Assignment2

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R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed           dist       
##  Min.   : 4.0   Min.   :  2.00  
##  1st Qu.:12.0   1st Qu.: 26.00  
##  Median :15.0   Median : 36.00  
##  Mean   :15.4   Mean   : 42.98  
##  3rd Qu.:19.0   3rd Qu.: 56.00  
##  Max.   :25.0   Max.   :120.00
```

Including Plots

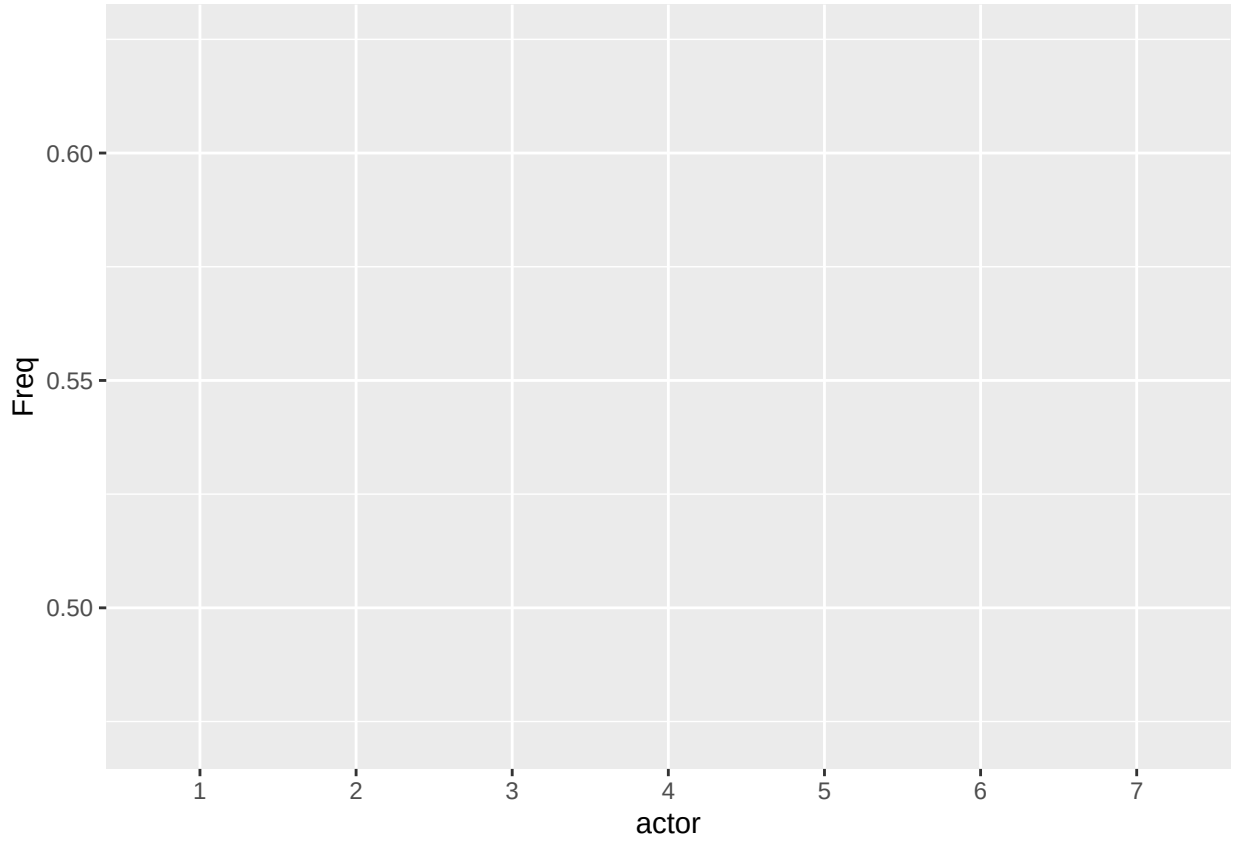
You can also embed plots, for example:

```
dataset = read.delim("assign2.txt", header = TRUE, sep = " ")
dataset['prosocial_action'] = (dataset$prosoc_left == dataset$pulled_left)
data1 = dataset[dataset$actor == 1,]
data2 = dataset[dataset$actor == 2,]
data3 = dataset[dataset$actor == 3,]
data4 = dataset[dataset$actor == 4,]
data5 = dataset[dataset$actor == 5,]
data6 = dataset[dataset$actor == 6,]
data7 = dataset[dataset$actor == 7,]
```

Using poisson regression to test three way contengency table

```
library(ggplot2)
prosocial = xtabs( ~ actor,prosocial_action, data = dataset)
prosocial_percentage = transform(prosocial, Freq=Freq/72)

ggplot(data=prosocial_percentage, aes(x=actor, y=Freq))
```




```
geom_bar(stat="identity", color="blue", fill="blue",width = 0.5)
```

```
## geom_bar: width = 0.5, na.rm = FALSE
## stat_identity: na.rm = FALSE
## position_stack
```

```
geom_hline(yintercept=0.5, linetype=1, color = "red",size = 2)
```

```
## mapping: yintercept = ~yintercept
## geom_hline: na.rm = FALSE
## stat_identity: na.rm = FALSE
## position_identity
```

```
ggtitle("Plot of the percentage of prosocial action for each actor")
```

```
## $title
## [1] "Plot of the percentage of prosocial action for each actor"
##
## attr(,"class")
## [1] "labels"
```

```
#actor
x = xtabs( ~ prosoc_left + condition + pulled_left, data = dataset)
x = data.frame(x)

model0 = glm(Freq~prosoc_left + condition + pulled_left, family = poisson,data = x )
deviance(model0)
```

```
## [1] 10.88825
```

```r
df.residual(model0)
```

```
## [1] 4
```

```r
pchisq(deviance(model0), df = df.residual(model0), lower.tail = FALSE)
```

```
## [1] 0.02784904
```

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

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