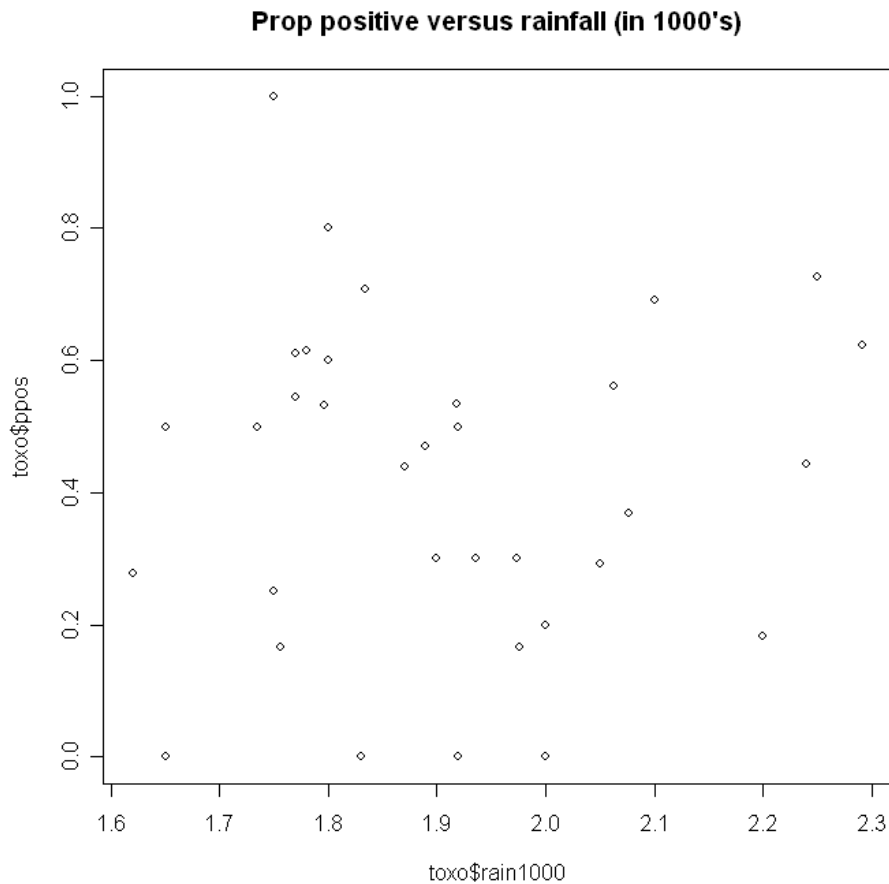
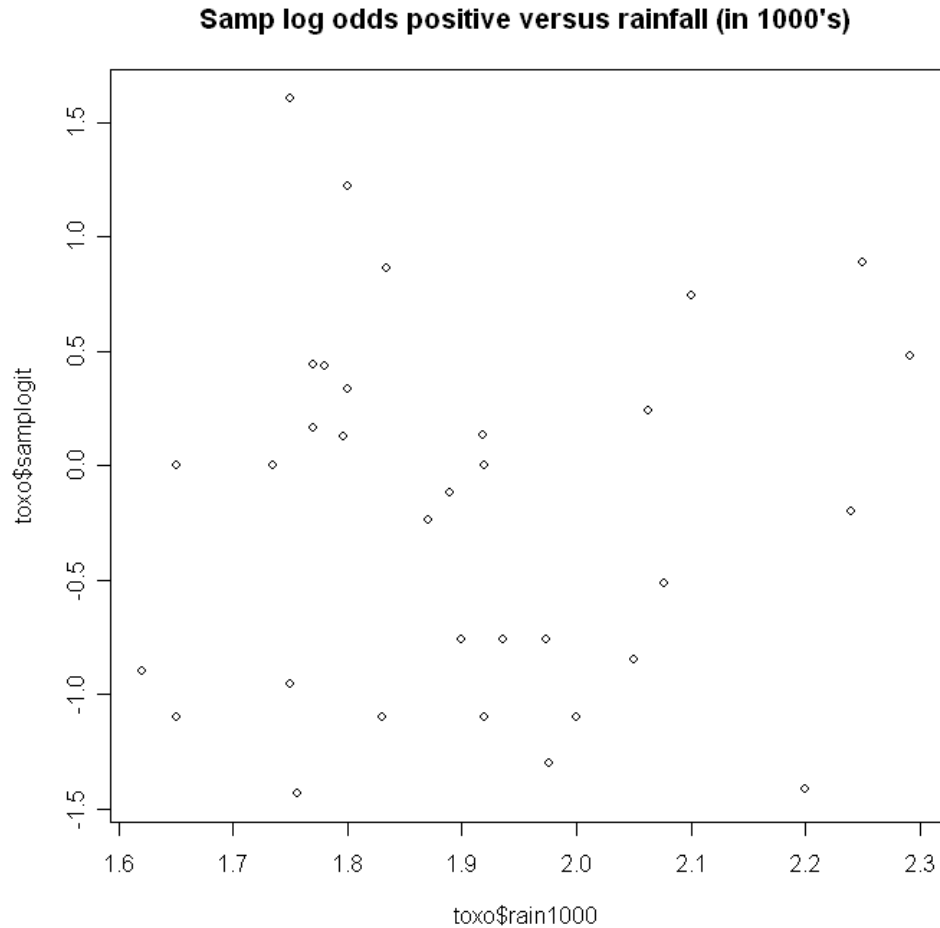


```
#####  
###      toxo.R      ###  
#####
```

```
> toxo <- read.table(file="N:\\courses\\stat8620\\Fall 08\\toxos.dat",header=T)  
> #toxo <- read.table(file="C:\\Documents and Settings\\dhall\\My Documents\\Dan's Work  
Stuff\\courses\\STAT8620\\Fall 08\\toxos.dat",header=T)  
> toxo$rain1000 <- toxo$rainf/1000  
> toxo$ypos <- round(toxo$ppos*toxo$n)  
> toxo$yneg <- toxo$n-toxo$ypos  
> toxo$samplogit <- log((toxo$ypos+0.5)/(toxo$n-toxo$ypos+0.5))  
> toxo[1:3,]  
  rainf  ppos  n  rain1000  ypos  yneg  samplogit  
1 1735 0.500  4   1.735    2    2  0.0000000  
2 1800 0.600  5   1.800    3    2  0.3364722  
3 2050 0.292 24   2.050   7   17 -0.8472979  
>  
>  
> plot(toxo$rain1000,toxo$ppos,main="Prop positive versus rainfall (in 1000's)")
```



```
> plot(toxo$rain1000,toxo$samplogit,main="Samp log odds positive versus rainfall (in 1000's)")
```



```
>  
> m1 <- glm(cbind(ypos,yneg)~poly(rain1000,5),data=tox,  
+ family=binomial(link="logit"))  
> summary(m1)
```

Call:
glm(formula = cbind(ypos, yneg) ~ poly(rain1000, 5), family = binomial(link = "logit"),
data = toxo)

Deviance Residuals:
Min 1Q Median 3Q Max
-2.9829 -1.2096 -0.4572 0.4160 2.8846

Coefficients:
Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.02505 0.07709 0.325 0.74524
poly(rain1000, 5)1 -0.24223 0.48608 -0.498 0.61825
poly(rain1000, 5)2 -0.23450 0.49023 -0.478 0.63240
poly(rain1000, 5)3 1.46167 0.43170 3.386 0.00071 ***

```
poly(rain1000, 5)4 -0.23823  0.47500 -0.502  0.61599
poly(rain1000, 5)5  0.51553  0.46234  1.115  0.26484
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 74.212 on 33 degrees of freedom
Residual deviance: 61.196 on 28 degrees of freedom
AIC: 163.89
```

Number of Fisher Scoring iterations: 3

```
>
> m2 <- glm(cbind(ypos,yneg)~poly(rain1000,3),data=tox,
+ family=binomial(link="logit"))
> summary(m2)
```

Call:

```
glm(formula = cbind(ypos, yneg) ~ poly(rain1000, 3), family = binomial(link = "logit"),
    data = tox)
```

Deviance Residuals:

```
Min      1Q  Median      3Q      Max
-2.7620 -1.2166 -0.5079  0.3538  2.6204
```

Coefficients:

```
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.02427   0.07693   0.315 0.752401
poly(rain1000, 3)1 -0.08606   0.45870  -0.188 0.851172
poly(rain1000, 3)2 -0.19269   0.46739  -0.412 0.680141
poly(rain1000, 3)3  1.37875   0.41150   3.351 0.000806 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 74.212 on 33 degrees of freedom
Residual deviance: 62.635 on 30 degrees of freedom
AIC: 161.33
```

Number of Fisher Scoring iterations: 3

```
> anova(m2,m1,test="Chisq")
Analysis of Deviance Table
```

```
Model 1: cbind(ypos, yneg) ~ poly(rain1000, 3)
Model 2: cbind(ypos, yneg) ~ poly(rain1000, 5)
```

```

  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1    30    62.635
2    28    61.196 2    1.438    0.487
>
> m0 <- glm(cbind(ypos,yneg)~1,data=toxos, family=binomial(link="logit"))
> anova(m0,m2,test="Chisq")
Analysis of Deviance Table

```

```

Model 1: cbind(ypos, yneg) ~ 1
Model 2: cbind(ypos, yneg) ~ poly(rain1000, 3)

```

```

  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1    33    74.212
2    30    62.635 3    11.577    0.009
>

```

```
> #deviance of model m2 is GOF statistic:
```

```
> deviance(m2)
```

```
[1] 62.6346
```

```
> #Pearson X^2 statistic:
```

```
> sum(resid(m2,type="pearson")^2)
```

```
[1] 58.21314
```

```
>
```

```
> m2q <- glm(cbind(ypos,yneg)~poly(rain1000,3),data=toxos,
```

```
+ family=quasibinomial(link="logit"))
```

```
> summary(m2q)
```

Call:

```
glm(formula = cbind(ypos, yneg) ~ poly(rain1000, 3), family = quasibinomial(link = "logit"),
    data = toxos)
```

Deviance Residuals:

```

  Min    1Q  Median    3Q   Max
-2.7620 -1.2166 -0.5079  0.3538  2.6204

```

Coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)    0.02427   0.10716   0.226  0.8224
poly(rain1000, 3)1 -0.08606   0.63897  -0.135  0.8938
poly(rain1000, 3)2 -0.19269   0.65108  -0.296  0.7693
poly(rain1000, 3)3  1.37875   0.57321   2.405  0.0225 *
---

```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for quasibinomial family taken to be 1.940446)

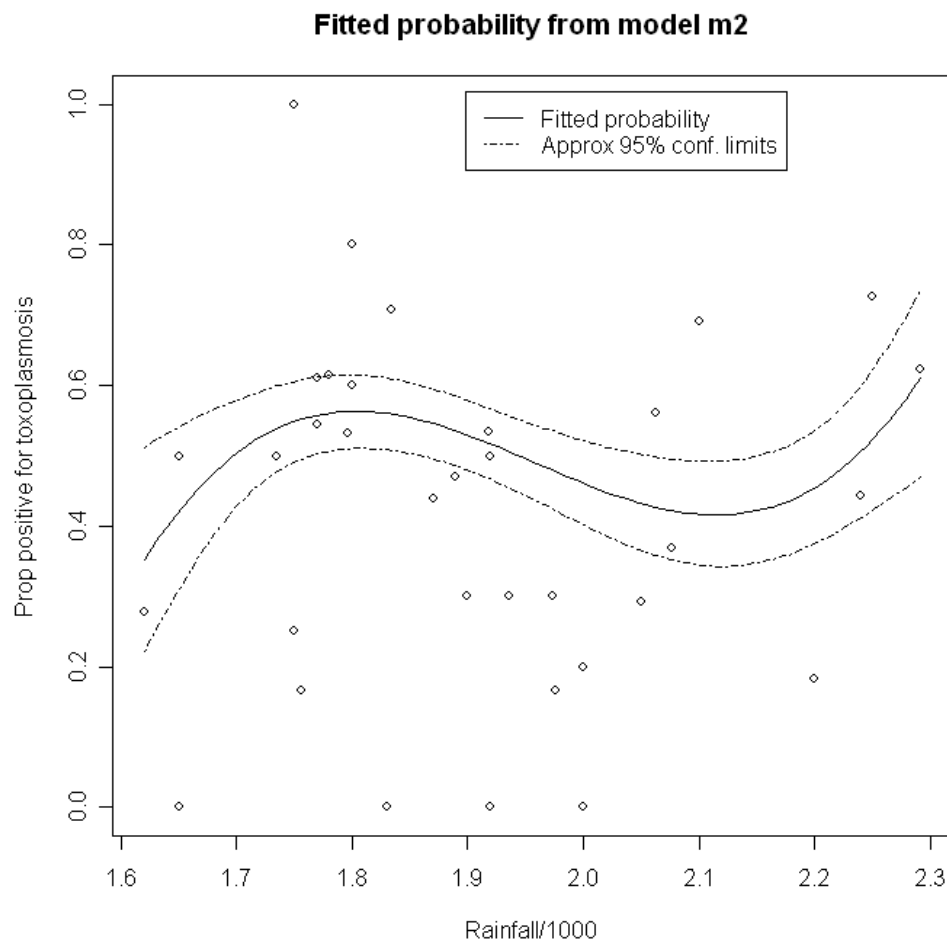
```

Null deviance: 74.212 on 33 degrees of freedom
Residual deviance: 62.635 on 30 degrees of freedom
AIC: NA

```

Number of Fisher Scoring iterations: 3

```
>
> r0 <- seq(from=min(toxo$rain1000),to=max(toxo$rain1000),length=100)
> expit <- function(x) {1/(1+exp(-x)) }
>
> pred.m2 <- predict(m2,data.frame(rain1000=r0),se.fit=T,type="link")
> L <- expit(pred.m2$fit-1.96*pred.m2$se.fit)
> U <- expit(pred.m2$fit+1.96*pred.m2$se.fit)
> plot(toxo$rain1000,toxo$ppos,type="p",xlab="Rainfall/1000",
+ ylab="Prop positive for toxoplasmosis",
+ main="Fitted probability from model m2")
> lines(r0,expit( pred.m2$fit ))
> lines(r0,L,lty=4)
> lines(r0,U,lty=4)
> legend(locator(1),lty=c(1,4),legend=c("Fitted probability","Approx 95% conf. limits"))
```



```
>
> pred.m2q <- predict(m2q,data.frame(rain1000=r0),se.fit=T,type="link")
> L <- expit(pred.m2q$fit-1.96*pred.m2q$se.fit)
> U <- expit(pred.m2q$fit+1.96*pred.m2q$se.fit)
```

```
> plot(toxo$rain1000,toxo$ppos,type="p",xlab="Rainfall/1000",
+ ylab="Prop positive for toxoplasmosis",
+ main="Fitted probability from model m2q")
> lines(r0,expit( pred.m2q$fit ))
> lines(r0,L,lty=4)
> lines(r0,U,lty=4)
> legend(locator(1),lty=c(1,4),legend=c("Fitted probability","Approx 95% conf. limits"))
>
```

