

# HomeworkAnswers4.R

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*Sun Mar 04 20:09:13 2018*

```
library(AER)
```

```
## Loading required package: car
## Loading required package: lmtest
## Loading required package: zoo
##
## Attaching package: 'zoo'
## The following objects are masked from 'package:base':
##
##   as.Date, as.Date.numeric
## Loading required package: sandwich
## Loading required package: survival
```

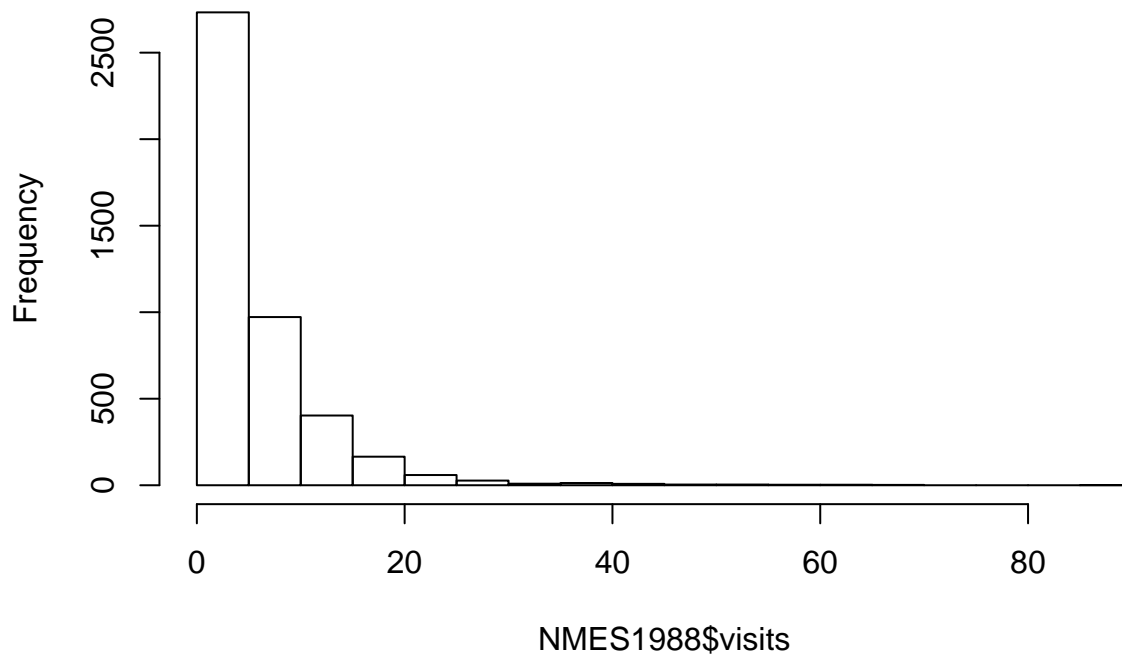
```
library(effects)
```

```
## Loading required package: carData
##
## Attaching package: 'carData'
## The following objects are masked from 'package:car':
##
##   Guyer, UN, Vocab
## lattice theme set by effectsTheme()
## See ?effectsTheme for details.
```

```
library(MASS)
data(NMES1988)
```

```
hist(NMES1988$visits)
```

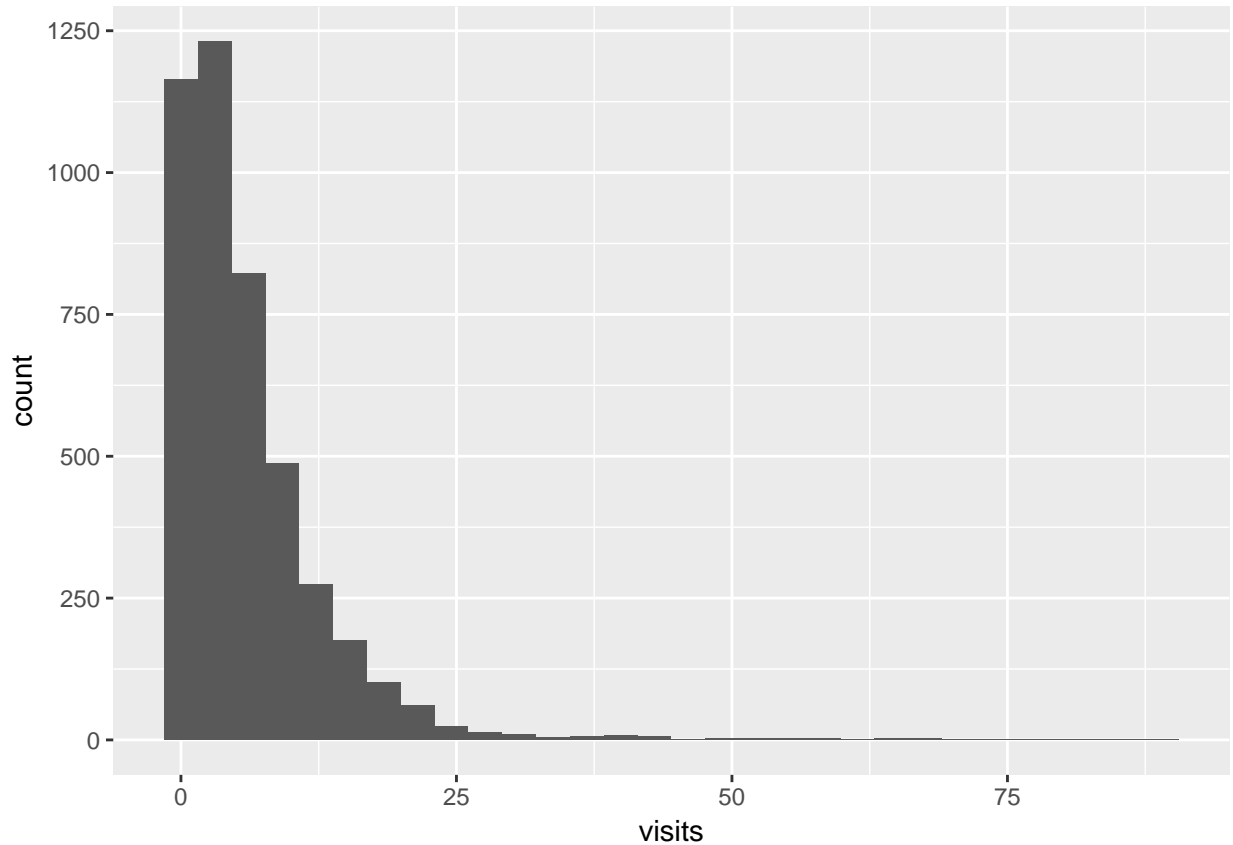
## Histogram of NMES1988\$visits



```
## Or, if you prefer ggplot:
```

```
library(ggplot2)  
ggplot(NMES1988, aes(x = visits)) + geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
xtabs(~ visits, data = NMES1988)
```

```
## visits
##  0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17
## 683 481 428 420 383 338 268 217 188 171 128 115 86 73 76 53 47 48
## 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35
## 30 24 16 18 16 10 12 3 9 7 4 3 4 4 4 1 1 2 1
## 36 37 38 39 40 41 42 43 44 47 48 49 50 51 53 55 56 58
## 1 3 2 5 2 1 4 2 1 1 1 1 1 1 1 2 1 1 2
## 61 63 65 66 68 89
## 1 1 1 1 1 1
```

```
summary(NMES1988)
```

```
##      visits      nvisits      ovisits      novisits
## Min.   : 0.000   Min.   : 0.000   Min.   : 0.0000   Min.   : 0.0000
## 1st Qu.: 1.000   1st Qu.: 0.000   1st Qu.: 0.0000   1st Qu.: 0.0000
## Median : 4.000   Median : 0.000   Median : 0.0000   Median : 0.0000
## Mean   : 5.774   Mean   : 1.618   Mean   : 0.7508   Mean   : 0.5361
## 3rd Qu.: 8.000   3rd Qu.: 1.000   3rd Qu.: 0.0000   3rd Qu.: 0.0000
## Max.   :89.000   Max.   :104.000   Max.   :141.0000   Max.   :155.0000
##      emergency      hospital      health      chronic
## Min.   : 0.0000   Min.   :0.000   poor      : 554   Min.   :0.000
## 1st Qu.: 0.0000   1st Qu.:0.000   average   :3509   1st Qu.:1.000
## Median : 0.0000   Median :0.000   excellent: 343   Median :1.000
## Mean   : 0.2635   Mean   :0.296           Mean   :1.542
## 3rd Qu.: 0.0000   3rd Qu.:0.000           3rd Qu.:2.000
```

```

## Max. :12.0000 Max. :8.000 Max. :8.000
## adl region age afam gender
## normal :3507 northeast: 837 Min. : 6.600 no :3890 female:2628
## limited: 899 midwest :1157 1st Qu.: 6.900 yes: 516 male :1778
## west : 798 Median : 7.300
## other :1614 Mean : 7.402
## 3rd Qu.: 7.800
## Max. :10.900
## married school income employed insurance
## no :2000 Min. : 0.00 Min. : -1.0125 no :3951 no : 985
## yes:2406 1st Qu.: 8.00 1st Qu.: 0.9122 yes: 455 yes:3421
## Median :11.00 Median : 1.6982
## Mean :10.29 Mean : 2.5271
## 3rd Qu.:12.00 3rd Qu.: 3.1728
## Max. :18.00 Max. :54.8351
## medicaid
## no :4004
## yes: 402
##
##
##
##

```

```
base <- glm(visits ~ 1, data = NMES1988, family = poisson())
```

```
summary(base)
```

```

##
## Call:
## glm(formula = visits ~ 1, family = poisson(), data = NMES1988)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -3.3984 -2.4580 -0.7821 0.8746 17.9001
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 1.753434 0.006269 279.7 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 26943 on 4405 degrees of freedom
## Residual deviance: 26943 on 4405 degrees of freedom
## AIC: 39720
##
## Number of Fisher Scoring iterations: 5

```

```
vis.step <- step(base, scope = ~ hospital + health + chronic + gender + school + insurance,
direction='forward', trace = 1)
```

```

## Start: AIC=39720.34
## visits ~ 1
##

```

```

##           Df Deviance  AIC
## + chronic  1   24768 37547
## + hospital 1   25449 38228
## + health   2   25715 38497
## + insurance 1  26774 39553
## + school   1  26797 39576
## + gender   1  26878 39657
## <none>     26943 39720
##
## Step: AIC=37546.91
## visits ~ chronic
##
##           Df Deviance  AIC
## + hospital  1   23982 36763
## + health    2   24391 37175
## + school    1   24524 37305
## + insurance 1   24526 37307
## + gender    1   24704 37485
## <none>     24768 37547
##
## Step: AIC=36763.28
## visits ~ chronic + hospital
##
##           Df Deviance  AIC
## + school    1   23722 36505
## + health    2   23730 36516
## + insurance 1   23752 36535
## + gender    1   23915 36698
## <none>     23982 36763
##
## Step: AIC=36505.47
## visits ~ chronic + hospital + school
##
##           Df Deviance  AIC
## + health    2   23382 36169
## + insurance 1   23609 36394
## + gender    1   23650 36435
## <none>     23722 36505
##
## Step: AIC=36169.44
## visits ~ chronic + hospital + school + health
##
##           Df Deviance  AIC
## + insurance 1   23244 36033
## + gender    1   23316 36105
## <none>     23382 36169
##
## Step: AIC=36033.15
## visits ~ chronic + hospital + school + health + insurance
##
##           Df Deviance  AIC
## + gender    1   23168 35959
## <none>     23244 36033
##

```

```
## Step: AIC=35959.23
## visits ~ chronic + hospital + school + health + insurance + gender
```

```
summary(vis.step)
```

```
##
## Call:
## glm(formula = visits ~ chronic + hospital + school + health +
## insurance + gender, family = poisson(), data = NMES1988)
##
## Deviance Residuals:
##   Min       1Q   Median       3Q      Max
## -8.4055  -1.9962  -0.6737   0.7049  16.3620
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.028874   0.023785  43.258 <2e-16 ***
## chronic       0.146639   0.004580  32.020 <2e-16 ***
## hospital      0.164797   0.005997  27.478 <2e-16 ***
## school        0.026143   0.001843  14.182 <2e-16 ***
## healthpoor    0.248307   0.017845  13.915 <2e-16 ***
## healthcellent -0.361993   0.030304 -11.945 <2e-16 ***
## insuranceyes  0.201687   0.016860  11.963 <2e-16 ***
## gendermale    -0.112320   0.012945  -8.677 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##   Null deviance: 26943  on 4405  degrees of freedom
## Residual deviance: 23168  on 4398  degrees of freedom
## AIC: 35959
##
## Number of Fisher Scoring iterations: 5
```

```
# All those variables are statistically significant
```

```
## Test for overdispersion by doing negative binomial regression
vis.nb <- glm.nb(visits ~ hospital + health + chronic + gender + school + insurance, data = NMES1988)
summary(vis.nb)
```

```
##
## Call:
## glm.nb(formula = visits ~ hospital + health + chronic + gender +
## school + insurance, data = NMES1988, init.theta = 1.206603534,
## link = log)
##
## Deviance Residuals:
##   Min       1Q   Median       3Q      Max
## -3.0469  -0.9955  -0.2948   0.2961   5.8185
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.929257   0.054591  17.022 < 2e-16 ***
## hospital      0.217772   0.020176  10.793 < 2e-16 ***
```

```
## healthpoor      0.305013   0.048511   6.288 3.23e-10 ***
## healthexcellent -0.341807   0.060924  -5.610 2.02e-08 ***
## chronic         0.174916   0.012092  14.466 < 2e-16 ***
## gendermale     -0.126488   0.031216  -4.052 5.08e-05 ***
## school         0.026815   0.004394   6.103 1.04e-09 ***
## insuranceeyes  0.224402   0.039464   5.686 1.30e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.2066) family taken to be 1)
##
## Null deviance: 5743.7 on 4405 degrees of freedom
## Residual deviance: 5044.5 on 4398 degrees of freedom
## AIC: 24359
##
## Number of Fisher Scoring iterations: 1
##
##
## Theta: 1.2066
## Std. Err.: 0.0336
##
## 2 x log-likelihood: -24341.1070
```

```
# You can see that Theta is much more than twice its standard error. Could do a likelihood ratio test.
# I'll illustrate how to write a function.
```

```
overdisp.test <- function(mod, alpha = 0.05){
  # mod is the result of running a glm.nb regression
  if (class(mod)[1] != 'negbin') stop('require model of class negbin\n')
  if (alpha < 0 | alpha > 1) stop('alpha must be in the range (0, 1)')
  # obtain Poissin regression results
  poisreg <- glm(formula = eval(mod$call$formula), data = eval(mod$call$data), family = poisson)
  llP <- logLik(poisreg)
  llNB <- logLik(mod)
  D <- 2 * (llNB - llP)
  cv <- qchisq(1 - (2 * alpha), df = 1)
  pval <- pchisq(D, df = 1, lower.tail = FALSE) / 2
  cat('Likelihood ratio test of H0: no overdispersion\n')
  cat('Test statistic: ', D, '\n')
  cat('Critical value of test statistic: ', cv, '\n')
  cat('p-value: ', pval, '\n')
  invisible(c(stat = D, critval = cv, pval = pval))
}
```

```
odt <- overdisp.test(vis.nb)
```

```
## Likelihood ratio test of H0: no overdispersion
## Test statistic: 11602.12
## Critical value of test statistic: 2.705543
## p-value: 0
```

```
# There is a similar function in the package pscl, called odTest
pscl::odTest(vis.nb)
```

```
## Likelihood ratio test of H0: Poisson, as restricted NB model:
## n.b., the distribution of the test-statistic under H0 is non-standard
```

```

## e.g., see help(odTest) for details/references
##
## Critical value of test statistic at the alpha= 0.05 level: 2.7055
## Chi-Square Test Statistic = 11602.1184 p-value = < 2.2e-16
# There is very clear evidence of overdispersion

summary(vis.nb)

##
## Call:
## glm.nb(formula = visits ~ hospital + health + chronic + gender +
## school + insurance, data = NMES1988, init.theta = 1.206603534,
## link = log)
##
## Deviance Residuals:
##   Min       1Q   Median       3Q      Max
## -3.0469  -0.9955  -0.2948   0.2961   5.8185
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.929257   0.054591  17.022 < 2e-16 ***
## hospital      0.217772   0.020176  10.793 < 2e-16 ***
## healthpoor    0.305013   0.048511   6.288 3.23e-10 ***
## healthexcellent -0.341807  0.060924  -5.610 2.02e-08 ***
## chronic       0.174916   0.012092  14.466 < 2e-16 ***
## gendermale    -0.126488   0.031216  -4.052 5.08e-05 ***
## school        0.026815   0.004394   6.103 1.04e-09 ***
## insuranceeyes  0.224402   0.039464   5.686 1.30e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.2066) family taken to be 1)
##
##   Null deviance: 5743.7  on 4405  degrees of freedom
## Residual deviance: 5044.5  on 4398  degrees of freedom
## AIC: 24359
##
## Number of Fisher Scoring iterations: 1
##
##              Theta:  1.2066
##            Std. Err.:  0.0336
##
## 2 x log-likelihood:  -24341.1070
# You can compare the Poisson & negbin results side by side like this:
compareCoefs(vis.step, vis.nb)

##
## Call:
## 1: glm(formula = visits ~ chronic + hospital + school + health +
## insurance + gender, family = poisson(), data = NMES1988)
## 2: glm.nb(formula = visits ~ hospital + health + chronic + gender +
## school + insurance, data = NMES1988, init.theta = 1.206603534, link =
## log)

```



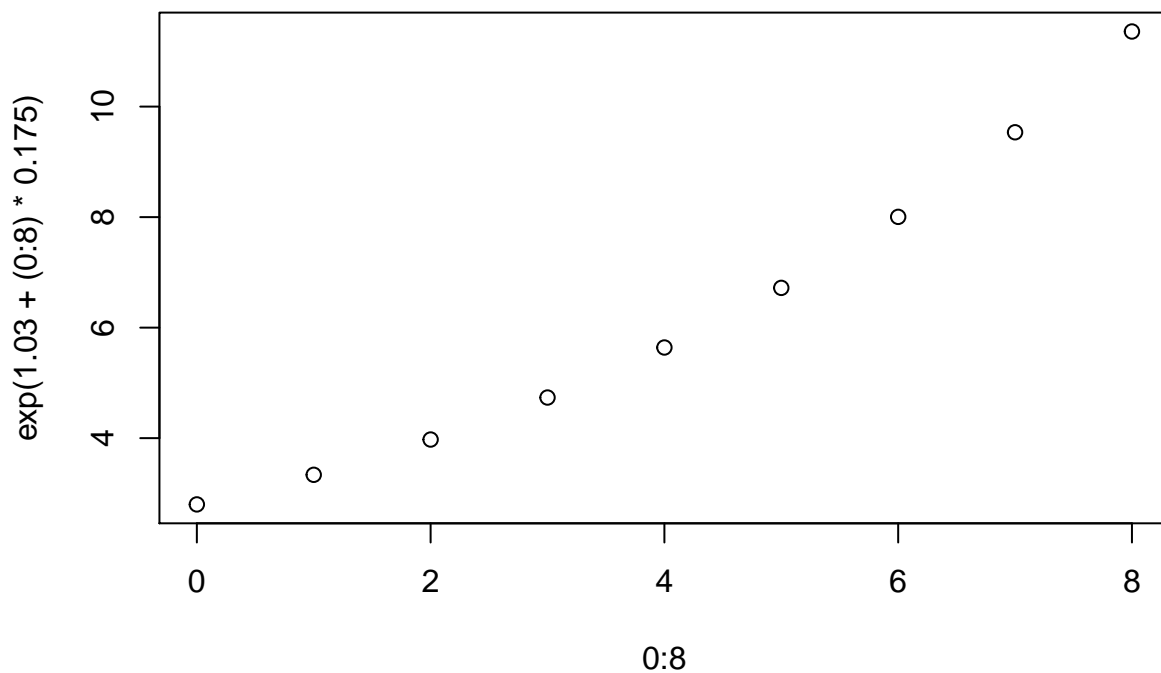
```
##           Est. 1    SE 1    Est. 2    SE 2
## (Intercept) 1.02887 0.02378 0.92926 0.05459
## chronic      0.14664 0.00458 0.17492 0.01209
## hospital     0.16480 0.00600 0.21777 0.02018
## school       0.02614 0.00184 0.02682 0.00439
## healthpoor   0.24831 0.01784 0.30501 0.04851
## healthexcellent -0.36199 0.03030 -0.34181 0.06092
## insuranceeyes 0.20169 0.01686 0.22440 0.03946
## gendermale   -0.11232 0.01295 -0.12649 0.03122
```

```
# Notice that all the standard errors are larger
```

```
# Interpretation
```

```
# Number of chronic conditions. This varies from 0 to 8. You can do an effect plot 'by hand' like this
```

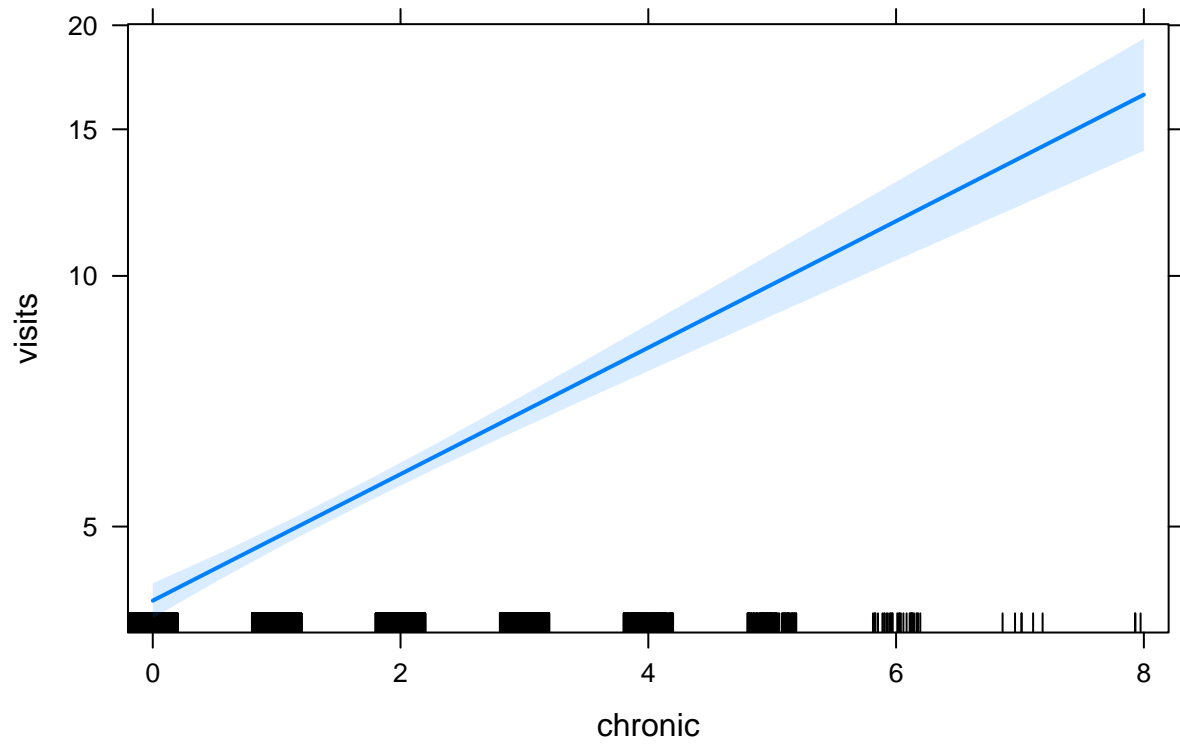
```
plot(0:8, exp(1.03 + (0:8) * 0.175))
```



```
# Or using the effects package (which also adds means of other variables)
```

```
plot(Effect('chronic', vis.nb))
```

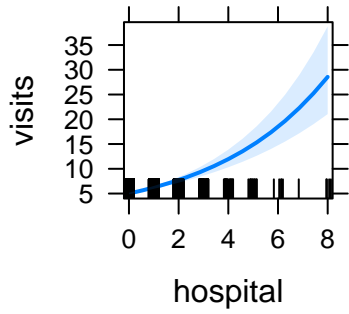
## chronic effect plot



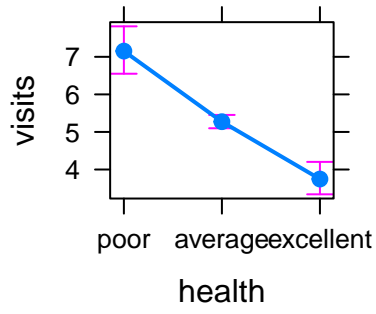
*# You can do them all at once like this:*

```
plot(allEffects(vis.nb), type = 'response')
```

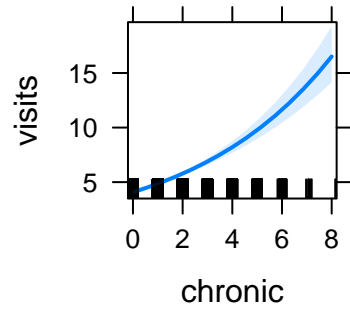
**hospital effect plot**



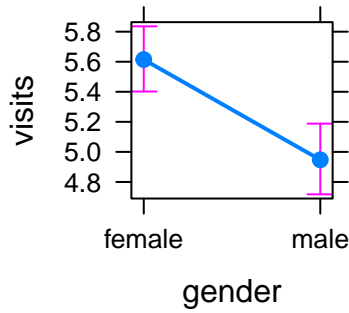
**health effect plot**



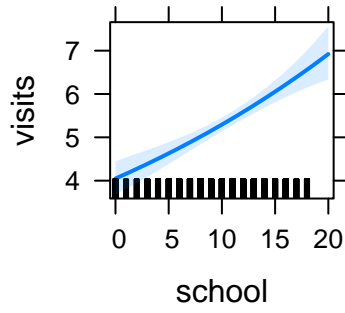
**chronic effect plot**



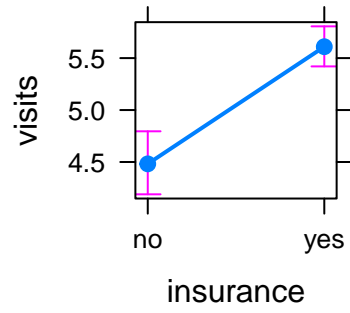
**gender effect plot**



**school effect plot**

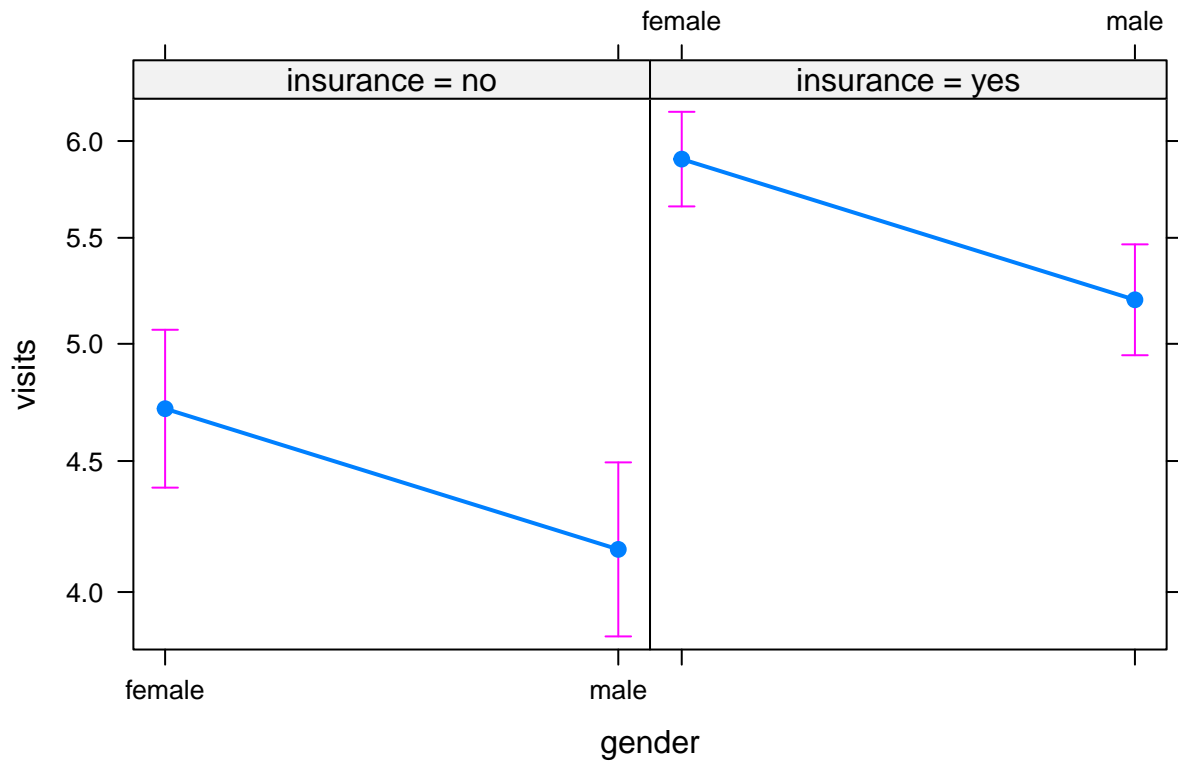


**insurance effect plot**



```
plot(Effect(c('gender','insurance'), vis.nb, multline = TRUE, type = 'response'))
```

## gender\*insurance effect plot



```
# So, for example we can see that women make on average 0.6 more visits than mens
```

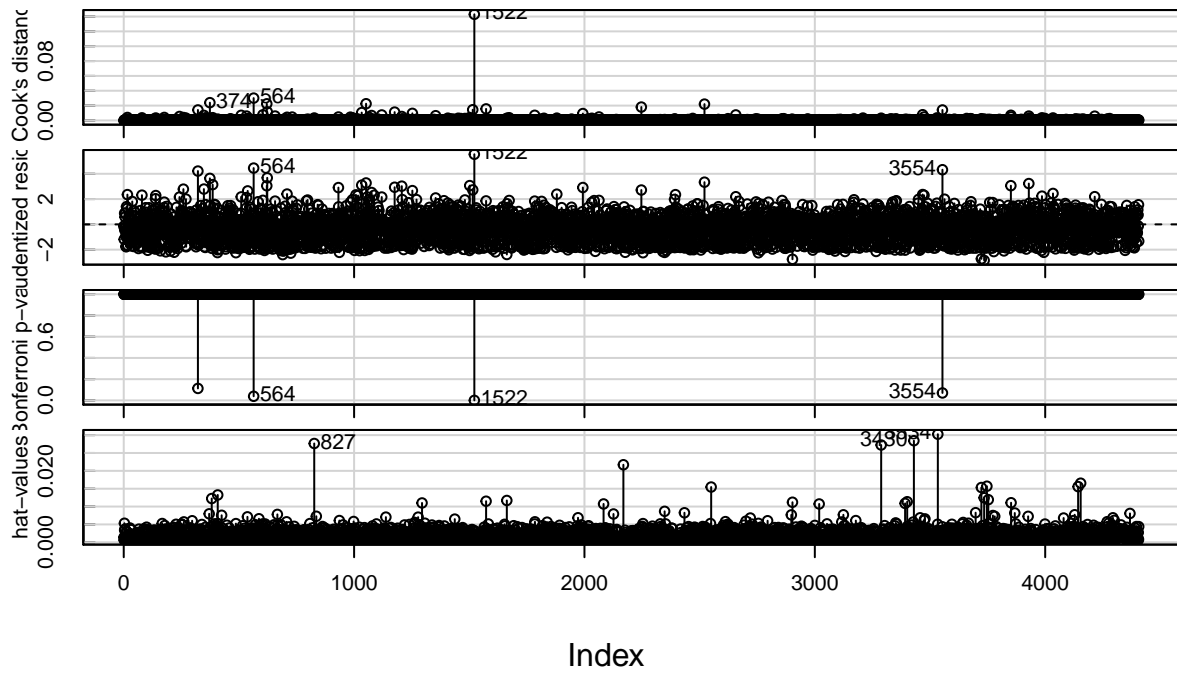
```
# Check for outliers
```

```
outlierTest(vis.nb)
```

```
##      rstudent unadjusted p-value Bonferonni p  
## 1522 5.541651      3.1715e-08  0.00013974  
## 564  4.449918      8.8028e-06  0.03878500
```

```
influenceIndexPlot(vis.nb, id.n = 3)
```

## Diagnostic Plots



```
residualPlot(vis.nb)
```

