GLM Assignment 1

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1 Introduction

In the given problem we are asked to model the proportion of people who pass the test using data about which treatments they were given and in what doses. There are 2 types of treatments being delivered to the patients, Treat1 and Treat2. In each treatment they are given one of two medicines, for Treat1, they are given medicines A or B and for Treat2 they are given medicines X or Y. We are also given the amount of dose of each treatment given to the subjects Dose1 and Dose2.

2 Models Tried

I tried 4 basic types of models and repeated these for all the 3 binomial link functions. These are as listed below:

2.1 Simple Sum

In this model I simply performed GLM regression on Pass/Total against the 4 columns of the data in a sum.

This model can be represented by the following R formula:

```
    Pass/Total ~ Treat1 + Dose1 + Treat2 + Dose2
```

2.2 Product of Treatment and Dose

In this model I regressed Pass/Total against:
Treat1AxDose1, Treat1BxDose1, Treat2XxDose2, Treat2YxDose2.
Where Treat1A is 1 when medicine A is given in treatment 1 and similarly for others. The reasoning behind this is that the amount of dose can have different

amount of effect based of if medicine A was given or B. In all the cases this reduces the residual Deviance.

This model is represented by the following R formula:

```
    Pass/Total ~ Treat1:Dose1 + Treat2:Dose2
```

2.3 Cross Terms

In this model I added all the cross terms of Treatment and Dose.
Pass/Total was regressed against the products of doses and treaments as in the previous model but the simple terms of Treat1, Treat2, Dose1 and Dose2 were also added. This model gives a further improvement in performance in all the link functions.

This model is represented by the following R formula:

```
    Pass/Total ~ Treat1*Dose1 + Treat2*Dose2
```

2.4 Partial Cross Terms

In the analysis of the previous model I observed that out of the linear terms only the coefficients for treatment terms were significant hence for finding a maximum parcimonious model I kept only those terms. This model has the same performance as the previous model but has lesser parameters. This can be interpreted as perhaps the effect increases linearly with dose but with non zero intercept.

This model is represented by the following R formula:

```
    Pass/Total ~ Treat1:Dose1 + Treat2:Dose2 + Treat1 + Treat2
```

3 Results

These models were evaulated for all 3 link functions, logit, probit and loglog. Out of these loglog gave the best performance with model 4.

The metrics of the fit are as follows:

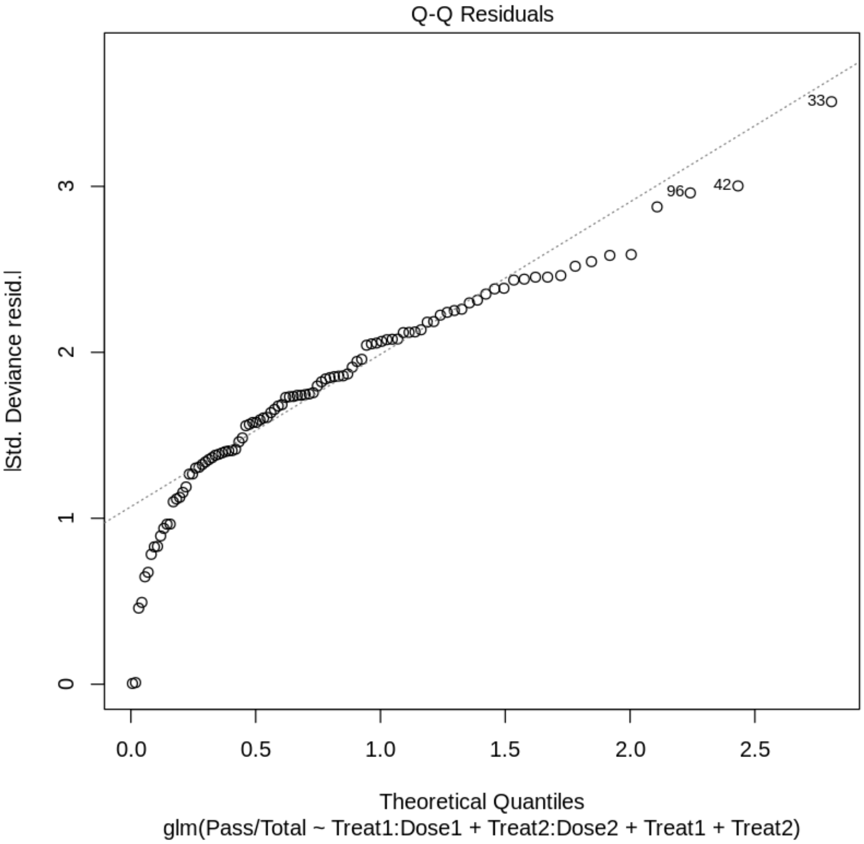
```
    glm(formula = Pass/Total ~ Treat1:Dose1 + Treat2:Dose2 + Treat1 +
    Treat2, family = binomial(link = "cloglog"), data = data,
    weights = Total)
```

```
Coefficients:
               Estimate Std. Error z value Pr(>|z|)    
(Intercept)    0.572205   0.201273   2.843  0.00447 ** 
Treat1B       -0.385280   0.135149  -2.851  0.00436 ** 
Treat2Y       -0.833672   0.276225  -3.018  0.00254 ** 
Treat1A:Dose1 -0.019452   0.013488  -1.442  0.14926    
Treat1B:Dose1  0.066677   0.013668   4.878 1.07e-06 ***
Treat2X:Dose2 -0.004866   0.025056  -0.194  0.84600    
Treat2Y:Dose2  0.020047   0.031990   0.627  0.53088    
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 658.51  on 99  degrees of freedom
Residual deviance: 311.62  on 93  degrees of freedom
AIC: 714.81

Number of Fisher Scoring iterations: 6
```

3.1 Plots

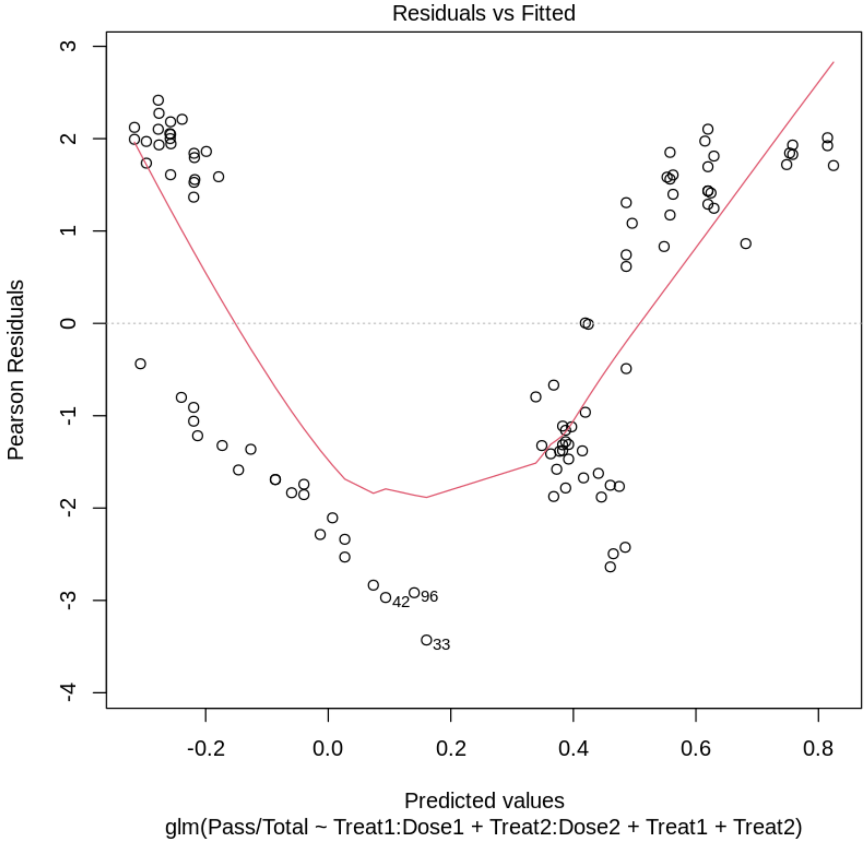
Here I have included 2 plots for the best model, the Residual vs Fitted Value plot and the QQ plot.

3.1.1 QQ-plot



Here we can see that the tails are slightly heavy but the center aligns very well with the theoretical distribution.

3.1.2 Residual vs Fitted value



This plot should be a flat line at 0 with points distributed around the line but as we can see it is far from it.

For more details about the parameters of each model please check attached R file.