

Example Report

Frank Harrell*

Fictitious Person[†]




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1 Descriptive Statistics

```
getHdata(FEV)
latex(describe(FEV), file='')
```

6 Variables						FEV 654 Observations								
id														
	n	missing	unique	Info	Mean	.05	.10	.25	.50	.75	.90	.95		
	654	0	654	1	37170	3142	6162	15811	36071	53638	73342	77706		
lowest :	201	202	301	341	351									
highest:	83841	83901	83951	83952	90001									
age [years]														
	n	missing	unique	Info	Mean	.05	.10	.25	.50	.75	.90	.95		
	654	0	17	0.99	9.931	5	6	8	10	12	14	15		
Frequency	3	4	5	6	7	8	9	10	11	12	13	14	15	
%	2	9	28	37	54	85	94	81	90	57	43	25	19	
	0	1	4	6	8	13	14	12	14	9	7	4	3	
fev [liters]														
	n	missing	unique	Info	Mean	.05	.10	.25	.50	.75	.90	.95		
	654	0	575	1	2.637	1.445	1.612	1.981	2.547	3.119	3.813	4.289		
lowest :	0.791	0.796	0.839	1.004	1.072									
highest:	5.102	5.224	5.633	5.638	5.793									
height [inches]														
	n	missing	unique	Info	Mean	.05	.10	.25	.50	.75	.90	.95		
	654	0	56	1	61.14	51.0	53.0	57.0	61.5	65.5	68.5	70.0		
lowest :	46.0	46.5	47.0	48.0	49.0	50.0	51.0	52.0	53.0	54.0	55.0	56.0		
highest:	72.0	72.5	73.0	73.5	74.0									
sex														
	n	missing	unique											
	654	0	2											
female (318, 49%), male (336, 51%)														

*Department of Biostatistics, Vanderbilt University School of Medicine, f.harrell@vanderbilt.edu

[†]Department of Irreproducible Research, Slapout College, fp@sloppy.com

smoke

```
n      missing  unique
654      0         2
non-current smoker (589, 90%), current smoker (65, 10%)
```

I have a question about the data. Do all the values make sense? Are these data applicable to our research question? Did we really land a man on the moon?

FH

No, I don't think we landed a man on the moon, but I do think that hundreds of aliens from an advanced civilization visited us in the 1950s and forgot to say hello.

FP

I'm convinced

FH

This section is for the Supplemental Material section. Code that goes below is executed in the original order of appearance, not at the end. But the code and its output appear only at the end.

```
%%_Here_jobname=spaper
%%_Creates_spaper2.sup
```

2 FEV vs. Age

Figure 1 shows the raw data for some of the key variables.

```
ggplot(FEV, aes(x=age, y=fev, color=sex)) + geom_point()
```

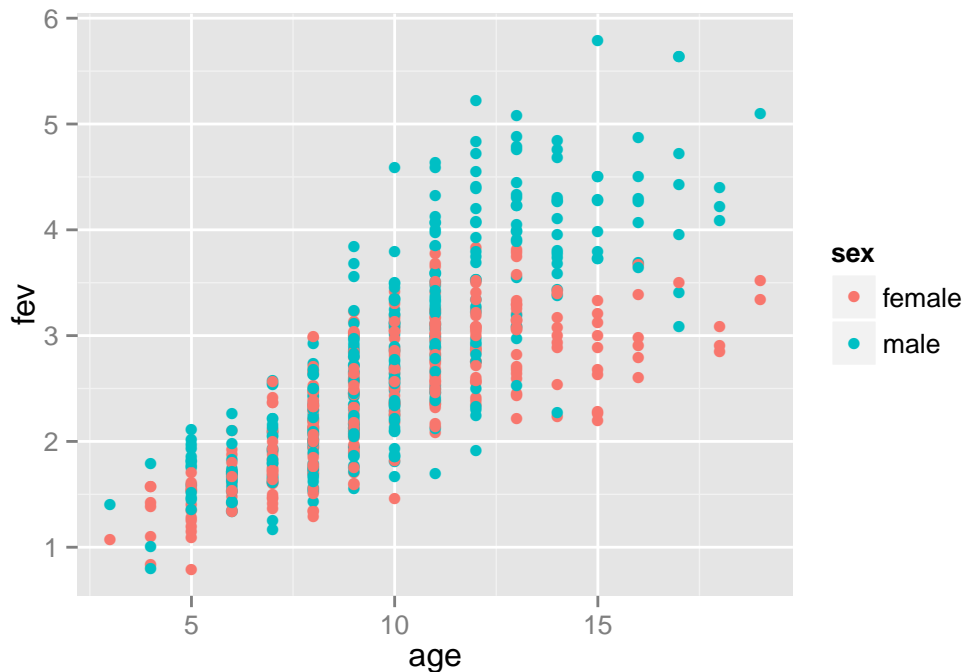


Figure 1: Scatterplot of age vs. FEV stratified by sex

TO DO:

1. See if other variables need to be accounted for
2. See if age and sex interact

FH

Bibliography

- [1] Frank E. Harrell. *Hmisc: A package of miscellaneous R functions*. 2015. URL: <http://biostat.mc.vanderbilt.edu/Hmisc>.
- [2] Frank E. Harrell. *rms: R functions for biostatistical/epidemiologic modeling, testing, estimation, validation, graphics, prediction, and typesetting by storing enhanced model design attributes in the fit*. Implements methods in *Regression Modeling Strategies, 2nd edition*. 2015. URL: <http://biostat.mc.vanderbilt.edu/rms>.
- [3] R Development Core Team. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing. Vienna, Austria, 2015. URL: <http://www.R-project.org>.
- [4] Yihui Xie. *knitr: A general-purpose package for dynamic report generation in R*. R package version 1.5. 2013. URL: <http://CRAN.R-project.org/package=knitr>.

3 Supplemental Material

3.1 Computing Environment

These analyses were done using the following versions of R³, the operating system, and add-on packages CHECK *Hmisc*¹, *rms*², and others:

- R version 3.2.2 (2015-08-14), x86_64-pc-linux-gnu
- Base packages: base, datasets, graphics, grDevices, grid, methods, stats, utils
- Other packages: Formula 1.2-1, ggplot2 1.0.1, Hmisc 3.17-0, knitr 1.11, lattice 0.20-33, rms 4.4-1, SparseM 1.7, survival 2.38-3
- Loaded via a namespace (and not attached): acepack 1.3-3.3, cluster 2.0.3, codetools 0.2-14, colorspace 1.2-6, digest 0.6.8, evaluate 0.8, foreign 0.8-66, formatR 1.2.1, gridExtra 2.0.0, gtable 0.1.2, labeling 0.3, latticeExtra 0.6-26, magrittr 1.5, MASS 7.3-44, Matrix 1.2-2, MatrixModels 0.4-1, multcomp 1.4-1, munsell 0.4.2, mvtnorm 1.0-3, nlme 3.1-122, nnet 7.3-11, plyr 1.8.3, polspline 1.1.12, proto 0.3-10, quantreg 5.19, RColorBrewer 1.1-2, Rcpp 0.12.1, reshape2 1.4.1, rpart 4.1-10, sandwich 2.3-4, scales 0.3.0, splines 3.2.2, stringi 0.5-5, stringr 1.0.0, TH.data 1.0-6, tools 3.2.2, zoo 1.7-12

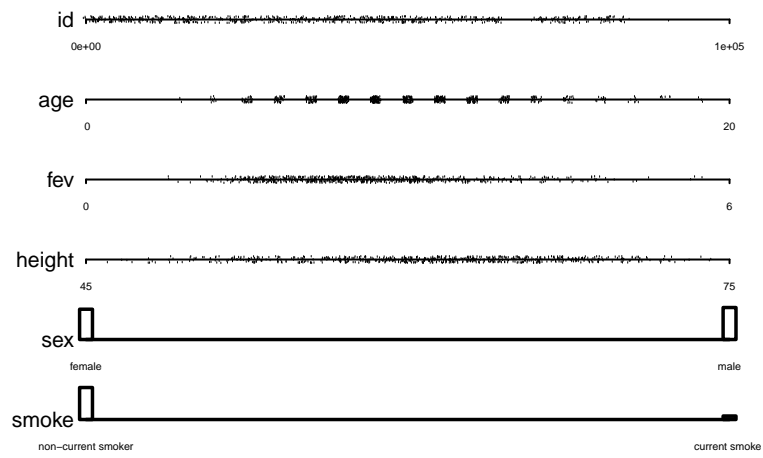
The reproducible research framework *knitr*⁴ was used.

3.2 All R Code

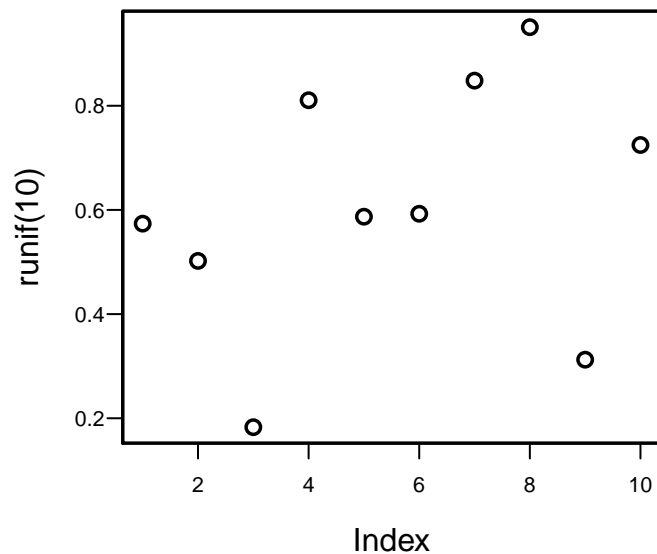
```
require(rms)
knitrSet(echo=TRUE) # set echo=FALSE to not print code
lan <- function(a, ...) latex(a, file='', table.env=FALSE, ...)
getHdata(FEV)
latex(describe(FEV), file='')
datadensity(FEV)
plot(runif(10))
plot(runif(10), col='red')
2*pi
ggplot(FEV, aes(x=age, y=fev, color=sex)) + geom_point()
toLatex(sessionInfo(), locale=FALSE)
```

3.3 Supplemental Analyses

```
datadensity(FEV)
```



```
plot(runif(10))
```



If you need to run R code in disconnected portions of the document, create new output file names as done here.

```
plot(runif(10), col='red')
2+pi
```

```
[1] 5.141593
```

