

MAST30027 Assignment 2: Statistical Report

Statistical Report: Summary

We are interested in whether chimpanzees behave in a human like way: that is pulling the prosocial lever, but only when another chimpanzee is present. This was measured using a binomial model, with the chimpanzee, the side the lever was on and the presence or absence of another chimpanzee as factors. There was no evidence that the chimpanzees were changing their behaviour based on the presence or absence of another chimpanzee.

Data categories

The data contained information of how many times each chimpanzee pulled the social lever out of 18 times, with and without another chimpanzee present, and with the prosocial lever on each side. Hence a binomial model was chosen. The response variable was set to be the number of times the chimpanzee pulled the prosocial lever out of 18 trials.

The dataset also contained information on two potential confounders: which chimpanzee performed the trial, and whether they had a preference for pulling the left or right lever. Three treatment groups were chosen, which together retained all the information in the dataset on these attributes. They were:

- 1) **condition**, which recorded whether the other chimpanzee was present or not (with “1” as present and “0” as absent)
- 2) **actor**, which recorded which chimpanzee performed the trials
- 3) **prosoc.left**, which recorded which side the prosocial lever was on (recorded as “1” when it was left, “0” when it was right)

The data was imported, a column called **social.choice** was added to record whether the chimpanzee pulled the prosocial lever in each trial. The data was then packaged into a table recording the number of times the chimpanzee pulled the prosocial lever for analysis.

```
data <- read.csv(file="assign2.txt", sep=" ") # import data
names(data)[names(data) == "prosoc_left"] <- "prosoc.left"

#Adding column "social.choice" to data to record when chimpanzee
#pulled the prosocial lever:
n <- length(data[,1]) #n is number of observations
data$social.choice <- rep(0, n)
for (i in 1:n){
  if (data$prosoc.left[i] == data$pulled_left[i]) {data$social.choice[i]<-1}}

#Putting data into a table for binomial analysis:
counts <- xtabs(social.choice ~ actor + condition + prosoc.left, data)
#Convert data into the right format for analysis:
counts <- as.data.frame(counts)
counts$actor <- as.factor(counts$actor)
counts$condition <- as.factor(counts$condition)
counts$prosoc.left <- as.factor(counts$prosoc.left)
```

Data visualisation

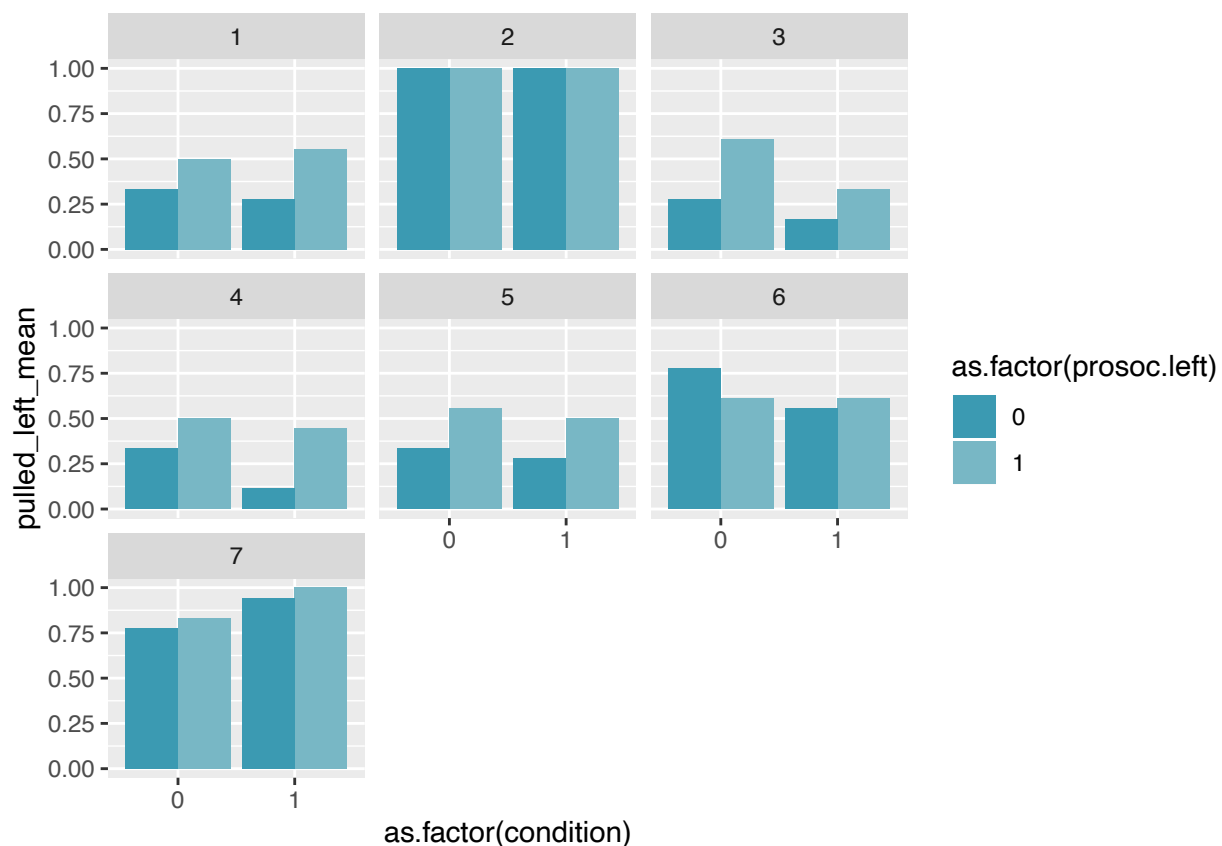
To start to visualise the Chimpanzees behaviour, a histogram was made measuring the mean number of times the each chimpanzee pulled left in all four experimental conditions. It shows the chimpanzees each have a preference for pulling the left lever or right lever - in particular, actor 2 always pulls the left lever, and actor 7 almost always does. Apart from actor 2, the chimpanzees almost always pulled left more frequently when the prosocial lever was on that side (the exception being actor 6 with no other chimpanzee present).

For most of the chimpanzees (actor 1, 2, 4 and 5), the pattern in the histogram is pretty similar when the other chimpanzee is present or not. The chimpanzee may be behaving in the same way, regardless of the presence or absence of other chimpanzees.

```
#Histogram of how many times each chimpanzee pulled left
n<-data%>%
group_by(prosoc.left, actor, condition)%>%
summarise(pulled_left_mean=mean(pulled_left))

p <- ggplot(n, aes(fill=as.factor(prosoc.left), y=pulled_left_mean, x=as.factor(condition))) +
  geom_bar(position="dodge", stat="identity") +
  scale_fill_manual(values = wes_palette("Zissou1", n=2))
)

p + facet_wrap(~as.factor(actor))
```



This is even more apparent when the number of times each chimpanzee pulled the prosocial lever is plotted in each experimental set up. Actors 1, 2, 4 and 5 do not appear to be behaving differently at all. There is a small difference in the way actors 3, 6 and 7 behave. This is the first sign that the results for this study may be negative.

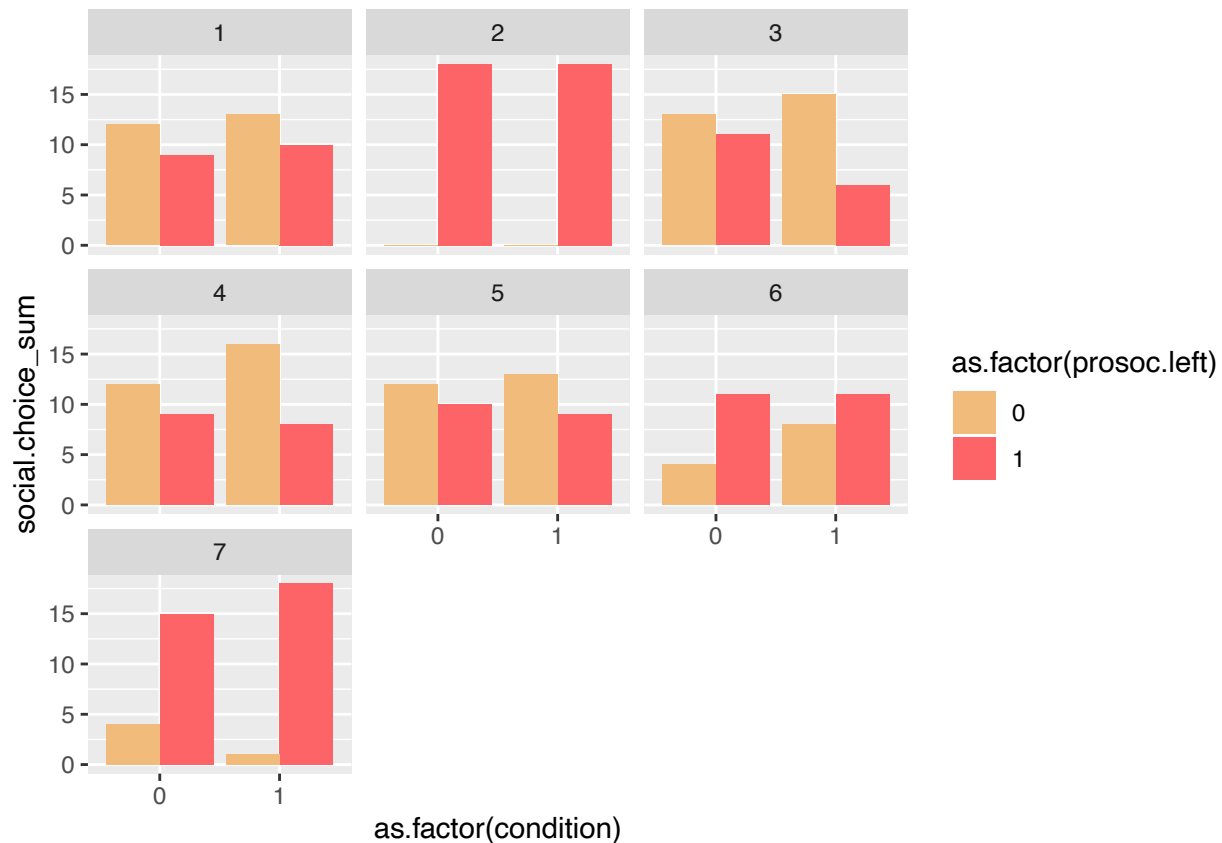
```

#Plot number of times each actor pulled the prosocial lever
n<-data%>%
group_by(prosoc.left, actor, condition)%>%
summarise(social.choice_sum=sum(social.choice))

p <- ggplot(n, aes(fill=as.factor(prosoc.left), y=social.choice_sum, x=as.factor(condition))) +
  geom_bar(position="dodge", stat="identity") +
  scale_fill_manual(values = wes_palette("GrandBudapest1", n=2)
  )

p + facet_wrap(~as.factor(actor))

```

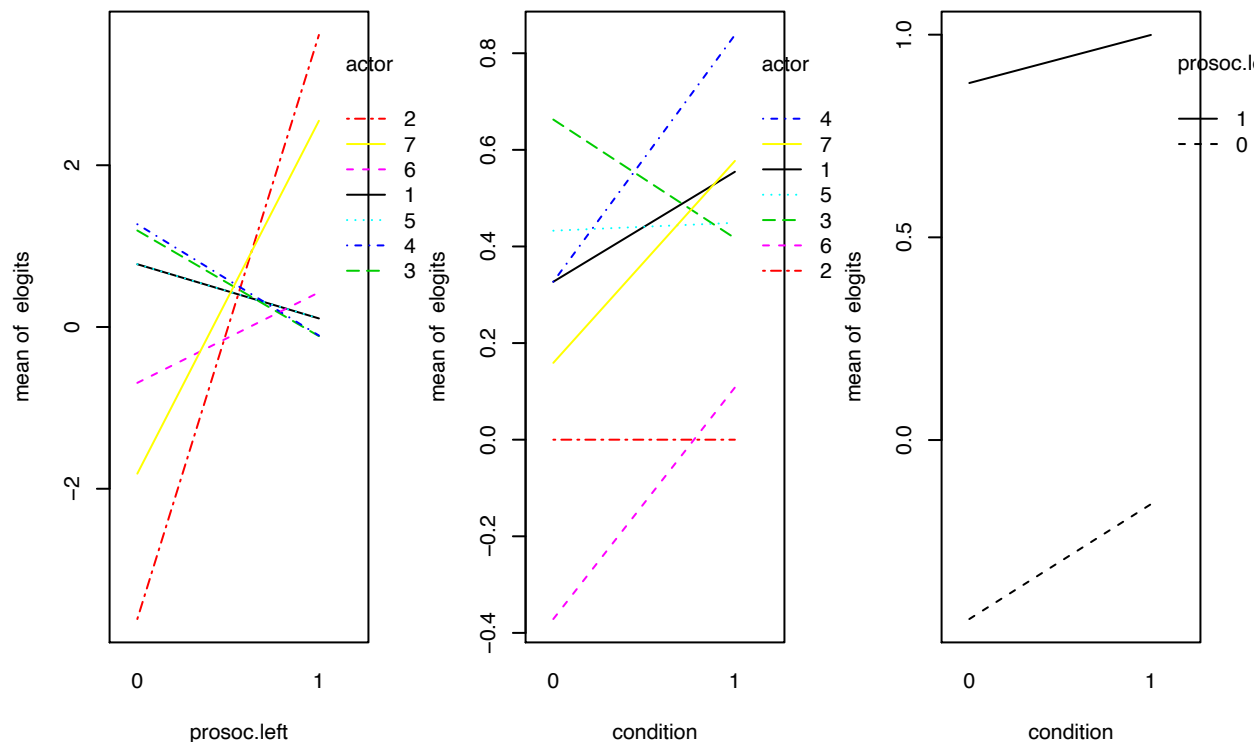


Three interaction plots (using the Empirical logits of the sample) were created to examine all possible interactions between the three factors.

```

#interaction plots with the empirical logits
par(mfrow=c(1,3))
elogits <- with(counts, log((Freq+0.5)/(18.5-Freq))) #Calculate the empirical logits
#Plot interaction plots for:
with(counts, interaction.plot(prosoc.left, actor, elogits,
                             col=c(1,2,3,4,5,6,7))) #prosoc.left and actor
with(counts, interaction.plot(condition, actor, elogits,
                             col=c(1,2,3,4,5,6,7))) #condition and actor
with(counts, interaction.plot(condition, prosoc.left, elogits)) #prosoc.left and actor

```



There is clearly potential interaction between `prosoc.left` and `actor`, and `condition` and “`actor`.” The first interaction is expected, as the histograms showed that chimpanzees have a preference for pulling left or right. The interaction `actor` and `condition` was also foreshadowed by the histograms and is quite interesting. If chimpanzees behave like humans, we would expect to see a positive gradient in all the lines in the plot, reflecting them pulling the prosocial lever more often when the other chimpanzee is present. However we see straight lines in two cases, and a negative gradient in one.

There is no sign of interaction between `condition` and `prosoc.left`. This indicates the chimpanzees are not more likely to change hand preference when the other chimp is present.

Model selection

As there were two potential interactions, a model called `larger.model` was fitted with them both, and found to be adequate with a Chi-squared test.

```
larger.model <- glm(cbind(Freq, 18-Freq) ~ actor*prosoc.left + actor*condition,
                    data=counts, family=binomial)
pchisq(deviance(larger.model), larger.model$df.residual, lower.tail = F)
```

```
## [1] 0.07169967
```

```
#Test for model adequacy
```

Then smaller models were sequentially fitted, and likelihood ratio tests were performed to find the most parsimonious model. In order:

- 1) a model called `wrong.model1` with `prosoc.left` as a factor and an interaction between `actor` and `condition` was fitted and failed a likelihood ratio test against `larger.model`:

```
wrong.model1 <- glm(cbind(Freq, 18-Freq) ~ condition * actor + prosoc.left,
  data=counts, family=binomial)
pchisq(deviance(wrong.model1) - deviance(larger.model),
  wrong.model1$df.residual - larger.model$df.residual, lower.tail=F) #LRT
```

```
## [1] 3.249123e-32
```

- 2) a model called `model` with `condition` as a factor and interactions between `actor` and `prosoc.left` was fitted and passed a likelihood ratio test against the `larger.model`:

```
model <- glm(cbind(Freq, 18-Freq) ~ condition + actor * prosoc.left,
  data=counts, family=binomial)
pchisq(deviance(model) - deviance(larger.model),
  model$df.residual - larger.model$df.residual, lower.tail=F) #LRT
```

```
## [1] 0.9210887
```

- 3) a model called `wrong.model2` with `condition`, `actor` and `prosoc.left` without any interactions failed a likelihood ratio test against `model`:

```
wrong.model2 <- glm(cbind(Freq, 18-Freq) ~ condition + actor + prosoc.left,
  data=counts, family=binomial)
pchisq(deviance(wrong.model2) - deviance(model),
  wrong.model2$df.residual - model$df.residual, lower.tail=F) #LRT
```

```
## [1] 3.303118e-32
```

So `model`, with `condition` and an interaction between `prosoc.left` and `actor`, was selected as the best model. The Wald tests for `condition` were not positive (see summary, below), so for inference alone, a likelihood ratio test was performed between the chosen model and a model with an interaction between `actor` and `prosoc.left` (ie not using `condition` as a predictor), and the smaller model was found to be more parsimonious.

```
no_condition <- glm(cbind(Freq, 18-Freq) ~ actor * prosoc.left,
  data=counts, family=binomial)
pchisq(deviance(no_condition) - deviance(model),
  no_condition$df.residual - model$df.residual, lower.tail=F) #LRT
```

```
## [1] 0.5205249
```

However `condition` measures what this experiment is examining, and cannot be removed from the model.

```
summary(model)
```

```
##
## Call:
## glm(formula = cbind(Freq, 18 - Freq) ~ condition + actor * prosoc.left,
##      family = binomial, data = counts)
##
```

```
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.3386  -0.3818   0.0000   0.3818   1.7108
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    7.531e-01  3.767e-01   1.999  0.04561 *
## condition1     1.377e-01  2.143e-01   0.642  0.52070
## actor2        -2.248e+01  5.084e+03  -0.004  0.99647
## actor3         4.322e-01  5.403e-01   0.800  0.42375
## actor4         4.322e-01  5.403e-01   0.800  0.42375
## actor5         1.296e-16  5.119e-01   0.000  1.00000
## actor6        -1.516e+00  5.062e-01  -2.995  0.00275 **
## actor7        -2.648e+00  6.029e-01  -4.392  1.12e-05 ***
## prosoc.left1   -7.105e-01  4.926e-01  -1.443  0.14916
## actor2:prosoc.left1  4.402e+01  7.190e+03   0.006  0.99512
## actor3:prosoc.left1 -6.549e-01  7.177e-01  -0.913  0.36150
## actor4:prosoc.left1 -6.549e-01  7.177e-01  -0.913  0.36150
## actor5:prosoc.left1 -7.807e-16  6.966e-01   0.000  1.00000
## actor6:prosoc.left1  1.857e+00  6.963e-01   2.667  0.00765 **
## actor7:prosoc.left1  4.937e+00  9.160e-01   5.390  7.06e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 197.206  on 27  degrees of freedom
## Residual deviance:  15.002  on 13  degrees of freedom
## AIC: 117.1
##
## Number of Fisher Scoring iterations: 18
```

The 0.95 confidence interval for the odds ratio of `condition` contains 1, which corresponds to the chimpanzees pulling the prosocial lever an equal proportion of times regardless of another chimpanzee being present. Hence the final model does not support chimpanzees behaving in a human-like way.

```
#Odds ratio confidence interval for "condition"
log_odds <- 0.1377 + c(-1,1)*qnorm(0.975)*0.2143 #Log Odds 95% Confidence Interval
exp(log_odds) #Odds Ratio 95% Confidence Interval
```

```
## [1] 0.7540321 1.7466860
```

Model adequacy

For goodness-of fit, a deviance test was done on the fitted model. The deviance was 0.30725, which corresponds with the model having the correct χ^2 distribution, so the model is adequate.

```
pchisq(deviance(model), model$df.residual, lower.tail = F) #Devaince test
```

```
## [1] 0.30725
```

$\hat{\Phi}$ was calculated to be 1.044518, so there is no evidence of overdispersion in the model.

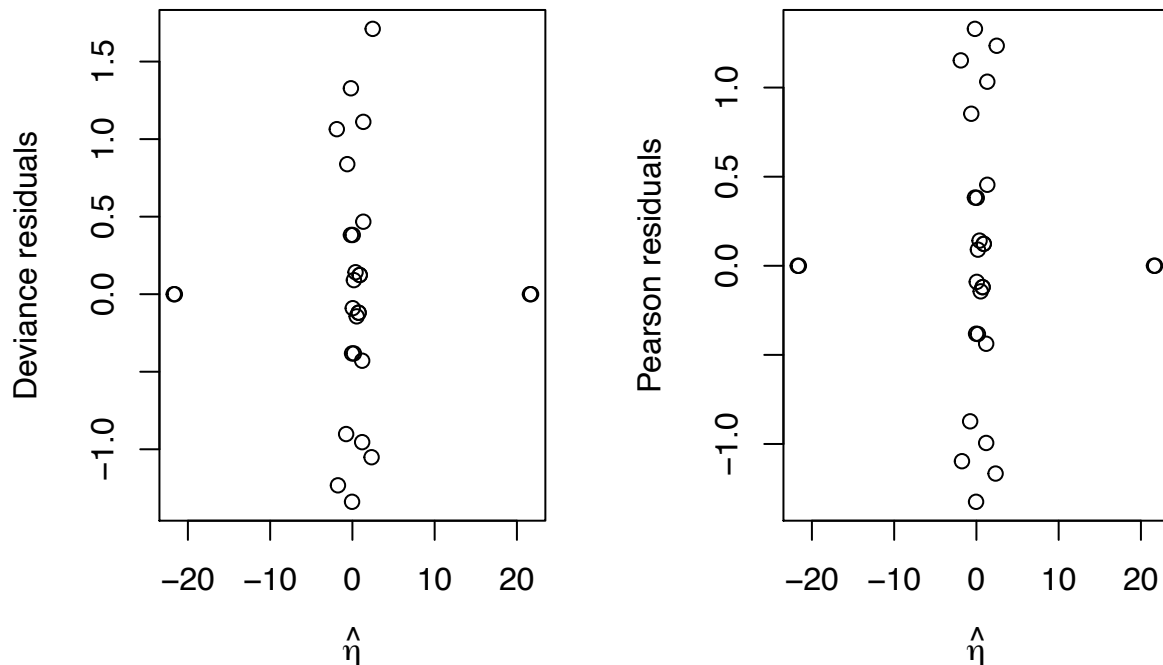
```
sum(residuals(model, type="pearson")^2)/13 #Calculate phi hat
```

```
## [1] 1.044518
```

Diagnostics

Whether using the Person's or Deviance residuals, the graph of the residuals vs the linear predictor (below) looks the same: it has a band of points down the middle, with two points at the left of the graph and two points to the right of the graph with a residual value of 0.

```
par(mfrow=c(1,2))
# deviance residuals vs linear fitted values
plot(residuals(model) ~ predict(model,type="link"),
     xlab=expression(hat(eta)), ylab="Deviance residuals")
# pearson residuals vs linear fitted values
plot(residuals(model,type="pearson") ~ predict(model, type="link"),
     xlab=expression(hat(eta)), ylab="Pearson residuals")
```



```
names(sort(predict(model,type="link"))[c(1,2,27,28)]) #Find which trials these came from
```

```
## [1] "2" "9" "16" "23"
```

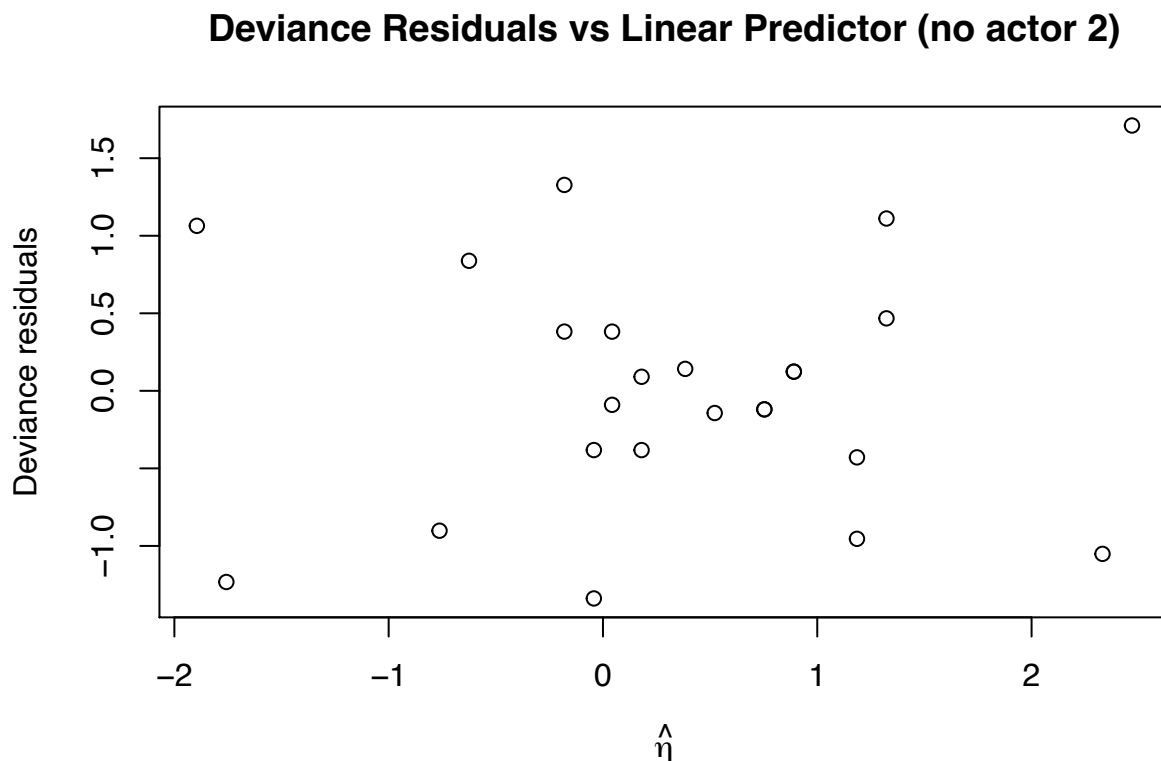
```
counts[c(2,9,16,23),] #All trials came from Actor 2
```

```
## actor condition prosoc.left Freq
## 2      2      0      0      0
```

```
## 9      2      1      0      0
## 16     2      0      1     18
## 23     2      1      1     18
```

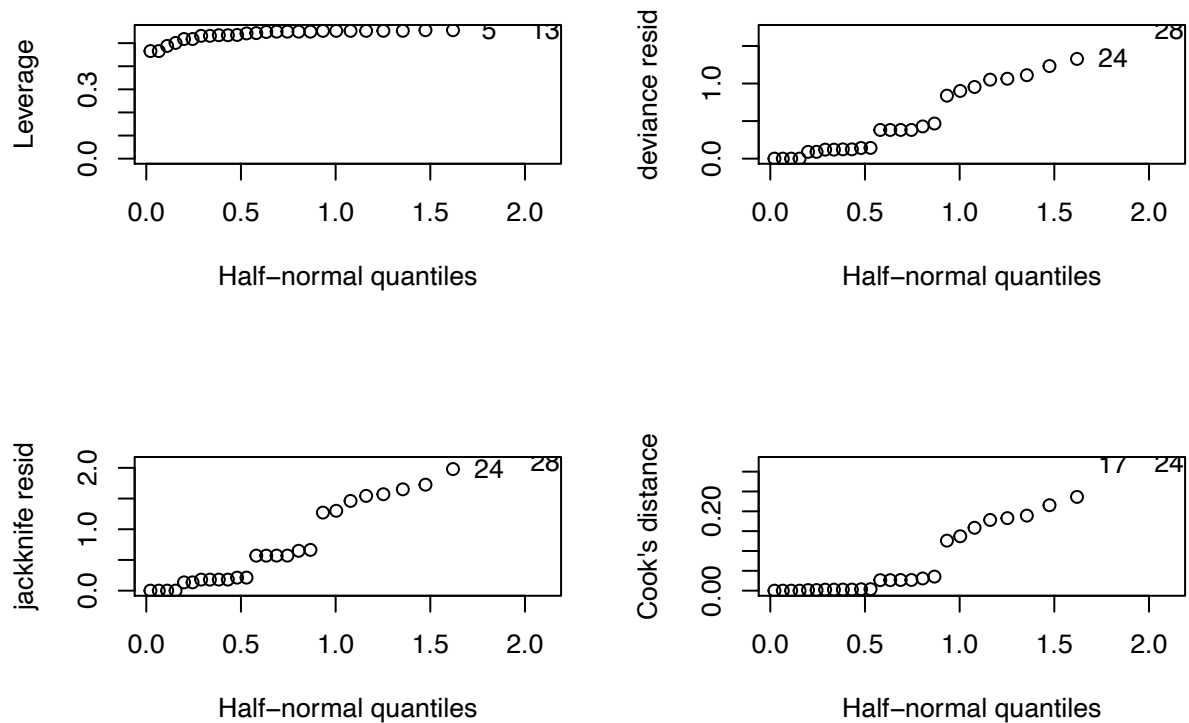
When these points were examined, above, it became clear they were all coming from actor 2, who always pulls the left lever. We designed to model to retain the information about the chimpanzees side preference, and actor 2's preference is so strong that the model should be fit to it perfectly. It makes sense that those points have residual values of 0. We also get extreme values for $\hat{\eta}$ for actor 2, because depending on the treatment group, it either chooses the social choice 18 times or 0 times. So the strong pattern in the linear fitted values vs. the residuals is because the $\hat{\eta}$ values for these points are spread so far from the other points on the x-axis. The greater variation in the other points is because they have some variation, unlike actor 2. When these points are removed from the plot, the pattern in the residuals vs. the linear predictors for the other points is easier to see, and it appears to be fine (see below).

```
plot(residuals(model)[-c(2,9,16,23)] ~ predict(model,type="link")[-c(2,9,16,23)],
     xlab=expression(hat(eta)), ylab="Deviance residuals",
     main="Deviance Residuals vs Linear Predictor (no actor 2)")
```



We also see actor 2 again when we examine the Halfnormal plots. Both the deviance residuals and the jackknife residuals looks good overall, but have a point towards the middle where the the residuals jump twice.

```
par(mfrow=c(2,2))
halfnorm(influence(model)$hat, ylab= "Leverage") #leverage
halfnorm(residuals(model), ylab="deviance resid") #deviance residual
halfnorm(rstudent(model), ylab="jackknife resid") #jackknife residual
halfnorm(cooks.distance(model), ylab="Cook's distance") #Cook's distance
```

Most of the points between the two jumps come from Actor 2, with two coming from actor 1:

```
names(sort(rstudent(model))[c(14:19)]) #Points of interest: deviance residuals
```

```
## [1] "2" "23" "16" "22" "12" "8"
```

```
names(sort(residuals(model))[c(13:19)]) #Points of interest: jakckknife residuals
```

```
## [1] "9" "2" "23" "16" "22" "8" "12"
```

```
counts[c(2,8,9,16,22,23),]
```

```
##      actor condition prosoc.left Freq
## 2      2          0           0     0
## 8      1          1           0    13
## 9      2          1           0     0
## 16     2          0           1    18
## 22     1          1           1    10
## 23     2          1           1    18
```

Luckily, these 6 points are amount the 8 points with the lowest Cook's distance in the model. If they are outliers, they are not exerting a huge amount of influence on the model.

```
names(sort(cooks.distance(model))[c(1:8)]) #Points with 4 lowest Cook's distances
```

```
## [1] "2" "23" "16" "9" "22" "15" "12" "8"
```

Apart from that, the leverages of all points is similar, and none of the points have a high Cook's distance.

Inference on the Model

What is this model measuring? The base case is actor 1, with no other chimpanzee present, with the prosocial lever on the right of the table. The model gives the change in log odds of the probability of a chimpanzee pulling the lever, based on whether another chimpanzee is present, which actor performs the trial and whether they tend to pull the left or right lever (as there is an interaction between `actor` and `prosoc.left`).

No significant result for condition

In the data visualisation section, we saw patterns consistent with the chimpanzees behaving in the same way, regardless of whether there was another chimp at the other side of the table or not. This suspicion was confirmed when the chosen model contained the value “1” in the confidence interval for the odds ratio of `condition` - meaning the model did not find a change in behaviour. Additionally, the most parsimonious model found for the data did not even contain the predictor `condition`, meaning other factors explain the variation in the data better. We have no evidence the chimpanzees are change behaviour when another chimpanzee is present.

Conclusion

We cannot say chimpanzees are more or less likely to pull the prosocial when another chimpanzee is present. If the chimpanzees were behaving like humans, we would expect more clear results, since humans only tend to pull the prosocial lever when another person is present. We have not found chimpanzees to behave in a human-like manner.

The model is capturing variation based individual preferences for pulling the left or right lever.