506CourseWork

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For the love of god don't forget

Do not display too much raw R output (e.g. don't display the full output of 'summary(model)'), but edit this down to the essentials. Ensure to include justification for each step of your analyses, providing comments alongside your R code to explain what you are doing and add appropriate titles and labelled axes to your plots.

Question 1

We have the model:

$Yi \sim N(\frac{\theta 1xi}{\theta 2+xi}, \sigma^2)$

Question 1 a)

Due to the visible non-linearity of the model, we would be required to significantly transform our data to get a linear model that would have an acceptable fit of the data. We can also see that the response data seems to be only positive while a normal distribution goes from]-∞,∞[. Such arbitrary transformation increases the complexity of the model, making it less interpretable and not respect the nature of the data.

Linear regression models are based on the assumption that the relationship between the independent and dependent variables is linear. If the relationship between the variables is non-linear, a linear regression model may not be appropriate to use. In such cases, transforming the data to make the relationship linear may not result in an accurate representation of the true relationship, and can lead to overfitting or underfitting. Additionally, transforming the data can result in a loss of interpretability of the results, as it can be difficult to understand the meaning of the transformed variables.

Another issue with using a linear regression model for non-linear data is that the residuals, which represent the difference between the observed and predicted values, may not be normally distributed, which is another assumption of linear regression models. This can lead to biased or incorrect results.

In conclusion, when the data is non-linear, a linear regression model may not be the best choice for modelling the relationship between the variables, and alternative methods need to be considered.

// make a graph to show the data is not linear

Question 1 b)

The Yi are independent so the likelihood is a product of the individual pdfs.

TODO GET BETTER WORDING FOR THE REPLACE PART

Likelihood of a normal distribution where $L(yi|\mu,\sigma^2) =$

$= \Pi_{i=1}^{n} fX(yi|\mu,\sigma^2)$

$= \Pi_{i=1}^{n} (2\pi\sigma^2)^{-\frac{1}{2}} * exp(-\frac{1}{2} * \frac{(yi-\mu)^2}{\sigma^2}) =$

$= (2\pi\sigma^2)^{-\frac{n}{2}} * exp(-\frac{1}{2\sigma^2} * \sum_{i=1}^{n}(yi-\mu)^2)$

Replacing the μ with the respective θs and n, we have the likelihood as:

$L(\beta 0, \beta 1, \sigma^2; x, y) =$

$= \prod_{i=1}^{n} p(\beta 0, \beta 1, \sigma^2; x, y) =$

$= (2\pi\sigma^2)^{-\frac{100}{2}} * exp(-\frac{1}{2\sigma^2} * \sum_{i=1}^{100}(yi - \frac{\theta 1xi}{\theta 2+xi})^2)$

The log-likelihood of a normal distribution is:

$l(yi|\mu, \sigma^2) =$

$= ln(L(yi|\mu, \sigma^2)) =$

$= ln((2\pi\sigma^2)^{-\frac{n}{2}} * exp(-\frac{1}{2\sigma^2} * \sum_{i=1}^{n}(yi - \mu)^2)) =$

$= ln((2\pi\sigma^2)^{-\frac{n}{2}}) + ln(exp(-\frac{1}{2\sigma^2} * \sum_{i=1}^{n}(yi - \mu)^2)) =$

$= -\frac{n}{2}ln(2\pi\sigma^2) - \frac{1}{2\sigma^2} * \sum_{i=1}^{n}(yi - \mu)^2) =$

$= -\frac{n}{2}ln(2\pi) - \frac{n}{2}ln(\sigma^2) - \frac{1}{2\sigma^2} * \sum_{i=1}^{n}(yi - \mu)^2)$

Once again replacing the μ with the respective θs and n, we have the log-likelihood as:

$l(\beta 0, \beta 1, \sigma^2; x, y) =$

$= -\frac{100}{2}ln(2\pi) - \frac{100}{2}ln(\sigma^2) - \frac{1}{2\sigma^2} * \sum_{i=1}^{100}(yi - \frac{\theta 1xi}{\theta 2+xi})^2) =$

$= -50ln(2\pi) - 50ln(\sigma^2) - \frac{1}{2\sigma^2} * \sum_{i=1}^{100}(yi - \frac{\theta 1xi}{\theta 2+xi})^2)$

Question 1 c)

```
n = nrow(nlmodel)


### Create a function to evaluate minus the log-likelihood
myLike = function(variables) {

    theta1 = variables[1]  #theta1
    theta2 = variables[2]  #theta2
    sigma = variables[3]  #sigma

    mu = ((theta1 * nlmodel$x)/(theta2 + nlmodel$x))

    # Log-likelihood
    result = (-(n/2) * log(2 * pi)) - ((n/2) * log(sigma^2)) - (1/(2 * (sigma^2))) *
        (sum((nlmodel$y - mu)^2))

    # Returning negative log-likelihood
    return(-result)
}
```

Question 1 d)

From the graph data we can clearly see that the deviantion is approximatly 15 from the value scatter which is easier to destinguish and measure between the $[0.5, 1]$ interval. We can observethat when x -> 1 y is approximately 210 and as x -> 0 y is approximately to 50

To determine the thetas we will first see see that when x approximates to zero we can observe that:

$\lim\limits_{x->0} \frac{\theta 1 xi}{\theta 2 + xi} \implies \frac{1}{\theta 2}$

As such \$ Y\$ ~ $N(\frac{\theta 1 xi}{\theta 2 + xi})$ becomes \$ 50\$ ~ $\frac{1}{\theta 2}$

Solving it for $\theta 2$ we get $\theta 2 = 1/50 \iff \theta 2 = 0.02$

Now that we have theta2 we can use the approximation of x to 1 to determine the value of $\theta 1$

$\lim\limits_{x->1} \frac{\theta 1 xi}{\theta 2 + xi} \implies \frac{\theta 1}{\theta 2 + x}$

As such \$ Y\$ ~ $N(\frac{\theta 1 xi}{\theta 2 + xi})$ becomes 215 ~ $\frac{\theta 1 * 1}{\theta 2 + 1}$

Solving it for $\theta 1$ we get $\theta 1 = 215/1.02 \iff \theta 1 \approx 210.7$

```
# Estimating the MLE
out <- nlm(myLike,
  p = c(210.7,0.02,15), #plugging in the starting values
  hessian = T,
  iterlim = 10000,
  steptol = 1e-10)

# Reporting estimates
variableEstimates = out$estimate
out$estimate
```

```
[1] 214.65008415   0.06353447  13.61564428
```

Question 1 e)

```
# Invert the negated Hessian to obtain the Observed Information Matrix
OIM <- solve(out$hessian)

# The diagonal entries are the variances of beta0 and beta1
# respectively so # obtain them
```

```r
VarianceBeta <- diag(OIM)

# and then square root them to obtain standard errors
stand_error <- sqrt(VarianceBeta)

# reporting standard errors
stand_error
```

```
[1] 2.674798031 0.005140379 0.963024267
```

The formula to calculate a 99% confidence interval is: $\pm$ 2.576 * SE( )

```r
# Estimating CIs
CIs <- cbind(variableEstimates - 2.576 * stand_error, variableEstimates +
    2.576 * stand_error)

# Reporting the CIs
CIs
```

```
             [,1]         [,2]
[1,] 207.75980442 221.54036388
[2,]   0.05029285   0.07677609
[3,]  11.13489377  16.09639479
```

Question 1 f)

H0 : $2 = 0{,}08$ vs. H1 : $2 \neq 0$

```r
## Hypothesis thesis without using confidence interval

z_stat <- (variableEstimates[2] - 0.08)/stand_error[2]

# Print the test values
z_stat  ## significance tests
```

```
[1] -3.203174
```

So now we need to decide if this value of the z-statistic is extreme at the 10% significance level

```r
### Note that equivalently we can look at the 95% quantile of N(0,1)
qnorm(0.95, 0, 1)
```

```
[1] 1.644854
```

```r
qnorm(0.05, 0, 1)
```

```
[1] -1.644854
```

As we can see the value from the z-statistician test is considerably lower than -1,645, meaning that it is an extreme value and therefore rejecting the null hypothesis that $\theta 2$ is 0,08.

Question 1 g)

```r
# Plotting initial starting guess
xx <- seq(0, 1, len = 200)

# Estimating mean relationship (mean mu = )
mu <- exp(out$estimate[1] * xx + out$estimate[2])

# Getting alpha (shape parameter)
shape <- out$estimate[3]

# Getting lambda (scale parameter)
scale <- mu/shape


## ploting associated mean relationship

# ggplot(data = nlmodel, aes(x = x, y = y)) + geom_point() +
# geom_smooth(method = 'lm', se = FALSE, color = 'red') + labs(title =
# 'Scatter Plot of y vs. x with Fitted Line and Prediction Intervals',
# x = 'x', y = 'y')
```

Question 2

Model 1:

$Yi \sim Pois(\lambda i)$

$log(\lambda i) = \beta 0 + \beta 1xi$

Model 2:

$Yi \sim N(\mu i, \sigma^2)$

$log(\mu i) = \gamma 0 + \gamma 1xi$

Question 2 a)

As we can from the graph and what we can determine from the nature of the data represented in such graph the recorded number of AIDS cases is a count variable and the counts are non-negative integers.

The first model, a Poisson distribution, would be a more appropriate choice. The Poisson distribution is a discrete distribution that models count data which respects the nature of the data

The second model, a Normal distribution, would not be the best fit since its range is from]-∞,∞[and expects continuous values, not respecting the nature of the data.

The log-link function in both models ensures that the predicted values are always positive. //TODO redo this pls

Question 2 b)

The Yi are independent so the likelihood is a product of the individual pdfs.

$L(\theta 1, theta2, \sigma^2; y, x)$

```
# Fitting in R model < -glm(< response > < covariates >,data = <data>,
# family = gaussian(link='identity')) model <- glm(<response>
# <covariates>, data = <data>, family = poisson(link='log'))


# Fitting model 2 pois.model <- glm(ca ~ offset(logcells) + doseamt +
# doserate, data = dicentric, family = poisson(link='log'))

model2 = glm(cases ~ date, data = aids, family = poisson(link = "log"))
```

```r
# Summarise the model
summary(model2)
```

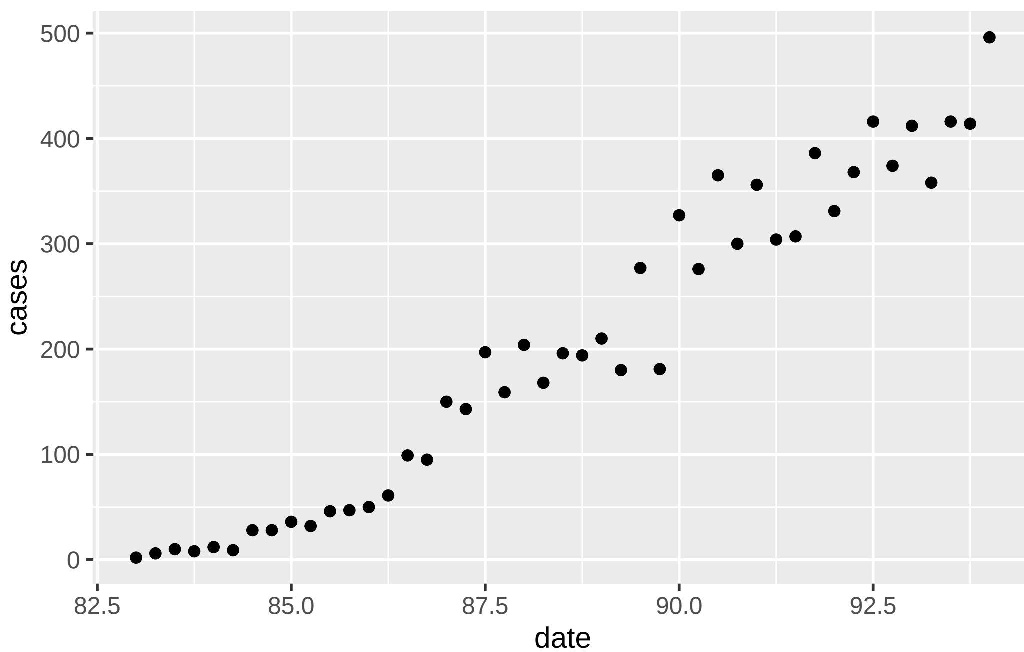
```
Call:
glm(formula = cases ~ date, family = poisson(link = "log"), data = aids)

Deviance Residuals: 
   Min      1Q  Median      3Q     Max  
-7.768  -4.042  -0.335   3.048   7.281  

Coefficients:
              Estimate Std. Error z value Pr(>|z|)    
(Intercept) -16.875879   0.350353  -48.17   <2e-16 ***
date          0.247169   0.003856   64.10   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 5738.16  on 44  degrees of freedom
Residual deviance:  854.02  on 43  degrees of freedom
AIC: 1153.9

Number of Fisher Scoring iterations: 5
```

```r
# Fitting model 1
model1 = glm(cases ~ date, data = aids, family = gaussian(link = "identity"))

# Summarise the model
summary(model1)
```

```
Call:
glm(formula = cases ~ date, family = gaussian(link = "identity"), 
    data = aids)

Deviance Residuals: 
    Min       1Q   Median       3Q      Max  
-75.018  -21.703   -4.756   25.350   75.824  

Coefficients:
```

```
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -3711.854    134.163  -27.67   <2e-16 ***
date           44.210      1.515   29.18   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 1088.729)

    Null deviance: 974004  on 44  degrees of freedom
Residual deviance:  46815  on 43  degrees of freedom
AIC: 446.33

Number of Fisher Scoring iterations: 2
```

```r
## plotting the models

## this is the original data to then plot the models on top of
ggplot(aids, aes(x = date, y = cases)) + geom_point()
```




```r
# plot(model2) plot(model1)
```

```r
confint(model1, level = 1 - 0.05)
```

```
Waiting for profiling to be done...
```

```
                  2.5 %      97.5 %
(Intercept) -3974.80950 -3448.89836
date           41.24102    47.17953
```

```r
confint(model2, level = 1 - 0.05)
```

```
Waiting for profiling to be done...
```

```
                 2.5 %     97.5 %
(Intercept) -17.564979 -16.191587
date          0.239636   0.254751
```

```r
# As we are modelling an unbounded count we use Poisson distribution.
# The data increases exponentially so we use a log-link with a model
# linear in time.
```