
## Simulate latex(summaryM(...)) :
tab ← tabulr(N + (bili + albumin + protime + age)*Heading()*trio +
  (sex + stage + spiders)*Heading()*freq ~
```

```
Heading()*drug + Heading('Combined')*1, data=pcb)
```

```
latex(tab)
```

	D-penicillamine	placebo	not randomized	Combined
	<i>n</i> = 154	<i>n</i> = 158	<i>n</i> = 106	<i>n</i> = 418
Serum Bilirubin mg/dl	0.7 1.3 3.6	0.8 1.4 3.2	0.7 1.4 3.1	0.8 1.4 3.4
Albumin gm/dl	3.3 3.5 3.8	3.2 3.6 3.8	3.1 3.5 3.7	3.2 3.5 3.8
Prothrombin Time sec.	10.0 10.6 11.4	10.0 10.6 11.0	10.1 10.6 11.0 (<i>n</i> = 104)	10.0 10.6 11.1 (<i>n</i> = 416)
Age	41.4 48.1 55.8	43.0 51.9 58.9	46.0 53.0 61.0	42.8 51.0 58.2
Sex	female 90% $\frac{139}{154}$	female 87% $\frac{137}{158}$	female 92% $\frac{98}{106}$	female 89% $\frac{374}{418}$
	male 10% $\frac{15}{154}$	male 13% $\frac{21}{158}$	male 8% $\frac{8}{106}$	male 11% $\frac{44}{418}$
Stage	1 3% $\frac{4}{154}$	1 8% $\frac{12}{158}$	1 5% $\frac{5}{100}$	1 5% $\frac{21}{412}$
	2 21% $\frac{32}{154}$	2 22% $\frac{35}{158}$	2 25% $\frac{25}{100}$	2 22% $\frac{92}{412}$
	3 42% $\frac{64}{154}$	3 35% $\frac{56}{158}$	3 35% $\frac{35}{100}$	3 38% $\frac{155}{412}$
	4 35% $\frac{54}{154}$	4 35% $\frac{55}{158}$	4 35% $\frac{35}{100}$	4 35% $\frac{144}{412}$
Spiders	absent 71% $\frac{109}{154}$	absent 72% $\frac{113}{158}$		absent 71% $\frac{222}{312}$
	present 29% $\frac{45}{154}$	present 28% $\frac{45}{158}$		present 29% $\frac{90}{312}$

```
with(subset(d, sex=='Female'), mean(preghx=='Yes'))
```

```
pc <- table_pc
```

```
z <- tabulr(sex*Heading()*Percent(fn=pc) +
  Heading('Females')*(sex=='Female')*1*preghx*
  Heading()*Percent(fn=pc) ~
  Heading()*(Country=country) + Heading('\textbf{Combined}')*1,
  data=d)
```

```
latex(z) # wrong denominators except for Combined
```

```
## Use built-in functions; also incorrect
```

```
z <- tabulr(sex*Heading()*Percent() +
  Heading('Females')*(sex=='Female')*1*preghx*
  Heading()*Percent() ~
  (Country=country)*1,
  data=d)
```

```
latex(z)
```