University of California, Davis

Take Home Project 2

Topic 1 Question 1: Helicopter Count & Shift
Topic 2 Question 1: Annual Salary & Profession, Region

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PROJECT 1 TOPIC 1 - Helicopter
Transformation of Variables

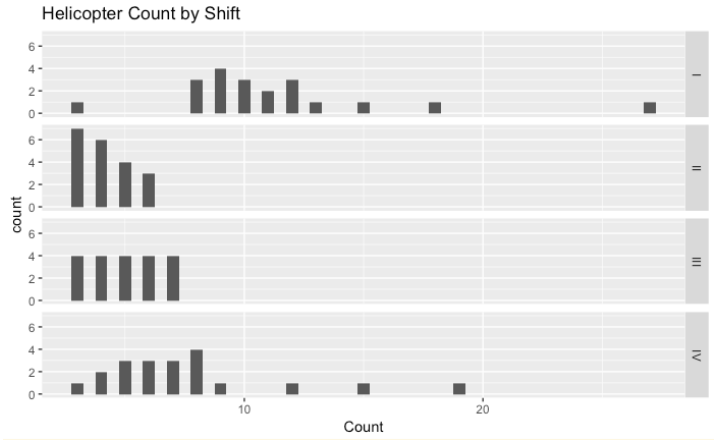
a. Introduction

Given data on the number of helicopters requested over different times of the day for a sheriff's office, the goal for this report is to transform the data so it best fits the ANOVA model. We will be looking at assumptions of normality and constant variance, the best transformation and if outliers must be removed using a Single Factor ANOVA model with variables Count (number of helicopters called) and Shift (I, II, III, IV).

b. Diagnostics

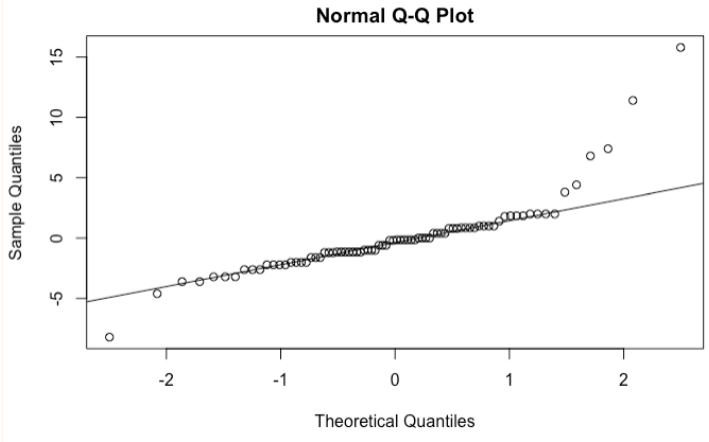
In this section we perform diagnostics to ensure that the data meets the assumptions of ANOVA which are that all Y_{ijk} are randomly sampled, all group levels of both factors are independent, and errors are distributed normally with mean of 0 and variance of σ^2_ε. Here we look at normality and constant variance.

1. Boxplot & Histogram



2. Testing for Normality

a. QQ Plot



There are clear outliers on this QQ plot as many values leave the perfect distribution Y=X line especially on the upper right side of the plot.

b. Shapiro-Wilkes Test

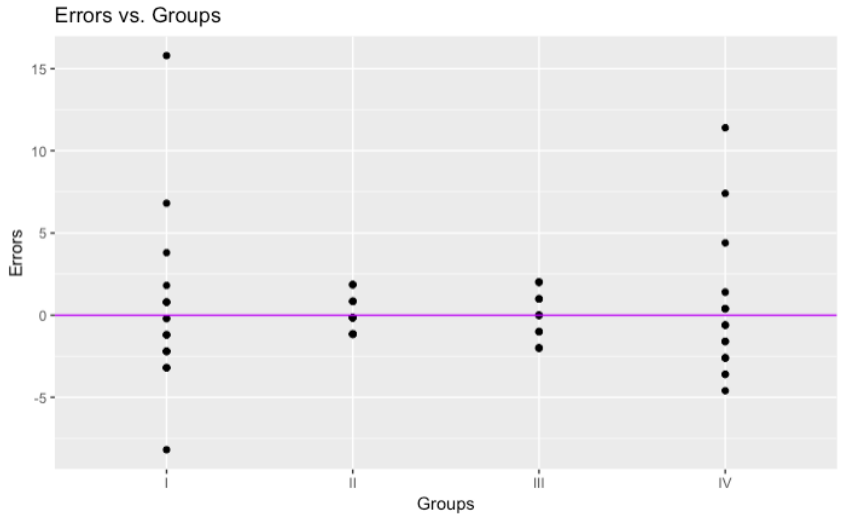
$Ho: Errors\ are\ normal$ $Ha: Errors\ are\ non-normal$

P-value: 3.945e-09

Because this p-value is less than alpha of 0.05, we reject the null and conclude there is evidence to suggest that the errors of the original dataset are non-normal.

3. Testing for Constant Variance

a. Errors Vs. Groups Plot



This plot shows a rather unequal spread of data.

b. Brown-Forsythe Test

$Ho: Residuals\ have\ equal\ variance$ $Ha: Residuals\ do\ not\ have\ equal\ variance$

P-value: 0.03185955

Because this p-value is less than an alpha value of 0.05, we reject the null hypothesis and there is evidence to conclude this data does not have equal variance.

4. Model Fit

Group Means Model: $Y=\mu_i+\varepsilon_{ij}$

We are using MSE to estimate the variance of the errors.

$\underline{Y}_I$	$\underline{Y}_{II}$	$\underline{Y}_{III}$	$\underline{Y}_{IV}$	MSE	Overall Mean
11.20	4.15	5.00	7.60	10.297	6.987

c. Outliers & Transformations

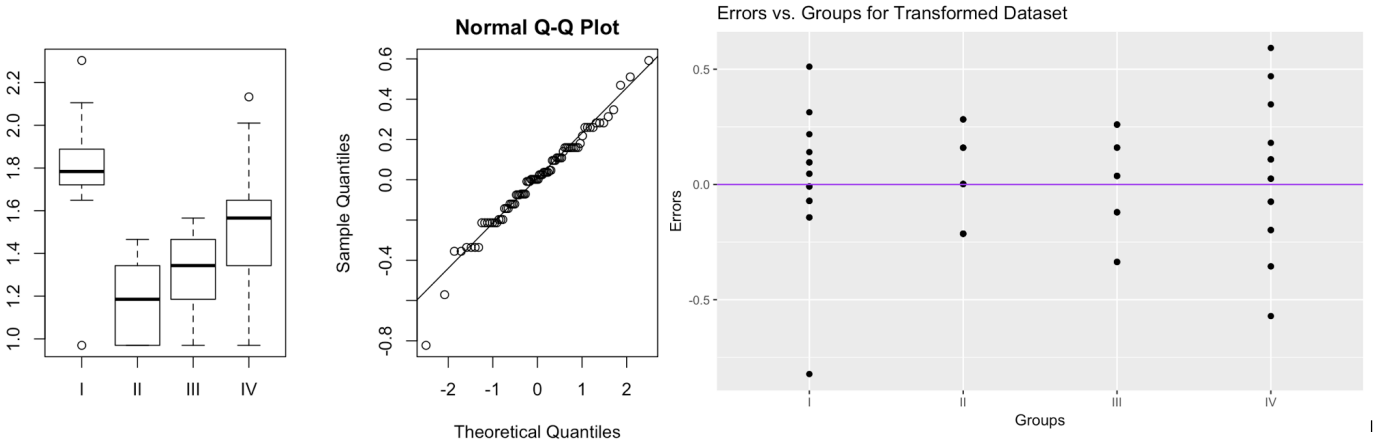
1. Box-Cox Transformations

a. Shapiro-Wilks

i.

Lambda: -0.2322012

ii. Plots



Here we can see that the data points are more closely aligned to the perfectly normal distribution X=Y line and vertical spread is more equal.

iii. Tests

Shapiro-Wilks P-value: 0.109024

Fail to reject the null at alpha of 0.05, so conclude this transformed data has normality.

Brown-Forsythe P-value: 0.6467526

Fail to reject the null at an alpha of 0.05, so we conclude constant variance.

b. Log-likelihood Transformation

i.

Lambda: -0.3964138

ii. Tests

Shapiro-Wilks P-value: 0.06738834

Fail to reject the null, so conclude this transformed data is normally distributed.

Brown-Forsythe P-value: 0.6596686

Fail to reject the null, so conclude constant variance.

Both transformations fulfill assumptions of normality and constant variance in the data. However, because the transformation using the Shapiro-Wilks transformation has a higher p-value for the Shapiro-

Wilks normality test and therefore is more likely to be normal, we will proceed with the data that has been transformed using the Shapiro-Wilks lambda. Plots are shown for only this transformation above.

2. Outliers

We did not find any outliers using the semi-studentized method and an alpha of 0.05 with the best model of Shapiro-Wilks transformed data so no data points were removed.

d. Discussion

Transforming the data did help. Some downsides are that it is hard to interpret as the units change and we cannot use old units to interpret the values. We do believe the transformed data is a better fit because the p-values testing for normality and constant variance both increase and we are able to reject the nulls so that assumptions for normality and constant variance are met. For a client who wants to use this data set for ANOVA, we would suggest to use the Shapiro-Wilks transformation and no outliers would need to be removed. Those who may be looking into how many helicopters sheriff's offices need on average may find this model useful to draw further conclusions from.

PROJECT 2 - Salary
Two Factor ANOVA

I. Introduction

The goal of this project is to build a model using data of annual salaries for Data Scientists, Software Engineers, and Bioinformatics Engineers in San Francisco and Seattle. We are using a Two Factor ANOVA approach and will test for various effects to build the best model, perform diagnostics, calculate confidence intervals and perform other statistical measures to analyze the data. People who are pursuing one of the professions we are looking at or students who are trying to get an idea of what to study may be interested in using this model to decide where they should work and which careers they can earn the most in.

II. Summary of Data

A. Summary Statistics

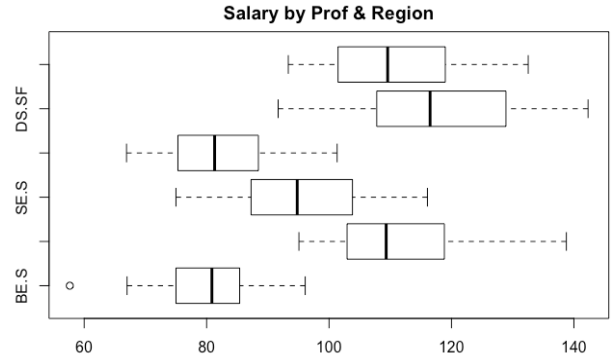
The first value in each box is the mean while the second value is the standard deviation. Units are in thousands of dollars.

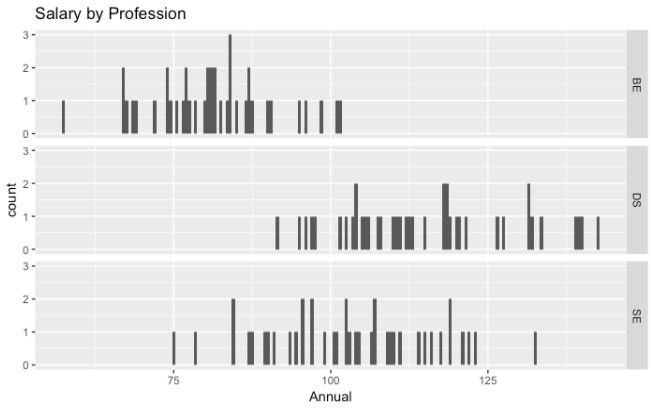
		j=1	j=2	
	(Units are thousands of dollars)	Seattle	San Francisco	Overall profession
i=1	BE	79.75485 (8.786628)	82.41914 (10.521476)	81.0870 (9.662515)
i=2	DS	112.52715 (12.838566)	117.76883 (14.289227)	115.1480 (13.668190)
i=3	SE	95.54875 (11.598722)	110.26412 (10.551705)	102.9064 (13.240313)

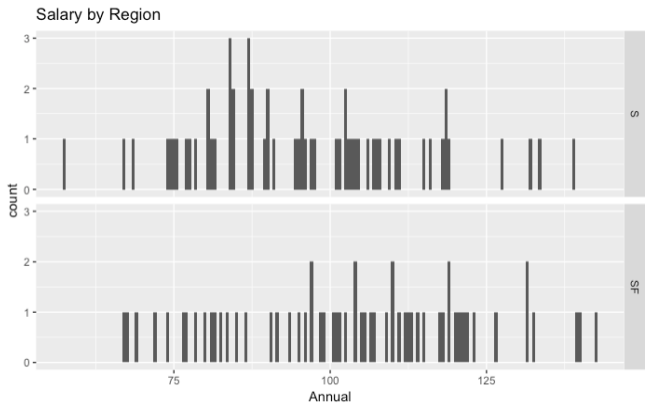
	Overall region means	95.94358 (17.41791)	103.48403 (19.29842)	Overall mean: 99.71381 Overall SD: 18.69226

Total sample size	Factor A level (Profession)	Factor B levels (Region)
120	3	2

B. Boxplot & Histograms





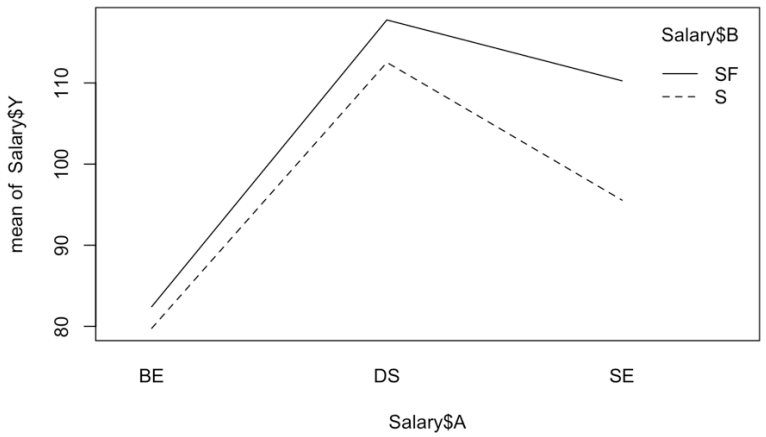


We can see from this section that salaries for Data Scientists have higher salaries on average than that of Bioinformatics Engineers and Software Engineers and Software Engineers have higher salaries on average than Bioinformatics Engineers. Another trend is that there is more variance in salaries in Seattle than in San Francisco.

III. Analysis & Interpretation: Model Fit

In this section we are choosing the best model to perform further analyses on. First we will test for interactions and if none are found, test for Profession effects and Region effects.

A. Interaction Plot



According to this interaction plot we can conclude that there are no interactions between profession and region. Furthermore to support this claim we can see in part IIA that the group means for each profession and region follow relatively the same trend.

B. Test for Interaction Effects

Full model**:** $Y_{ijk}= \mu.. + \gamma_i + \delta_j+(\gamma\delta)_{ij}+ \varepsilon_{ijk}$

Reduced model: $Y_{ijk}= \mu.. + \gamma_i + \delta_j+\varepsilon_{ijk}$

$Ho: \delta$ **δδδδδδδδδδδδδδδδ** $\gamma\delta = 0$ **δδδδ**

$Ha: \ \gamma\delta \neq \ 0$

F-statistic	P-value
3.0098	0.05324

Because the p-value is greater than alpha 0.05, we fail to reject the null hypothesis and conclude that there is no interaction between profession and region.

If in reality the reduced model with no interaction term between Profession and Region was a better statistical fit, we would see our data or more extreme 5.32% of the time.

Because we have concluded a no interactions model, next we must test for Profession and Region effects.

C. Test for Factor A Effects

Full model : $Y_{ijk}= \mu.. + \gamma i+\boldsymbol{\delta}j +\varepsilon_{ijk}$

Reduced model: $Y_{ijk}= \mu.. +\boldsymbol{\delta}j +\varepsilon_{ijk}$

$Ho: \gamma i = 0$

$Ha: At\ least\ one\ \gamma i \neq 0$

F-statistic	P-value
86.014	2.2e-16

Because the p-value is less than alpha of 0.05 we reject the null hypothesis and conclude that Profession (Factor A) effects exist and so the full model with Profession effects fits significantly better than the reduced model.

1. **Partial R^2**

   $R^2\{A+B|B\} = 0.5972622$

When we add Profession to a model that already contains Region we reduce error by 59.7%. This further shows that Profession is an important factor for this model since we significantly reduced the error.

D. Test for Factor B effects

Full model : $Y_{ijk}= \mu.. + \gamma_i + \delta_j+\varepsilon_{ijk}$
Reduced model: $Y_{ijk}= \mu.. + \gamma_i + \varepsilon_{ijk}$
$Ho: \boldsymbol{\delta}\delta j = 0$

$Ha : At\ least\ one\ \delta j \neq 0$

F-stat	P-value
6.2561	0.0005712

Because the p-value is less than alpha of 0.05 we reject the null and there is sufficient evidence to conclude that Region (Factor B) effects exist and so the full model with Region effects fits significantly better than the reduced model.

1. **Partial R^2**
   $R^2\{A+B|A\} = 0.09602243$
   When we add Region (Factor B) to a model that already has Profession (Factor A) effects we reduce our error by 9.6%. Although this value may seem small in comparison to the previous, it still shows a significant reduction in error.

E. Final Model

According to the above tests we can conclude that the best model is one with no interaction effect between profession and region but with both variables still in the model. Thus, the best model is:

$$Y_{ijk}= \mu.. + \gamma_i + \delta_j+ \varepsilon_{ijk}$$

Where the Gammas are:

BE (γ_1)	DS (γ_2)	SE (γ_3)
-18.626812	15.434183	3.192629

And the Deltas are:

Seattle (δ_1)	San Francisco (δ_2)
-3.770225	3.770225

A general interpretation of a gamma would be the change in the overall average salary when a Bioinformatic Engineer, Data Scientist, or Software Engineer ignoring interactions effects or effects of region.
For example the interpretation of BE would be: The average change in overall average salary when a subject is a Bioinformatic Engineer is a decrease of $18,626.81.

A general interpretation of a delta would be the change in overall average salary when in Seattle or San Francisco, ignoring effects of Profession.

For example the interpretation of Seattle would be: The average change in overall average salary when a subject works in Seattle is a decrease of $3,770.26.

IV. Diagnostics

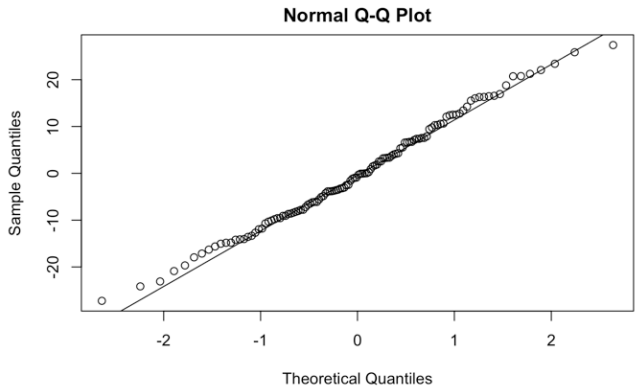
With our "best" model of no interaction effects, we will perform diagnostics to ensure that it meets the assumptions of ANOVA which are that all Y_{ijk} are randomly sampled, all group levels of both factors are independent, and errors are distributed normally with mean of 0 and variance of σ^2_ε. In this section we will be testing the assumptions of normality and constant variance.

A. Outliers

Using the Studentized and Semi-Studentized method, we found no outliers using alpha of 0.05 so we will not remove any data points.

B. Testing for Normality

1. QQ Plot



The residuals looks rather normal as the data points are lying very close to the perfect distribution Y=X line.

2. Shapiro-Wilks

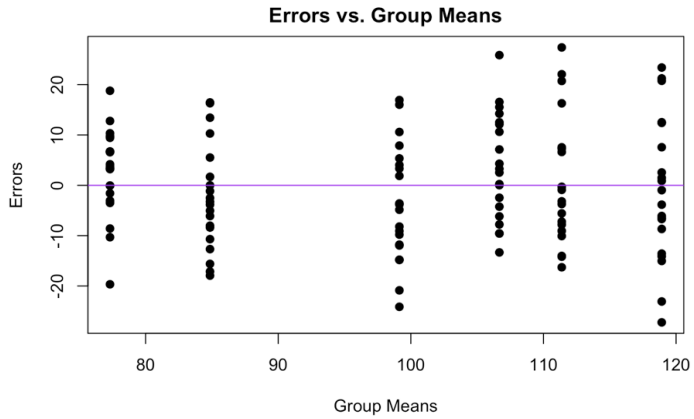
$$Ho: Errors\ are\ normal \qquad Ha: Errors\ are\ non-normal$$

P-value: 0.6698

Because our p-value is greater than the alpha of 0.05, there is evidence to fail to reject the null and we conclude that the errors are approximately normally distributed.

C. Testing for Constant Variance

1. Errors vs. Groups



This plot shows a rather equal spread of data across the plot.

2. Brown-Forsythe Test

Ho: Residuals have equal variance *Ha: Residuals do not have equal variance*

P-value: 0.3048319

Because this p-value is greater than an alpha value of 0.05, we fail to reject the null hypothesis and there is evidence to conclude there is equal variance.

D. Conclusion

From this section we can conclude assumptions of normality and constant variance are met and no outliers need to be removed. We do not need to look at transformations of the data.

V. Analysis & Interpretation: Confidence Intervals & Regression

Now that we have concluded our model is reliable, we can draw conclusions from the data such as confidence intervals to further analyze the data of salaries.

Since there are equal sample sizes for each factor level we can use the equal weights formula.

1. Pairwise Confidence Intervals

a. Multipliers

alpha	Bonferroni	Tukey	Scheffe
0.05	2.429	2.374	2.480

For pairwise confidence intervals we can use either the Bonferroni, Tukey or Scheffe multiplier so in this case we will use Tukey because that is the smallest of the three for intervals i-iii.

b. Intervals

i) BE-SE	Lower Bound	Upper Bound
-21.81944	-28.10459	-15.53429

ii) BE-DS	Lower Bound	Upper Bound
-34.06100	-40.34614	-27.77585

iii) DS-SE	Lower Bound	Upper Bound
12.241555	5.956406	18.526703

iv) S-SF	Lower Bound	Upper Bound
-7.540449	-11.724029	-3.356869

i) We are overall 95% confident that the true average annual salary for Software Engineers is greater than that of a Bioinformatics Engineer by between $28,104.59 and $15,534.29 thousands of dollars.
ii) We are overall 95% confident that the true average annual salary for Data Scientists is greater than that of Bioinformatics Engineers by between $27,775.85 and $40,346.14.
iii) We are overall 95% confident that the true average annual salary for Data Scientists is greater than that of Software Engineers by between $5,956.41 and $18,526.70.
iv) For this interval we assumed the number of intervals (g) is 1 and a multiplier of 1.981. We are overall 95% confident that the true average annual salary for those who reside in San Francisco is greater than that of those who reside in Seattle by between $3,356.87 and $11,724.03.

2. Contrast Confidence Intervals

a. Multipliers

Bonferroni	Tukey	Scheffe
2.271	2.374	2.480

Because contrast intervals are of interest we will choose between Bonferroni or Scheffe. Typically Scheffe is more commonly used for contrasts, however, because Bonferroni is smaller we will be using that value for the following CI.

b. Intervals

i) $\mu_{31}-\frac{\mu 11+\mu 21}{2}$	Lower bound	Upper bound
-0.592250	-7.786276	6.601776

ii) $\mu_{22}-\frac{\mu 11+\mu 31}{2}$	Lower bound	Upper bound
30.11703	22.92301	37.31106

i) We are overall 95% confident that there is no significant difference between the mean salary of Software Engineers in Seattle and the average of the mean salaries for Bioinformatic Engineers and Data Scientists in Seattle.
ii) We are overall 95% confident that the true mean salary for Data Scientists in San Francisco is higher than the average of the mean salaries for Bioinformatic Engineers and Software Engineers in Seattle by between $22,923.01 and $37,311.06.

C. Regression Formation

Using regression formation, we can make further analyses which compare the different professions and regions to one another.

The line of best fit:

$$\hat{Y} = 77.316771 + 34.060995XA,DS + 21.819441XA,SE + 7.540449XB,SF$$

(i) **(ii)** **(iii)** **(iv)**

i) The estimated average salary for Bioinformatic Engineers in Seattle is $77,316.77.
ii) Holding region in Seattle constant, the estimated difference in average salary for Data Scientists versus Bioinformatic Engineers is $34,061.
iii) Holding region in Seattle constant, the estimated difference in average salary for Software Engineers versus Bioinformatic Engineers is $21,819.44.

iv) Holding profession at Bioinformatic engineer constant, the estimated difference in average salary in San Francisco versus Seattle is $7,540.45.

V. Conclusion

Through this project we have found that an ANOVA Two Factor Model without interactions but with individual effects from Profession and Region have statistical significance in determining annual salary using this dataset. After performing diagnostics with that model in mind, we concluded assumptions of normality and constant variance were met and no outliers needed to be removed so we proceeded without performing transformations. Through calculating six confidence intervals, we formed various conclusions about salary in San Francisco and Seattle for the different professions. We then used regression formation to find average differences for various combinations between the variables. Those who are interested in these professions will be able to use this model to good use in determining where they should pursue their career.

R Appendix

PROJECT 1

b. Diagnostics

Boxplot

```
boxplot(Count ~ Shift, data = Helicopter, main = "Helicopter Count by Shift", horizontal = TRUE)
```

Histogram

```
library(ggplot2)
ggplot(Helicopter, aes(x = Count)) + geom_histogram(binwidth = 0.5) + facet_grid(Shift ~.) +ggtitle("Helicopter Count by Shift")
```

Diagnostics

Testing for Normality

QQ Plot

```
h.model = lm(Count ~ Shift, data = Helicopter)
qqnorm(h.model$residuals)
qqline(h.model$residuals)
```

Shapiro-Wilkes Test

```
h.ei = h.model$residuals
the.SWtest = shapiro.test(h.ei)
the.SWtest
```

Testing for Constant Variance

Errors Vs. Groups

```
qplot(Shift, h.ei, data = Helicopter) + ggtitle("Errors vs. Groups") + xlab("Groups") + ylab("Errors") + geom_hline(yintercept = 0,col = "purple")
```

Brown-Forsythe Test

Model Fit

```
aggregate(Count ~ Shift, data = Helicopter, mean)
sd(Helicopter$Count)
anova.table = anova(h.model)
Anova.table
SSE= anova.table[2,2]
SSE
```

Outliers and Transformations

Box-Cox

```
library(EnvStats)
h.model = lm(Count ~ Shift, data = Helicopter)
boxcox(h.model ,objective.name = "PPCC")
boxcox(h.model ,objective.name = "Shapiro-Wilk")
boxcox(Helicopter$Count,objective.name = "Log-Likelihood")
L2 = boxcox(h.model ,objective.name = "Shapiro-Wilk",optimize = TRUE)$lambda
L3 = boxcox(Helicopter$Count,objective.name = "Log-Likelihood",optimize = TRUE)$lambda
L2
L3
```

Transformed data(SW)

```
par(mfrow = c(1,2))
YTS = (Helicopter$Count^(L2)-1)/L2
tS.data = data.frame(Count = YTS, Shift = Helicopter$Shift)
tS.model = lm(Count~Shift,data = tS.data)
plot(tS.data$Shift, tS.data$Count)
qqnorm(tS.model$residuals)
qqline(tS.model$residuals)
```

Transformed data (LL)

```
qqnorm(t.model$residuals)
qqline(t.model$residuals)
qplot(Shift, h.ei, data = t.data) +  ggtitle("Errors vs. Groups") + xlab("Groups") + ylab("Errors") + geom_hline(yintercept = 0,col = "purple")
h.ei.t = t.model$residuals
the.SWtest.t = shapiro.test(h.ei.t)
the.SWtest.t
library(car)
the.BFtest.t = leveneTest(h.ei.t~ Shift, data=t.data, center=median)
p.val.t = the.BFtest.t[[3]][1]
P.val.t
```

Outliers

```
t.data$ei = t.model$residuals
nt = nrow(t.data) #Calculates the total sample size
a = length(unique(t.data$Shift)) #Calculates the value of a
SSE.t = sum(t.data$ei^2) #Sums and squares the errors (finds SSE)
MSE.t = SSE.t/(nt-a) #Finds MSE
```

```
eij.star = t.model$residuals/sqrt(MSE.t)
alpha = 0.05
t.cutoff= qt(1-alpha/(2*nt), nt-a)
CO.eij = which(abs(eij.star) > t.cutoff)
CO.eij
```

PROJECT 2

Summary of the data

```
aggregate(Y ~ A + B, data = Salary, sd)
sd(Salary$Y)
aggregate(Y ~ A, data = Salary, sd)
aggregate(Y ~ B, data = Salary, sd)
find.means = function(the.data,fun.name = mean){
 a = length(unique(the.data[,2]))
b = length(unique(the.data[,3]))
means.A = by(the.data[,1], the.data[,2], fun.name)
means.B = by(the.data[,1],the.data[,3],fun.name)
means.AB = by(the.data[,1],list(the.data[,2],the.data[,3]),fun.name)
MAB = matrix(means.AB,nrow = b, ncol = a, byrow = TRUE)
colnames(MAB) = names(means.A)
rownames(MAB) = names(means.B)
MA = as.numeric(means.A)
names(MA) = names(means.A)
MB = as.numeric(means.B)
names(MB) = names(means.B)
MAB = t(MAB)
results = list(A = MA, B = MB, AB = MAB)
return(results)
}
the.means = find.means(the.data)
the.model = lm(Y ~ A*B, data = the.data)
SSE = sum(the.model$residuals^2)
MSE = SSE/(nt-a*b)
the.means
mean(the.data$Y)
the.data = Salary
nt = nrow(the.data)
nt
a = length(unique(the.data[,2]))
a
b = length(unique(the.data[,3]))
b
names(the.data) = c("Y","A","B")
Boxplot: boxplot(Annual ~ Prof + Region, data = Salary, main = "Salary by Prof & Region",
horizontal = TRUE)
```

I. Model Fit

A. Interaction Plot

```
names(Salary) = c("Y","A","B")
interaction.plot(Salary$A, Salary$B, Salary$Y)
```

B. Testing for interaction effect

```
names(Salary) = c("Y","A","B")
AB = lm(Y ~ A*B,Salary)
A.B = lm(Y ~ A + B,Salary)
A = lm(Y ~ A,Salary)
B = lm(Y ~ B,Salary)
N = lm(Y ~ 1,Salary)

all.models = list(AB,A.B,A,B,N)
SSE = t(as.matrix(sapply(all.models,function(M) sum(M$residuals^2))))
colnames(SSE) = c("AB","(A+B)","A","B","Empty/Null")
rownames(SSE) = "SSE"
SSE
anova(A.B,AB)
```

C. Test for Factor A effects

```
anova(B,A.B)
```

1. **Partial R^2**

```
Partial.R2 = function(small.model,big.model){
SSE1 = sum(small.model$residuals^2)
SSE2 = sum(big.model$residuals^2)
PR2 = (SSE1 - SSE2)/SSE1
return(PR2)
}
Partial.R2(B,A.B)
```

D.Test for Factor B effects

```
anova(A,AB)
```

1. **Partial R^2**

```
Partial.R2 = function(small.model,big.model){
SSE1 = sum(small.model$residuals^2)
SSE2 = sum(big.model$residuals^2)
PR2 = (SSE1 - SSE2)/SSE1
return(PR2)
```

```
}
Partial.R2(A,A.B)
```

E. Final model

```
A.B = lm(Y ~ A+B,Salary)
get.gamma.delta =
function(the.model,the.data){
 nt = nrow(the.data)
 a = length(unique(the.data[,2]))
 b = length(unique(the.data[,3]))
 the.data$hat = the.model$fitted.values
 the.ns = find.means(the.data,length)
 a.vals = sort(unique(the.data[,2]))
 b.vals= sort(unique(the.data[,3]))
 muij = matrix(nrow = a, ncol = b)
 rownames(muij) = a.vals
 colnames(muij) = b.vals
 for(i in 1:a){
  for(j in 1:b){
   muij[i,j] =
the.data$hat[which(the.data[,2] == a.vals[i] &
the.data[,3] == b.vals[j])[1]]
  }
 }
 mi. = rowMeans(muij)
 m.j = colMeans(muij)
 mu.. = sum(muij)/(a*b)
 gammai = mi. - mu..
 deltaj = m.j - mu..
 gmat = matrix(rep(gammai,b),nrow =
a, ncol = b, byrow= FALSE)
 dmat = matrix(rep(deltaj,a),nrow = a,
ncol = b,byrow=TRUE)
 gamma.deltaij =round(muij -(mu.. +
gmat + dmat),8)
 results = list(Gam = gammai, Del =
deltaj, GamDel = gamma.deltaij)
 return(results)
}
Wow = get.gamma.delta(A.B, the.data)
Wow
```

II. Diagnostics

A. Outliers

```
theS.model = lm(Annual ~
Prof+Region, data = Salary)
Salary$ei = the.model$residuals
nt = nrow(Salary) #Calculates the total
sample size
a = length(unique(Salary$Prof))
SSE = sum(Salary$ei^2) #Sums and
squares the errors (finds SSE)
MSE = SSE/(nt-a) #Finds MSE
eij.star = the.model$residuals/sqrt(MSE)
alpha = 0.05
t.cutoff=qt(1-0.01,nt -a)
t.cutoff= qt(1-alpha/(2*nt), nt-a)
CO.eij = which(abs(eij.star) > t.cutoff)
CO.eij
rij = rstandard(the.model)
CO.rij = which(abs(rij) > t.cutoff)
CO.rij
```

B. Testing for Normality

1. **QQ plot**

```
qqnorm(theS.model$residuals)
qqline(theS.model$residuals)
```

2. **SW test**

```
ei = theS.model$residuals
the.SWtest = shapiro.test(ei)
the.SWtest
```

C. Testing for Constant Variance

1. **Errors vs Groups**

```
plot(theS.model$fitted.values,
theS.model$residuals, main = "Errors
vs. Group Means",xlab = "Group
Means",ylab = "Errors",pch = 19)
abline(h = 0,col = "purple")
```

2. **BF test**

```
the.BFtest = leveneTest(ei~
Prof*Region, data=Salary, center=median)
p.val = the.BFtest[[3]][1]
p.val
```

Confidence Intervals

A. Check for equal weight

```
sum(the.data$A=="BE"&
the.data$B=="SF")
sum(the.data$A=="SE"&
the.data$B=="SF")
sum(the.data$A=="DS"&
the.data$B=="SF")
sum(the.data$A=="BE"&
the.data$B=="S")
sum(the.data$A=="DS"&
the.data$B=="S")
sum(the.data$A=="SE"&
the.data$B=="S")
```

B. Multipliers

```
all.mult = find.mult(alpha  = 0.05, a = 3,
b = 2, dfSSE = nt-a-b+1, g = 3, group = "A")
All.mult
```

C.Pairwise

```
scary.CI =
function(the.data,MSE,equal.weights =
TRUE,multiplier,group,cs){
```

```
 if(sum(cs) != 0 & sum(cs !=0 ) != 1){
return("Error - you did not input a valid
contrast")
}else{
the.means = find.means(the.data)
 the.ns =find.means(the.data,length)
 nt = nrow(the.data)
 a = length(unique(the.data[,2]))
 b = length(unique(the.data[,3]))
if(group =="A"){
if(equal.weights == TRUE){
 a.means = rowMeans(the.means$AB)
 est = sum(a.means*cs)
mul = rowSums(1/the.ns$AB)
SE = sqrt(MSE/b^2 * (sum(cs^2*mul)))
 N = names(a.means)[cs!=0]
CS = paste("(",cs[cs!=0],")",sep = "")
fancy = paste(paste(CS,N,sep
=""),collapse = "+")
 names(est) = fancy
 } else{
 a.means = the.means$A
est = sum(a.means*cs)
SE =
sqrt(MSE*sum(cs^2*(1/the.ns$A)))
N = names(a.means)[cs!=0]
CS = paste("(",cs[cs!=0],")",sep = "")
fancy = paste(paste(CS,N,sep
=""),collapse = "+")
names(est) = fancy
 }
 }else if(group == "B"){
  if(equal.weights == TRUE){
 b.means = colMeans(the.means$AB)
 est = sum(b.means*cs)
 mul = colSums(1/the.ns$AB)
SE = sqrt(MSE/a^2 * (sum(cs^2*mul)))
N = names(b.means)[cs!=0]
CS = paste("(",cs[cs!=0],")",sep = "")
fancy = paste(paste(CS,N,sep
=""),collapse = "+")
 names(est) = fancy
 } else{
b.means = the.means$B
est = sum(b.means*cs)
SE =
sqrt(MSE*sum(cs^2*(1/the.ns$B)))
N = names(b.means)[cs!=0]
CS = paste("(",cs[cs!=0],")",sep = "")
fancy = paste(paste(CS,N,sep
=""),collapse = "+")
names(est) = fancy
}
} else if(group == "AB"){
est = sum(cs*the.means$AB)
SE = sqrt(MSE*sum(cs^2/the.ns$AB))
names(est) = "someAB"
 }
the.CI = est + c(-1,1)*multiplier*SE
results = c(est,the.CI)
names(results) = c(names(est),"lower
bound","upper bound")
return(results)
 }
}
Tuk = find.mult(alpha  = 0.05, a = 3, b =
2, df{SSE} = nt - a*b, g = 3, group = "A")[1]
A.cs.1 = c(1,0,-1)
A.cs.2 = c(1,-1,0)
A.cs.3=c(0,1,-1)
scary.CI(the.data,MSE,equal.weights =
TRUE,Tuk,"A",A.cs.1)
scary.CI(the.data,MSE,equal.weights =
TRUE,Tuk,"A",A.cs.2)
scary.CI(the.data,MSE,equal.weights =
TRUE,Tuk,"A",A.cs.3)
all.mult = find.mult(alpha  = 0.05, a = 3,
b = 2, dfSSE = nt-a-b+1, g = 1, group = "B")
all.mult
Bon = find.mult(alpha  = 0.05, a = 3, b =
2, dfSSE = nt - a-b+1, g = 1, group = "B")[1]
A.cs.1 = c(1,-1)
scary.CI(the.data,MSE,equal.weights =
TRUE,Bon,"B",A.cs.1)
```

D. Contrasts

```
all.mult = find.mult(alpha  = 0.05, a = 3,
b = 2, dfSSE =nt-a-b+1, g = 2, group = "AB")
All.mult
AB.cs = matrix(0,nrow = a, ncol = b)
AB.cs
the.means$AB
AB.cs[3,1] = 1
AB.cs[1,1] = -1/2
AB.cs[2,1]=-1/2
scary.CI(Salary,MSE,equal.weights =
TRUE,Bon,"AB",AB.cs)
AB.cs = matrix(0,nrow = a, ncol = b)
AB.cs
the.means$AB
AB.cs[2,2] = 1
AB.cs[1,1] = -1/2
AB.cs[3,1]=-1/2
```

```
        scary.CI(Salary,MSE,equal.weights =
TRUE,Bon,"AB",AB.cs)
```

D. Regression Formation

```
        names(Salary) = c("Y","A","B")
        thebestS.model = lm(Y ~ A+B,data =
Salary)
        thebestS.model$coefficients
```