



# Example Enhanced Report

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Changes for 2014-10-02 are marked by  as a vertical line in the right margin  
Changes for 2014-10-04 are marked by  as a vertical line in the right margin

## 1 Descriptive Statistics

```
require(rms) # Get access to rms and Hmisc packages

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='')
```

10 Variables <sup>d</sup>  
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

Frequency	ARF/MOSF	w/Sepsis	COPD	CHF	Cirrhosis	Coma	Colon	Cancer	Lung	Cancer
%	391	116	143		55	60		49		100
Frequency	MOSF	w/Malig								
%	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 ← transform(d, race = combine.levels(race, minlev = 0.05))
```

Summaries of variables stratified by sex are below.

```
latex(summaryM(age + race + edu + income + slos + dzgroup +
  meanbp + hrt ~ sex, data=d, test=TRUE),
  npct='both', file='', landscape=TRUE, round=1)
```

Table 1: Descriptive Statistics ( $N = 1000$ ).  $a$   $b$   $c$  represent the lower quartile  $a$ , the median  $b$ , and the upper quartile  $c$  for continuous variables.  $N$  is the number of non-missing values. Tests used: <sup>1</sup>Wilcoxon test; <sup>2</sup>Pearson test

	N	female $N = 438$	male $N = 562$	Test Statistic
Age	1000	51.5 64.9 75.9	52.1 64.9 72.7	$F_{1,998} = 1.6, P = 0.206^1$
race : OTHER	995	0.06 <sup>27</sup> / <sub>435</sub>	0.05 <sup>30</sup> / <sub>560</sub>	$\chi^2_2 = 3.89, P = 0.143^2$
white		0.76 <sup>329</sup> / <sub>435</sub>	0.81 <sup>452</sup> / <sub>560</sub>	
black		0.18 <sup>79</sup> / <sub>435</sub>	0.14 <sup>78</sup> / <sub>560</sub>	
Years of Education	798	10 12 14	9 12 14	$F_{1,796} = 0.66, P = 0.416^1$
income : under \$11k	651	0.54 <sup>161</sup> / <sub>298</sub>	0.42 <sup>148</sup> / <sub>353</sub>	$\chi^2_3 = 11.59, P = 0.009^2$
\$11-\$25k		0.21 <sup>63</sup> / <sub>298</sub>	0.28 <sup>98</sup> / <sub>353</sub>	
\$25-\$50k		0.16 <sup>48</sup> / <sub>298</sub>	0.16 <sup>58</sup> / <sub>353</sub>	
>\$50k		0.09 <sup>26</sup> / <sub>298</sub>	0.14 <sup>49</sup> / <sub>353</sub>	
Days from Study Entry to Discharge	1000	7 12 21	6 10 19	$F_{1,998} = 9.11, P = 0.003^1$
dzgroup : ARF/MOSF w/Sepsis	1000	0.41 <sup>181</sup> / <sub>438</sub>	0.37 <sup>210</sup> / <sub>562</sub>	$\chi^2_7 = 15.95, P = 0.026^2$
COPD		0.14 <sup>61</sup> / <sub>438</sub>	0.10 <sup>55</sup> / <sub>562</sub>	
CHF		0.11 <sup>46</sup> / <sub>438</sub>	0.17 <sup>97</sup> / <sub>562</sub>	
Cirrhosis		0.05 <sup>21</sup> / <sub>438</sub>	0.06 <sup>34</sup> / <sub>562</sub>	
Coma		0.06 <sup>27</sup> / <sub>438</sub>	0.06 <sup>33</sup> / <sub>562</sub>	
Colon Cancer		0.05 <sup>21</sup> / <sub>438</sub>	0.05 <sup>28</sup> / <sub>562</sub>	
Lung Cancer		0.09 <sup>38</sup> / <sub>438</sub>	0.11 <sup>62</sup> / <sub>562</sub>	
MOSF w/Malig		0.10 <sup>43</sup> / <sub>438</sub>	0.08 <sup>43</sup> / <sub>562</sub>	
Mean Arterial Blood Pressure Day 3	1000	64 77 107	65 79 107	$F_{1,998} = 0.16, P = 0.687^1$
Heart Rate Day 3	1000	74 105 122	71 100 118	$F_{1,998} = 3.86, P = 0.05^1$

## 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
0	0	5	202	349	0	0
hrt						
0						

```
Transformation of target variables forced to be linear
```

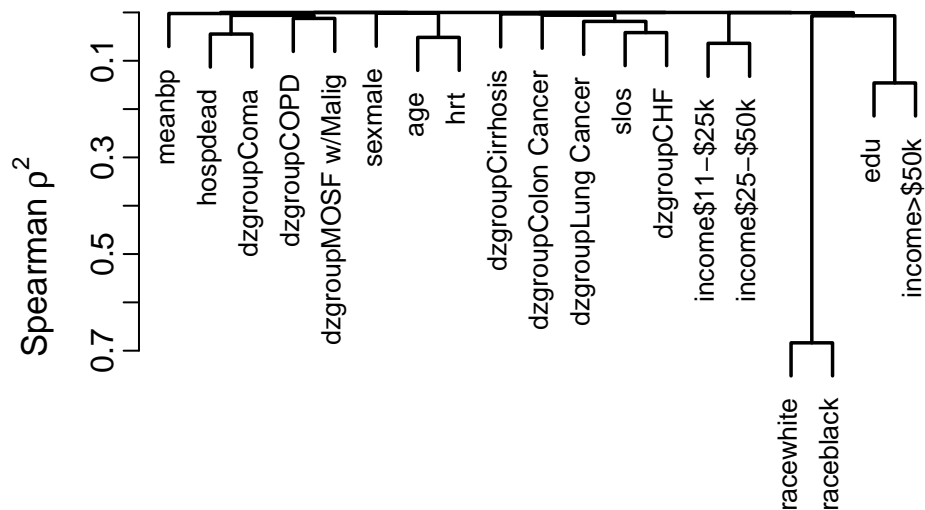
```
R2 cutoff: 0.9 Type: ordinary
```

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

age	sex	race	edu	income	dzgroup	meanbp
0.196	0.088	0.120	0.284	0.339	0.253	0.067
hrt						
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 (... is printed in their place). Artificially create more missing data so that a dot chart showing frequencies of missings will be printed when the `latex` version of the output appears later.

```
dd <- datadist(d); options(datadist='dd')
d$age[1:10] <- d$meanbp[1:13] <- d$hospdead[1:7] <- NA
f <- lrm(hospdead ~ rcs(age,4) + sex + race + dzgroup + rcs(meanbp,5),
        data=d) # see Section 1 for descriptive statistics
f
```

```
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
       7      10       0       5      0       13

                Model Likelihood      Discrimination      Rank Discrim.
                Ratio Test              Indexes              Indexes
Obs           982    LR  $\chi^2$     241.21     $R^2$     0.322     $C$     0.800
0             735    d.f.           17         $g$     1.604     $D_{xy}$   0.599
1             247    Pr(>  $\chi^2$ ) < 0.0001     $g_r$   4.972     $\gamma$   0.601
max |deriv| 1e-09                                 $g_p$   0.227     $\tau_a$   0.226
                                                Brier  0.144
...
```

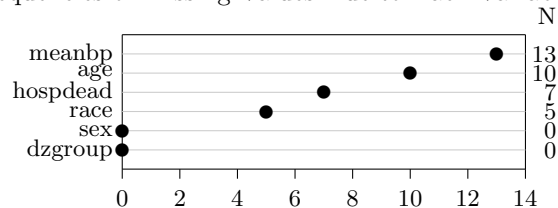
Better: Directly output model statistics as L<sup>A</sup>T<sub>E</sub>X markup and easily suppress coefficients.

```
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



	Model Likelihood	Discrimination	Rank Discrim.
	Ratio Test	Indexes	Indexes
Obs	982	LR $\chi^2$ 241.21	$R^2$ 0.322
0	735	d.f. 17	$C$ 0.800
1	247	Pr(> $\chi^2$ ) < 0.0001	$D_{xy}$ 0.599
max $ \frac{\partial \log L}{\partial \beta} $	$1 \times 10^{-9}$	$g_r$ 4.972	$\gamma$ 0.601
		$g_p$ 0.227	$\tau_a$ 0.226
		Brier 0.144	

The mean arterial blood pressure effect is shown below, on the probability scale. **Note:** `knitr` was told to automatically use a L<sup>A</sup>T<sub>E</sub>X floating `figure` environment since a caption was given.

```
p <- Predict(f, meanbp, fun=plogis)
```

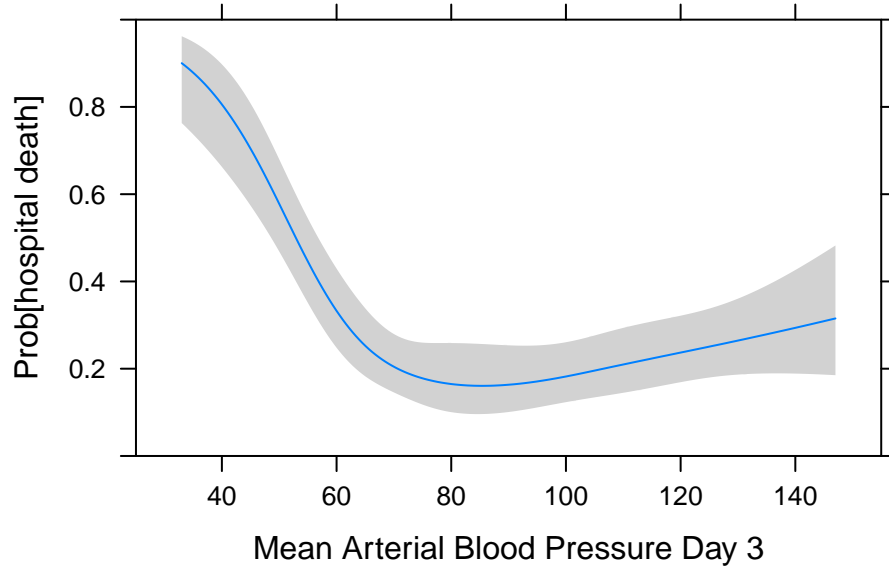


Figure 1: Partial effect of mean arterial blood pressure adjusted to age=64.9 sex=male race=white dzgroup=ARF/MOSF w/Sepsis

```
plot(p, ylab='Prob[hospital death]', adj.subtitle=FALSE)
# Figure 1
```

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

Table 2: Wald Statistics for hospdead

	$\chi^2$	<i>d.f.</i>	<i>P</i>
age	7.26	3	0.0640
<i>Nonlinear</i>	3.04	2	0.2192
sex	2.19	1	0.1386
race	1.51	2	0.4700
dzgroup	78.22	7	< 0.0001
meanbp	63.33	4	< 0.0001
<i>Nonlinear</i>	47.35	3	< 0.0001
TOTAL NONLINEAR	49.45	5	< 0.0001
TOTAL	148.51	17	< 0.0001

The likelihood ratio  $\chi^2$  statistic is 241.21 on 17 d.f. The fitted model in algebraic form is found below.

```
latex(f, file='')
```

$$\text{Prob}\{\text{hospdead} = 1\} = \frac{1}{1 + \exp(-X\hat{\beta})}, \text{ where}$$

$$X\hat{\beta} = 6.47 - 0.01516\text{age} + 1.877 \times 10^{-5}(\text{age} - 33.8)_+^3 - 7.492 \times 10^{-5}(\text{age} - 58.4)_+^3$$

$$\begin{aligned}
& +6.878 \times 10^{-5}(\text{age} - 70.2)_+^3 - 1.264 \times 10^{-5}(\text{age} - 86.07)_+^3 \\
& +0.2572\{\text{male}\} \\
& -0.4244\{\text{white}\} - 0.3205\{\text{black}\} \\
& -0.975\{\text{COPD}\} - 2.396\{\text{CHF}\} + 0.4155\{\text{Cirrhosis}\} + 1.392\{\text{Coma}\} - 1.788\{\text{Colon Cancer}\} \\
& -0.447\{\text{Lung Cancer}\} + 0.7479\{\text{MOSF w/Malig}\} \\
& -0.111\text{meanbp} + 4.588 \times 10^{-5}(\text{meanbp} - 47)_+^3 - 7.526 \times 10^{-5}(\text{meanbp} - 65)_+^3 \\
& +1.241 \times 10^{-5}(\text{meanbp} - 78)_+^3 + 1.909 \times 10^{-5}(\text{meanbp} - 106.9)_+^3 \\
& -2.107 \times 10^{-6}(\text{meanbp} - 128.7)_+^3
\end{aligned}$$

and  $\{c\} = 1$  if subject is in group  $c$ , 0 otherwise;  $(x)_+ = x$  if  $x > 0$ , 0 otherwise.

## 4 Computing Environment

These analyses were done using the following versions of R<sup>1</sup>, the operating system, and add-on packages Hmisc<sup>2</sup>, rms<sup>3</sup>, and others:

- R version 3.1.1 (2014-07-10), x86\_64-pc-linux-gnu
- Base packages: base, datasets, graphics, grDevices, grid, methods, splines, stats, utils
- Other packages: Formula 1.1-2, Hmisc 3.14-6, knitr 1.6, lattice 0.20-29, rms 4.2-2, SparseM 1.05, survival 2.37-7
- Loaded via a namespace (and not attached): acepack 1.3-3.3, cluster 1.15.3, evaluate 0.5.5, foreign 0.8-61, formatR 1.0, latticeExtra 0.6-26, multcomp 1.3-6, mvtnorm 1.0-0, nlme 3.1-117, nnet 7.3-8, polspline 1.1.9, quantreg 5.05, RColorBrewer 1.0-5, rpart 4.1-8, sandwich 2.3-2, stringr 0.6.2, tcltk 3.1.1, TH.data 1.0-3, tools 3.1.1, zoo 1.7-11

## References

- [1] R Development Core Team. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria, 2013.
- [2] Frank E. Harrell. *Hmisc: A package of miscellaneous R functions*, 2014.
- [3] 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*, 2013. Implements methods in *Regression Modeling Strategies*, New York:Springer, 2001.

## 5 Source Code for This Report

```

%Usage: knitr sweaveEx
%   rubber -d sweaveEx
%   (= pdflatex sweaveEx + bibtex sweaveEx sufficiently many times)
% To get .R file: R CMD Stangle sweaveEx.Rnw = Stangle sweaveEx
\documentclass{article}
\usepackage{resize,setspace} % used by latex(describe( ))
\usepackage{url}             % used in bibliography
\usepackage[superscript,nomove]{cite} % use if \cite is used and superscripts wanted
% Remove nomove if you want superscripts after punctuation in citations
\usepackage{lscap}          % for landscape mode tables
\usepackage{calc,epic,color} % used for latex(..., dotchart=TRUE)
\usepackage{moreverb}       % handles verbatiminput

```

```

% Macro changes: defines commands \cbstart* to use the changebar
% package to draw vertical change bars for different edits (e.g. on
% different days) having their own color/line thickness. A key is
% generated in the text at the point at which \changes is called.
% Change marking can be turned off without removing /cbstart* and
% /cbend commands from the text.
%
% Usage:
% \def\showchanges{1} or {0} to turn off change marking
% \changes{suffix}{color}{thickness in pts}{description}
% \changes{another suffix}{color}{thickness}{description}
% . . .
% Note that suffixes must contain only letters (single or multiple).
% Suffixes are appended to \cbstart. \changes appears after
% \begin{document}.
%
\usepackage[color]{changebar}
\newcommand{\changes}[4]{%
  \ifnum\showchanges=1
  \expandafter\newcommand\csname cbstart#1\endcsname{\cbstart[#3pt]\cbcolor{#2}}%
  \noindent Changes for #4 are marked by %
  \textcolor{#2}{\rule[0.05in]{.25in}{#3pt}} as a vertical line in the
  right margin\\
  \else
  \expandafter\newcommand\csname cbstart#1\endcsname{}%
  \def\cbend{}
  \fi
}

\textwidth 6.75in           % set dimensions before fancyhdr
\textheight 9.25in
\topmargin -.875in
\oddsidemargin -.125in
\evensidemargin -.125in
\usepackage{fancyhdr}      % this and next line are for fancy headers/footers
\pagestyle{fancy}
\newcommand{\bc}{\begin{center}} % abbreviate
\newcommand{\ec}{\end{center}}
\newcommand{\code}[1]{\smaller\texttt{#1}}
\newcommand{\R}{\normalfont\textsf{R}}{}}

% Define the following only if you put figures in a figure environment
%\fg{basefilename}{label}{caption}
\newcommand{\fg}[3]{\begin{figure}[htbp]%
  \leavevmode\centerline{\includegraphics{graphics/#1}}%
  \caption{\smaller #3\label{#2}\end{figure}}

\usepackage{Sweavel}
% Uncomment some of the following to use some alternatives:
% \def\Sweavesize{\normalsize} (changes size of typeset R code and output)
% \def\Rcolor{\color{black}}
% \def\Routcolor{\color{green}}
% \def\Rcommentcolor{\color{red}}

```



```

% To change background color or R code and/or output, use e.g.:
% \def\Rbackground{\color{white}}
% \def\Routbackground{\color{white}}
% To use rgb specifications use \color[rgb]{ , , }
% To use gray scale use e.g. \color[gray]{0.5}
% If you change any of these after the first chunk is produced, the
% changes will have effect only for the next chunk.

<<echo=FALSE>>=
knitrSet(w=5, h=3.5) # function is defined in my .Rprofile
# To omit code and its output throughout, use
# knitrSet(echo=FALSE, results='hide')
@

%\SweaveOpts{prefix.string=graphics/plot, eps = FALSE, pdf = TRUE}

\title{Example Enhanced Report}
\author{Frank E Harrell Jr\\\smaller Department of Biostatistics\\\smaller Vanderbilt University School of
\begin{document}
\maketitle
\def\showchanges{1}
\changes{a}{blue}{1}{2014-10-02}
\changes{b}{red}{2}{2014-10-04}

% Use the following 3 lines for long reports needing navigation
%\tableofcontents
%\listoftables
%\listoffigures % not used unless figure environments used

\section{Descriptive Statistics}\label{descStats}
<<results='asis'>>=
require(rms) # Get access to rms and Hmisc packages
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='')
@
Race is reduced to three levels (white, black, OTHER) because of low
frequencies in other levels (minimum relative frequency set to 0.05).
<<>>=
d <- transform(d, race = combine.levels(race, minlev = 0.05))
@
\cbstarta
Summaries of variables stratified by sex are below.
<<results='asis'>>=
latex(summaryM(age + race + edu + income + slos + dzgroup +
meanbp + hrt ~ sex, data=d, test=TRUE),
npct='both', file='', landscape=TRUE, round=1)
@
\cbend

\section{Redundancy Analysis and Variable Interrelationships}
\bc
% Note: giving a chunk name to each code chunk that produces a figure
% makes it easy to know which plots to send to a collaborator, and

```

% will not allow numbered orphan plots to be left when code chunks are  
 % inserted into the file. The default in knitr is for plots to be  
 % numbered by the chunks producing them.

```
\cbstartb
<<vc>>=
v <- varclus(~., data=d)
plot(v)
redun(~ age + sex + race + edu + income + dzgroup + meanbp + hrt, data=d)
# Alternative: redun(~., data=subset(d, select=-c(hospdead,slos)))
@
\ec
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.
\cbend
\section{Logistic Regression Model}
Here we fit a tentative binary logistic regression model. The
coefficients are not very useful so they are not printed (\dots is
printed in their place). Artificially create more missing data so
that a dot chart showing frequencies of missings will be printed when
the \code{latex} version of the output appears later.
<<z,eval=FALSE,echo=TRUE>>=
dd <- datadist(d); options(datadist='dd')
d$age[1:10] <- d$meanbp[1:13] <- d$hospdead[1:7] <- NA
f <- lrm(hospdead ~ rcs(age,4) + sex + race + dzgroup + rcs(meanbp,5),
        data=d) # see Section (*\ref{descStats}*) for descriptive statistics
f
<<echo=FALSE>>=
z <- capture.output( {
<<z>>
  } )
prselect(z, 'S.E.') # keep only summary stats; or:
# prselect(z, stop='S.E.', j=-1) # keep only coefficients
@
Better: Directly output model statistics as \LaTeX\ markup and easily
suppress coefficients.
<<results='asis'>>=
print(f, latex=TRUE, coefs=FALSE)
@
```

The mean arterial blood pressure effect is shown below, on the  
 probability scale. \textbf{Note}: \code{knitr} was told to  
 automatically use a \LaTeX\ floating \code{figure} environment since a  
 caption was given.

```
<<<pmeanbp>>=
p <- Predict(f, meanbp, fun=plogis)
<<meanbp,cap=paste('Partial effect of mean arterial blood pressure adjusted to',attr(p, 'info')$adjust)>>=
plot(p, ylab='Prob[hospital death]', adj.subtitle=FALSE)
# Figure (*\ref{fig:meanbp}*)
<<results='asis'>>=
latex(anova(f), where='h', file='') # can also try where='htbp'
@
```

The likelihood ratio  $\chi^2$  statistic is  
 $\text{Sexpr}\{\text{round}(f\$stats['\text{Model L.R.}'],2)\}$  on  $\text{Sexpr}\{f\$stats['\text{d.f.}']\}$  d.f.

The fitted model in algebraic form is found below.

```
<<results='asis'>>=
latex(f, file='')
@

\section{Computing Environment}
These analyses were done using the following versions of \R\cite{Rsystem}, the
operating system, and add-on packages \code{Hmisc}\cite{Hmisc},
\code{rms}\cite{rrms}, and others:
<<echo=FALSE,results='asis'>>=
toLatex(sessionInfo(), locale=FALSE)
@

% Note: Rsystem reference is defined inside feh.bib. It is a slightly
% edited version of the output of citation().
\bibliography{/home/harrelfe/bib/harrelfe.bib}
\bibliographystyle{unsrt}
% Use \bibliographystyle{abbrv} if want references alphabetized

\section{Source Code for This Report}
\verbatiminput{sweaveEx.Rnw}

\section{\code{Sweavel.sty}}
\verbatiminput{/home/harrelfe/doc/latex/texinput/Sweavel.sty}

\end{document}
```

## 6 Sweavel.sty

```
% Usage: \usepackage{Sweavel}
% To change size of R code and output, use e.g.: \def\Sweavesize{\normalsize}
% To change just the size of output, use e.g.: \def\Routsize{\smaller[2]}
% To change colors of R code, output, and commands, use e.g.:
% \def\Rcolor{\color{black}}
% \def\Routcolor{\color{green}}
% \def\Rcommentcolor{\color{red}}
% To change background color or R code and/or output, use e.g.:
% \def\Rbackground{\color{white}}
% \def\Routbackground{\color{white}}
% To use rgb specifications use \color[rgb]{ , , }
% To use gray scale use e.g. \color[gray]{0.5}
% If you change any of these after the first chunk is produced, the
% changes will have effect only for the next chunk.
```

```
\NeedsTeXFormat{LaTeX2e}
\ProvidesPackage{Sweavel}{} % substitute for Sweave.sty using
% listings package with relsize
\RequirePackage{listings,fancyvrb,color,relsize,ae}
\RequirePackage[T1]{fontenc}
\IfFileExists{upquote.sty}{\RequirePackage{upquote}}{}

\providecommand{\Sweavesize}{\smaller}
\providecommand{\Routsize}{\Sweavesize}
```

---

```

\providecommand{\Rcolor}{\color[rgb]{0, 0.5, 0.5}}
\providecommand{\Routcolor}{\color[rgb]{0.461, 0.039, 0.102}}
\providecommand{\Rcommentcolor}{\color[rgb]{0.101, 0.043, 0.432}}

\providecommand{\Rbackground}{\color[gray]{0.91}}
\providecommand{\Routbackground}{\color[gray]{0.935}}
% Can specify \color[gray]{1} for white background or just \color{white}

\lstdefinestyle{Rstyle}{fancyvrb=false,escapechar=`,language=R,%
    basicstyle={\Rcolor\Sweavesize},% some want \ttfamily too
    backgroundcolor=\Rbackground,%
    showstringspaces=false,%
    keywordstyle=\Rcolor,%
    commentstyle={\Rcommentcolor\ttfamily\itshape},%
    literate={<-}{\leftarrow}2{<<-}{\twoheadleftarrow}2{~}{\sim}1{<=}{\leq}
    alsoother={\$},%
    alsoletter={.<-},%
    otherkeywords={!,!=,~, $,*, \&, \%/\%, \%*\%, \%\\%, <-, <<- , /},%
    escapeinside={(*}{*)}}%

% Other options of interest:
% frame=single,framerule=0.1pt,framesep=1pt,rulecolor=\color{blue},
% numbers=left,numberstyle=\tiny,stepnumber=1,numbersep=7pt,
% keywordstyle={\bf\Rcolor}

\lstdefinestyle{Routstyle}{fancyvrb=false,literate={~}{\sim}1{R^2}{R^2}2{~}{\scriptstyle\we
    frame=single,framerule=0.2pt,framesep=1pt,basicstyle=\Routcolor\Routsize\ttfamily,%
    backgroundcolor=\Routbackground}

\newenvironment{Schunk}{}{}
\lstnewenvironment{Sinput}{\lstset{style=Rstyle}}{}
\lstnewenvironment{Scode}{\lstset{style=Rstyle}}{}
\lstnewenvironment{Soutput}{\lstset{style=Routstyle}}{}
\lstnewenvironment{Sinputsmall}{%
    \lstset{style=Rstyle,basicstyle={\small}}}{%
\lstnewenvironment{Sinputsmaller}{%
    \lstset{style=Rstyle,basicstyle={\smaller}}}{%

\endinput

sudo cp ~/doc/latex/texinput/Sweavel.sty /usr/share/R/share/texmf/.
sudo mktexlsr

```