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))
```

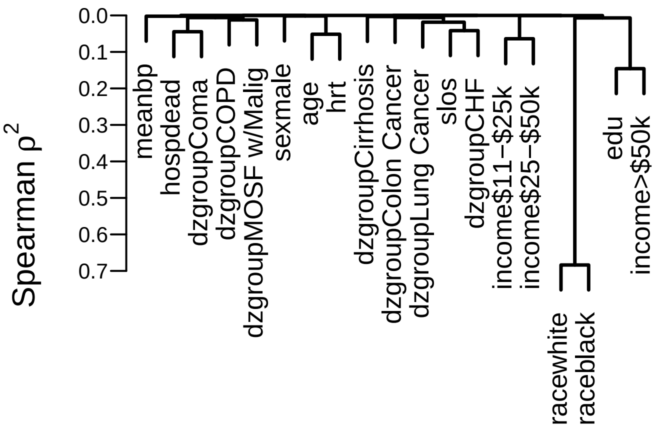
```
Input object size:       107336 bytes;   10 variables    1000 observations
Modified variable        race
New object size:         107216 bytes;   10 variables    1000 observations
```

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

R^2 cutoff: 0.9  Type: ordinary

R^2 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. Note: the symbolic section reference below was created by the following R comment:
`# see Section (*\ref{descStats}*) for descriptive statistics`
The label was defined in an earlier section using
`\section{Descriptive Statistics}\label{descStats}`

```
require(rms)
```

```
dd ← datadist(d); options(datadist='dd')
f ← lrm(hospdead ∼ rcs(age,4) + sex + race + dzgroup + rcs(meanbp,5),
          data=d) # see Section 1 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
```

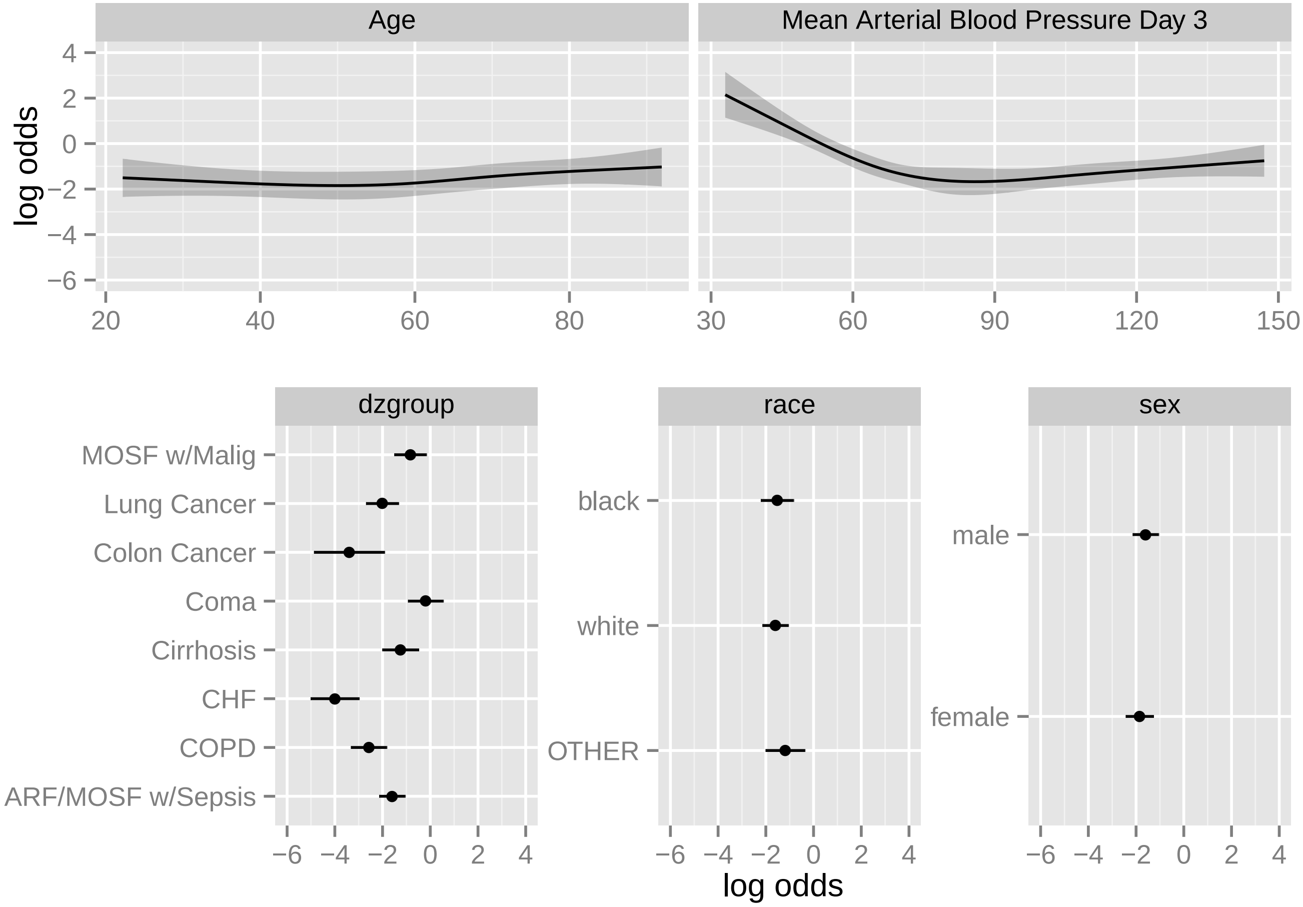
		Model Likelihood Ratio Test		Discrimination Indexes		Rank Discrim. Indexes	
Obs	995	LR χ^2	245.83	R^2	0.323	C	0.800
0	744	d.f.	17	g	1.605	D_{xy}	0.601
1	251	$\Pr(>\chi^2)$	< 0.0001	g_r	4.980	γ	0.602
$\max \lvert \frac{\partial \log L}{\partial \beta} \rvert$	1×10^{-9}			g_p	0.228	τ_a	0.227
				Brier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

```
ggplot(Predict(f), sepdiscrete='vertical')
```



4 Test Calculations

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

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

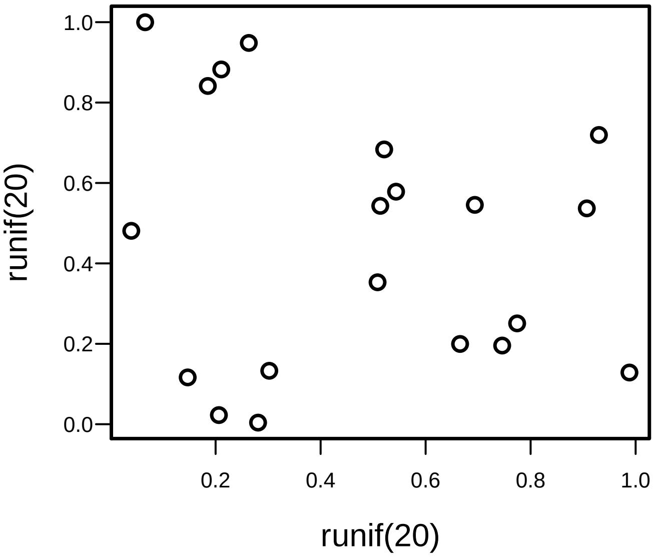
```
if(y ≥ x) 'that' else 'this'
```

```
[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:

```
toLatex(sessionInfo(), locale=FALSE)
```

- 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 1.0-1, stringr 1.0.0, TH.data 1.0-6, tools 3.2.2, zoo 1.7-12

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`.