An Analysis

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March 19, 2011

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	Mean	.05	.10	.25	.50	.75	.90	.95
1000	0	970	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	Mean	.05	.10	.25	.50	.75	.90	.95
798	202	25	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	Sum	Mean
1000	0	2	253	0.253

slos : Days from Study Entry to Discharge

n	missing	unique	Mean	.05	.10	.25	.50	.75	.90	.95
1000	0	88	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	Mean	.05	.10	.25	.50	.75	.90	.95
1000	0	122	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	Mean	.05	.10	.25	.50	.75	.90	.95
1000	0	124	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))
```

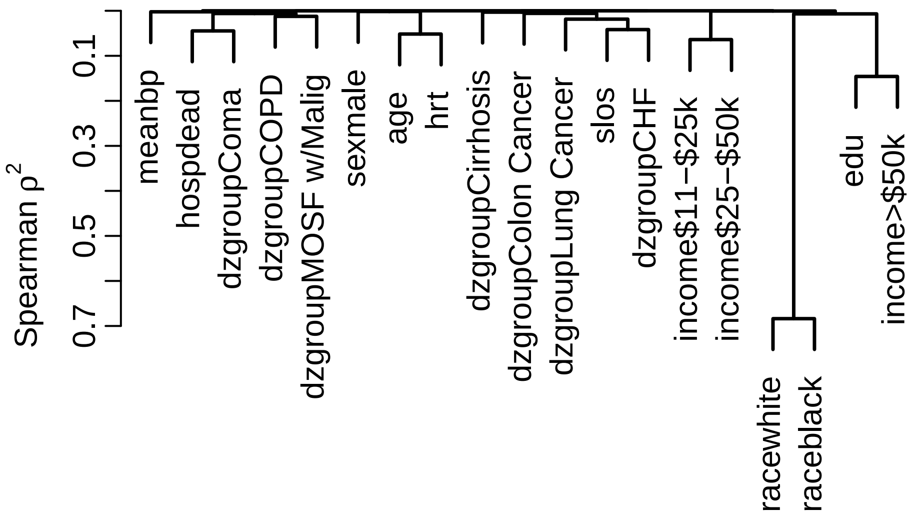
```
Input object size:      107000 bytes;   10 variables
Modified variable       race
New object size:        106880 bytes;   10 variables
```

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}
```

```
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
```

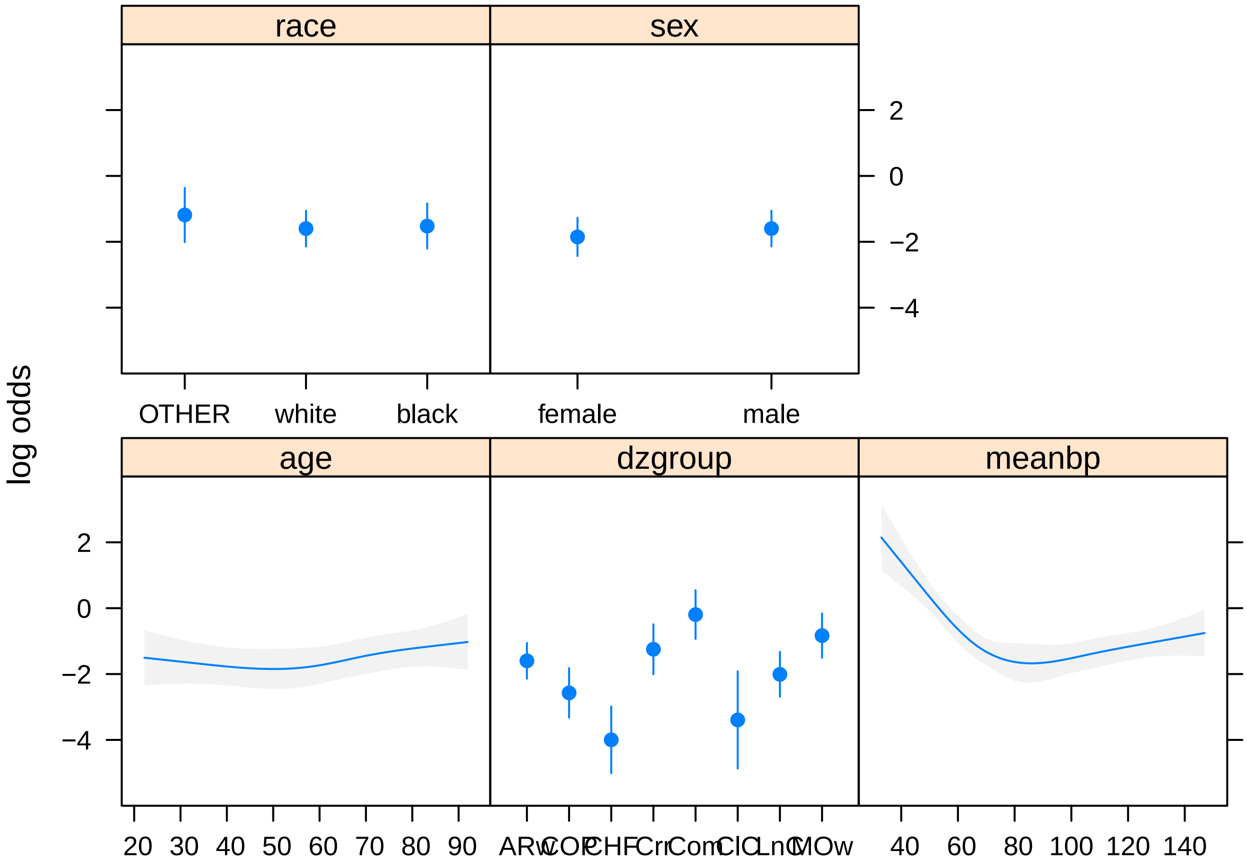
		Model Likelihood Ratio Test		Discrimination Indexes		Rank Discrim. Indexes	
Obs	995	LR χ^2	245.83	R^2	0.323	C	0.800
0	744	d.f.	17	g	1.605	D_{xy}	0.601
1	251	Pr($>\chi^2$)	<0.0001	g_r	4.980	γ	0.602
max |deriv|	1×10^{-9}			g_p	0.228	τ_a	0.227
				Brier	0.144		

```
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

```
print(plot(Predict(f)))
```



4 Test Calculations

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

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

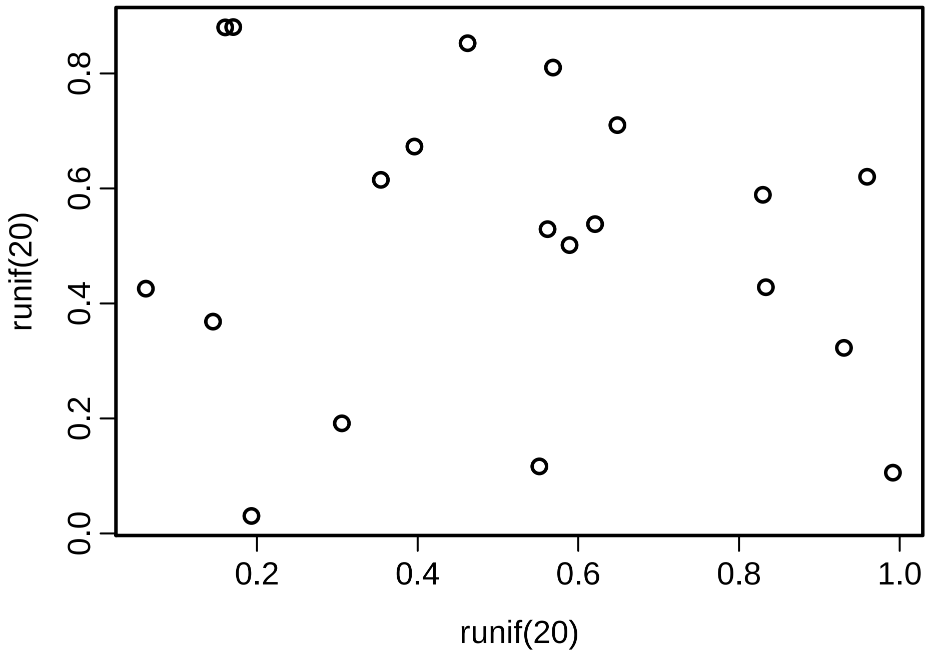
```
if(y ≥ x) 'that' else 'this'
```

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

```
x^y
```

```
[1] 9
```

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



5 Computing Environment

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

- R version 2.12.2 (2011-02-25), `x86_64-pc-linux-gnu`
- Base packages: base, datasets, graphics, grDevices, grid, methods, splines, stats, utils
- Other packages: Hmisc 3.8-3, lattice 0.19-17, rms 3.3-0, survival 2.36-5
- Loaded via a namespace (and not attached): cluster 1.13.3

References

[1] R Development Core Team. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria, 2010. ISBN 3-900051-07-0, available from `www.R-project.org`.

[2] Frank E. Harrell. `Hmisc`: A package of miscellaneous S functions. Available from `biostat.mc.vanderbilt.edu/s/Hmisc`, 2011.

[3] Frank E. Harrell. `rms`: S functions for biostatistical/epidemiologic modeling, testing, estimation, validation, graphics, prediction, and typesetting by storing enhanced model design attributes in the fit. Available from `biostat.mc.vanderbilt.edu/rms`, 2011. Implements methods in *Regression Modeling Strategies*, New York:Springer, 2001.