The Relationship Between Arsenic Concentrations and Well Usage

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Introduction

Araihazar, Bangladesh

Many of the wells used for drinking water in Bangladesh and other South Asian countries are contaminated with natural arsenic, affecting an estimated 100 million people. Arsenic is a cumulative poison, and exposure increases the risk of cancer and other diseases, with risks estimated to be proportional to exposure. Any locality can include wells with a range of arsenic levels, as can be seen from the map in Figure 5.7 of all the wells in a collection of villages in a small area of Bangladesh. The bad news is that even if your neighbor's well is safe, it does not mean that yours is safe. However, the corresponding good news is that, if your well has a high arsenic level, you can probably find a safe well nearby to get your water from—if you are willing to walk the distance and your neighbor is willing to share. (The amount of water needed for drinking is low enough that adding users to a well would not exhaust its capacity, and the surface water in this area is subject to contamination by microbes, hence the desire to use water from deep wells.) In the area shown in Figure 5.7, a research team from the United States and Bangladesh measured all the wells and labeled them with their arsenic level as well as a characterization as "safe" (below 0.5 in units of hundreds of micrograms per liter, the Bangladesh standard for arsenic in drinking water) or "unsafe" (above 0.5). People with unsafe wells were encouraged to switch to nearby private or community wells or to new wells of their own construction. A few years later, the researchers returned to find out who had switched wells. We shall perform a logistic regression analysis to understand the factors predictive of well switching among the users of unsafe wells. In the notation of the previous section, our outcome variable is

yi = 1 if household i switched to a new well yi = 0 if household i continued using its own well

We consider the following inputs: • A constant term • The distance (in meters) to the closest known safe well • The arsenic level of respondent's well • Whether any members of the household are active in community organizations • The education level of the head of household.

We shall first fit the model just using distance to nearest well and then put in arsenic concentration, organizational membership, and education.

```
# Set up cleaned dataset for Bangladesh well-switching

# Read in the data
```

```
all <- read.dta ("all.dta", convert.factors=F)

# For simplicity, pull out all wells with missing data in the variables that we will b

# according to well owner's wife/sister-in-law
# survey of laypersons, not scientific experts

missing <- is.na (all[,"func"] + all[,"as"] + all[,"distnearest"] + all[,"assn"] + all[,
table(missing)
```

```
## missing
## FALSE  TRUE
##  6498    12
```

```
# with the added predictors, still only 12 missing out of 6510

# recode change and shifted to 0/1

# https://www.ldeo.columbia.edu/~avangeen/publications/documents/vanGeen_JESH_07.pdf

# PREDICTIVE ACCURACY

# try recoding: the levels of education among the 3020 respondents varied from 0 to 18

# ed4: ed/4 - if ed is not a multiple of 4, ed4 truncates the quotient, e.g. ed = 10,

# perception of well safety; not based on arsenic concentrations (already know that ev

# Include only the wells that are functioning (func==1) - analysis does not consider p
keep <- all[,"func"]==1 & all[,"as"]>50
attach.all (all[!missing & keep,])
```

```
## The following object is masked from package:MASS:
##
##     survey
```

```
# Give convenient names to the variables

switch <- switch
arsenic <- as/100
dist <- distnearest
assoc <- ifelse (assn > 0, 1, 0)
educ <- ed
```

```r
educ4 <- ed4
use <- drink
status_perceived <- status
well_change <- ifelse(change > 0, 1, 0)
well_shift <- shifted

wells.data <- cbind (switch, arsenic, dist, assoc, educ, educ4, use, status_perceived, w
write.table (wells.data, "wells.dat")

wells <- read.table("wells.dat", header = TRUE)

drinkorcook_wells <- wells[wells$use!=0,]
## Stopping point
```

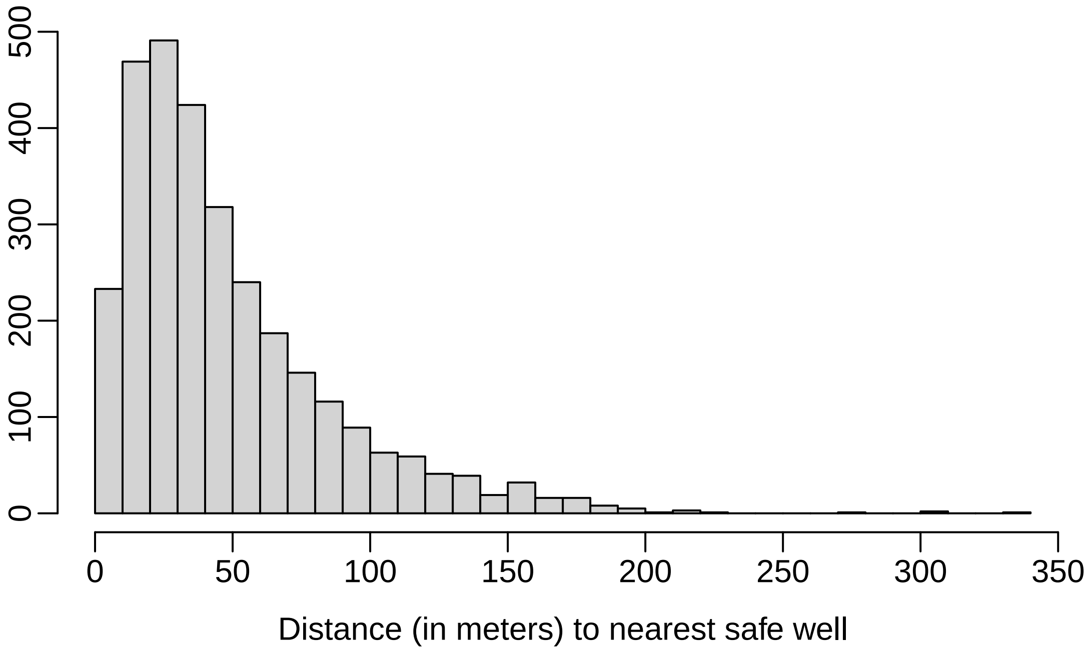
```r
# Logistic regression of switching on distance to nearest safe well

seed <- 200

fit.1 <- stan_glm(switch ~ dist, data = wells,
                 family = binomial(link = "logit"),
                 prior = normal(0,1), prior_intercept = normal(0,1),
                 seed = seed,
                 refresh = 0)

print(fit.1$stanfit)
```

```
## Inference for Stan model: bernoulli.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##                   mean se_mean   sd     2.5%      25%      50%      75%
## (Intercept)       0.61    0.00 0.06     0.49     0.57     0.61     0.65
## dist             -0.01    0.00 0.00    -0.01    -0.01    -0.01    -0.01
## mean_PPD          0.58    0.00 0.01     0.55     0.57     0.57     0.58
## log-posterior -2041.03    0.03 1.04 -2043.84 -2041.43 -2040.70 -2040.29
##                  97.5% n_eff Rhat
## (Intercept)       0.73  1409    1
## dist              0.00  3112    1
## mean_PPD          0.60  1373    1
## log-posterior -2040.03   904    1
##
## Samples were drawn using NUTS(diag_e) at Thu Apr 29 15:54:55 2021.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

```
### END of edited code

# Redefine distance in 100-meter units and fit the model again

dist100 <- dist/100
fit.2 <- glm (switch ~ dist100, family=binomial(link="logit"))
display (fit.2)
```

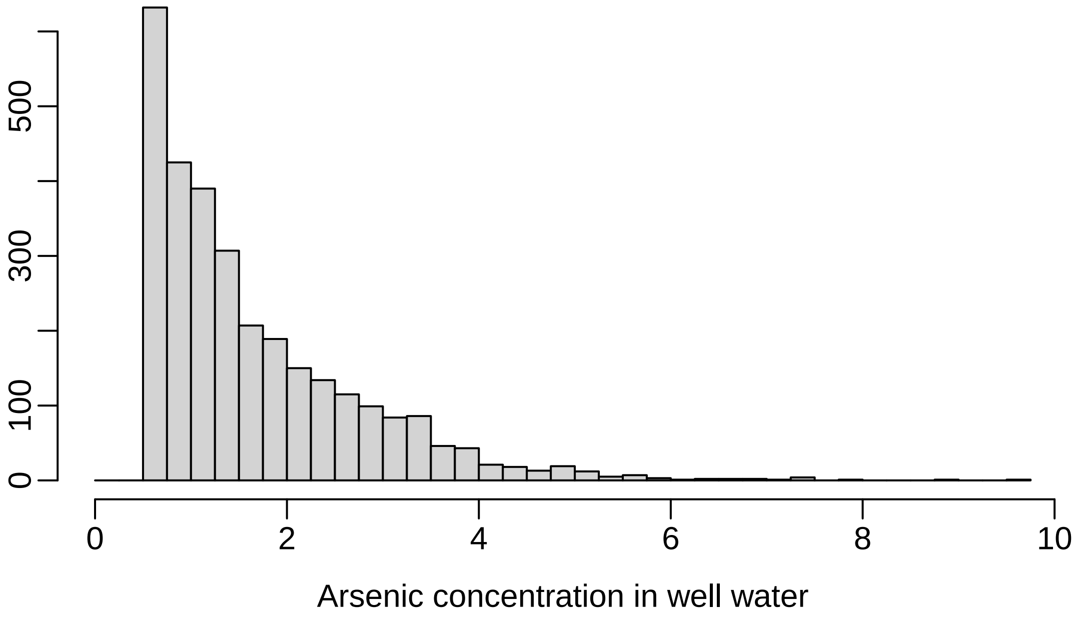
```
## glm(formula = switch ~ dist100, family = binomial(link = "logit"))
##             coef.est coef.se
## (Intercept)  0.61     0.06
## dist100     -0.62     0.10
## ---
##   n = 3020, k = 2
##   residual deviance = 4076.2, null deviance = 4118.1 (difference = 41.9)
```

```
# histogram of distances

#postscript ("c:/books/multilevel/arsenic.distances.bnew.ps", height=3, width=4, horiz
hist (dist, breaks=seq(0,10+max(dist[!is.na(dist)]),10), freq=TRUE, xlab="Distance (in m
```



```
#dev.off ()

# plots of model fit
```

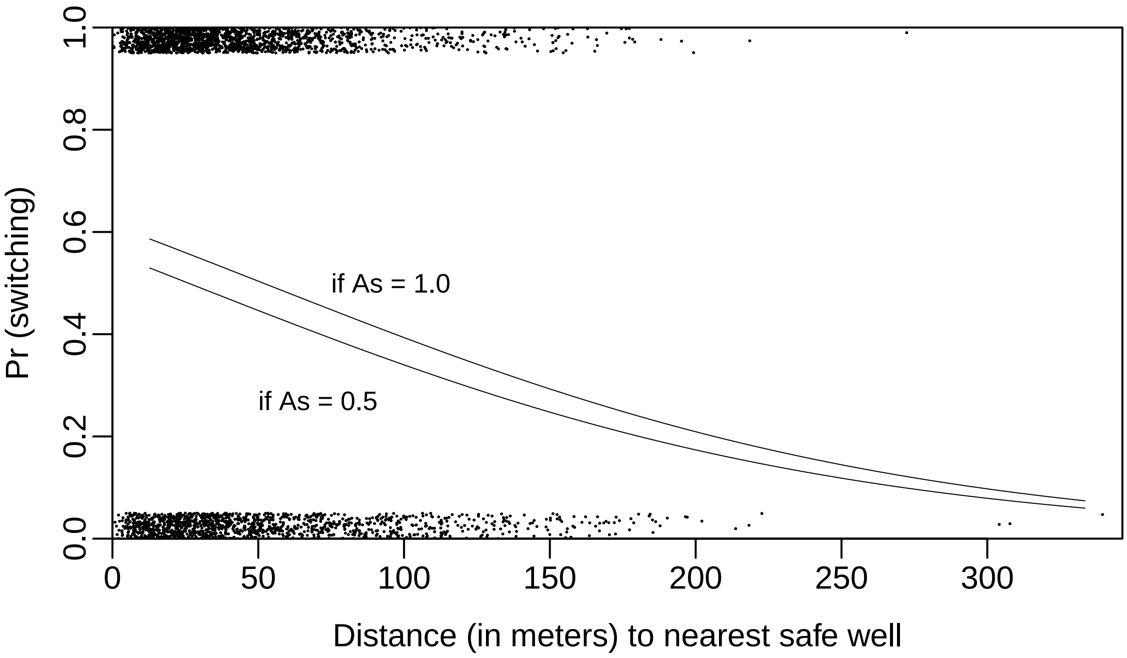
```
jitter.binary <- function(a, jitt=.05){
  a + (1-2*a)*runif(length(a),0,jitt)
}

#postscript ("c:/books/multilevel/arsenic.logitfit.1new.a.ps", height=3.5, width=4, ho
#plot(c(0,max(dist, na.rm=TRUE)*1.02), c(0,1), xlab="Distance (in meters) to nearest s
#curve (invlogit(coef(fit.1)[1]+coef(fit.1)[2]*x), lwd=1, add=TRUE)
#points (dist, jitter.binary(switch), pch=20, cex=.1)
#dev.off ()

# histogram of As levels

#postscript ("c:/books/multilevel/arsenic.levels.a.ps", height=3, width=4, horizontal=
hist (arsenic, breaks=seq(0,.25+max(arsenic[!is.na(arsenic)]),.25), freq=TRUE, xlab="Ars
```



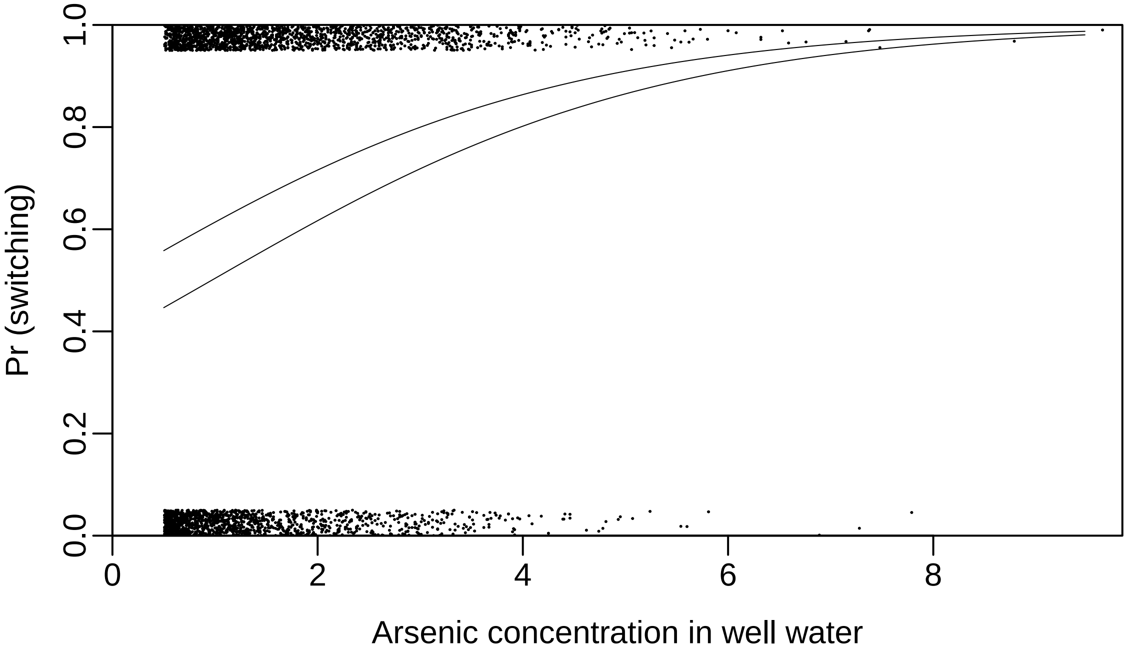
```
#dev.off ()

# model with 2 predictors

fit.3 <- glm (switch ~ dist100 + arsenic, family=binomial(link="logit"))
display (fit.3)
```

```
## glm(formula = switch ~ dist100 + arsenic, family = binomial(link = "logit"))
##             coef.est coef.se
## (Intercept)  0.00     0.08
## dist100     -0.90     0.10
## arsenic      0.46     0.04
## ---
##   n = 3020, k = 3
##   residual deviance = 3930.7, null deviance = 4118.1 (difference = 187.4)
```

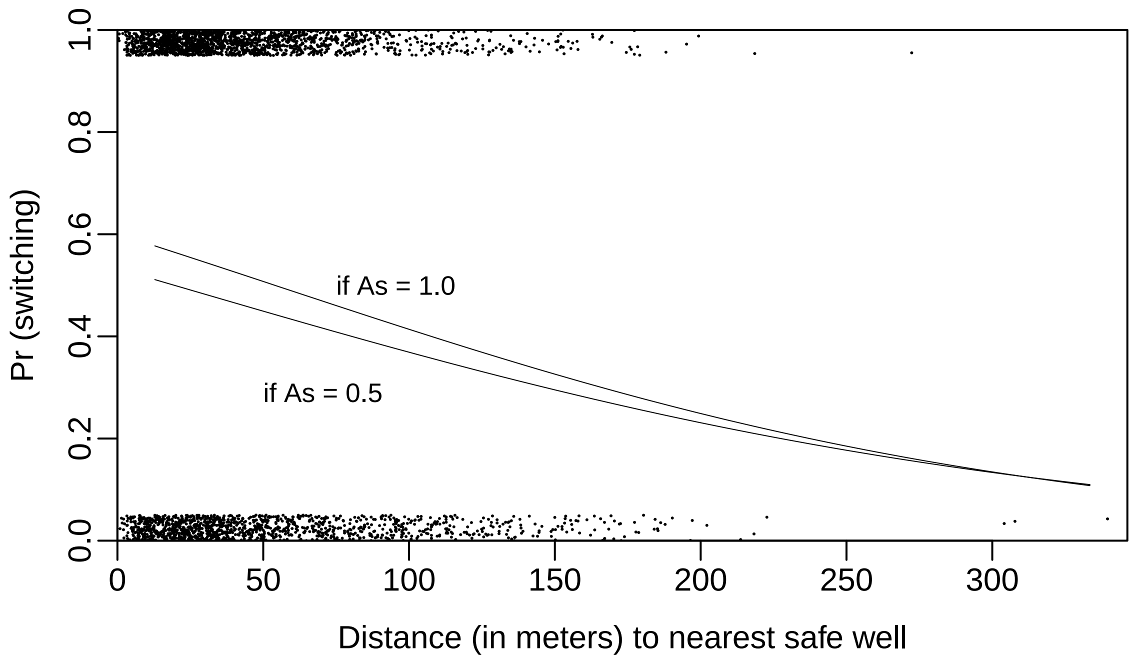
```
#postscript ("c:/books/multilevel/arsenic.2variables.a.ps", height=3.5, width=4, horiz
plot(c(0,max(dist,na.rm=TRUE)*1.02), c(0,1), xlab="Distance (in meters) to nearest safe
points (dist, jitter.binary(switch), pch=20, cex=.1)
curve (invlogit(coef(fit.3)[1]+coef(fit.3)[2]*x/100+coef(fit.3)[3]*.50), lwd=.5, add=TRU
curve (invlogit(coef(fit.3)[1]+coef(fit.3)[2]*x/100+coef(fit.3)[3]*1.00), lwd=.5, add=TI
text (50, .27, "if As = 0.5", adj=0, cex=.8)
text (75, .50, "if As = 1.0", adj=0, cex=.8)
```



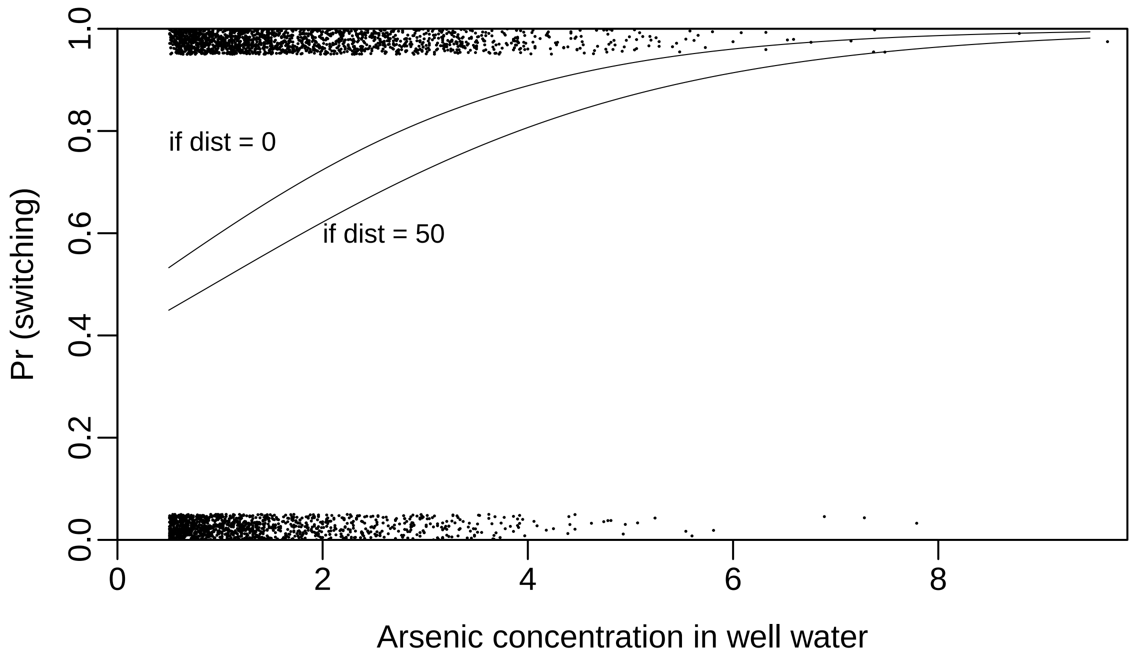
```
#dev.off ()

#postscript ("c:/books/multilevel/arsenic.2variables.b.ps", height=3.5, width=4, horiz
plot(c(0,max(arsenic,na.rm=TRUE)*1.02), c(0,1), xlab="Arsenic concentration in well wate
points (arsenic, jitter.binary(switch), pch=20, cex=.1)
curve (invlogit(coef(fit.3)[1]+coef(fit.3)[2]*0+coef(fit.3)[3]*x), from=0.5, lwd=.5, ado
curve (invlogit(coef(fit.3)[1]+coef(fit.3)[2]*0.5+coef(fit.3)[3]*x), from=0.5, lwd=.5, a
text (50, .78, "if dist = 0", adj=0, cex=.8)
text (200, .6, "if dist = 50", adj=0, cex=.8)
```



```
#dev.off ()

# including an interaction

fit.4 <- glm (switch ~ dist100 + arsenic + dist100:arsenic,
  family=binomial(link="logit"))

# centering the input variables

c.dist100 <- dist100 - mean (dist100)
c.arsenic <- arsenic - mean (arsenic)

fit.5 <- glm (switch ~ c.dist100 + c.arsenic + c.dist100:c.arsenic,
  family=binomial(link="logit"))

#postscript ("c:/books/multilevel/arsenic.interact.a.ps", height=3.5, width=4, horizon
plot(c(0,max(dist,na.rm=TRUE)*1.02), c(0,1), xlab="Distance (in meters) to nearest safe
points (dist, jitter.binary(switch), pch=20, cex=.1)
curve (invlogit(coef(fit.4)[1]+coef(fit.4)[2]*x/100+coef(fit.4)[3]*.50+coef(fit.4)[4]*(
curve (invlogit(coef(fit.4)[1]+coef(fit.4)[2]*x/100+coef(fit.4)[3]*1.00+coef(fit.4)[4]*
text (50, .29, "if As = 0.5", adj=0, cex=.8)
text (75, .50, "if As = 1.0", adj=0, cex=.8)
```



```
#dev.off ()

#postscript ("c:/books/multilevel/arsenic.interact.b.ps", height=3.5, width=4, horizon
plot(c(0,max(arsenic,na.rm=TRUE)*1.02), c(0,1), xlab="Arsenic concentration in well wate
points (arsenic, jitter.binary(switch), pch=20, cex=.1)
curve (invlogit(coef(fit.4)[1]+coef(fit.4)[2]*0+coef(fit.4)[3]*x+coef(fit.4)[4]*0*x), f
curve (invlogit(coef(fit.4)[1]+coef(fit.4)[2]*0.5+coef(fit.4)[3]*x+coef(fit.4)[4]*0.5*x
text (.50, .78, "if dist = 0", adj=0, cex=.8)
text (2.00, .6, "if dist = 50", adj=0, cex=.8)
```



```r
#dev.off ()

# adding social predictors

educ4 <- educ/4

fit.6 <- glm (switch ~ c.dist100 + c.arsenic + c.dist100:c.arsenic +
  assoc + educ4, family=binomial(link="logit"))
display (fit.6)
```

```
## glm(formula = switch ~ c.dist100 + c.arsenic + c.dist100:c.arsenic +
##     assoc + educ4, family = binomial(link = "logit"))
##                     coef.est coef.se
## (Intercept)          0.20     0.07
## c.dist100           -0.88     0.11
## c.arsenic            0.48     0.04
## assoc               -0.12     0.08
## educ4                0.17     0.04
## c.dist100:c.arsenic -0.16     0.10
## ---
##   n = 3020, k = 6
##   residual deviance = 3905.4, null deviance = 4118.1 (difference = 212.7)
```

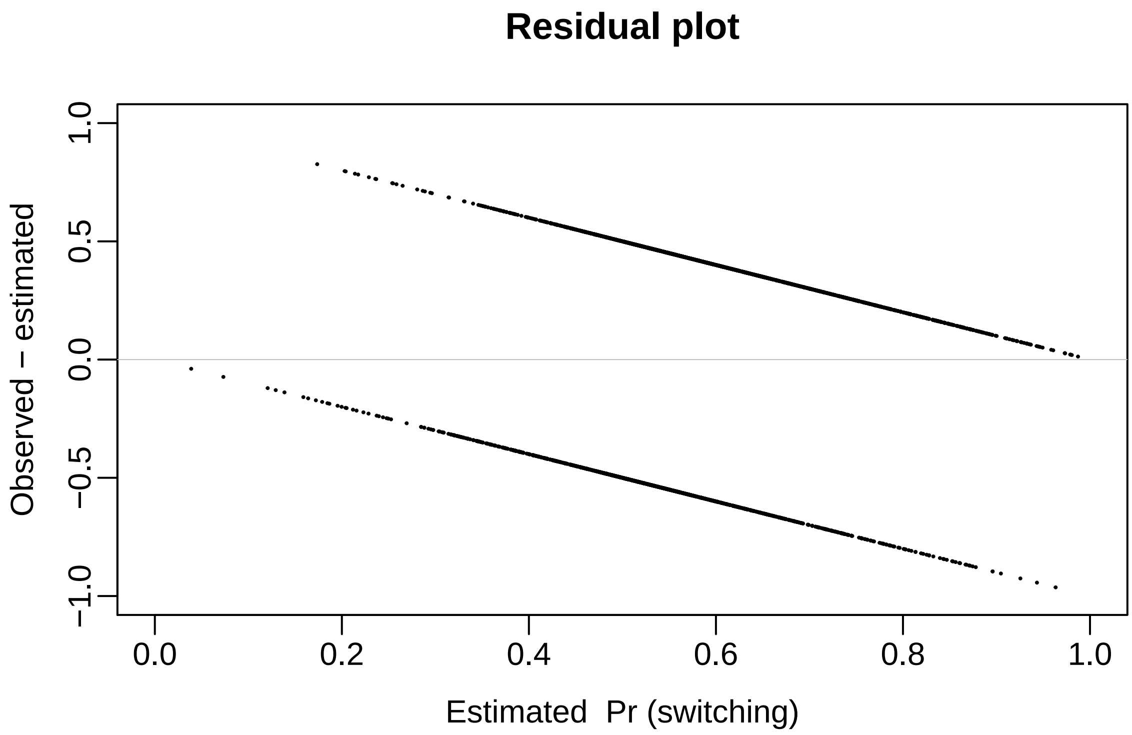
```r
fit.7 <- glm (switch ~ c.dist100 + c.arsenic + c.dist100:c.arsenic +
  educ4, family=binomial(link="logit"))
display (fit.7)
```

```
## glm(formula = switch ~ c.dist100 + c.arsenic + c.dist100:c.arsenic +
##     educ4, family = binomial(link = "logit"))
##                     coef.est coef.se
## (Intercept)          0.15     0.06
## c.dist100           -0.87     0.11
## c.arsenic            0.48     0.04
## educ4                0.17     0.04
## c.dist100:c.arsenic -0.16     0.10
## ---
##   n = 3020, k = 5
##   residual deviance = 3907.9, null deviance = 4118.1 (difference = 210.2)
```

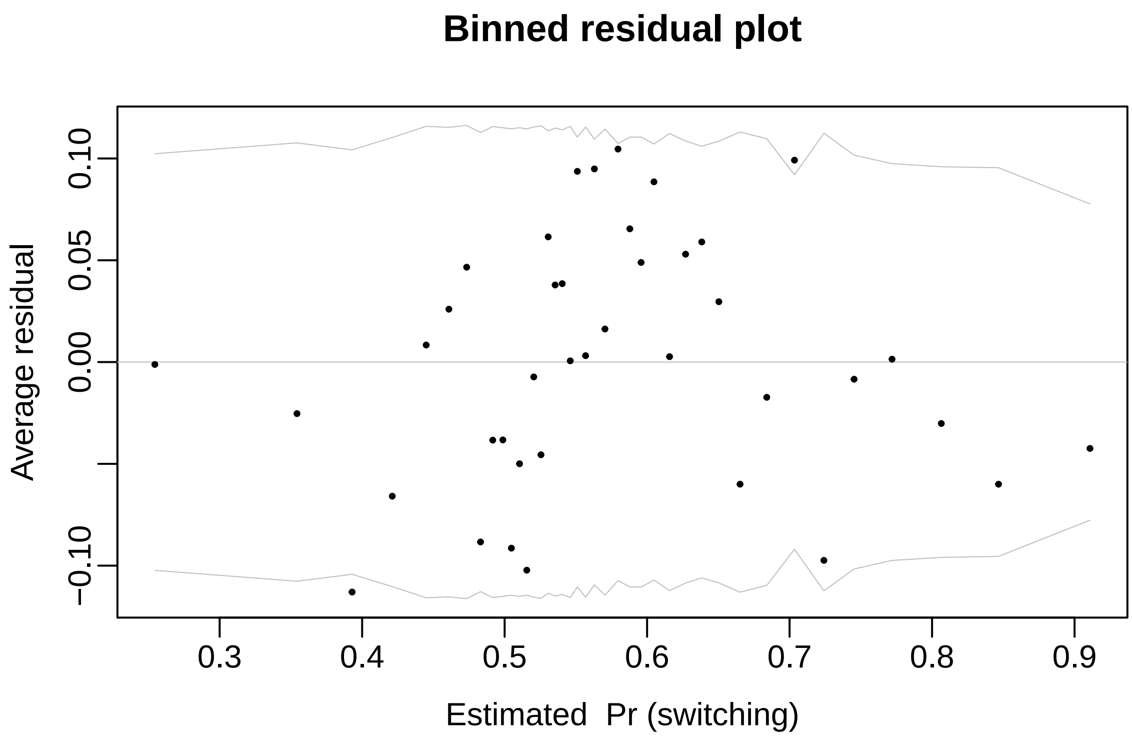
```r
c.educ4 <- educ4 - mean(educ4)

fit.8 <- glm (switch ~ c.dist100 + c.arsenic + c.educ4 + c.dist100:c.arsenic +
  c.dist100:c.educ4 + c.arsenic:c.educ4, family=binomial(link="logit"))
display (fit.8)
```

```
## glm(formula = switch ~ c.dist100 + c.arsenic + c.educ4 + c.dist100:c.arsenic +
##     c.dist100:c.educ4 + c.arsenic:c.educ4, family = binomial(link = "logit"))
##                     coef.est coef.se
## (Intercept)          0.36     0.04
## c.dist100           -0.90     0.11
## c.arsenic            0.49     0.04
## c.educ4              0.18     0.04
## c.dist100:c.arsenic -0.12     0.10
## c.dist100:c.educ4    0.32     0.11
## c.arsenic:c.educ4    0.07     0.04
## ---
##   n = 3020, k = 7
##   residual deviance = 3891.7, null deviance = 4118.1 (difference = 226.4)
```

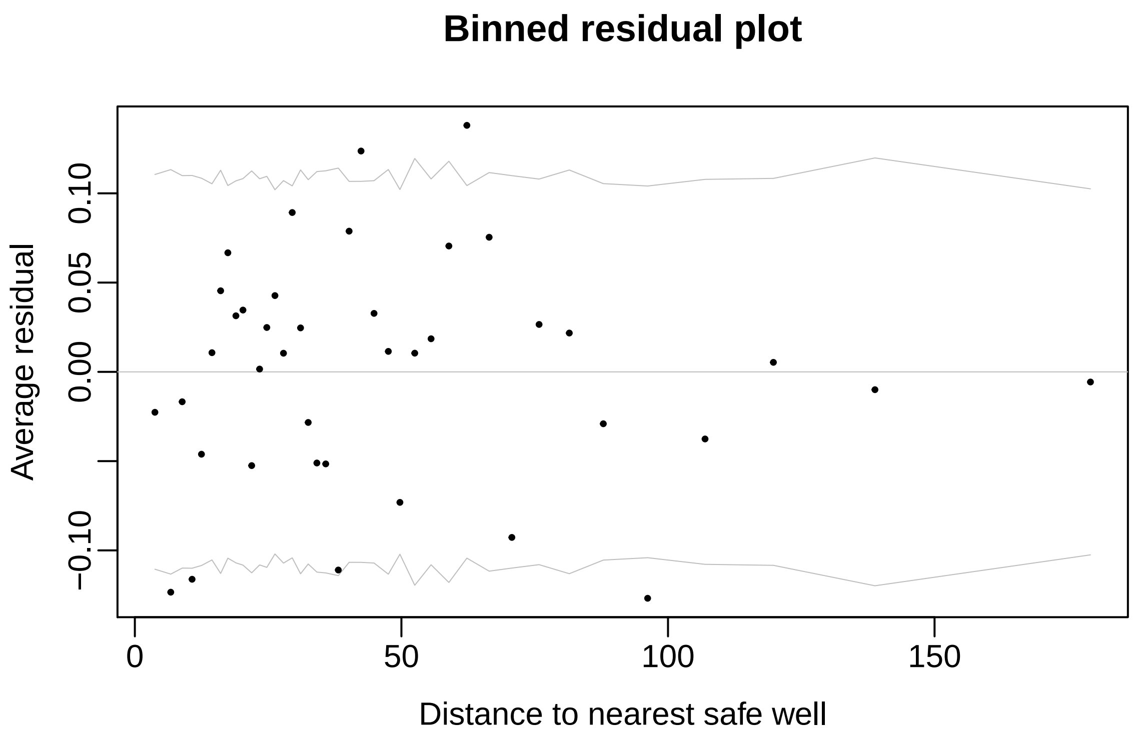
```
# plots of residuals

pred.8 <- fit.8$fitted.values

#postscript ("c:/books/multilevel/arsenic.logitresidsa.ps", height=3.5, width=4, horiz
plot(c(0,1), c(-1,1), xlab="Estimated  Pr (switching)", ylab="Observed - estimated", typ
abline (0,0, col="gray", lwd=.5)
points (pred.8, switch-pred.8, pch=20, cex=.2)
```



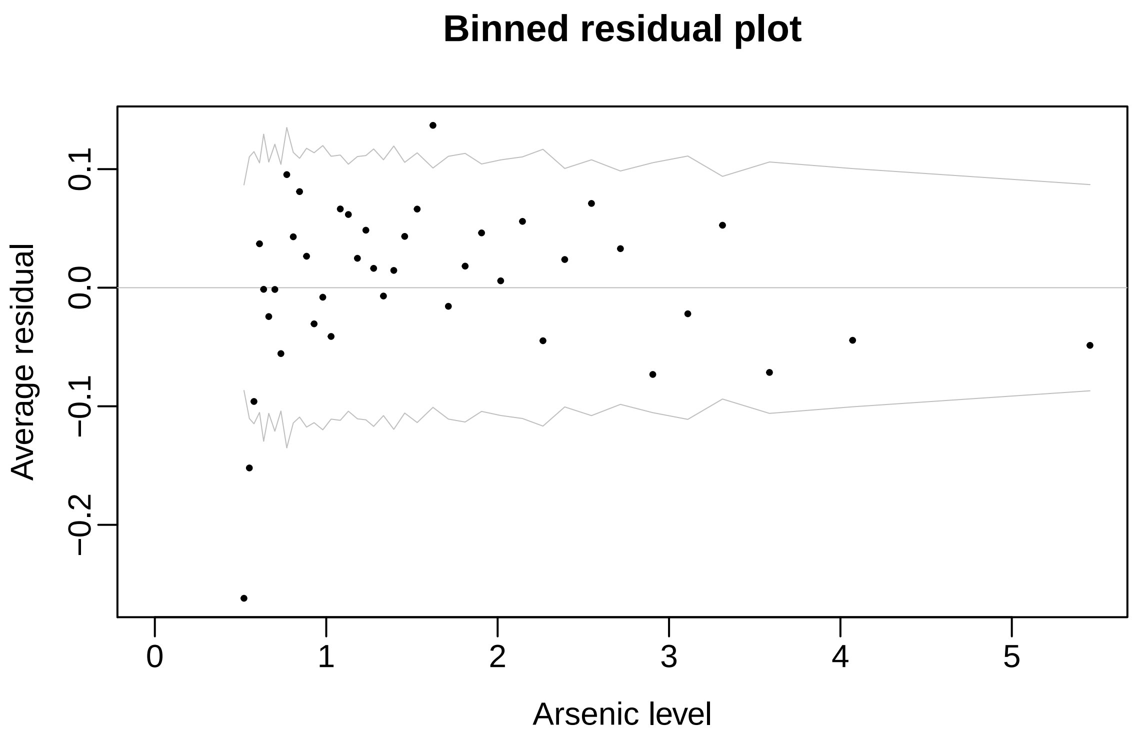
```
#dev.off ()

binned.resids <- function (x, y, nclass=sqrt(length(x))){
  breaks.index <- floor(length(x)*(1:(nclass-1))/nclass)
  breaks <- c (-Inf, sort(x)[breaks.index], Inf)
  output <- NULL
  xbreaks <- NULL
  x.binned <- as.numeric (cut (x, breaks))
  for (i in 1:nclass){
    items <- (1:length(x))[x.binned==i]
    x.range <- range(x[items])
    xbar <- mean(x[items])
    ybar <- mean(y[items])
    n <- length(items)
    sdev <- sd(y[items])
    output <- rbind (output, c(xbar, ybar, n, x.range, 2*sdev/sqrt(n)))
  }
  colnames (output) <- c ("xbar", "ybar", "n", "x.lo", "x.hi", "2se")
  return (list (binned=output, xbreaks=xbreaks))
}

#postscript ("c:/books/multilevel/arsenic.logitresidsb.ps", height=3.5, width=4, horiz
br.8 <- binned.resids (pred.8, switch-pred.8, nclass=40)$binned
plot(range(br.8[,1]), range(br.8[,2],br.8[,6],-br.8[,6]), xlab="Estimated  Pr (switching
abline (0,0, col="gray", lwd=.5)
lines (br.8[,1], br.8[,6], col="gray", lwd=.5)
lines (br.8[,1], -br.8[,6], col="gray", lwd=.5)
points (br.8[,1], br.8[,2], pch=20, cex=.5)
```



```
#dev.off ()

# compute error rates

error.rate <- mean(round(abs(switch-pred.8)))
error.rate.null <- mean(round(abs(switch-mean(pred.8))))

# more residual plots

#postscript ("c:/books/multilevel/arsenic.logitresids.2a.ps", height=3.5, width=4, hor
br <- binned.resids (dist, switch-pred.8, nclass=40)$binned
plot(range(br[,1]), range(br[,2],br[,6],-br[,6]), xlab="Distance to nearest safe well",
abline (0,0, col="gray", lwd=.5)
n.within.bin <- length(y)/nrow(br)
lines (br[,1], br[,6], col="gray", lwd=.5)
lines (br[,1], -br[,6], col="gray", lwd=.5)
points (br[,1], br[,2], pch=20, cex=.5)
```



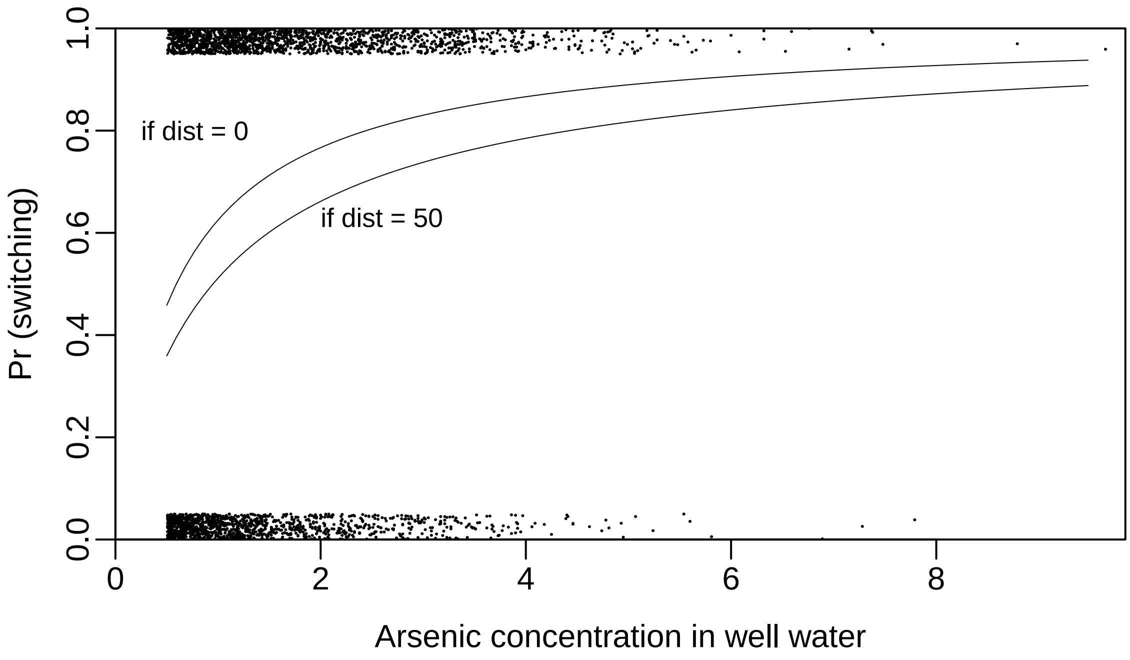
```
#dev.off ()

#postscript ("c:/books/multilevel/arsenic.logitresids.2b.ps", height=3.5, width=4, hor
br <- binned.resids (arsenic, switch-pred.8, nclass=40)$binned
plot(range(0,br[,1]), range(br[,2],br[,6],-br[,6]), xlab="Arsenic level", ylab="Average
abline (0,0, col="gray", lwd=.5)
lines (br[,1], br[,6], col="gray", lwd=.5)
lines (br[,1], -br[,6], col="gray", lwd=.5)
points (br[,1], br[,2], pch=20, cex=.5)
```



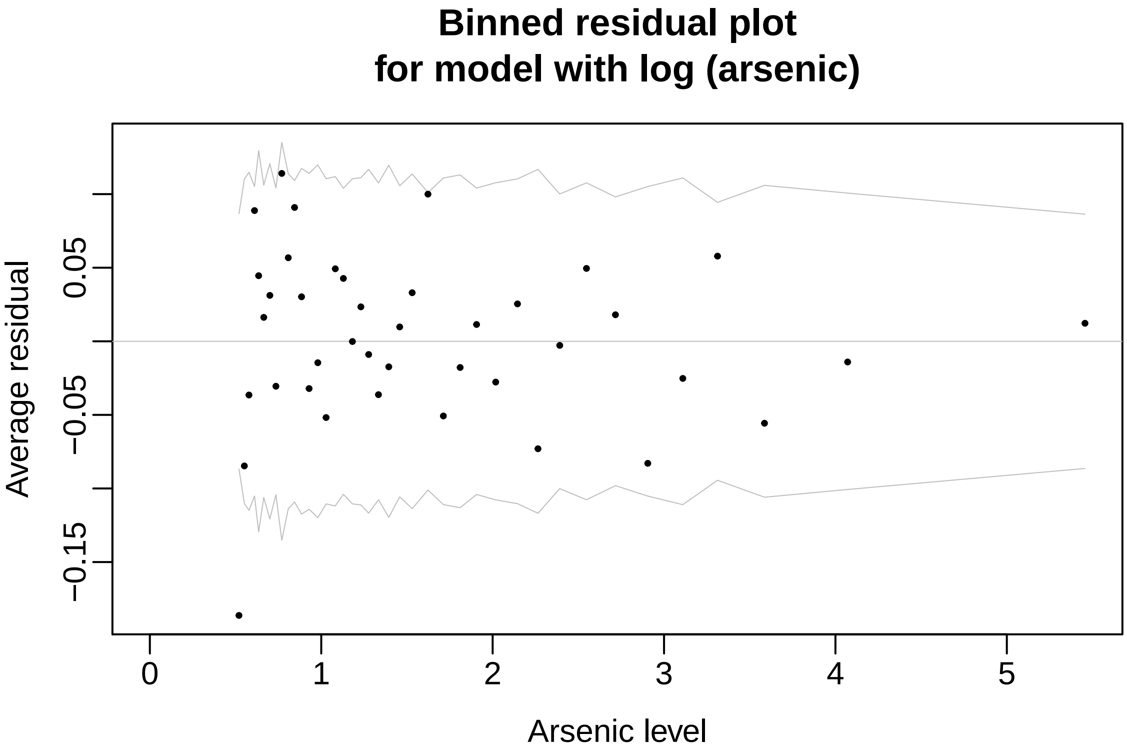
```
#dev.off ()

# new model on log scale

log.arsenic <- log (arsenic)
c.log.arsenic <- log.arsenic - mean (log.arsenic)

fit.9 <- glm (switch ~ c.dist100 + c.log.arsenic + c.educ4 +
  c.dist100:c.log.arsenic + c.dist100:c.educ4 + c.log.arsenic:c.educ4,
  family=binomial(link="logit"))
display (fit.9)
```

```
## glm(formula = switch ~ c.dist100 + c.log.arsenic + c.educ4 +
##     c.dist100:c.log.arsenic + c.dist100:c.educ4 + c.log.arsenic:c.educ4,
##     family = binomial(link = "logit"))
##                         coef.est coef.se
## (Intercept)              0.35     0.04
## c.dist100               -0.98     0.11
## c.log.arsenic            0.90     0.07
## c.educ4                  0.18     0.04
## c.dist100:c.log.arsenic -0.16     0.19
## c.dist100:c.educ4        0.34     0.11
## c.log.arsenic:c.educ4    0.06     0.07
## ---
##   n = 3020, k = 7
##   residual deviance = 3863.1, null deviance = 4118.1 (difference = 255.0)
```

```
fit.9a <- glm (switch ~ dist100 + log.arsenic + educ4 +
  dist100:log.arsenic + dist100:educ4 + log.arsenic:educ4,
  family=binomial(link="logit"))

# graphs for log model

#postscript ("c:/multilevel/arsenic.logmodel.ps", height=3.5, width=4, horizontal=TRUE
plot(c(0,max(arsenic,na.rm=TRUE)*1.02), c(0,1), xlab="Arsenic concentration in well wate
points (arsenic, jitter.binary(switch), pch=20, cex=.1)
curve (invlogit(coef(fit.9a)[1]+coef(fit.9a)[2]*0+coef(fit.9a)[3]*log(x)+coef(fit.9a)[4
curve (invlogit(coef(fit.9a)[1]+coef(fit.9a)[2]*.5+coef(fit.9a)[3]*log(x)+coef(fit.9a)[
text (.25, .80, "if dist = 0", adj=0, cex=.8)
text (2.00, .63, "if dist = 50", adj=0, cex=.8)
```



```
#dev.off ()

pred.9 <- fit.9$fitted.values

#postscript ("c:/books/multilevel/arsenic.logitresids.3b.ps", height=3.5, width=4, hor
br <- binned.resids (arsenic, switch-pred.9, nclass=40)$binned
plot(range(0,br[,1]), range(br[,2],br[,6],-br[,6]), xlab="Arsenic level", ylab="Average
abline (0,0, col="gray", lwd=.5)
n.within.bin <- length(y)/nrow(br)
lines (br[,1], br[,6], col="gray", lwd=.5)
lines (br[,1], -br[,6], col="gray", lwd=.5)
points (br[,1], br[,2], pch=20, cex=.5)
```



```
#dev.off ()

# calculations for average predictive differences

# simple model
fit.10 <- glm (switch ~ dist100 + arsenic + educ4,
  family=binomial(link="logit"))
display (fit.10)
```

```
## glm(formula = switch ~ dist100 + arsenic + educ4, family = binomial(link = "logit"))
##             coef.est coef.se
## (Intercept) -0.21     0.09  
## dist100     -0.90     0.10  
## arsenic      0.47     0.04  
## educ4        0.17     0.04  
## ---
##   n = 3020, k = 4
##   residual deviance = 3910.4, null deviance = 4118.1 (difference = 207.7)
```

```
# avg pred diffs for distance to nearest safe well
b <- coef (fit.10)
hi <- 1
lo <- 0
delta <- invlogit (b[1] + b[2]*hi + b[3]*arsenic + b[4]*educ4) -
         invlogit (b[1] + b[2]*lo + b[3]*arsenic + b[4]*educ4)
print (mean(delta))
```

```
## [1] -0.2044681
```

```
# avg pred diffs for arsenic level
hi <- 1.0
lo <- 0.5
delta <- invlogit (b[1] + b[2]*dist100 + b[3]*hi + b[4]*educ4) -
         invlogit (b[1] + b[2]*dist100 + b[3]*lo + b[4]*educ4)
print (mean(delta))
```

```
## [1] 0.05643807
```

```
# avg pred diffs for education
hi <- 3
lo <- 0
delta <- invlogit (b[1]+b[2]*dist100+b[3]*arsenic+b[4]*hi) -
         invlogit (b[1]+b[2]*dist100+b[3]*arsenic+b[4]*lo)
print (mean(delta))
```

```
## [1] 0.1167189
```

```
# example model with interaction
fit.11 <- glm (switch ~ dist100 + arsenic + educ4 + dist100:arsenic,
  family=binomial(link="logit"))
display (fit.11)
```

```
## glm(formula = switch ~ dist100 + arsenic + educ4 + dist100:arsenic,
##     family = binomial(link = "logit"))
##                 coef.est coef.se
## (Intercept)     -0.35     0.13
## dist100         -0.60     0.21
## arsenic          0.56     0.07
## educ4            0.17     0.04
## dist100:arsenic -0.16     0.10
## ---
##   n = 3020, k = 5
##   residual deviance = 3907.9, null deviance = 4118.1 (difference = 210.2)
```

```
b <- coef (fit.11)
hi <- 1
lo <- 0
delta <- invlogit (b[1] + b[2]*hi + b[3]*arsenic + b[4]*educ4 +
                   b[5]*hi*arsenic) -
         invlogit (b[1] + b[2]*lo + b[3]*arsenic + b[4]*educ4 +
                   b[5]*lo*arsenic)
print (mean(delta))
```

```
## [1] -0.1944495
```