R lecture notes 2023-11-29

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```
knitr::opts_chunk$set(echo = TRUE)
library(tidyverse)
```

```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✓ dplyr     1.1.3     ✓ readr     2.1.4
## ✓ forcats   1.0.0     ✓ stringr   1.5.0
## ✓ ggplot2   3.4.4     ✓ tibble    3.2.1
## ✓ lubridate 1.9.3     ✓ tidyr     1.3.0
## ✓ purrr     1.0.2
## ── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(lattice)
library(Rling)
library(languageR)
library(nhstplot)
library(reshape)
```

```
##
## Attaching package: 'reshape'
##
## The following object is masked from 'package:lubridate':
##
##     stamp
##
## The following object is masked from 'package:dplyr':
##
##     rename
##
## The following objects are masked from 'package:tidyr':
##
##     expand, smiths
```

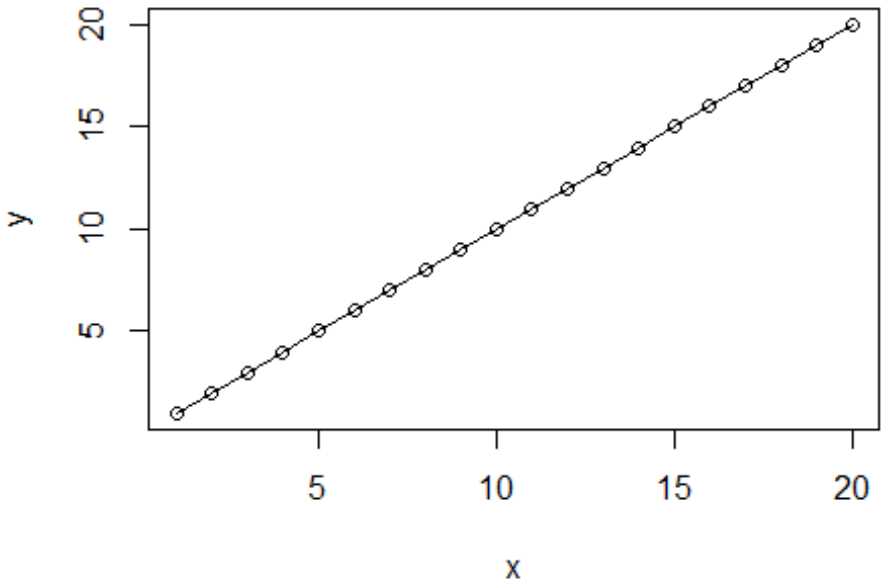
```
elp.df <- read.csv("/Users/Adan Tallman/Desktop/ELP_full_length_frequency.csv")
senses <- read.csv("/Users/Adan Tallman/Desktop/winter_2016_senses_valence.csv")
```

```
data(ldt)
data(sharedref)
```

Linear models

A deductive versus a statistical model can be seen by simulation.

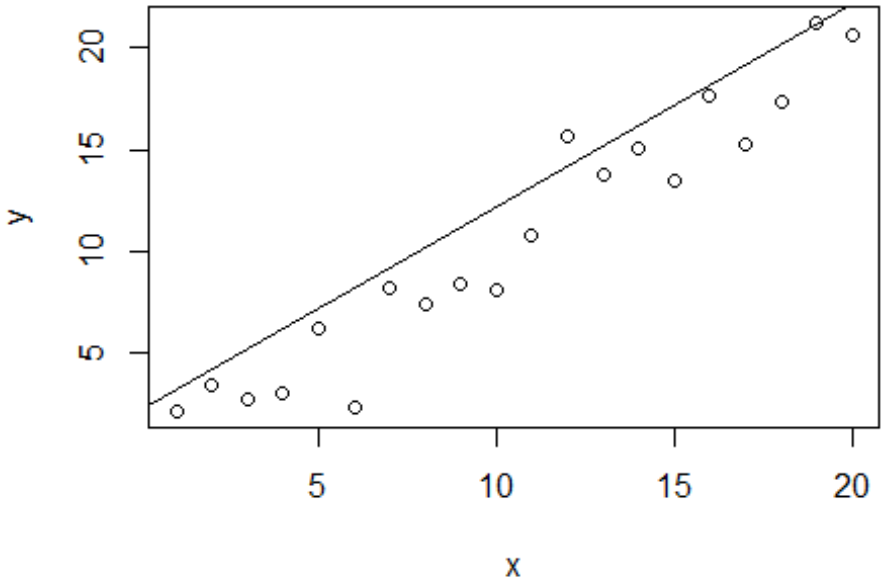
```
##Deductive model
x <- seq(from=1, to=20)
b <- 1
a <- 0
y <- a + b*x
plot(y~x)+lines(y,x)
```




```
## integer(0)
```

Simulating a stochastic model would look like this.

```
##Statistical model
set.seed(12345)
x <- seq(from=1, to=20)
b <- 1
a <- 0
e <- rnorm(m=0,sd=2, n=20)
y <- a + b*x + e
plot(y~x)+abline(y,x)
```




```
## integer(0)
```

Those error terms are the `residuals" that we discussed last lecture.

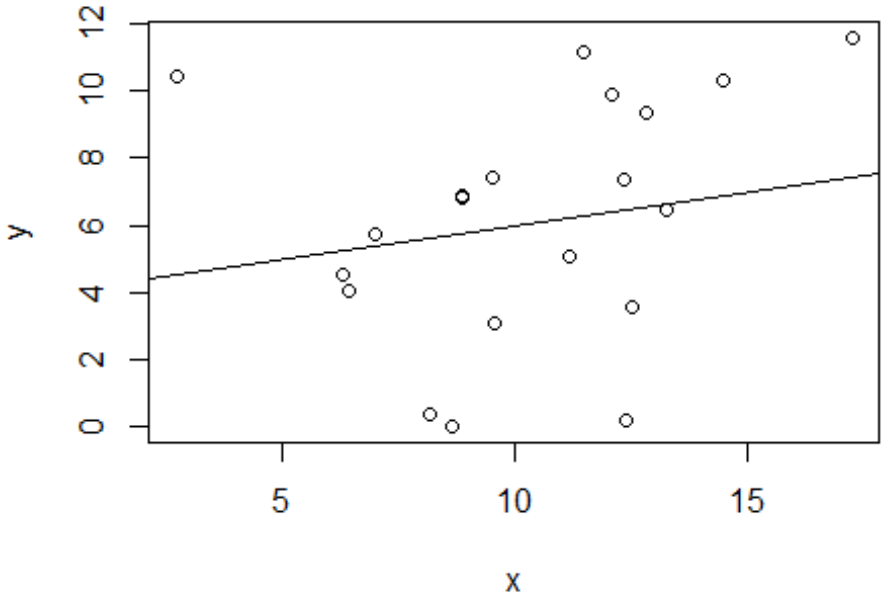
```
y_hat <- predict(lm(y~x))
residuals <- y - y_hat

error_residuals <- make.groups(e, residuals)

ggplot(error_residuals, aes(x=data, fill=which))+
  geom_density(alpha=0.3)
```

How do I know that my line is making predictions

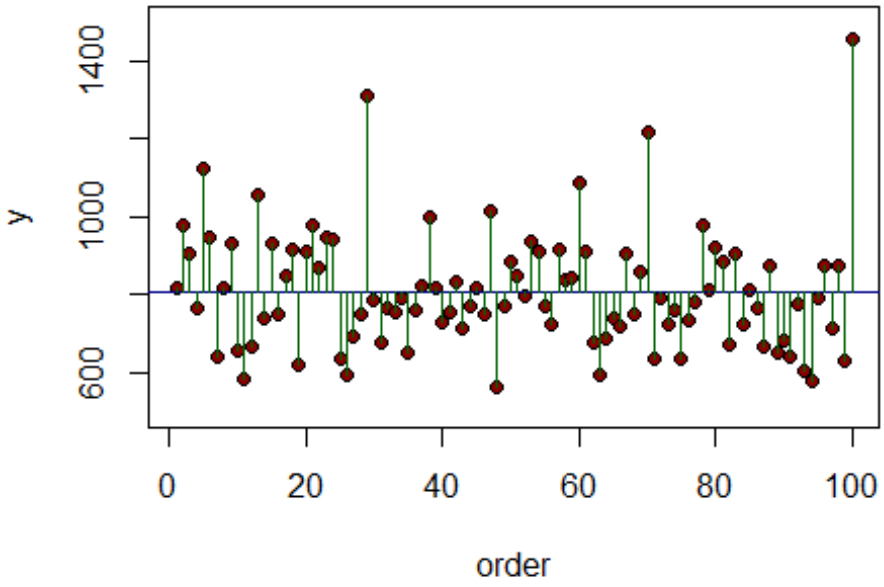
```
##Line through unrelated vectors
set.seed(12345)
x <- rnorm(20, 10, 4)
y <- rnorm(20, 5, 3)
plot(y~x)+abline(a=4, b=0.2)
```




```
## integer(0)
```

How do we know when our line explains anything? Let's look at the ldt database. We can visualize the variance by using a straight line through the datapoints. The x-axis is just the order of elements in the vector.

```
data(ldt)
RT <- ldt$Mean_RT
plot(1:100,RT,ylim=c(500,1500),ylab="y",xlab="order",pch=21,bg="darkred")
abline(h=mean(RT),col="darkblue")
for(i in 1:100) lines(c(i,i),c(mean(RT),RT[i]),col="darkgreen")
```

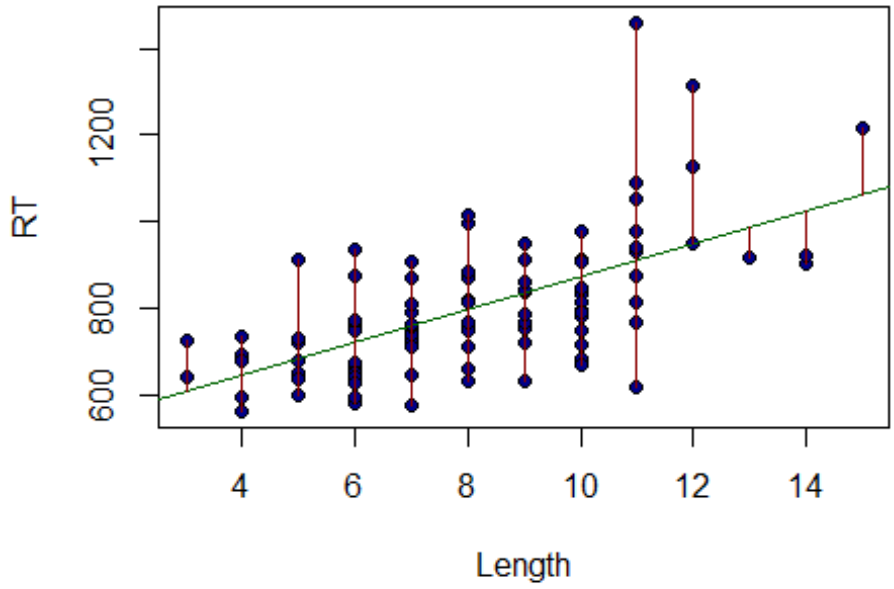


You are calculating the overall distance the points are from the mean.

```
var(RT)

## [1] 23472.17

Length <- ldt$Length
plot(Length,RT,pch=21,bg="darkblue")
abline(lm(RT~Length),col="darkgreen")
fitted <- predict(lm(RT~Length))
lines(c(0,0),c(12,11.755556))
for (i in 1:100)
  lines (c(Length[i],Length[i]),c(RT[i],fitted[i]),col="darkred")
```




```
sqrt(sum((RT-fitted)^2))
```

```
## [1] 1202.32
```

I will give an overview of how to read an lm() model below.

```
model_1 <- lm(Mean_RT~Length, data=ldt)
summary(model_1)
```

```
##
## Call:
## lm(formula = Mean_RT ~ Length, data = ldt)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -291.74  -77.81   -3.69   47.92  546.22
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  498.443     41.949  11.882  < 2e-16 ***
## Length        37.644      4.879   7.716 1.02e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 121.5 on 98 degrees of freedom
## Multiple R-squared:  0.3779, Adjusted R-squared:  0.3716
## F-statistic: 59.53 on 1 and 98 DF,  p-value: 1.019e-11
```

Analysis of Variance

```
head(senses)
```

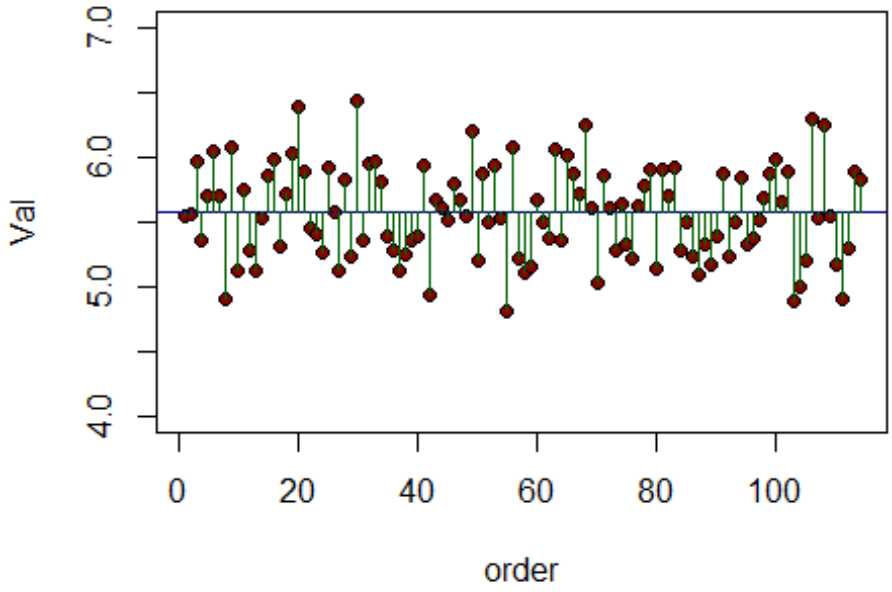
```
##        Word Modality      Val
## 1  abrasive    Touch 5.398113
## 2 absorbent    Sight 5.876667
## 3    aching    Touch 5.233370
## 4    acidic    Taste 5.539592
## 5     acrid    Smell 5.173947
## 6  adhesive    Touch 5.240000
```

```
tail(senses)
```

```
##        Word Modality      Val
## 400    wide    Sight 5.450416
## 401    wiry    Sight 5.665333
## 402   wispy    Sight 5.678721
## 403 wizened    Sight 5.733333
## 404  woolly    Touch 5.503770
## 405  yellow    Sight 5.451604
```

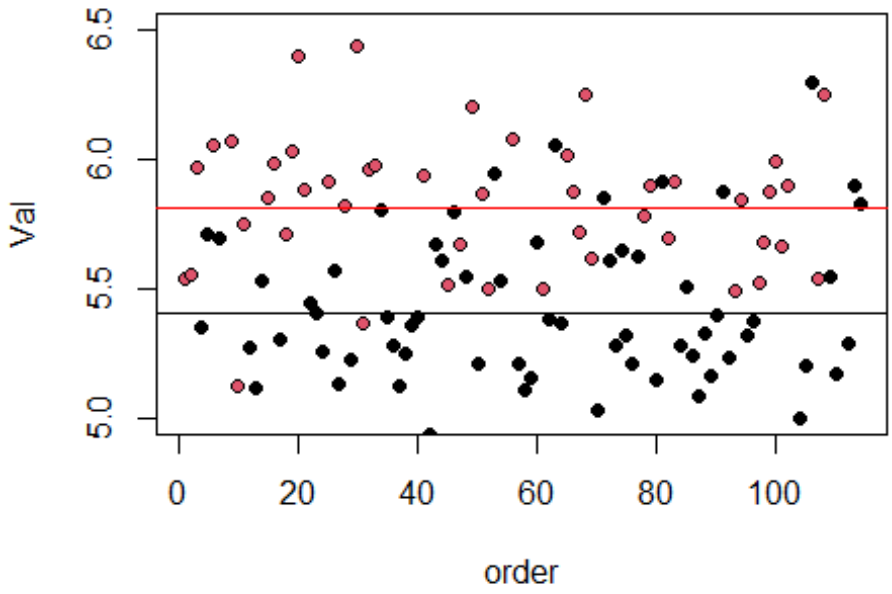
How to imagine your null model? It would just be a model that tried to predict every VAL from the mean of all the values. You can visual this as a line going through the mean.

```
senses_01 <- filter(senses, Modality =="Taste" | Modality =="Sound")
modality <- senses_01$Modality
Val <- senses_01$Val
plot(1:114,Val,ylim=c(4,7),ylab="Val",xlab="order",pch=21,bg="darkred")
abline(h=mean(Val),col="darkblue")
for(i in 1:114)
  lines(c(i,i),c(mean(Val),Val[i]),col="darkgreen")
```

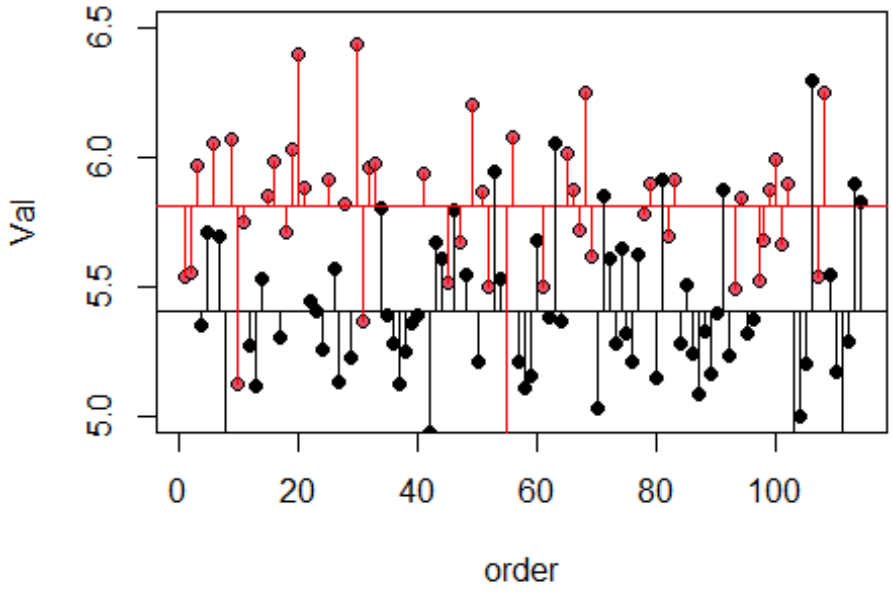


The variances are distances from the mean visualized as lines in the plot above. The overall varianxes will be difference if you split the data into groups, which can be visualized as different lines.

```
senses_01 <- filter(senses, Modality =="Taste" | Modality =="Sound")
modality <- senses_01$Modality
Val <- senses_01$Val
plot(1:114,Val,ylim=c(5,6.5),ylab="Val",xlab="order", pch=21,bg=
as.numeric(as.factor(modality)))
#abline(h=mean(Val[modality=="Sight"]),col="darkgreen")
#abline(h=mean(Val[modality=="Smell"]), col="darkred")
abline(h=mean(Val[modality=="Sound"]), col="black")
#abline(h=mean(Val[modality=="Taste"]), col="cornflowerblue")
abline(h=mean(Val[modality=="Taste"]), col="red")
```




```
senses_01 <- filter(senses, Modality =="Taste" | Modality =="Sound")
modality <- senses_01$Modality
Val <- senses_01$Val
plot(1:114,Val,ylim=c(5,6.5),ylab="Val",xlab="order", pch=21,bg=
as.numeric(as.factor(modality)))
#abline(h=mean(Val[modality=="Sight"]),col="darkgreen")
#abline(h=mean(Val[modality=="Smell"]), col="darkred")
abline(h=mean(Val[modality=="Sound"]), col="black")
#abline(h=mean(Val[modality=="Taste"]), col="cornflowerblue")
abline(h=mean(Val[modality=="Taste"]), col="red")
index <- 1:length(Val)
for (i in 1:length(index)){
if (modality[i] == "Sound")
  lines(c(index[i],index[i]),c(mean(Val[modality=="Sound"]),Val
[i]))
else
  lines(c(index[i],index[i]),c(mean(Val[modality=="Taste"]),Val
[i]), col="red")
}
```



The difference can be formalized as the error sum of squares.

$$SSE = \sum_{j=1}^{k} \Sigma \left(y - \overline{y}_j \right)^2$$

Here's a way of calculating it using base R functions

```
sound <- senses_01[senses_01$Modality=="Sound",]
taste <- senses_01[senses_01$Modality=="Taste",]
residuals_Sound <- sound$Val - mean(sound$Val)
residuals_Taste <- taste$Val - mean(taste$Val)
error_sum_of_squares <- sum(residuals_Sound^2) + sum(residuals_Taste^2)
error_sum_of_squares
```

```
## [1] 10.13909
```

The `analysis' part of the`Analysis of Variance' involves comparing this number to the total sum of squares.

```
total_sum_of_squares <- sum((senses_01$Val - mean(senses_01$Val))^2)
```

The part of the variance that is explained by the different is called the ``treatment sum of squares', and that's just the the total sum of squares minus the error sum of squares.

```
treatment_sum_of_squares <- total_sum_of_squares - error_sum_of_squares
```

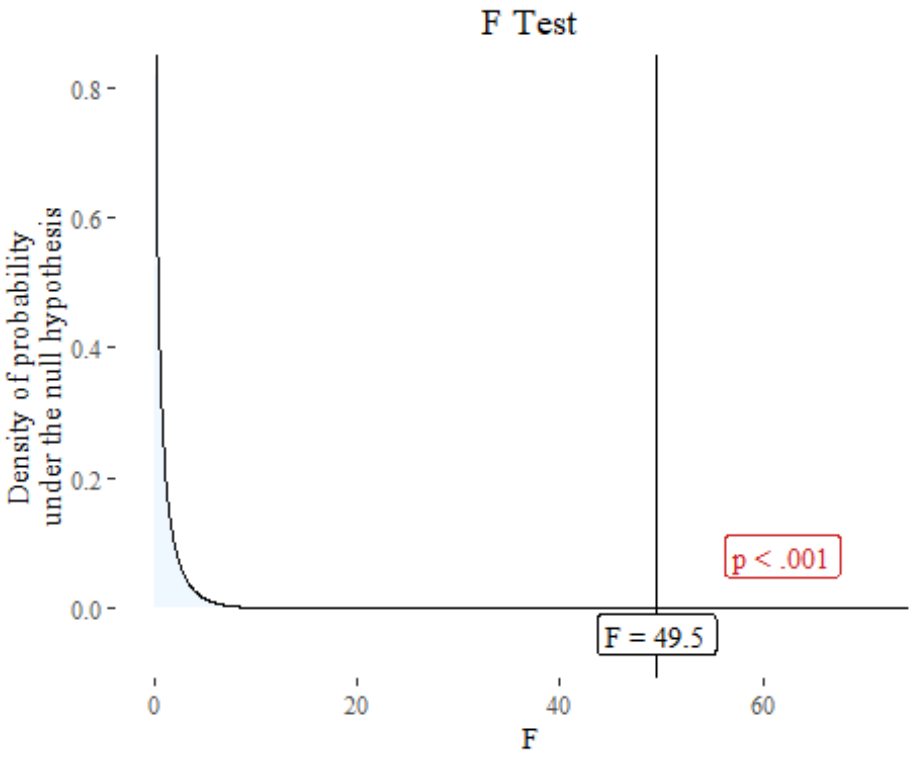
Basically the F-statistic is as follows

$$F = \frac{\text{Variance explained}}{\text{Variance of error}}$$

You calculate the variance by dividing the sum of squares by their degrees of freedom.

```
F_ratio <- treatment_sum_of_squares / (error_sum_of_squares/112)

plotftest(f = 49.54, dfnum = 1, dfdenom = 112)
```



And there is a function in R that can do this.

```
summary(aov(Val~Modality, data=senses_01))

##              Df Sum Sq Mean Sq F value   Pr(>F)
## Modality      1  4.485   4.485   49.54 1.65e-10 ***
## Residuals   112 10.139   0.091
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Chi-squared test

Let's take a look at some of the data from Matthew Dryer's paper on word order correlations.

```
adpos <- matrix(c(107,12,7,70),ncol=2,byrow=TRUE)
rownames(adpos)<-c("PostP","Prep")
```

```
colnames(adpos)<-c("OV","VO")
adpos
```

```
##        OV VO
## PostP 107 12
## Prep    7 70
```

```
wordorder <- cbind(c(107, 7), c(12, 70))
rownames(wordorder) <- c("Postp", "Prep")
colnames(wordorder) <- c("OV", "VO")
wordorder <- rbind(wordorder, c(114,82))
wordorder <- cbind(wordorder, c(119,77,196))
rownames(wordorder) <- c("PostP", "Prep", "Column Total")
colnames(wordorder) <- c("OV", "VO", "Row total")
wordorder
```

```
##               OV VO Row total
## PostP        107 12       119
## Prep           7 70        77
## Column Total 114 82       196
```

Here's how we create the expected frequencies

```
E <- cbind(c((114*119)/196, (114*77)/196),
           c(82*119/196,(82*77)/196))
rownames(E) <- c("Postp", "Prep")
colnames(E) <- c("OV", "VO")
E
```

```
##             OV       VO
## Postp 69.21429 49.78571
## Prep  44.78571 32.21429
```

```
E.df <- melt(E)
```

```
## Warning in type.convert.default(X[[i]], ...): 'as.is' should be
specified by
## the caller; using TRUE
```

```
## Warning in type.convert.default(X[[i]], ...): 'as.is' should be
specified by
## the caller; using TRUE
```

```
colnames(E.df)<-c("Adposition", "Verb.Object", "Expected.Frequency")
E.df$Observed.Frequency <- c(107,7,12,70)
E.df
```

```
##   Adposition Verb.Object Expected.Frequency Observed.Frequency
## 1      Postp          OV           69.21429                107
## 2       Prep          OV           44.78571                  7
## 3      Postp          VO           49.78571                 12
## 4       Prep          VO           32.21429                 70
```

$$\chi^2 = \sum \frac{(Observed - Expected)^2}{Expected}$$

```
E.df$oe <- ((E.df$Observed.Frequency - E.df$Expected.Frequency)^2) /
E.df$Expected.Frequency
sum(E.df$oe)

## [1] 125.5068

chisq.test(adpos)

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  adpos
## X-squared = 122.21, df = 1, p-value < 2.2e-16
```