

An {arsenal} of R Functions for Statistical Summaries

<https://github.com/mayoverse/arsenal>

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- ▶ Mayo Clinic: 3-site research hospital
- ▶ Historically a SAS shop
- ▶ Now ~500 R users
- ▶ A SAS license negotiation revealed our dependency on SAS
- ▶ How to port in-house macros and other SAS procedures to R?

- ▶ First started with an internal-only package: `rlocal`
- ▶ Contained some “private” functions, some “public” functions
- ▶ Decided to separate “public” into a CRAN package

- ▶ Goal: mimic and improve SAS functionality “easily”
- ▶ v0.1.2 on CRAN Dec 30, 2016
- ▶ Major releases Feb 2018, Jan 2019, and March 2019
- ▶ Minor releases every couple of months

- ▶ `tableby() ≡ %table()`: create a table 1
- ▶ `paired() ≡ %paired()`: create a table 1 for paired data
- ▶ `modelsum() ≡ %modelsum()`: fit models over a set of independent variables
- ▶ `freqlist() ≡ PROC FREQ`: compile frequency table
- ▶ `comparedf() ≡ PROC COMPARE`: compare two datasets
- ▶ `write2*() ≈ ODS OUTPUT`: output results to a file

The dataset

```
library(arsenal)
data(mockstudy)
str(mockstudy)
```

```
## 'data.frame':    1499 obs. of  14 variables:
## $ case      : int  110754 99706 105271 105001 112263 86205 99508 90158 88989 90515 ...
## $ age       : int  67 74 50 71 69 56 50 57 51 63 ...
## $.- attr(*, "label")= chr "Age in Years"
## $ arm       : chr  "F: FOLFOX" "A: IFL" "A: IFL" "G: IROX" ...
## $.- attr(*, "label")= chr "Treatment Arm"
## $ sex       : Factor w/ 2 levels "Male","Female": 1 2 2 2 2 1 1 1 2 1 ...
## $ race      : chr  "Caucasian" "Caucasian" "Caucasian" "Caucasian" ...
## $.- attr(*, "label")= chr "Race"
## $ fu.time   : int  922 270 175 128 233 120 369 421 387 363 ...
## $ fu.stat   : int  2 2 2 2 2 2 2 2 2 2 ...
## $ ps        : int  0 1 1 1 0 0 0 0 1 1 ...
## $ hgb       : num  11.5 10.7 11.1 12.6 13 10.2 13.3 12.1 13.8 12.1 ...
## $ bmi       : num  25.1 19.5 NA 29.4 26.4 ...
## $.- attr(*, "label")= chr "Body Mass Index (kg/m^2)"
## $ alk.phos  : int  160 290 700 771 350 569 162 152 231 492 ...
## $ ast       : int  35 52 100 68 35 27 16 12 25 18 ...
## $ mdquality.s: int  NA 1 1 1 NA 1 1 1 1 1 ...
## $ age.ord   : Ord.factor w/ 8 levels "10-19"<"20-29"<...: 6 7 4 7 6 5 4 5 5 6 ...
```

A simple pipe table:

```
tb <- tableby(arm ~ sex + age, data = mockstudy)
summary(tb, text = TRUE)
```

```
##
##
## |           | A: IFL (N=428) | F: FOLFOX (N=691) | G: IROX (N=380) | Total (N=1499) | p value|
## |-----| :-----: | :-----: | :-----: | :-----: | :-----:|
## |sex      |           |           |           |           |           | 0.190|
## |- Male  | 277 (64.7%) | 411 (59.5%) | 228 (60.0%) | 916 (61.1%) |         |
## |- Female | 151 (35.3%) | 280 (40.5%) | 152 (40.0%) | 583 (38.9%) |         |
## |Age in Years |           |           |           |           |           | 0.614|
## |- Mean (SD) | 59.673 (11.365) | 60.301 (11.632) | 59.763 (11.499) | 59.985 (11.519) |         |
## |- Range   | 27.000 - 88.000 | 19.000 - 88.000 | 26.000 - 85.000 | 19.000 - 88.000 |         |
```

The markdown equivalent:

```
tb <- tableby(arm ~ sex + age, data = mockstudy)
summary(tb)
```

	A: IFL (N=428)	F: FOLFOX (N=691)	G: IROX (N=380)	Total (N=1499)	p value
sex					0.190
Male	277 (64.7%)	411 (59.5%)	228 (60.0%)	916 (61.1%)	
Female	151 (35.3%)	280 (40.5%)	152 (40.0%)	583 (38.9%)	
Age in Years					0.614
Mean (SD)	59.673 (11.365)	60.301 (11.632)	59.763 (11.499)	59.985 (11.519)	
Range	27.000 - 88.000	19.000 - 88.000	26.000 - 85.000	19.000 - 88.000	

Notice that sex (a categorical) is treated differently from age (continuous). `tableby()` supports categoricals (character, logical, factor), numerics, ordered factors, `survival::Surv()` objects, dates, and results from `arsenal::selectall()`.

Common requests:

- ▶ Change labels: `set_labels()`, `labels()<-`, `labelTranslations=`
- ▶ Change summary statistics: `tableby.control()` or `inline`
- ▶ Change statistical test (p-value): `tableby.control()` or `inline`, or `modpval.tableby()`.
- ▶ Change decimal points: `tableby.control()` or `inline`

```
tb <- tableby(arm ~ fe(sex, digits.pct = 0) + notest(age, digits = 1, "median", "q1q3"),
              data = mockstudy)
summary(tb, pfootnote = TRUE)
```

	A: IFL (N=428)	F: FOLFOX (N=691)	G: IROX (N=380)	Total (N=1499)	p value
sex					0.190 ¹
Male	277 (65%)	411 (59%)	228 (60%)	916 (61%)	
Female	151 (35%)	280 (41%)	152 (40%)	583 (39%)	
Age in Years					
Median	61.0	61.0	61.0	61.0	
Q1, Q3	53.0, 68.0	52.0, 69.0	52.0, 68.0	52.0, 68.0	

1. Fisher's Exact Test for Count Data

Without a by-variable:

```
tb <- tableby( ~ sex + age, data = mockstudy)
summary(tb)
```

Overall (N=1499)	
sex	
Male	916 (61.1%)
Female	583 (38.9%)
Age in Years	
Mean (SD)	59.985 (11.519)
Range	19.000 - 88.000

A stratified, subsetted, and multiple endpoint summary:

```
tb <- tableby(list(arm, sex) ~ age, strata = ps, data = mockstudy, subset = ps %in% 0:1)
summary(tb)
```

ps		A: IFL (N=340)	F: FOLFOX (N=521)	G: IROX (N=305)	Total (N=1166)	p value
0	Age in Years					0.740
	Mean (SD)	60.101 (10.948)	60.173 (11.096)	59.361 (11.904)	59.935 (11.261)	
	Range	27.000 - 81.000	22.000 - 82.000	26.000 - 85.000	22.000 - 85.000	
1	Age in Years					0.582
	Mean (SD)	60.579 (12.026)	61.342 (11.918)	60.081 (11.037)	60.800 (11.721)	
	Range	28.000 - 88.000	26.000 - 88.000	28.000 - 84.000	26.000 - 88.000	

ps		Male (N=720)	Female (N=446)	Total (N=1166)	p value
0	Age in Years				0.614
	Mean (SD)	59.757 (11.031)	60.221 (11.637)	59.935 (11.261)	
	Range	27.000 - 85.000	22.000 - 82.000	22.000 - 85.000	
1	Age in Years				0.045
	Mean (SD)	61.599 (11.748)	59.500 (11.588)	60.800 (11.721)	
	Range	26.000 - 88.000	28.000 - 88.000	26.000 - 88.000	

Other features:

- ▶ `as.data.frame()`, `as.data.frame(summary())`
- ▶ Subset variables, change the order, delete variable: `[`, `head()`, `tail()`
- ▶ Sort by p-value: `sort()`
- ▶ Filter by p-value: `<`, `<=`, `>`, `>=`, etc.
- ▶ Merge two tables: `merge()`
- ▶ Custom p-values and user statistics

The basic table (modeling `alk.phos ~ arm` and `alk.phos ~ ps`)

```
ms <- modelsum(alk.phos ~ arm + ps, data = mockstudy)
summary(ms)
```

	estimate	std.error	p.value	adj.r.squared	Nmiss
(Intercept)	175.577	6.779	< 0.001	0.001	266
Treatment Arm F: FOLFOX	-13.593	8.715	0.119		
Treatment Arm G: IROX	-2.070	9.842	0.833		
(Intercept)	143.772	4.813	< 0.001	0.046	266
ps	46.719	5.979	< 0.001		

Add common adjusters:

```
ms <- modelsum(alk.phos ~ arm + ps, data = mockstudy, adjust = ~ sex + age)
summary(ms)
```

	estimate	std.error	p.value	adj.r.squared	Nmiss
(Intercept)	175.548	20.587	< 0.001	-0.001	266
Treatment Arm F: FOLFOX	-13.701	8.730	0.117		
Treatment Arm G: IROX	-2.245	9.860	0.820		
sex Female	3.016	7.521	0.688		
Age in Years	-0.017	0.319	0.956		
(Intercept)	148.391	19.585	< 0.001	0.045	266
ps	46.721	5.987	< 0.001		
sex Female	1.169	7.343	0.874		
Age in Years	-0.084	0.311	0.787		

Don't show common adjusters:

```
ms <- modelsum(alk.phos ~ arm + ps, data = mockstudy, adjust = ~ sex + age)
summary(ms, show.adjust = FALSE, show.intercept = FALSE)
```

	estimate	std.error	p.value	adj.r.squared	Nmiss
Treatment Arm F: FOLFOX	-13.701	8.730	0.117	-0.001	266
Treatment Arm G: IROX	-2.245	9.860	0.820		
ps	46.721	5.987	< 0.001	0.045	266

Other options:

- ▶ Change model “family”: Poisson, Binomial, Survival, Negative Binomial, Ordinal, Conditional Logistic, Relative Risk
- ▶ Change labels: `labels()<-`, `set_labels()`, `labelTranslations=`
- ▶ Change decimal places: `modelsum.control()`
- ▶ Change summary statistics: `modelsum.control()`
- ▶ `as.data.frame()`, `as.data.frame(summary())`
- ▶ Subset variables, change the order, delete variable: `[`, `head()`, `tail()`
- ▶ Merge two tables: `merge()`

freqlist

```
f1 <- freqlist(~ sex + arm + ps, data = mockstudy)
summary(f1)
```

sex	Treatment Arm	ps	Freq	Cumulative Freq	Percent	Cumulative Percent
Male	A: IFL	0	122	122	8.14	8.14
		1	101	223	6.74	14.88
		2	8	231	0.53	15.41
		NA	46	277	3.07	18.48
	F: FOLFOX	0	168	445	11.21	29.69
		1	148	593	9.87	39.56
		2	16	609	1.07	40.63
		NA	79	688	5.27	45.90
	G: IROX	0	101	789	6.74	52.64
		1	80	869	5.34	57.97
		2	10	879	0.67	58.64
		NA	37	916	2.47	61.11
Female	A: IFL	0	66	982	4.40	65.51
		1	51	1033	3.40	68.91
		2	11	1044	0.73	69.65
		NA	23	1067	1.53	71.18
	F: FOLFOX	0	110	1177	7.34	78.52
		1	95	1272	6.34	84.86
		2	13	1285	0.87	85.72
		NA	62	1347	4.14	89.86
	G: IROX	0	68	1415	4.54	94.40
		1	56	1471	3.74	98.13
		2	9	1480	0.60	98.73
		NA	19	1499	1.27	100.00

Sorted by frequency:

```
f1 <- freqlist(~ sex + arm + ps, data = mockstudy)
summary(sort(f1), dupLabels = TRUE)
```

sex	Treatment Arm	ps	Freq	Cumulative Freq	Percent	Cumulative Percent
Male	A: IFL	2	8	8	0.53	0.53
Female	G: IROX	2	9	17	0.60	1.13
Male	G: IROX	2	10	27	0.67	1.80
Female	A: IFL	2	11	38	0.73	2.54
Female	F: FOLFOX	2	13	51	0.87	3.40
Male	F: FOLFOX	2	16	67	1.07	4.47
Female	G: IROX	NA	19	86	1.27	5.74
Female	A: IFL	NA	23	109	1.53	7.27
Male	G: IROX	NA	37	146	2.47	9.74
Male	A: IFL	NA	46	192	3.07	12.81
Female	A: IFL	1	51	243	3.40	16.21
Female	G: IROX	1	56	299	3.74	19.95
Female	F: FOLFOX	NA	62	361	4.14	24.08
Female	A: IFL	0	66	427	4.40	28.49
Female	G: IROX	0	68	495	4.54	33.02
Male	F: FOLFOX	NA	79	574	5.27	38.29
Male	G: IROX	1	80	654	5.34	43.63
Female	F: FOLFOX	1	95	749	6.34	49.97
Male	A: IFL	1	101	850	6.74	56.70
Male	G: IROX	0	101	951	6.74	63.44
Female	F: FOLFOX	0	110	1061	7.34	70.78
Male	A: IFL	0	122	1183	8.14	78.92
Male	F: FOLFOX	1	148	1331	9.87	88.79
Male	F: FOLFOX	0	168	1499	11.21	100.00

Other options:

- ▶ `as.data.frame()`, `as.data.frame(summary())`
- ▶ Change labels: `labels()<-`, `set_labels()`,
`labelTranslations=`
- ▶ Subset variables, change the order, delete variable: `[`, `head()`,
`tail()`
- ▶ Merge two tables: `merge()`

```
mockstudy2 <- muck_up_mockstudy()
cdf <- comparedf(mockstudy, mockstudy2, by = "case")
cdf
```

```
## Compare Object
##
## Function Call:
## comparedf(x = mockstudy, y = mockstudy2, by = "case")
##
## Shared: 9 non-by variables and 1495 observations.
## Not shared: 7 variables and 4 observations.
##
## Differences found in 3/7 variables compared.
## 3 variables compared have non-identical attributes.
```

```
# summary(cdf)
```

Three main functions: `write2word()`, `write2pdf()`,
`write2html()`

Can use other output formats supported by R Markdown.

```
write2pdf(list(  
  tb,  
  summary(lm(age ~ sex, data = mockstudy)),  
  "\\newpage",  
  "# My modelsum table",  
  ms,  
  code.chunk(1 + 1)  
) , file = "test.pdf")
```

Docs: <https://mayoverse.github.io/arsenal/>

Issues: <https://github.com/mayoverse/arsenal/>

This presentation: https://github.com/eheinzen/2021_arsenal_RMedicine/tree/Recording

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