PS1

# Problems 3-6

## Problem 3

### 3a)

probit = glm(dead~alcohol+dmage+dmage2+dmar+dmeduc+foreignb+tobacco+mblack+motherr+mhispan,  
 family = binomial(link = "probit"), data = d)  
(summary(probit))

##   
## Call:  
## glm(formula = dead ~ alcohol + dmage + dmage2 + dmar + dmeduc +   
## foreignb + tobacco + mblack + motherr + mhispan, family = binomial(link = "probit"),   
## data = d)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.3024 -0.1468 -0.1151 -0.1016 3.3642   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.9197032 0.0930779 -20.625 < 2e-16 \*\*\*  
## alcohol 0.0645402 0.0285995 2.257 0.02403 \*   
## dmage -0.0298198 0.0071779 -4.154 3.26e-05 \*\*\*  
## dmage2 0.0005278 0.0001309 4.032 5.53e-05 \*\*\*  
## dmar 0.0978295 0.0133972 7.302 2.83e-13 \*\*\*  
## dmeduc -0.0175084 0.0024660 -7.100 1.25e-12 \*\*\*  
## foreignb -0.0596650 0.0187627 -3.180 0.00147 \*\*   
## tobacco 0.1524062 0.0139106 10.956 < 2e-16 \*\*\*  
## mblack 0.2545930 0.0135147 18.838 < 2e-16 \*\*\*  
## motherr 0.1472550 0.0469987 3.133 0.00173 \*\*   
## mhispan 0.0242961 0.0216295 1.123 0.26132   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 55255 on 565942 degrees of freedom  
## Residual deviance: 54098 on 565932 degrees of freedom  
## AIC: 54120  
##   
## Number of Fisher Scoring iterations: 7

From the coefficients and standard errors in the regression output, it appears that education and foreign birth have a significant negative effect on infant mortality. In other words, if a mother is more educated or she is foreign born,there is a smaller chance of her baby dying, all else equal. On the flip side, being unmarried,black, neither black nor white, and consuming tobacco or alcohol during pregnancy all have a significant positive effecton infant mortality. All else equal, having one of these attributes will increase the chances of the mother's baby dying. Age and age squared have opposite effects on the chances of infant mortality. whether or not the mother is hispanic does not appear to have a significant effect on infant mortality.

### 3b)

(waldtest(probit))

## Wald test  
##   
## Model 1: dead ~ alcohol + dmage + dmage2 + dmar + dmeduc + foreignb +   
## tobacco + mblack + motherr + mhispan  
## Model 2: dead ~ 1  
## Res.Df Df F Pr(>F)   
## 1 565932   
## 2 565942 -10 117.9 < 2.2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

The wald test performed tells us that we can be confident that at least one of the coefficients in the regression is statistically different from zero.

betap = probit$coefficients[-1] #gets estimated betas (w/o constant)  
valsp = pnorm(as.matrix(d[,1:10])%\*%betap) #multiplies betas by given data  
predictp = numeric(nrow(valsp))  
  
for(i in 1:length(predictp)){ #predicts dead = 1 if x'beta is greater than 0.5  
 if(valsp[i]>0.5){  
 predictp[i] = 1  
 }  
}  
boundp = cbind(d$dead,predictp)   
boundp = boundp[which(boundp[,1]==boundp[,2]),]  
  
perccorrectp = length(boundp[,1])/length(d$dead)  
(perccorrectp)

## [1] 0.9905697

The percentage correctly predicted calculated above seems too high to be the true percentage that we could actually predict given the regression results. This may be because we are predicting a lot of zero outcomes (a lot of values of x'beta are less than .5) and infant mortality rates in the US are very low. Therefore, we are predicting many zero outcomes when, in fact, there are many zero outcomes because of the nature of the data. This would lead to a high percentage correctly predicted even though we are not necessarily predicting a 1 outcome.

### 3c)

pdfp = mean(dnorm(cbind(ones,as.matrix(d[,-c(11,12)]))%\*%probit$coefficients)) #calculates mean of density of all x'betas  
avgeffectsp = pdfp\*probit$coefficients #multiplies mean by beta hat  
(avgeffectsp)

## (Intercept) alcohol dmage dmage2 dmar   
## -4.349118e-02 1.462170e-03 -6.755720e-04 1.195734e-05 2.216344e-3  
## dmeduc foreignb tobacco mblack motherr   
## -3.966562e-04 -1.351720e-03 3.452787e-03 5.767846e-03 3.336086e-3  
## mhispan   
## 5.504314e-04

(margins(probit,factors = "continuous", atmeans = F,type = "response")[[1]]) #uses a function to get the same result

## Warning in margins.glm(probit, factors = "continuous", atmeans = F, type =  
## "response"): Variances for marginal effects on response scale are incorrect

## Factor dy/dx Std.Err. z value Pr(>|z|) 2.50% 97.50%  
## alcohol 0.0015 0.0006 2.2567 0.0240 0.0002 0.0027  
## dmage -0.0007 0.0002 -4.1544 0.0000 -0.0010 -0.0004  
## dmage2 0.0000 0.0000 4.0318 0.0001 0.0000 0.0000  
## dmar 0.0022 0.0003 7.3022 0.0000 0.0016 0.0028  
## dmeduc -0.0004 0.0001 -7.1001 0.0000 -0.0005 -0.0003  
## foreignb -0.0014 0.0004 -3.1800 0.0015 -0.0022 -0.0005  
## tobacco 0.0035 0.0003 10.9561 0.0000 0.0028 0.0041  
## mblack 0.0058 0.0003 18.8383 0.0000 0.0052 0.0064  
## motherr 0.0033 0.0011 3.1332 0.0017 0.0012 0.0054  
## mhispan 0.0006 0.0005 1.1233 0.2613 -0.0004 0.0015

### 3d)

means = c(1,colMeans(d[,1:10])) #calculataes means of each independent variable  
effatmean = dnorm(t(as.matrix(means))%\*%probit$coefficients)\*probit$coefficients #calculates effects at the mean  
  
(effatmean)

## [1] -4.046003e-02 1.360263e-03 -6.284875e-04 1.112397e-05 2.061874e-03  
## [6] -3.690110e-04 -1.257511e-03 3.212142e-03 5.365851e-03 3.103575e-03  
## [11] 5.120687e-04

The effects at the mean are smaller than the average effects calculated above, but barely. Since the estimate of the effect of the mean are misleading and do not differ very much from the mean effect, I would prefer to use the mean effect rather than the effect at the mean.

### 3e)

alcp = probit$coefficients[2]\*ones #creates a vector of betas for alcohol  
tobacp = probit$coefficients[8]\*ones #creates a vector of betas for tobacco  
noalc = cbind(ones,d[,-c(1,11,12)]) #creates a data frame that doesn't include alcohol   
notob = cbind(ones,d[,-c(8,11,12)]) #creates a data frame that doesn't include tobacco  
acteffalcp = mean(pnorm(as.matrix(noalc)%\*%as.matrix(probit$coefficients[-c(2)])+alcp)-  
 pnorm(as.matrix(noalc)%\*%probit$coefficients[-c(2)]))  
#^calculates actual effect of alcohol using the formula from class  
actefftobacp = mean(pnorm(as.matrix(notob)%\*%as.matrix(probit$coefficients[-c(8)])+tobacp)-  
 pnorm(as.matrix(notob)%\*%probit$coefficients[-c(8)]))  
(acteffalcp)

## [1] 0.001569307

(actefftobacp)

## [1] 0.003696319

In this particular application, the effect of alcohol and tobacco calculated using a continuous approximation understates the actual effect by a only very small amount, so the continuous approximation was a good estimation of the actual effect.

## Problem 4

### 4a)

##Below code re-calculates all of the measures from problem 3, but using a logit model rather than a probit model  
logit = glm(dead~alcohol+dmage+dmage2+dmar+dmeduc+foreignb+tobacco+mblack+tobacco+motherr+mhispan,  
 family = binomial(link = "logit"), data = d)  
(summary(logit))

##   
## Call:  
## glm(formula = dead ~ alcohol + dmage + dmage2 + dmar + dmeduc +   
## foreignb + tobacco + mblack + tobacco + motherr + mhispan,   
## family = binomial(link = "logit"), data = d)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.3221 -0.1460 -0.1148 -0.1023 3.3521   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.5470664 0.2460432 -14.416 < 2e-16 \*\*\*  
## alcohol 0.1674730 0.0743974 2.251 0.024382 \*   
## dmage -0.0769192 0.0191073 -4.026 5.68e-05 \*\*\*  
## dmage2 0.0013552 0.0003499 3.874 0.000107 \*\*\*  
## dmar 0.2625815 0.0362390 7.246 4.30e-13 \*\*\*  
## dmeduc -0.0476287 0.0066583 -7.153 8.47e-13 \*\*\*  
## foreignb -0.1666520 0.0513482 -3.246 0.001172 \*\*   
## tobacco 0.4113891 0.0371749 11.066 < 2e-16 \*\*\*  
## mblack 0.6813733 0.0361173 18.866 < 2e-16 \*\*\*  
## motherr 0.4086585 0.1283388 3.184 0.001451 \*\*   
## mhispan 0.0652053 0.0596765 1.093 0.274550   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 55255 on 565942 degrees of freedom  
## Residual deviance: 54104 on 565932 degrees of freedom  
## AIC: 54126  
##   
## Number of Fisher Scoring iterations: 8

(waldl)

## Wald test  
##   
## Model 1: dead ~ alcohol + dmage + dmage2 + dmar + dmeduc + foreignb +   
## tobacco + mblack + tobacco + motherr + mhispan  
## Model 2: dead ~ 1  
## Res.Df Df F Pr(>F)   
## 1 565932   
## 2 565942 -10 119.67 < 2.2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

print("Percentage correctly predicted:")

## [1] "Percentage correctly predicted:"

(perccorrectl)

## [1] 0.9901651

pdfl = mean(dlogis(cbind(ones,as.matrix(d[,-c(11,12)]))%\*%logit$coefficients))  
avgeffectsl = pdfl\*logit$coefficients  
(avgeffectsl) #gives average effects with logistic assumption

## (Intercept) alcohol dmage dmage2 dmar   
## -2.969769e-02 1.402162e-03 -6.440031e-04 1.134663e-05 2.198454e-3   
## dmeduc foreignb tobacco mblack motherr   
## -3.987693e-04 -1.395288e-03 3.444341e-03 5.704774e-03 3.421479e-3   
## mhispan   
## 5.459287e-04

(margins(logit,factors = "discrete", atmeans = F,type = "response")[[1]])#uses a built in function to get the actual (discrete) effects of tobacco and alcohol

## Warning in margins.glm(logit, factors = "discrete", atmeans = F, type =  
## "response"): Variances for marginal effects on response scale are incorrect

## Factor dy/dx Std.Err. z value Pr(>|z|) 2.50% 97.50%  
## alcohol 0.0014 0.0006 2.2511 0.0244 0.0002 0.0026  
## dmage -0.0006 0.0002 -4.0256 0.0001 -0.0010 -0.0003  
## dmage2 0.0000 0.0000 3.8736 0.0001 0.0000 0.0000  
## dmar 0.0022 0.0003 7.2458 0.0000 0.0016 0.0028  
## dmeduc -0.0004 0.0001 -7.1533 0.0000 -0.0005 -0.0003  
## foreignb -0.0014 0.0004 -3.2455 0.0012 -0.0022 -0.0006  
## tobacco 0.0034 0.0003 11.0663 0.0000 0.0028 0.0041  
## mblack 0.0057 0.0003 18.8655 0.0000 0.0051 0.0063  
## motherr 0.0034 0.0011 3.1842 0.0015 0.0013 0.0055  
## mhispan 0.0005 0.0005 1.0926 0.2745 -0.0004 0.0015

### 4b)

The coefficients generated by the logit model are different from those of the probit model, however, all logit coefficients have the same sign as well as the same level of significance as their corresponding probit counterparts. The average effects calculated using the logit model also have the same signs as the probit average effects. The effects are very close in magnitude to each other as well, but the estimated effects are very slightly higher using probit rather than logit

### 4c)

predicted = numeric(1)  
i = min(d$dmage)  
while(i <= max(d$dmage)){ #calculataes probability of infant mortality at each age and saves results  
 x00 = data.frame(alcohol = 0,dmage=i, dmage2=i^2,dmar=0,dmeduc=12,foreignb=0,tobacco=1,mblack=0,motherr=0,mhispan=0)  
 prediction = predict(logit,x00, type = "response")  
 predicted = c(predicted, prediction)  
 i = i+1  
}  
predicted = predicted[-1]  
bestage = which(predicted == min(predicted))+min(d$dmage)  
(bestage)  
## 29

CI4c = c(bestage-1.96\*pred29$se.fit,bestage+1.96\*pred29$se.fit)  
(CI4c)

## 1 1   
## 28.99944 29.00056

The method for estimating the best age for a mother to have a baby shown above makes use of a loop where the probability of infant mortality is calculatedfor each age between the min and max in the given data. The main issue with this method is that it assumes that all other covariates are equal to the onesgiven in part d). When trying to estimate this at the means of the covariates, I received errors in the predict function.Therefore, this result can be interpreted as the best age to have a baby if the mother has all the other given characteristics.There is also an isssue with the confidence interval that I calculated. This CI uses the standard errors on the probability of infant mortality given an age of 29, which clearly is the wrong se to use. I was unable to back out this probability se to get one for age, so this CI is not very meaningful.

### 

### 4d)

xo = c(1,0,25,25^2,0,12,1,0,0,0,0)  
  
betal = logit$coefficients  
probl = plogis(t(xo)%\*%betal) #calculates probability of having a baby die within a year of birth given supplied characteristics  
(probl)

## [,1]  
## [1,] 0.004673224

x00 = data.frame(alcohol = 0,dmage=25, dmage2=25^2,dmar=0,dmeduc=12,foreignb=0,tobacco=1,mblack=0,motherr=0,mhispan=0)  
  
pred = predict(logit,x00,type = "response",se.fit = TRUE )  
(pred) #^uses a built in function to acheive the same result

## $fit  
## 1   
## 0.00829987   
##   
## $se.fit  
## 1   
## 0.000295174   
##   
## $residual.scale  
## [1] 1

CI4d = c(probl-1.96\*pred$se.fit, probl+1.96\*pred$se.fit) #calculates 95%CI based on estimate  
(CI4d)

## [1] 0.004094683 0.005251765

### 4e)

effatmeanl = dlogis(t(as.matrix(means))%\*%logit$coefficients)\*logit$coefficients  
 #^calculates effects using fomula from class  
x1 = data.frame(alcohol = 0,dmage=28, dmage2=28^2,dmar=0,dmeduc=17,foreignb=0,tobacco=0,mblack=0,motherr=0,mhispan=0)  
  
pdfx1 = mean(dlogis(cbind(1,as.matrix(x1))%\*%logit$coefficients))  
avgeffectsx1 = pdfx1\*logit$coefficients #calculataes average effects using formula from class  
  
(effatmeanl)

## [1] -2.666510e-02 1.258980e-03 -5.782404e-04 1.018796e-05 1.973958e-03  
## [6] -3.580487e-04 -1.252807e-03 3.092621e-03 5.122229e-03 3.072093e-03  
## [11] 4.901809e-04

(avgeffectsx1)

## (Intercept) alcohol dmage dmage2 dmar   
## -1.513933e-02 7.147959e-04 -3.283007e-04 5.784298e-06 1.120731e-3  
## dmeduc foreignb tobacco mblack motherr   
## -2.032851e-04 -7.112916e-04 1.755861e-03 2.908187e-03 1.744206e-3   
## mhispan   
## 2.783042e-04

The marginal effects for a mother with covariates equal to the mean are higher than those of the mother given in the problem. In fact, they seem to be roughly twice as large.This is because there is more mass in the density function around the mean than there is at points that are farther away from the mean. To get the asymptotic variance of the estimates of these effects, I would employ the delta method because we are looking for the variance of a function of our parameters. This would involve taking the derivative of the pdf of a logistic distribution with respect to the parametersand squaring it, and then multiplying this function by 1/n.

### 4f)

lpm = lm(dead~alcohol+dmage+dmage2+dmar+dmeduc+foreignb+tobacco+mblack+motherr+mhispan, data = d )  
coeftest(lpm, vcov = vcovHC(lpm, "HC1")) #computes robust standard errors, requires "plm"

##   
## t test of coefficients:  
##   
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 2.0599e-02 2.6772e-03 7.6941 1.428e-14 \*\*\*  
## alcohol 2.2874e-03 8.6840e-04 2.6341 0.0084373 \*\*   
## dmage -7.9008e-04 1.9852e-04 -3.9799 6.895e-05 \*\*\*  
## dmage2 1.3989e-05 3.5214e-06 3.9724 7.115e-05 \*\*\*  
## dmar 2.4870e-03 3.5531e-04 6.9995 2.571e-12 \*\*\*  
## dmeduc -3.5879e-04 5.7107e-05 -6.2828 3.328e-10 \*\*\*  
## foreignb -1.4312e-03 4.2022e-04 -3.4059 0.0006594 \*\*\*  
## tobacco 3.6107e-03 3.7567e-04 9.6115 < 2.2e-16 \*\*\*  
## mblack 6.8402e-03 4.0209e-04 17.0116 < 2.2e-16 \*\*\*  
## motherr 3.3310e-03 1.0497e-03 3.1732 0.0015079 \*\*   
## mhispan 6.8197e-04 4.5545e-04 1.4974 0.1342978   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(avgeffectsp)

## (Intercept) alcohol dmage dmage2 dmar   
## -4.349118e-02 1.462170e-03 -6.755720e-04 1.195734e-05 2.216344e-3   
## dmeduc foreignb tobacco mblack motherr   
## -3.966562e-04 -1.351720e-03 3.452787e-03 5.767846e-03 3.336086e-3   
## mhispan   
## 5.504314e-04

(avgeffectsl)

## (Intercept) alcohol dmage dmage2 dmar   
## -2.969769e-02 1.402162e-03 -6.440031e-04 1.134663e-05 2.198454e-3  
## dmeduc foreignb tobacco mblack motherr   
## -3.987693e-04 -1.395288e-03 3.444341e-03 5.704774e-03 3.421479e-3  
## mhispan   
## 5.459287e-04

Overall, the average effects of the covariates calculated using the linear probability model are actually very close to the marginal effects for both the probit and logit models. The coefficient estimates created in the linear probability model also share the same level of significance as the estimates created through probit and logit. It does appear that, on average, the linear probability model overstates the effects of the covariates, but only by a small amount. Though the difference does not seem very significant in this case, it may be that the difference between a linear probability model and probit/logit grows when the covariates have a larger effect on the outcome variable. Here, the covariates that we use to estimate infant mortality have very small effects because (1) infant mortality is very rare in the US (4790 of over 500k observations) so it is hard to find data that will predict it and (2) there are a huge range of factors not considered in the model that may also contribute. Had we modeled an outcome that could be boiled down to only a few contributing factors, we may expect that the disparity between estimates in the linear probability model and probit/logit would be greater.

lpmeffatmean = means\*lpm$coefficients  
lpmeffx1 = cbind(1,x1)\*lpm$coefficients  
(lpmeffatmean)

## alcohol dmage dmage2 dmar   
## 2.059852e-02 6.746127e-05 -2.073564e-02 1.010423e-02 7.724554e-4   
## dmeduc foreignb tobacco mblack motherr   
## -4.435499e-03 -2.735333e-04 6.515758e-04 1.569931e-03 4.902285e-5   
## mhispan   
## 9.521833e-05

(effatmeanl)

## [1] -2.666510e-02 1.258980e-03 -5.782404e-04 1.018796e-05 1.973958e-03  
## [6] -3.580487e-04 -1.252807e-03 3.092621e-03 5.122229e-03 3.072093e-03  
## [11] 4.901809e-04

(lpmeffx1)

## const. alcohol dmage dmage2 dmar dmeduc foreignb  
## 0.02059852 0 -0.02212 0.01096704 0 -0.006099399 0   
## tobacco mblack motherr mhispan  
## 0 0 0 0

(avgeffectsx1)

## (Intercept) alcohol dmage dmage2 dmar   
## -1.513933e-02 7.147959e-04 -3.283007e-04 5.784298e-06 1.120731e-3   
## dmeduc foreignb tobacco mblack motherr   
## -2.032851e-04 -7.112916e-04 1.755861e-03 2.908187e-03 1.744206e-3  
## mhispan   
## 2.783042e-04

It appears that once we try to calculate marginal effects given a certain set of characteristics, the linear probability model starts to fail a bit more. The LPM overstates the effects quite a bit given covariates equal to the average, and fails to create marginal effects for many covariates given the "x1" characteristics because some of these characteristics took a value of zero. This resulted in multiplying the estimated coefficient by zero, which ultimately suggests that not drinking alcohol, smoking, not being black, being married etc. has no effect on infant mortality. This clearly is not accurate because these factors would surely have some effect, however small or insignificant, and in fact they do based on the estimates from our other models.

xo = c(1,0,25,25^2,1,12,0,1,0,0,0)  
prob4f = sum(xo\*lpm$coefficients)  
(prob4f)

## [1] 0.01138163

x0 = data.frame(alcohol = 0,dmage=25, dmage2=25^2,dmar=1,dmeduc=12,foreignb=0,tobacco=1,mblack=0,motherr=0,mhispan=0)  
pred4f=predict(lpm,x0,type = "response",se.fit = T)  
  
CI4f = c(prob4f-1.96\*pred4f$se.fit,prob4f+1.96\*pred4f$se.fit)  
(CI4f)

## [1] 0.01063420 0.01212906

(CI4d)

## [1] 0.004094683 0.005251765

The probability of infant mortality for a mother with the characteristics given in 4d) is roughly the same when predicted using a linear probability model as when using a logit model. The LPM slightly overstates the probability, however, and has a narrower CI because of its lower standard error estimate.

### 5.

R's glm() function can be used to find ML estimates of probit and logit models. This function, by default, uses iteratively weighted least squares as the numerical method. This method creates estimates by minimizing the least absolute error (in this case). It does this by calculating the absolute error based on the current error (y-f(x'B)) and a weight for the beta calculated in the previous iteration. The method converges to a solution when the absolute differences in deviances between the current and last interation divided by the current deviation +0.1 is less than a given epsilon, which is 1e-8 by default. This convergence criteria seems to be a good one, as the differences between deviations become very small and therefore are likely to converge in probability to the true value. This convergence criteria can easily be changed by specifying a new value of epsilon in the function call, or providing a maximum number of iterations. The numerical method of glm can be changed, but doing so is difficult. It requires the user to write a function of the numerical method that takes the same arguments as the default method. In this case, it may not be worth it because numerical methods will likely provide similar estimates.

### 6a)

\*See back of first sheet

### 6b)

ordered = polr(factor(adequacy, levels = c(0,1,2),ordered = T) ~alcohol+dmage+dmage2+dmar+dmeduc+foreignb+tobacco+mblack+motherr+mhispan,  
 data = d, method = "probit") #requires "MASS" package, estimates an ordered probit   
summary(ordered)

##   
## Re-fitting to get Hessian

## Call:  
## polr(formula = factor(adequacy, levels = c(0, 1, 2), ordered = T) ~   
## alcohol + dmage + dmage2 + dmar + dmeduc + foreignb + tobacco +   
## mblack + motherr + mhispan, data = d, method = "probit")  
##   
## Coefficients:  
## Value Std. Error t value  
## alcohol -0.238392 9.844e-03 -24.217  
## dmage 0.085038 7.787e-04 109.198  
## dmage2 -0.001204 1.628e-05 -73.932  
## dmar -0.423941 4.019e-03 -105.481  
## dmeduc 0.089812 7.767e-04 115.629  
## foreignb -0.050447 5.787e-03 -8.717  
## tobacco -0.345858 4.553e-03 -75.969  
## mblack -0.354444 4.484e-03 -79.045  
## motherr -0.307537 1.470e-02 -20.923  
## mhispan -0.212578 6.465e-03 -32.880  
##   
## Intercepts:  
## Value Std. Error t value   
## 0|1 0.6228 0.0003 2248.3833  
## 1|2 1.6510 0.0025 657.6512  
##   
## Residual Deviance: 842693.14   
## AIC: 842717.14

Most of the coefficients from the regression output are negative, and it appears that all of the estimated coefficients are significant at some level. These coefficients can be interpreted as the effect on some unobserved "parental care index" given the covariate in question. For example, consuming alcohol during pregnancy is associated with a .238 decrease in the parental care index, which lowers the chances of being a "good" or "average" parent during pregnancy, all else equal. An extra year of education is associated with a .0898 increase in the parental care index, which incrases the mother's chances of being a "good" parent (Y=2), all else equal.

### 6c)

#Below code calculates average effects at each outcome category using formulas from class  
xs = as.matrix(d[,-c(11,12)])  
avgeffectso0 = mean(dnorm(ordered$zeta[1]-xs%\*%as.matrix(ordered$coefficients)))\*-(ordered$coefficients)  
  
avgeffectso2 = mean(-dnorm(ordered$zeta[2]-xs%\*%as.matrix(ordered$coefficients)))\*-(ordered$coefficients)  
  
avgeffectso1 = mean(dnorm(ordered$zeta[1]-xs%\*%as.matrix(ordered$coefficients))  
 -dnorm(ordered$zeta[2]-xs%\*%as.matrix(ordered$coefficients)))\*ordered$coefficients  
  
(avgeffectso0)

## alcohol dmage dmage2 dmar dmeduc   
## 0.0337925061 -0.0120542174 0.0001706114 0.0600943528 0.0127309341   
## foreignb tobacco mblack motherr mhispan   
## 0.0071509445 0.0490258545 0.0502430387 0.0435938183 0.0301332600

(avgeffectso1)

## alcohol dmage dmage2 dmar dmeduc   
## 0.0415860477 -0.0148342729 0.0002099594 0.0739538706 0.0156670603   
## foreignb tobacco mblack motherr mhispan   
## 0.0088001617 0.0603326524 0.0618305549 0.0536478296 0.0370828723

(avgeffectso2)

## alcohol dmage dmage2 dmar dmeduc   
## -0.0753785537 0.0268884903 -0.0003805707 -0.1340482234 0.0283979944   
## foreignb tobacco mblack motherr mhispan   
## -0.0159511063 -0.1093585069 -0.1120735935 -0.0972416480 0.0672161322

The numbers provided by these calculations can be interpreted as a specific covariate's effect on the probability that a mother exhibited one of the three levels of parental care during pregnancy. For example, the number 0.03379 in "avgeffectso0" tells us that a mother who drank during pregnancy had a 3% higher chance of being in the "0" category of parental care than a mother who did not. Overall, these effects reverse in sign as we move across adequacy categories. For example, being unmarried has a positive effect on being a "bad" parent (0.06), but a large negative effect on being a "good" parent (-0.134). These make intuitive sense because one could assume that being married provides better parental support, so being unmarried reduces the ability to use such parental support, ultimately decreasing the chances of being a "good" parent (Y =2). One more thing to note is that effects of covariates on being in category 1 are larger than the effects on being in category 0. This goes against intuition because one would think that, for example, smoking would increase the probability of being a "bad" parent more than it would increase the probability of being an "average" parent.

### 6d)

#Calculates probability of being in category 1 based on given characteristics  
xoo = c(0,25,25^2,1,12,0,1,0,0,0)  
betao = ordered$coefficients  
probo = pnorm(ordered$zeta[2]-t(xoo)%\*%betao)-pnorm(ordered$zeta[1]-t(xoo)%\*%betao)  
(probo)

## [,1]  
## [1,] 0.342945

predo = predict(ordered,x0,se.fit=T,type = "probs")   
(predo)

## 0 1 2   
## 0.1448395 0.3429450 0.5122155

Unfortunately, I was unable to calculate the standard errors for this estimate and the function used is limited in that it can't generate anything besides a prediction for a polr object class, so I wasn't able to create a confidence interval.