An Analysis

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Contents

1 Descriptive Statistics

```
getHdata(support)    # Use Hmisc/getHdata to get dataset from VU DataSets wiki
d ← subset(support, select=c(age,sex,race,edu,income,hospdead,slos,dzgroup,
                            meanbp,hrt))
latex(describe(d), file='')
```

d
10 Variables 1000 Observations

---

age : Age

n	missing	unique	Info	Mean	.05	.10	.25	.50	.75	.90	.95
1000	0	970	1	62.47	33.76	38.91	51.81	64.90	74.50	81.87	86.00

```
lowest :  18.04  18.41  19.76  20.30  20.31
highest:  95.51  96.02  96.71 100.13 101.85
```

---

sex

n	missing	unique
1000	0	2

```
female (438, 44%), male (562, 56%)
```

---

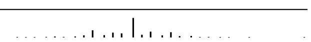
race

n	missing	unique
995	5	5

	white	black	asian	other	hispanic
Frequency	781	157	9	12	36
%	78	16	1	1	4

---

edu : Years of Education



n	missing	unique	Info	Mean	.05	.10	.25	.50	.75	.90	.95
798	202	25	0.97	11.78	6	8	10	12	14	16	18

```
lowest :  0  1  2  3  4, highest: 20 21 22 24 30
```

---

income

n	missing	unique
651	349	4

```
under $11k (309, 47%), $11-$25k (161, 25%), $25-$50k (106, 16%)
>$50k (75, 12%)
```

hospdead : Death in Hospital

```
        n   missing    unique      Info       Sum      Mean
     1000         0         2      0.57       253     0.253
```

slos : Days from Study Entry to Discharge

```
        n   missing    unique      Info      Mean       .05       .10       .25       .50       .75       .90       .95
     1000         0        88         1     17.86         4         4         6        11        20        37        53
lowest :   3   4   5   6   7, highest: 145 164 202 236 241
```

dzgroup

```
        n   missing    unique
     1000         0         8

          ARF/MOSF w/Sepsis COPD CHF Cirrhosis Coma Colon Cancer Lung Cancer
Frequency               391  116 143        55   60           49         100
%                        39   12  14         6    6            5          10
          MOSF w/Malig
Frequency           86
%                    9
```

meanbp : Mean Arterial Blood Pressure Day 3

```
        n   missing    unique      Info      Mean       .05       .10       .25       .50       .75       .90       .95
     1000         0       122         1     84.98     47.00     55.00     64.75     78.00    107.00    120.00    128.05
lowest :   0  20  27  30  32, highest: 155 158 161 162 180
```

hrt : Heart Rate Day 3

```
        n   missing    unique      Info      Mean       .05       .10       .25       .50       .75       .90       .95
     1000         0       124         1     97.87      54.0      60.0      72.0     100.0     120.0     135.0     146.1
lowest :   0  11  30  35  36, highest: 189 193 199 232 300
```

Race is reduced to three levels (white, black, OTHER) because of low frequencies in other levels (minimum relative frequency set to 0.05).

```
d ← upData(d,
           race = combine.levels(race, minlev = 0.05))
```

```
Input object size:       107336 bytes;   10 variables    1000 observations
Modified variable        race
New object size:         107216 bytes;   10 variables    1000 observations
```

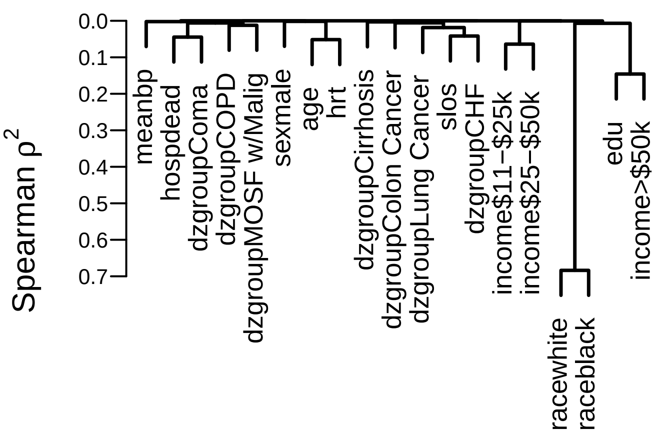
2 Redundancy Analysis and Variable Interrelationships

```
v ← varclus(~., data=d)
plot(v)
redun(~age+sex+race+edu+income+dzgroup+meanbp+hrt, data=d)
```

```

Redundancy Analysis

redun(formula = ~age + sex + race + edu + income + dzgroup +
    meanbp + hrt, data = d)

n: 617  p: 8    nk: 3

Number of NAs:   383
Frequencies of Missing Values Due to Each Variable
    age     sex    race     edu  income dzgroup  meanbp     hrt
      0       0       5     202     349       0       0       0


Transformation of target variables forced to be linear

R2 cutoff: 0.9  Type: ordinary

R2 with which each variable can be predicted from all other variables:
```

```
   age     sex    race     edu  income dzgroup  meanbp     hrt
 0.196   0.088   0.120   0.284   0.339   0.253   0.067   0.163

No redundant variables
```

```
# Alternative: redun(~., data=subset(d, select=-c(hospdead,slos)))
```



Note that the clustering of black with white is not interesting; this just means that these are mutually exclusive higher frequency categories, causing them to be negatively correlated.

3 Logistic Regression Model

Here we fit a tentative binary logistic regression model. The coefficients are not very useful so they are not printed.

```
dd ← datadist(d); options(datadist='dd')
f ← lrm(hospdead ~ rcs(age,4) + sex + race + dzgroup + rcs(meanbp,5),
        data=d) # see Section \ref{descStats} for descriptive statistics
print(f, latex=TRUE, coefs=FALSE)
```

Logistic Regression Model

```
lrm(formula = hospdead ~ rcs(age, 4) + sex + race + dzgroup +
    rcs(meanbp, 5), data = d)
```

Frequencies of Missing Values Due to Each Variable

```
hospdead      age      sex     race  dzgroup   meanbp
       0        0        0        5        0        0
```

		Model Likelihood Ratio Test		Discrimination Indexes		Rank Discrim. Indexes	
Obs	995	LR χ^2	245.83	R^2	0.323	C	0.800
0	744	d.f.	17	g	1.605	D_{xy}	0.601
1	251	$\Pr(>\chi^2)$	<0.0001	g_r	4.980	γ	0.602
$\max\lvert\frac{\partial \log L}{\partial \beta}\rvert$	1×10^{-9}			g_p	0.228	τ_a	0.227
				Brier	0.144		

```
latex(anova(f), where='h', file='')    # can also try where='htbp'
```

Table 1: Wald Statistics for `hospdead`

	χ^2	d.f.	P
age	7.12	3	0.0683
Nonlinear	2.91	2	0.2338
sex	2.16	1	0.1413
race	1.38	2	0.5005
dzgroup	78.77	7	< 0.0001
meanbp	65.62	4	< 0.0001
Nonlinear	48.11	3	< 0.0001
TOTAL NONLINEAR	50.15	5	< 0.0001
TOTAL	151.71	17	< 0.0001

4 Test Calculations

```
x ← 3; y ← 2
if(x ≤ y) 'this' else 'that'
```

```
[1] "that"
```

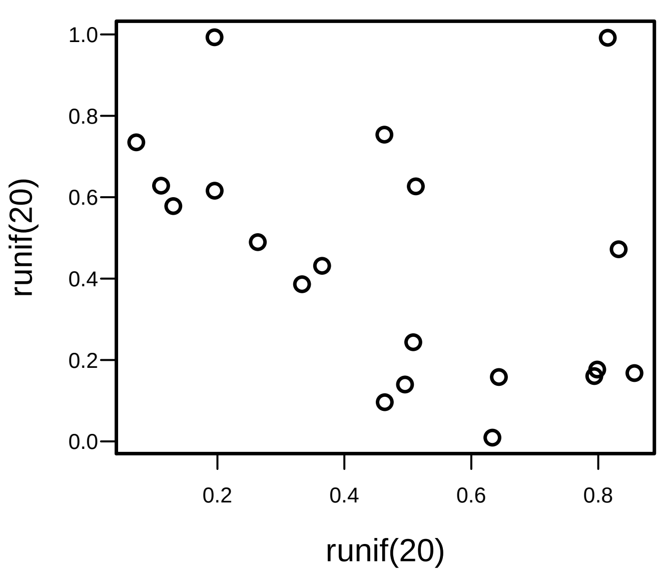
```
if(y ≥ x) 'that' else 'this'
```

```
[1] "this"
```

```
x^y
```

```
[1] 9
```

```
plot(runif(20),runif(20))
```



5 Computing Environment

These analyses were done using the following versions of R[3], the operating system, and add-on packages `Hmisc`[1], `rms`[2], and others:

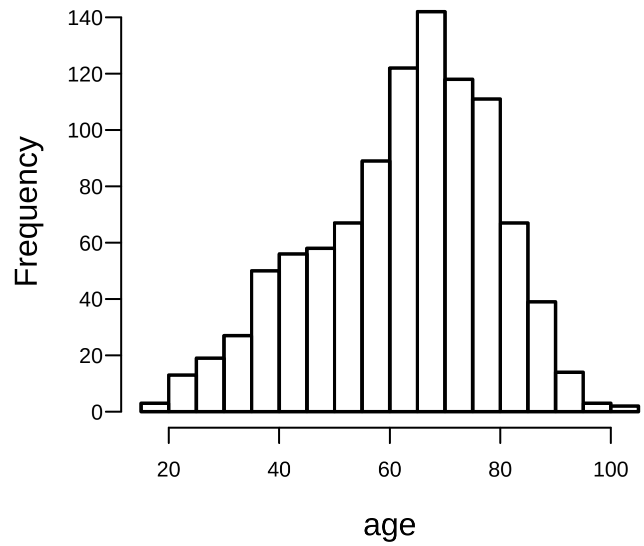
- R version 3.2.2 (2015-08-14), `x86_64-pc-linux-gnu`
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: Formula 1.2-1, ggplot2 2.0.0, Hmisc 3.17-2, knitr 1.12, lattice 0.20-33, rms 4.4-1, SparseM 1.7, survival 2.38-3
- Loaded via a namespace (and not attached): acepack 1.3-3.3, cluster 2.0.3, codetools 0.2-14, colorspace 1.2-6, evaluate 0.8, foreign 0.8-66, formatR 1.2.1, grid 3.2.2, gridExtra 2.0.0, gtable 0.1.2, latticeExtra 0.6-26, magrittr 1.5, Matrix 1.2-3, MatrixModels 0.4-1, multcomp 1.4-1, munsell 0.4.2, mvtnorm 1.0-3, nlme 3.1-123, nnet 7.3-11, plyr 1.8.3, polspline 1.1.12, quantreg 5.19, RColorBrewer 1.1-2, Rcpp 0.12.3, rpart 4.1-10, sandwich 2.3-4, scales 0.3.0, splines 3.2.2, stringi 1.0-1, stringr 1.0.0, TH.data 1.0-6, tools 3.2.2, zoo 1.7-12

6 Descriptive Statistics Again

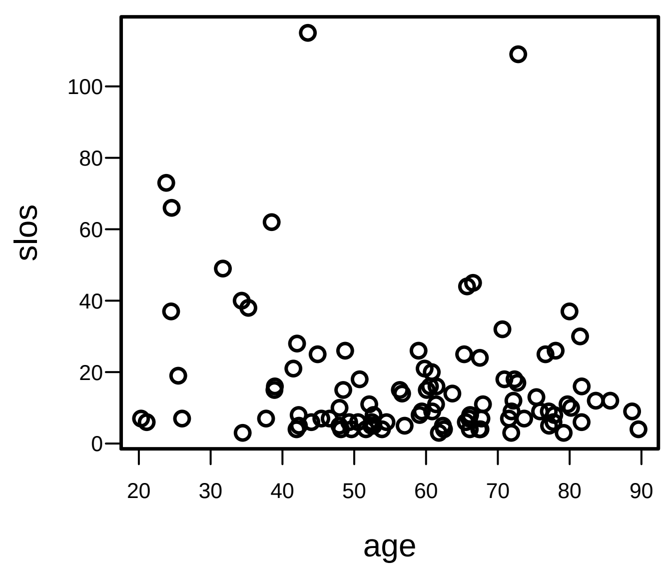
```
getHdata(support)   # Use Hmisc/getHdata to get dataset from VU DataSets wiki
d ← subset(support, select=c(age,sex,race,edu,income,hospdead,slos,dzgroup,
                            meanbp,hrt))
summary(d)
```

```
      age             sex             race           edu       
 Min.   : 18.04   female:438   white   :781   Min.   : 0.00  
 1st Qu.: 51.81   male  :562   black   :157   1st Qu.:10.00  
 Median : 64.90                asian   :  9   Median :12.00  
 Mean   : 62.47                other   : 12   Mean   :11.78  
 3rd Qu.: 74.50                hispanic: 36   3rd Qu.:14.00  
 Max.   :101.85                NA's    :  5   Max.   :30.00  
                                              NA's   :202    
         income        hospdead          slos                      dzgroup   
 under $11k:309   Min.   :0.000   Min.   :  3.00   ARF/MOSF w/Sepsis:391  
 $11-$25k  :161   1st Qu.:0.000   1st Qu.:  6.00   CHF              :143  
 $25-$50k  :106   Median :0.000   Median : 11.00   COPD             :116  
 >$50k     : 75   Mean   :0.253   Mean   : 17.86   Lung Cancer      :100  
 NA's      :349   3rd Qu.:1.000   3rd Qu.: 20.00   MOSF w/Malig     : 86  
                  Max.   :1.000   Max.   :241.00   Coma             : 60  
                                                   (Other)          :104  
     meanbp            hrt        
 Min.   :  0.00   Min.   :  0.00  
 1st Qu.: 64.75   1st Qu.: 72.00  
 Median : 78.00   Median :100.00  
 Mean   : 84.98   Mean   : 97.87  
 3rd Qu.:107.00   3rd Qu.:120.00  
 Max.   :180.00   Max.   :300.00  
```

```
with(d, hist(age, nclass=25, main=''))
```




```
with(d[1:100,], plot(age, slos))
```



That was a very concise set of descriptive statistics.

References

[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`.