Assignment4_stat359

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#Q1. In a study examining smoking and lung cancer, a random sample of men #between the ages of 55 and 60 was obtained. The smoking and disease status of #each sampled subject was ascertained. For each subject, a '1' is assigned if #the subject had lung cancer (case) and a '0' if not. Similarly, a '1' #indicates that a subject is a smoker and a '0' indicates a nonsmoker. #The data are found in the Excel file 'LungCancer'.

#• Read the data into R, and use table() function to produce a contingency #table summarizing these data.

```
LungCancer<-read.csv(file='~/Desktop/stat359/data/LungCancer.csv',header =
TRUE)
observed<-table(LungCancer)
observed

##     Smoker
## Case   0   1
##    0  60 650
##    1  22 687

#• Assuming that there is no association between smoking and lung cancer,
#compute a table of 'expected' counts.

expected <- round(chisq.test(observed)$expected,2)
expected

##     Smoker
## Case     0      1
##    0 41.03 668.97
##    1 40.97 668.03

#I also did this by hand in a different file.


#• By hand, compute the observed value of the test statistic for testing
#association between lung cancer and smoking.
#The result is in a different file

#• Assuming there is no association, what is the distribution of
#the test statistic?

#If there is no association,the distribution of
#the test statistic follows a chi-squared distribution with degrees
```

```
#of freedom equal to (r-1)(c-1) = (2-1)(2-1) = 1

#• Using R, compute the p-value for a test of association, and give a
#detailed conclusion based on the p-value and a comparison of the tables
#observed and expected counts.
1-pchisq(18.63,df = 1)

## [1] 1.587034e-05

#Since p-value = 1.587034e-05 << a = 0 .05, we reject Ho. There is a
significant
#evidence that there is an association between Smokers and Cases of lung
cancer.
#Also from 2 tables I created above, you can see that the number of cases of
the
#lung cancers whose patients are smokers is at least 10 times higher than the
#number of cases of the lung cancers whose patients are non-smokers.
#Therefore the number of cases of the lung cancers is associated with
smoking.
```

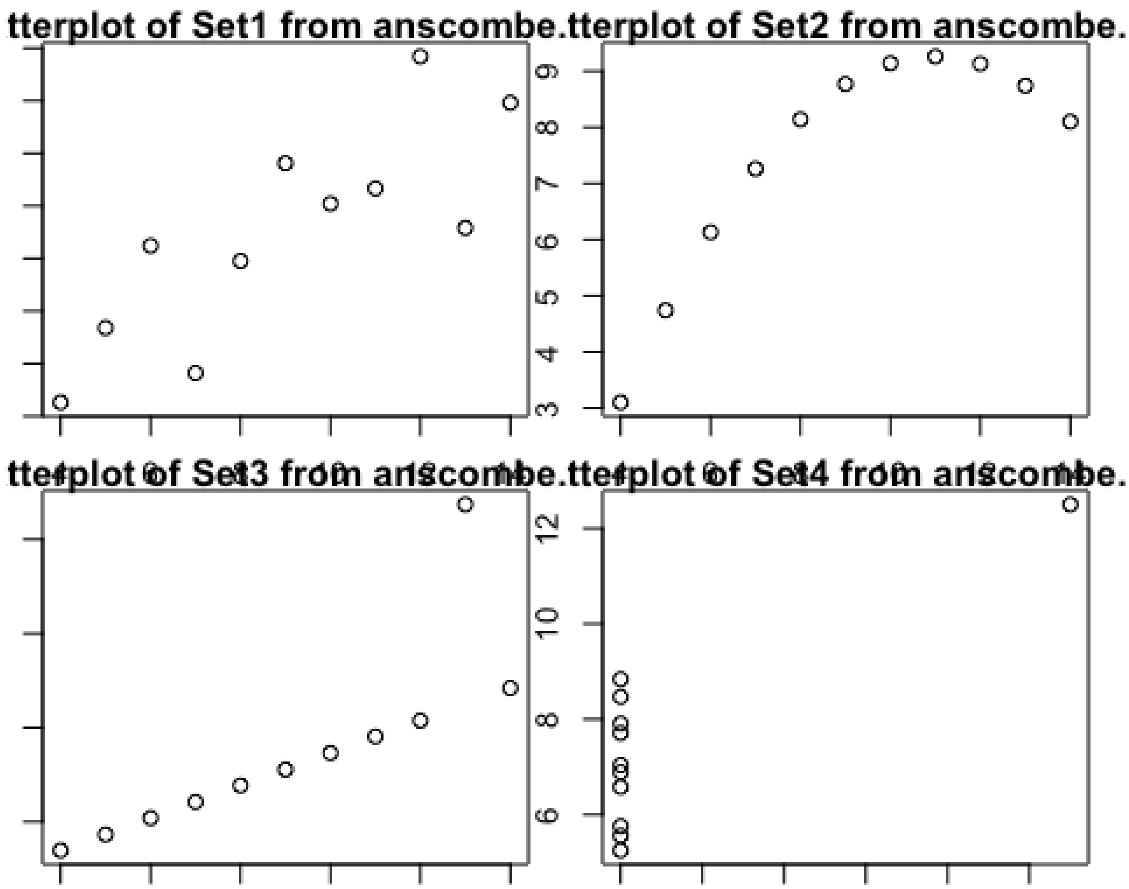
#2. The following data are from a study examining the incidence of tuberculosis #in relation to blood groups in a sample of Eskimos. It is of interest to #determine if there is any association between the disease and blood group #within the ABO system. #Severity O A AB B #Moderate-advanced 7 7 7 13 #Minimal 27 34 12 18 #Not Present 55 52 11 24 #• Assuming that there is no association between disease and blood group, #compute a table of 'expected' counts.

```
data <- c(7,7,7,13,27,34,12,18,55,52,11,24)

data <- c(7, 7, 7, 13, 27, 34, 12, 18, 55, 52, 11, 24)
mat <- matrix(data, nrow = 3, ncol = 4, byrow = TRUE)

# Calculate the expected counts
row_totals <- rowSums(mat)
col_totals <- colSums(mat)
grand_total <- sum(mat)
e_row <- matrix(row_totals, nrow = nrow(mat), ncol = ncol(mat), byrow = TRUE)
e_col <- matrix(col_totals, nrow = nrow(mat), ncol = ncol(mat), byrow =
FALSE)
mat_expected <- e_row * e_col / grand_total

print(mat_expected)
```

```
##           [,1]     [,2]      [,3]     [,4]
## [1,] 11.33333 18.74532 15.955056 11.84270
## [2,] 31.69663 47.33333  7.003745 10.22472
## [3,] 15.95506 11.84270 30.333333 29.25094

#• By hand, compute the observed value of the test statistic for testing association between
#disease and blood group.

#• Assuming there is no association, what is the distribution of the test statistic?
#If there is no association between the disease and blood group,the distribution of
#the test statistic follows a chi-squared distribution with degrees
#of freedom equal to (r-1)(c-1) = (3-1)(4-1) = 6
#• Using R, compute the p-value for a test of association, and give a detailed conclusion
#based on the p-value and a comparison of the tables observed and expected counts.

1-pchisq(q = 16.1427,df=6)

## [1] 0.01300819

#Since p-value = 0.01300819 < a = 0 .05, we reject Ho. There is a significant
#evidence that there is an association between disease and blood group.
#Also from 2 tables,When I see the row Minimal, The number of cases, which severty
# is Minimal, of people whose blood types arebO and A have almost two time as much as
#people whose blood type is AB or B.
```

#3. The file ‘Anscombe’ contains 4 diferent datasets, each of which are based on a response Y, #and a covariate X.

```
ancombe<-read.csv('~/Desktop/stat359/data/anscombe.csv',header=TRUE)




#(a) Produce 4 scatter plots (one for each dataset), on the same page,
#illustrating the relationship between Y and X. Describe each of these
briefly,
#and state if you think a linear
#model of the form yi = a + bxi + ≤i would be appropriate.
#4
ancombe[45:55,2]

##  [1] "6.58" "5.76" "7.71" "8.84" "8.47" "7.04" "5.25" "12.5" "5.56" "7.91"
## [11] "6.89"

par(mar = c(1,1,1,1))
par(mfrow = c(2,2))
plot(ancombe[2:12,1],ancombe[2:12,2], xlab = "The value of x",
     ylab = "The value of y", main = "Scatterplot of Set1 from anscombe.csv",
     sub = "Written by Koki Itagaki")
plot(ancombe[16:26,1],ancombe[16:26,2], xlab = "The value of x",
     ylab = "The value of y", main = "Scatterplot of Set2 from anscombe.csv",
     sub = "Written by Koki Itagaki")
plot(ancombe[30:40,1],ancombe[30:40,2], xlab = "The value of x",
     ylab = "The value of y", main = "Scatterplot of Set3 from anscombe.csv",
     sub = "Written by Koki Itagaki")
plot(ancombe[45:55,1],ancombe[45:55,2], xlab = "The value of x",
     ylab = "The value of y", main = "Scatterplot of Set4 from anscombe.csv",
     sub = "Written by Koki Itagaki")
```




```
#According to the graphs, we can see the different trend of the data.
#Graph 1 shows that there is a positive linear relationships between x and y.
#However, graph 2 is a quadric equation.
#The data from graph 3 also have a  positive relationships between x and y
with
#a outlier at arount x = 13 and y = 14.
#There is not a linear relationships in graph 4.The x value of all data is 8
#except one outlier. it means it does not show any correlation between x and
y.
#Therefore, in my opinion,Graph1 and Graph 3 can be shown as yi = a + bxi +
error


#(b) Perform 4 separate simple linear regressions (one for each dataset)and
#produce a table (in your text editor (ie. word)) that shows the R2 value.
#Discuss what is happening here (hint: for simple linear regression, R2 is
just
#the square of the sample correlation coe±cient).

set1_x<-ancombe[2:12,1]
set1_x<-as.numeric(set1_x)
set1_y<-ancombe[2:12,2]
set1_y<-as.numeric(set1_y)
```

```r
re_set1<-lm(set1_x~set1_y)
re_set1

##
## Call:
## lm(formula = set1_x ~ set1_y)
##
## Coefficients:
## (Intercept)       set1_y
##     -0.9975       1.3328

set2_x<-ancombe[16:26,1]
set2_x<-as.numeric(set2_x)
set2_y<-ancombe[16:26,2]
set2_y<-as.numeric(set2_y)
re_set2<-lm(set2_x~set2_y)
re_set2

##
## Call:
## lm(formula = set2_x ~ set2_y)
##
## Coefficients:
## (Intercept)       set2_y
##     -0.9948       1.3325

set3_x<-ancombe[30:40,1]
set3_x<-as.numeric(set3_x)
set3_y<-ancombe[30:40,2]
set3_y<-as.numeric(set3_y)
re_set3<-lm(set3_x~set3_y)
re_set3

##
## Call:
## lm(formula = set3_x ~ set3_y)
##
## Coefficients:
## (Intercept)       set3_y
##      -1.000        1.333

set4_x<-ancombe[45:55,1]
set4_x<-as.numeric(set4_x)
set4_y<-ancombe[45:55,2]
set4_y<-as.numeric(set4_y)
re_set4<-lm(set4_x~set4_y)
re_set4

##
## Call:
## lm(formula = set4_x ~ set4_y)
```

```
##
## Coefficients:
## (Intercept)       set4_y
##      -1.004        1.334
```

```
summary(re_set1)
```

```
##
## Call:
## lm(formula = set1_x ~ set1_y)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.6522 -1.5117 -0.2657  1.2341  3.8946
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.9975     2.4344  -0.410  0.69156
## set1_y        1.3328     0.3142   4.241  0.00217 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.019 on 9 degrees of freedom
## Multiple R-squared:  0.6665, Adjusted R-squared:  0.6295
## F-statistic: 17.99 on 1 and 9 DF,  p-value: 0.00217
```

```
summary(re_set2)
```

```
##
## Call:
## lm(formula = set2_x ~ set2_y)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.8516 -1.4315 -0.3440  0.8467  4.2017
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.9948     2.4354  -0.408  0.69246
## set2_y        1.3325     0.3144   4.239  0.00218 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.02 on 9 degrees of freedom
## Multiple R-squared:  0.6662, Adjusted R-squared:  0.6292
## F-statistic: 17.97 on 1 and 9 DF,  p-value: 0.002179
```

```
summary(re_set3)
```

```
##
## Call:
```

```
## lm(formula = set3_x ~ set3_y)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.9869 -1.3733 -0.0266  1.3200  3.2133
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.0003     2.4362  -0.411  0.69097
## set3_y        1.3334     0.3145   4.239  0.00218 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.019 on 9 degrees of freedom
## Multiple R-squared:  0.6663, Adjusted R-squared:  0.6292
## F-statistic: 17.97 on 1 and 9 DF,  p-value: 0.002176
```

```
summary(re_set4)
```

```
##
## Call:
## lm(formula = set4_x ~ set4_y)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.7859 -1.4122 -0.1853  1.4551  3.3329
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.0036     2.4349  -0.412  0.68985
## set4_y        1.3337     0.3143   4.243  0.00216 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.018 on 9 degrees of freedom
## Multiple R-squared:  0.6667, Adjusted R-squared:  0.6297
## F-statistic:    18 on 1 and 9 DF,  p-value: 0.002165
```

```
#Dataset R^2
# 1.   0.67
# 2.   0.67
# 3    0.67
# 4.   0.67

#The Rs of all datasets is the same even though the shapes of 4 graphs are
#totally different. For examle, the first graph shows that there is a linear
#moderate relationship and the third graph shows that there is a strong
linear
#relationships with only one outlier. This means if the data set has at least
#one outlier, the correlation rate between x and y changes considerably.
```

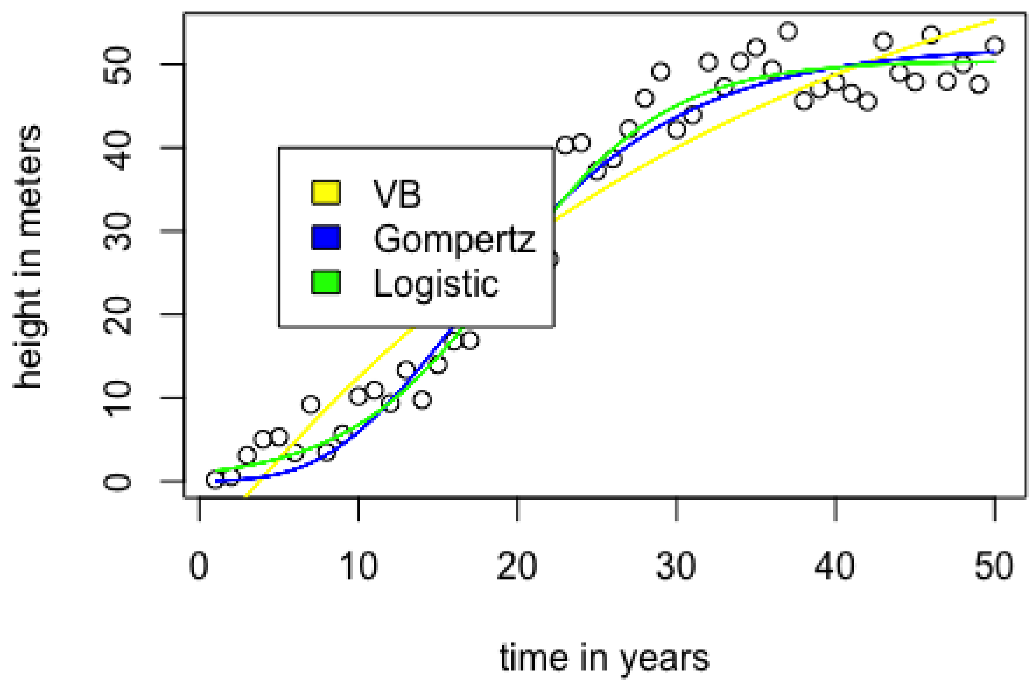
```
#Moreover, the data set 4 shows that quadratic curve and the correlation rate
is also the same as the dataset 1 and 3.
```

#4. The file ‘growth’ gives data on the height of a white spruce #tree measured annually for 50 years. Letting Yt denote the height of the #tree at year t > 0, we consider describing the growth of the tree over time #with a non-linear model Yt = f(t) + ≤t, ≤t iidª N(0;, æ2). Three growth #curves are considered for f(t) #(a) Logistic: f(t) = a/(1 + b § exp{°ct}) #(b) Gompertz: f(t) = a exp{°b exp{°ct}} #(c) Von BertalanÆy: f(t) = a ° a exp{°b(t + c)} #• Fit all three models using the non-linear least squares function nls() in R. #Explain how you are choosing the starting values for nls() in each case. #Produce a figure depicting the estimated curves all on the same plot, along #with the observed data. Be sure to include a legend to distinguish the #diÆerent curves.

```
data <- read.table(file='~/Desktop/stat359/data/growth.txt',header=TRUE)
y <- data$height
t <- data$t
a.start <- max(y)

# Logistic
b.start <- a.start/(min(y))
c.start <- -log((a.start-mean(y))/(b.start*mean(y)))/mean(t)

# Fit logistic model using nls()
logistic <- nls(y ~ a/(1+b*exp(-c*t)),
                start=list(a=a.start, b=b.start, c=c.start),
                trace=TRUE)

## 2180.554    (1.84e+00): par = (53.95014 269.7507 0.2328016)
## 846.6886    (9.29e-01): par = (53.10289 109.7646 0.2177264)
## 495.3645    (3.38e-01): par = (51.69629 64.09383 0.2088176)
## 445.9083    (8.97e-02): par = (50.37352 47.11803 0.2013761)
## 442.5841    (1.02e-02): par = (50.45075 46.50495 0.1984343)
## 442.5424    (1.38e-03): par = (50.41649 47.14147 0.1993367)
## 442.5417    (1.68e-04): par = (50.42135 47.12783 0.1992812)
## 442.5417    (2.05e-05): par = (50.42068 47.13808 0.1992959)
## 442.5417    (2.50e-06): par = (50.42076 47.13769 0.1992949)

# Gompertz
b.start <- -log(min(t)/a.start)
c.start <- -log(-log(mean(y)/a.start)/b.start)/mean(t)
```

```r
# Fit gompertz model using nls()
gompertz <- nls(y ~ a*exp(-b*exp(-c*t)),
                start=list(a=a.start, b=b.start, c=c.start),
                trace=TRUE)

## 1517.220    (1.21e+00): par = (53.95014 3.98806 0.07855924)
## 971.6970    (7.44e-01): par = (48.08192 5.698813 0.1185395)
## 626.9119    (1.35e-01): par = (52.89492 6.410667 0.1143171)
## 616.5275    (4.82e-02): par = (52.14363 7.238899 0.1233726)
## 614.9412    (1.27e-02): par = (52.29073 7.417474 0.1237323)
## 614.8192    (3.98e-03): par = (52.22642 7.534484 0.1246399)
## 614.8067    (1.22e-03): par = (52.22317 7.563496 0.1248037)
## 614.8055    (3.79e-04): par = (52.21911 7.574479 0.1248795)
## 614.8054    (1.18e-04): par = (52.21833 7.577643 0.1248995)
## 614.8054    (3.67e-05): par = (52.21801 7.578676 0.1249064)
## 614.8054    (1.14e-05): par = (52.21792 7.57899 0.1249084)
## 614.8054    (3.54e-06): par = (52.21789 7.579089 0.1249091)

# VB
b.start <- -log((mean(y)-a.start)/(min(y)-a.start))/mean(t)
c.start <- -log((a.start-min(y))/a.start)/b.start

# Fit VB model using nls()
vb <- nls(y ~ a*(1-exp(-b*(t+c))),
          start=list(a=a.start, b=b.start, c=c.start),
          trace=TRUE)

## 3380.398    (1.23e+00): par = (53.95014 0.03424298 0.1084606)
## 2144.571    (7.68e-01): par = (75.10794 0.02491852 -4.467943)
## 1384.782    (1.55e-01): par = (70.49888 0.03103404 -3.733227)
## 1354.408    (3.20e-02): par = (74.91996 0.02883085 -3.728334)
## 1353.121    (5.14e-03): par = (74.15239 0.0295587 -3.772171)
## 1353.094    (1.40e-03): par = (74.48107 0.02933935 -3.757477)
## 1353.093    (4.14e-04): par = (74.39064 0.02940495 -3.761695)
## 1353.092    (1.23e-04): par = (74.41844 0.02938538 -3.760418)
## 1353.092    (3.68e-05): par = (74.41021 0.02939122 -3.760798)
## 1353.092    (1.10e-05): par = (74.41267 0.02938948 -3.760684)
## 1353.092    (3.32e-06): par = (74.41194 0.02939 -3.760718)

#I basically find the unknown parameters:a,b,and c for each cases and pass 
the
#values to the nls function  to calculate



# Define a function to generate predictions from a model
predict_model <- function(model, t_values) {
  predicted_values <- predict(model, list(t = t_values))
  return(predicted_values)
}
```

```r
plot(t, y, xlab = "time in years", ylab = "height in meters")
# predict values for different models
t_seq <- seq(min(t), max(t), 0.01)
H.vb <- predict(vb, list(t = t_seq))
H.gompertz <- predict(gompertz, list(t = t_seq))
H.logistic <- predict(logistic, list(t = t_seq))

# add lines to the plot for each model
lines(t_seq, H.vb, col = "yellow")
lines(t_seq, H.gompertz, col = "blue")
lines(t_seq, H.logistic, col = "green")

# add a legend to the plot
legend(x = 5, y = 40, legend = c("VB", "Gompertz", "Logistic"), fill =
c("yellow", "blue", "green"))
```




```r
#• For each of the three models, give a 95% confidence interval for
limt!1f(t).
#What doest his represent?
z<-1.96
paste("95% CI for the first model is: ",74.411938 -z*9.950934 , 74.411938
+z*9.950934,
  "95% CI for the second model is: ",50.4208-z*0.8473 , 50.4208 +z*0.8473,
```

```
  "95% CI for the third model is: ",52.21789 -z*1.33361 , 52.21789 +z*1.33361
)

## [1] "95% CI for the first model is:  54.90810736 93.91576864 95% CI for
the second model is:  48.760092 52.081508 95% CI for the third model is:
49.6040144 54.8317656"

t.plot <- seq(min(t), max(t), 0.01)



#• Select the best of the three models, and plot an estimate of the
#derivative df(t) dt , which represents the rate of growth over time.

# define variables a, b, and c
a <- 50.4208; b <- 47.1377; c <- 0.1993

# calculate the derivative of Y with respect to time
deriva <- a*b*c*exp(-c * t.plot) / ((1 + b * exp(-c * t.plot))^2)

plot(deriva,main = "estimate of the derivative")
```