Covid-19 Predictions and Time Series Forecasting

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The goal of this project is to make predictions about Covid-19. It is made up of three parts

I) Investigating the number of hospitalizations

2) Predicting who will be hospitalized

3) Forecasting when a country will peak

First, importing and reading the data.

In [159]:
```
data <- read.csv('diagnosis-of-covid-19-and-its-clinical-spectrum.csv')
```

In [160]:
```
head(data)
length(data)
```

	patient_id	patient_age_quantile	sars_cov_2_exam_result	patient_addmite
	<fct>	<int>	<fct>	<fct>
1	44477f75e8169d2	13	negative	f
2	126e9dd13932f68	17	negative	f
3	a46b4402a0e5696	8	negative	f
4	f7d619a94f97c45	5	negative	f
5	d9e41465789c2b5	15	negative	f
6	75f16746216c4d1	9	negative	f

111

Checking for missing values using the 'questionr' library.

In [47]:
```
#if not already installed please install package
install.packages('questionr')
```

```
The downloaded binary packages are in
        /var/folders/hb/6zq315r16hn_lj34r4s5cqhh0000gn/T//RtmpAGtdO
M/downloaded_packages
```

In [161]:
```
library(questionr)
missingvaluestable <- freq.na(data)
missingvaluestable
```

	missing	%
mycoplasma_pneumoniae	5644	100
urine_sugar	5644	100
partial_thromboplastin_time_ptt	5644	100
prothrombin_time_pt_activity	5644	100
d_dimer	5644	100
fio2_venous_blood_gas_analysis	5643	100
vitamin_b12	5641	100
lipase_dosage	5636	100
albumin	5631	100
arteiral_fio2	5624	100
phosphor	5624	100
ferritin	5621	100
arterial_lactic_acid	5617	100
hb_saturation_arterial_blood_gases	5617	100
pco2_arterial_blood_gas_analysis	5617	100
base_excess_arterial_blood_gas_analysis	5617	100
ph_arterial_blood_gas_analysis	5617	100
total_co2_arterial_blood_gas_analysis	5617	100
hco3_arterial_blood_gas_analysis	5617	100
po2_arterial_blood_gas_analysis	5617	100

cto2_arterial_blood_gas_analysis	5617	100
magnesium	5604	99
ionized_calcium	5594	99
urine_density	5574	99
urine_red_blood_cells	5574	99
relationship_patient_normal	5553	98
rods	5547	98
segmented	5547	98
promyelocytes	5547	98
metamyelocytes	5547	98
⋮	⋮	⋮
coronavirus_hku1	0	0
parainfluenza_3	0	0
chlamydophila_pneumoniae	0	0
adenovirus	0	0
parainfluenza_4	0	0
coronavirus229e	0	0
coronavirusoc43	0	0
inf_a_h1n1_2009	0	0
bordetella_pertussis	0	0
metapneumovirus	0	0
parainfluenza_2	0	0
influenza_b_rapid_test	0	0
influenza_a_rapid_test	0	0
strepto_a	0	0
myeloblasts	0	0
urine_esterase	0	0
urine_aspect	0	0
urine_ph	0	0

urine_hemoglobin	0	0
urine_bile_pigments	0	0
urine_ketone_bodies	0	0
urine_nitrite	0	0
urine_urobilinogen	0	0
urine_protein	0	0
urine_leukocytes	0	0
urine_crystals	0	0
urine_hyaline_cylinders	0	0
urine_granular_cylinders	0	0
urine_yeasts	0	0
urine_color	0	0

About half of the dataset is near 100% missing values. Since I will be examning hospitalizations I will slect the relevant variables that do not have the majority of their values missing.

In [49]:
```
install.packages('dplyr')
```

```
The downloaded binary packages are in
        /var/folders/hb/6zq315r16hn_lj34r4s5cqhh0000gn/T//RtmpAGtdO
M/downloaded_packages
```

In [50]:
```
library(dplyr)
data1 <- data[,1:6]
#data1 <- data %>% select(patient_id, patient_age_quantile, sars_co
v_2_exam_result,
                #patient_addmited_to_regular_ward_1_yes_0_no, patie
nt_addmited_to_semi_intensive_unit_1_yes_0_no,
                #patient_addmited_to_intensive_care_unit_1_yes_0_no
)
```

Next, I will examine the structure of the variables in our dataframe.

In [51]:
```
str(data1)
```

```
'data.frame':   5644 obs. of  6 variables:
 $ patient_id                                          : Factor w/ 56
44 levels "001646dfe0e98df",..: 1589 452 3670 5458 4844 2666 1009 1
833 3122 2187 ...
 $ patient_age_quantile                                : int  13 17 8
5 15 9 13 16 1 17 ...
 $ sars_cov_2_exam_result                              : Factor w/ 2
levels "negative","positive": 1 1 1 1 1 1 1 1 1 1 ...
 $ patient_addmited_to_regular_ward_1_yes_0_no         : Factor w/ 2
levels "f","t": 1 1 1 1 1 1 1 1 1 1 ...
 $ patient_addmited_to_semi_intensive_unit_1_yes_0_no: Factor w/ 2
levels "f","t": 1 1 1 1 1 1 1 1 2 1 ...
 $ patient_addmited_to_intensive_care_unit_1_yes_0_no: Factor w/ 2
levels "f","t": 1 1 1 1 1 1 1 1 1 1 ...
```

Next, I will encode variables as numeric values. This way calculations can be done with the values. Later on in the project I will be using Random Forest to train and make predictions. It is important to note there is no need for encoding when using Random Forest.

In [52]:
```
data1$sars_cov_2_exam_result <- as.numeric(data1$sars_cov_2_exam_re
sult)
data1$patient_addmited_to_regular_ward_1_yes_0_no <- as.numeric(dat
a1$patient_addmited_to_regular_ward_1_yes_0_no)
data1$patient_addmited_to_semi_intensive_unit_1_yes_0_no <- as.nume
ric(data1$patient_addmited_to_semi_intensive_unit_1_yes_0_no)
data1$patient_addmited_to_intensive_care_unit_1_yes_0_no <- as.nume
ric(data1$patient_addmited_to_intensive_care_unit_1_yes_0_no)
```

In [53]:
```
data1 <- data1[-1] #removing PatientID: not helpful when making pre
dictinos
str(data1)
```

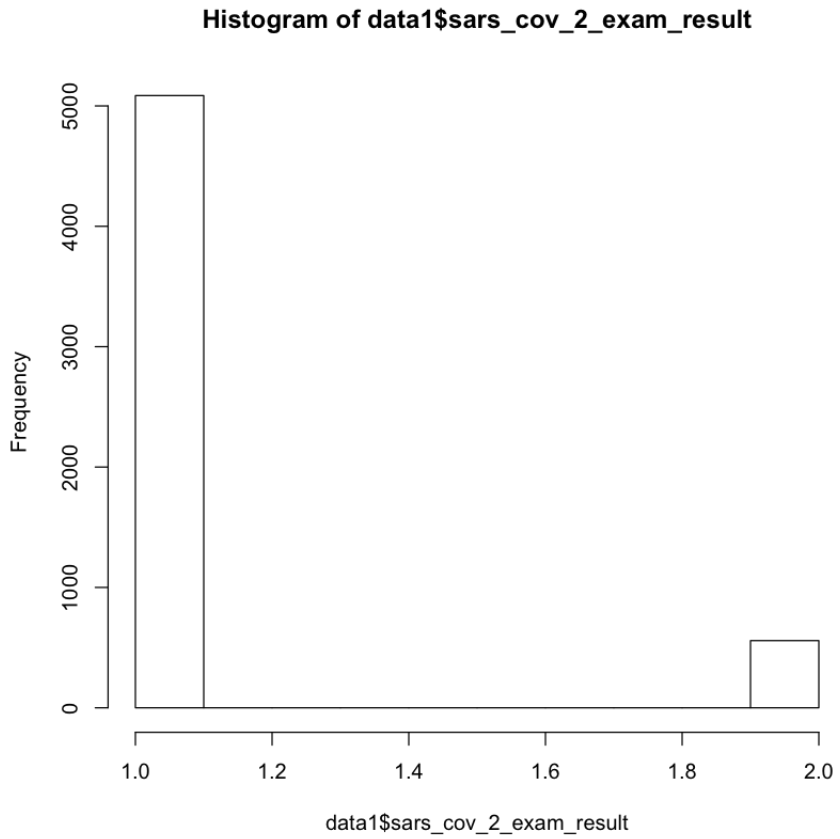
```
'data.frame':   5644 obs. of  5 variables:
 $ patient_age_quantile                                : int  13 17 8
5 15 9 13 16 1 17 ...
 $ sars_cov_2_exam_result                              : num  1 1 1 1
1 1 1 1 1 1 ...
 $ patient_addmited_to_regular_ward_1_yes_0_no         : num  1 1 1 1
1 1 1 1 1 1 ...
 $ patient_addmited_to_semi_intensive_unit_1_yes_0_no: num  1 1 1 1
1 1 1 1 2 1 ...
 $ patient_addmited_to_intensive_care_unit_1_yes_0_no: num  1 1 1 1
1 1 1 1 1 1 ...
```

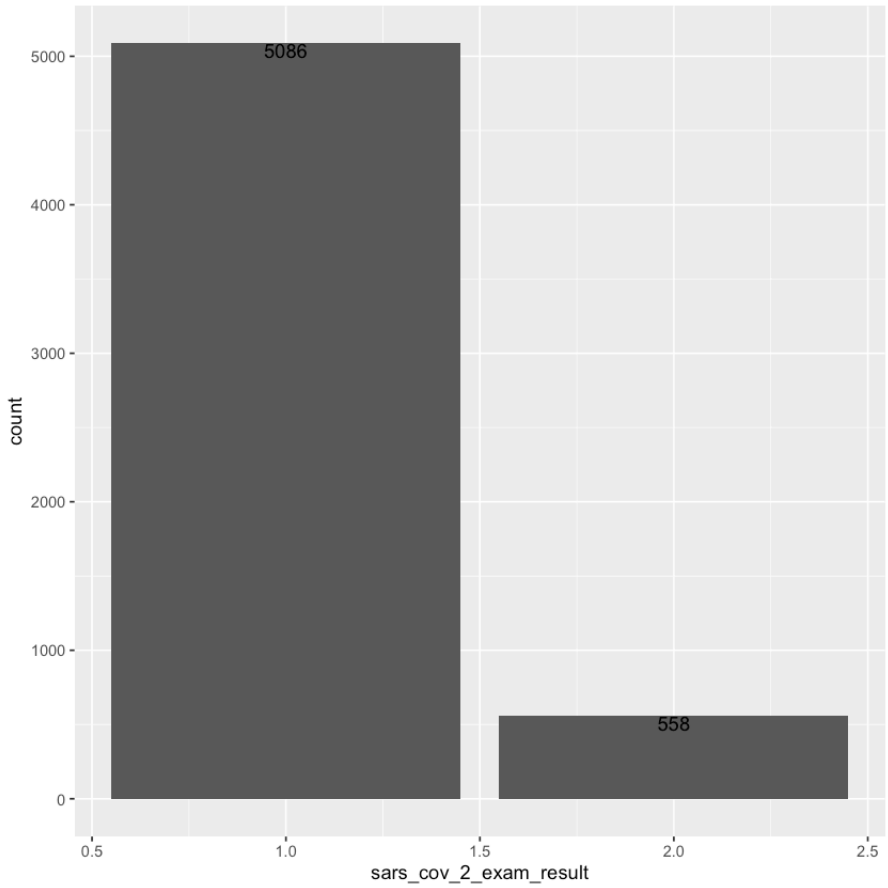
Now that the data is structured properly, the number of hospitalizations can be investigated.

I) Investigating the number of hospitalizations

First I will attempt to plot the exam results

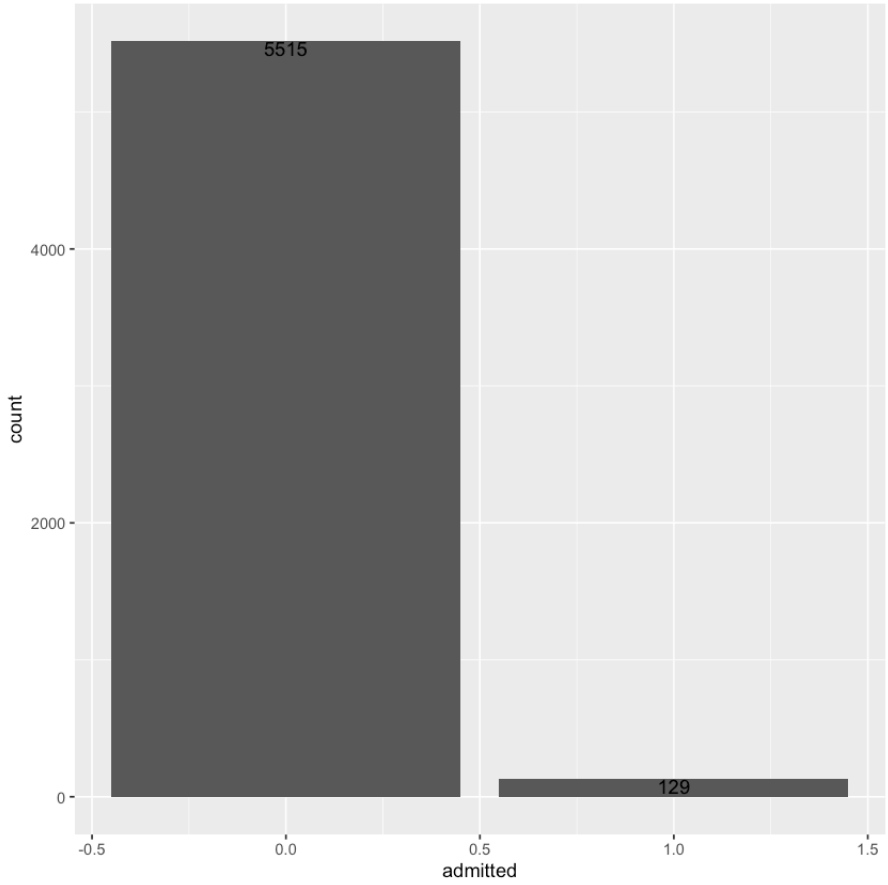
In [54]:
```
hist(data1$sars_cov_2_exam_result) #the plot is viewing this as num
eric
library(ggplot2)
plot1 <- ggplot(data=data1, aes(x=sars_cov_2_exam_result, fill=sars
_cov_2_exam_result)) + geom_bar()
plot1 <- plot1 +geom_text(stat = 'count', aes(label = ..count..),
vjust=1) #Adding data labels here
plot1
```





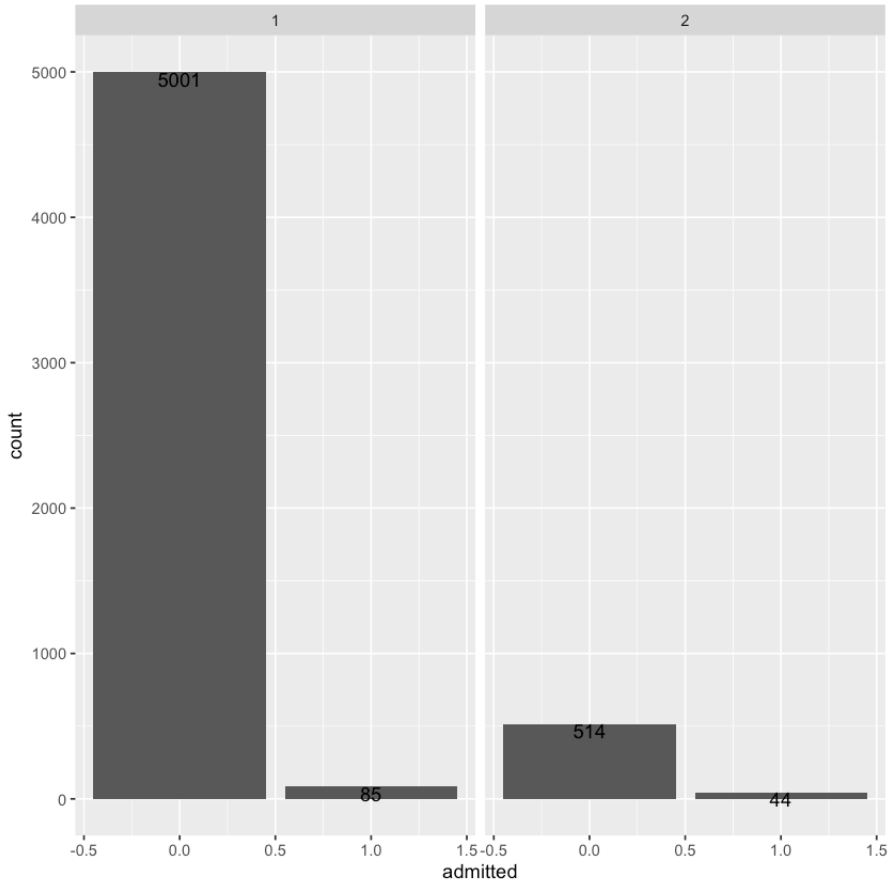
The plot is currently being viewed as numeric. I would like to know who out of these individuals were admitted for hospitalization. For this reason, I will create a colum describing whether a person has been admitted or not. Then, I will plot the admitted column

In [55]:
```
data1$admitted <- ifelse(data1$patient_addmited_to_regular_ward_1_yes_0_no+data1$patient_addmited_to_regular_ward_1_yes_0_no+
                           data1$patient_addmited_to_semi_intensive_unit_1_yes_0_no>3, 1, 0)
plot2 <- ggplot(data=data1, aes(x=admitted, fill=admitted)) +
geom_bar()
plot2 <- plot2 +geom_text(stat = 'count', aes(label = ..count..), vjust=1) #Adding data labels here
plot2
```



Now, the admitted colum can be segmented by the individuals exam result. This will be done using facet_wrap.

In [56]:
```
plot3 <- ggplot(data=data1, aes(x=admitted, fill=admitted)) +
geom_bar() +facet_wrap(~sars_cov_2_exam_result)
plot3 <- plot3 + geom_text(stat = 'count', aes(label = ..count..),
vjust=1) #Adding data labels here
plot3
```



I would like to understand the relationship between testing and admittance. For correlation, the variable has to be numeric (it is not compatable with binary or categorical variables). Since testing and admittance are binomial you would need to preform regression and calssification.

To deal with this, I will change the admitted coloum to categorical.

In [121]:
```
data1$admitted <- as.factor(data1$admitted)
```

2) Predicting who will be hospitalized

To make predictions on who will be admitted, I need to preform classification. Classification is a good fit when the response variable is categorical.

To fully understand the power and weaknesses of forecasting I will do the following:

1) Use a decision trees classifier

2) Use random forest classifier

3) Examine the ROC curve

4) Fix the unbalanced data set

5) Preform K-fold validation

6) Make predictions!!!

Decision Tree:

In [58]:
```
require(tree)
```

In [59]:
```
tree.admitted <- tree(admitted~ sars_cov_2_exam_result +
patient_age_quantile, data=data1)
summary(tree.admitted)
```

```
Classification tree:
tree(formula = admitted ~ sars_cov_2_exam_result + patient_age_quan
tile,
    data = data1)
Number of terminal nodes:  5
Residual mean deviance:  0.1898 = 1070 / 5639
Misclassification error rate: 0.02286 = 129 / 5644
```

Interpretation of the mean deviance: The mean deviance is a measure of the error in the tree after construction. The residual mean deviance here is about 0.189 Next, I would like to check the accuracy of our prediction. To do this I will subract the misclassification error rate by 1.

In [60]:
```
acc <- 1-0.022
acc
```

```
0.978
```

An accuracy around 98% tells me something is wrong within the data itself. One reason for this could be an imbalanced dataset. If 99% of the response variable is 1(admitted) and only 1% is 0(not admitted) then the decision tree may classify everyone as admitted. The tree here does not really learn the pattern. To take care of this issue the data needs to be balanced.

Lets make predictions just for fun!

In [61]:
```
y_pred <- predict(tree.admitted, newdata=data1)
y_pred # woops our class(data1$admitted) is numeric. This means the
decision tree regressed not classified
```

	0	1
1	0.9900332	0.009966777
2	0.9900332	0.009966777
3	0.9900332	0.009966777
4	0.9900332	0.009966777
5	0.9900332	0.009966777
6	0.9900332	0.009966777
7	0.9900332	0.009966777
8	0.9900332	0.009966777
9	0.9900332	0.009966777
10	0.9900332	0.009966777
11	0.9900332	0.009966777
12	0.9900332	0.009966777
13	0.9900332	0.009966777
14	0.9900332	0.009966777
15	0.9900332	0.009966777
16	0.9900332	0.009966777
17	0.9900332	0.009966777
18	0.9900332	0.009966777
19	0.9900332	0.009966777
20	0.9900332	0.009966777
21	0.9339339	0.066066066

22	0.9900332	0.009966777
23	0.9900332	0.009966777
24	0.9900332	0.009966777
25	0.9900332	0.009966777
26	0.9900332	0.009966777
27	0.9900332	0.009966777
28	0.9900332	0.009966777
29	0.9900332	0.009966777
30	0.9900332	0.009966777
⋮	⋮	⋮
5615	0.9243697	0.075630252
5616	0.9900332	0.009966777
5617	0.9900332	0.009966777
5618	0.9900332	0.009966777
5619	0.9900332	0.009966777
5620	0.8612100	0.138790036
5621	0.9900332	0.009966777
5622	0.9900332	0.009966777
5623	0.9900332	0.009966777
5624	0.9900332	0.009966777
5625	0.8612100	0.138790036
5626	0.9900332	0.009966777
5627	0.9819495	0.018050542
5628	0.9819495	0.018050542
5629	0.9900332	0.009966777
5630	0.8612100	0.138790036
5631	0.9900332	0.009966777
5632	0.8612100	0.138790036
5633	0.8612100	0.138790036

5634	0.9819495	0.018050542
5635	0.8612100	0.138790036
5636	0.9900332	0.009966777
5637	0.9900332	0.009966777
5638	0.9900332	0.009966777
5639	0.9900332	0.009966777
5640	0.9819495	0.018050542
5641	0.9900332	0.009966777
5642	0.9900332	0.009966777
5643	0.9900332	0.009966777
5644	0.8612100	0.138790036

Splitting the data into training and test sets using caTools library

In [65]:
```
library(caTools)
set.seed(123)
split <- sample.split(data1$admitted, SplitRatio=0.75)
training_set <- subset(data1, split==TRUE)
test_set <- subset(data1, split==FALSE)
```

Checking that the data was split properly!

In [66]:
```
nrow(training_set)
nrow(test_set)
```

4233

1411

I could apply decision trees again but I will move onto Random Forest. Random Forest is an ensembling technique that creates multiple decision trees. Random Forest is capable of regression and classification. Random Forest's forecasting ability will be tested later on.

Random Forest:

In [68]:
```
library(randomForest)
set.seed(123)
classifier <- randomForest(admitted~ sars_cov_2_exam_result+
patient_age_quantile, data=data1,
                           ntree=400, importance=TRUE)
```

Next, I will make predictions on the test results

In [70]:
```
y_pred <- predict(classifier, newdata=test_set[,-6])
```

Examining the results using a confusion matrix:

In [71]:
```
con_matrix <- table(y_pred, test_set[,6])
con_matrix #Making one sided prediction
accuracy <- ((con_matrix[[1,1]]+con_matrix[[2,2]])/sum(con_matrix))
accuracy
```

```
y_pred    0    1
     0 1379   32
     1    0    0
```

0.977321048901488

Again, the accuracy is a bit concerning. I will take a look at the ROC curve.

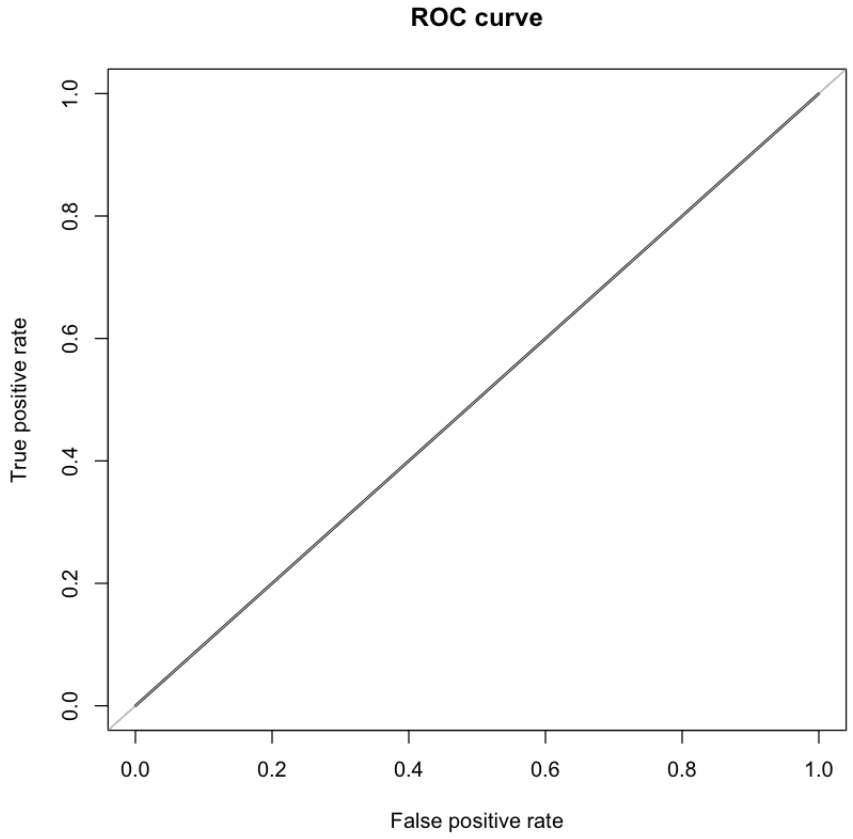
ROC Analysis:

In [72]:
```
install.packages('ROSE')
```

```
The downloaded binary packages are in
        /var/folders/hb/6zq315r16hn_lj34r4s5cqhh0000gn/T//RtmpAGtdO
M/downloaded_packages
```

In [73]:
```
library(ROSE)
roc.curve(test_set[,6], y_pred, plotit = TRUE)
```

```
Loaded ROSE 0.0-3


Area under the curve (AUC): 0.500
```



ROC Analysis: The area under the curve is .5. This is the worst possible situation to be in. It means that the model is unable to distinguish between the positive and negative class.

I will attempt to balance the dataset.

Balancing Data: An over sampling method

In [74]:
```
library(caret)
library(rpart)
tab <- table(data1$admitted)
tab #the current imbalanced data
```

```
Loading required package: lattice


   0    1 
5515  129 
```

In [76]:
```
data2<-data1[,c(1,2,6)]
data2$sars_cov_2_exam_result <- as.factor(data2$sars_cov_2_exam_res
ult)
tab <- table(data2$admitted)
tab
```

```
   0    1 
5515  129 
```

In [77]:
```
data.over <- ovun.sample(admitted~. , data=data2, method="over", N=
11030)$data
tab <- table(data.over$admitted)
tab
```

```
   0    1 
5515 5515 
```

Now, I can apply Random Forest again and compare the results with the unbalanced classifier.

In [78]:
```
library(caTools)
split = sample.split(data.over, SplitRatio = 0.75)
training_set = subset(data.over, split==TRUE)
test_set = subset(data.over, split==FALSE)
```

In [82]:
```
library(randomForest)
set.seed(123)
classifier = randomForest(admitted~., data= training_set,
                          ntree = 400, imporance=TRUE)
```

Now, I will preict results

In [84]:
```
y_pred = predict(classifier, newdata = test_set[,-3]) #3 is where a
dmitted (response) var is
```

Creating a confusion matric to see predictions

In [85]:
```
con_matrix <- table(y_pred, test_set[,3])
con_matrix
accuracy <- ((con_matrix[[1,1]]+con_matrix[[2,2]])/sum(con_matrix))
accuracy
```

```
y_pred    0    1
     0 1535  645
     1  304 1193
```

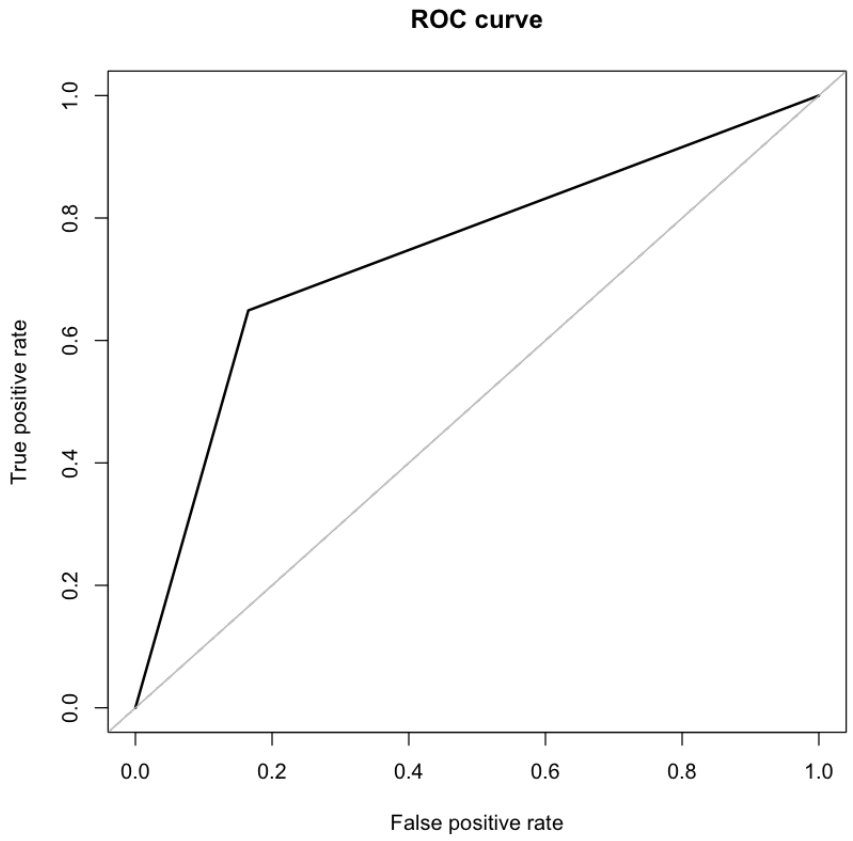
0.741909165080228

This looks much better. Although the accuracy decreased, the model is actually showing it can distinguish between predicting the outcome. Accuracy is now 74%

Let's investigate the precision and recall

In [86]:
```
accuracy.meas(test_set[,3], y_pred)
roc.curve(test_set[,3], y_pred, plotit = TRUE)
```

```
Call:
accuracy.meas(response = test_set[, 3], predicted = y_pred)

Examples are labelled as positive when predicted is greater than 0.
5

precision: 0.500
recall: 1.000
F: 0.333
Area under the curve (AUC): 0.742
```



The ROC curve now shows an AUC of .742. This is an accuracy of about 74% As you can see, this is a much better model then before. The model has about a 74% chance of distinguishing between the positive and negative class.

Further Analysis:

If a patient is in the 17th age quantile and goes in for the test , will they be admitted?

There are two different ways to approach this question. One, I could make my own data row to predict: this is difficult because to compare results you will need to assume a value for admitted. Two, I could filter out the criteria I want from the test set! I will chose to show example two.

Filtering out the criteria from the test set

In [116]:
```
test3 <-  filter(test_set, patient_age_quantile== 17)
```

Next, predict results

In [117]:
```
y_pred3 = predict(classifier, newdata = test3[,-3])
```

In [118]:
```
con_matrix <- table(y_pred3, test3[,3])
con_matrix
accuracy <- ((con_matrix[[1,1]]+con_matrix[[2,2]])/sum(con_matrix))
accuracy
```

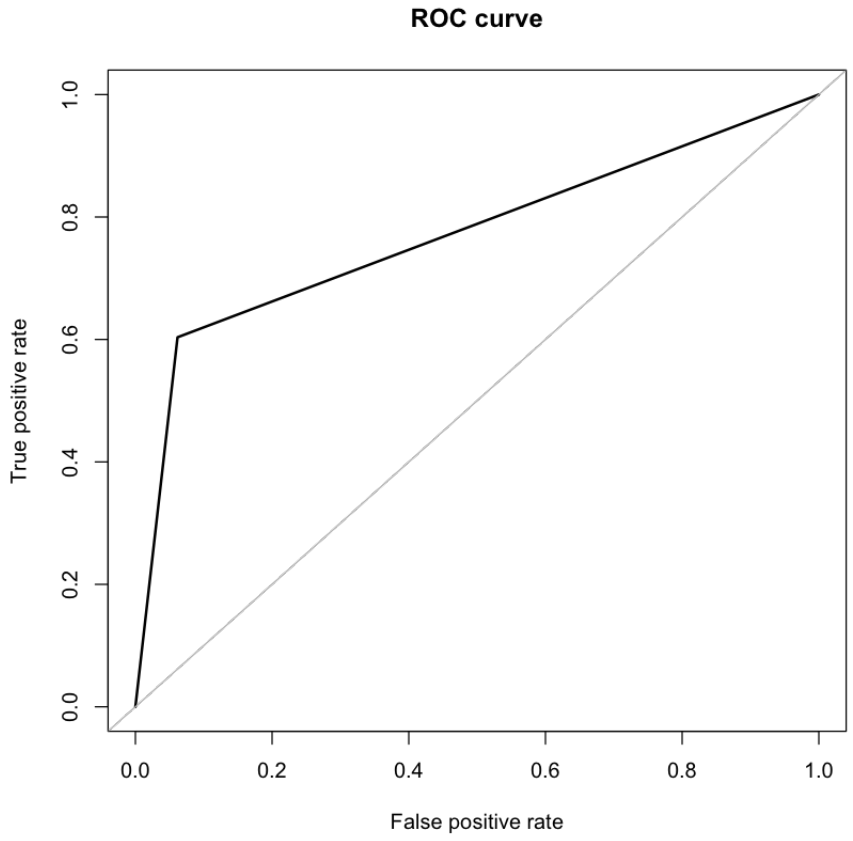
```
y_pred3  0  1
      0 76 44
      1  5 67
```

0.744791666666667

Here the accuracy is about 74.4%. This is a pretty good prediction.

In [119]:
```
roc.curve(test3[,3], y_pred3, plotit = TRUE)
```

```
Area under the curve (AUC): 0.771
```



The ROC curve again, reasures us that the model is making a good prediction.

Finaly, I will preform K-Fold Validation

In [120]:
```
library(caret)
set.seed(123)
train.control <- trainControl(method = "cv", number = 10)

#Train the model
model <- train(admitted ~ patient_age_quantile +
sars_cov_2_exam_result, data = data2,
               method = "rf", trControl = train.control)

#Summarize the results
print(model)
```

```
note: only 1 unique complexity parameters in default grid. Truncati
ng the grid to 1 .

Random Forest

5644 samples
   2 predictor
   2 classes: '0', '1'

No pre-processing
Resampling: Cross-Validated (10 fold)
Summary of sample sizes: 5079, 5079, 5080, 5080, 5079, 5080, ...
Resampling results:

  Accuracy   Kappa
  0.9771443  0

Tuning parameter 'mtry' was held constant at a value of 2
```

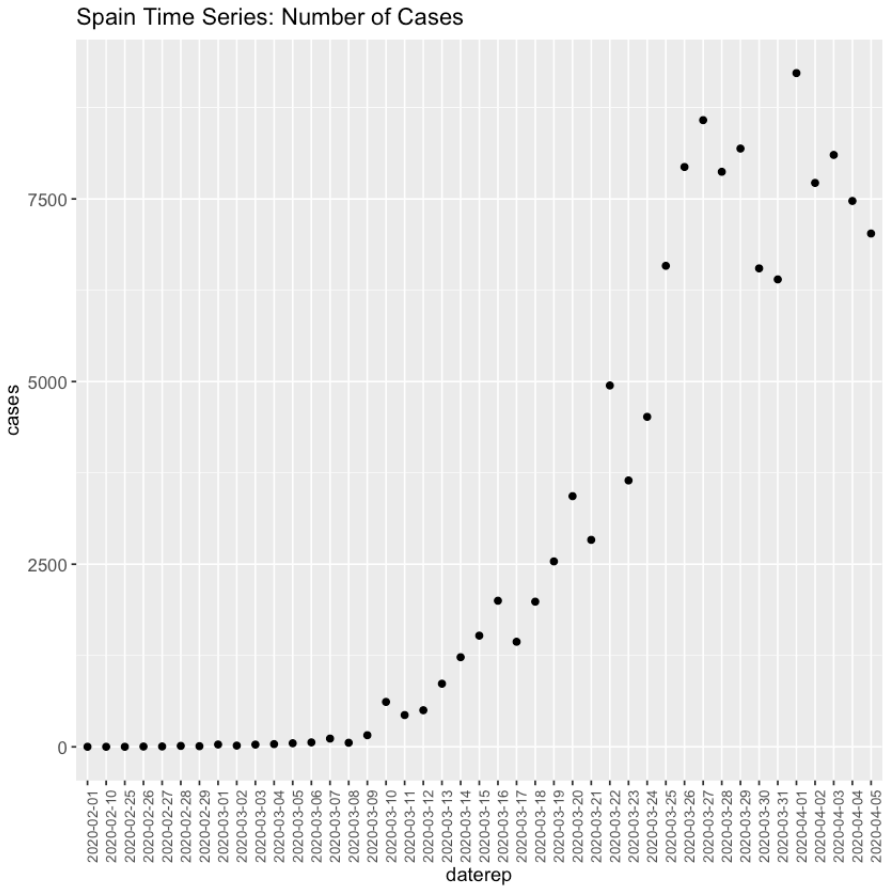
3) Forecasting when a country will peak in their number of cases

I will be working with a new dataset that includes Covid-19 information on different countries

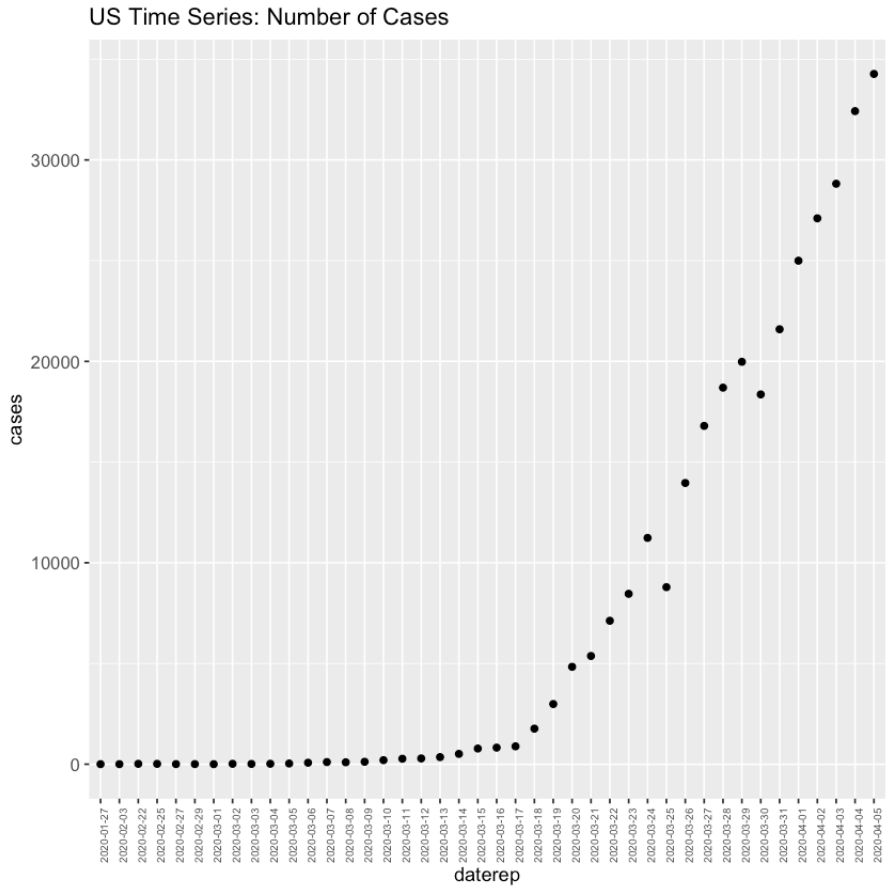
In [123]:
```
spread <- read.csv('geoCovid.csv')
```

I will split the data into 3 datasets so that forecasting can be done by Country. The dataframes will be made for the US, Spain, and South Korea.

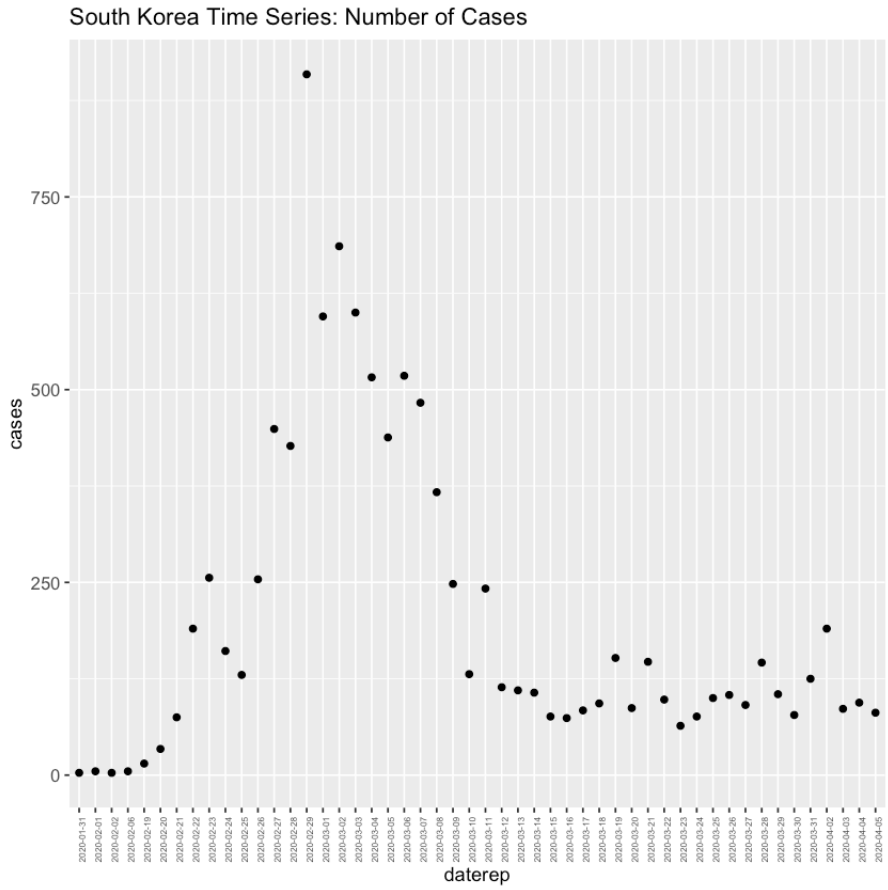
In [124]:
```
library(dplyr)
spreadinspain <- filter(spread, geoid == "ES")
spreadinspain2 <- filter(spreadinspain, cases>0)
#plot using dates and number of cases in spain
library(ggplot2)
sp <- ggplot(data=spreadinspain2, aes(x=daterep, y=cases)) +
geom_point()
sp <- sp + labs(title = "Spain Time Series: Number of Cases")
sp <- sp + theme(axis.text.x = element_text(size=8, angle=90))
sp <- sp + theme(axis.text.y = element_text(size=10))
sp
```



In [125]:
```
spreadinus <- filter(spread, geoid == "US")
spreadinus2<- filter(spreadinus, cases>2)
us <- ggplot(data=spreadinus2, aes(x=daterep, y=cases)) +
geom_point()
us <- us + labs(title = "US Time Series: Number of Cases")
us <- us + theme(axis.text.x = element_text(size=6, angle=90))
us <- us + theme(axis.text.y = element_text(size=10))
us
```



In [126]:
```
spreadinsouthkorea <- filter(spread, geoid == "KR")
spreadinsouthkorea2<- filter(spreadinsouthkorea, cases>2)
kr <- ggplot(data=spreadinsouthkorea2, aes(x=daterep, y=cases)) +
geom_point()
kr <- kr + labs(title = "South Korea Time Series: Number of Cases")
kr <- kr + theme(axis.text.x = element_text(size=5, angle=90))
kr <- kr + theme(axis.text.y = element_text(size=10))
kr
```



The spreads for each country look pretty different. Since I would like to predict when a country's number of cases will peak, I will focus mainly on the US (South Korea and Spain have already peaked).

How much time was there between the first case and case 34272?

In [127]:
```
firstcase<- filter(spreadinus, cases>0)
firstcase<- filter(spreadinus, cases<34272)
firstcase$daterep <- as.Date(firstcase$daterep)
with(firstcase, difftime(max(daterep), min(daterep)))
```

```
Time difference of 95 days
```

Now, I will investigate the forecasting power of Random Forest.

In [131]:
```
spreadinus <- spreadinus[,c(1:5, 10)] #Can use select feature in dp
lyr
spreadinus$day <- as.factor(spreadinus$day)
spreadinus$month <- as.factor(spreadinus$month)
spreadinus$year <- as.factor(spreadinus$year)
```

Next, I will regress using RF

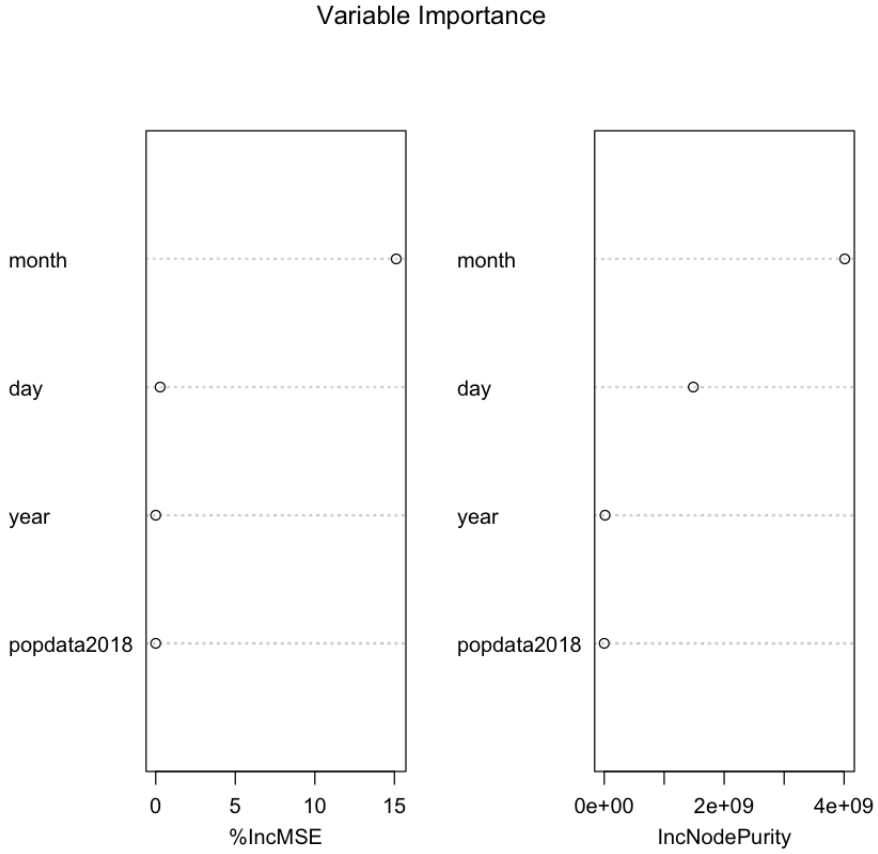
In [132]:
```
install.packages('randomForest')
```

```
The downloaded binary packages are in
        /var/folders/hb/6zq315r16hn_lj34r4s5cqhh0000gn/T//RtmpAGtdO
M/downloaded_packages
```

In [133]:
```
library(randomForest)
spreadinus <- spreadinus[order(spreadinus$daterep),] #Ordering data
for ascending order
```

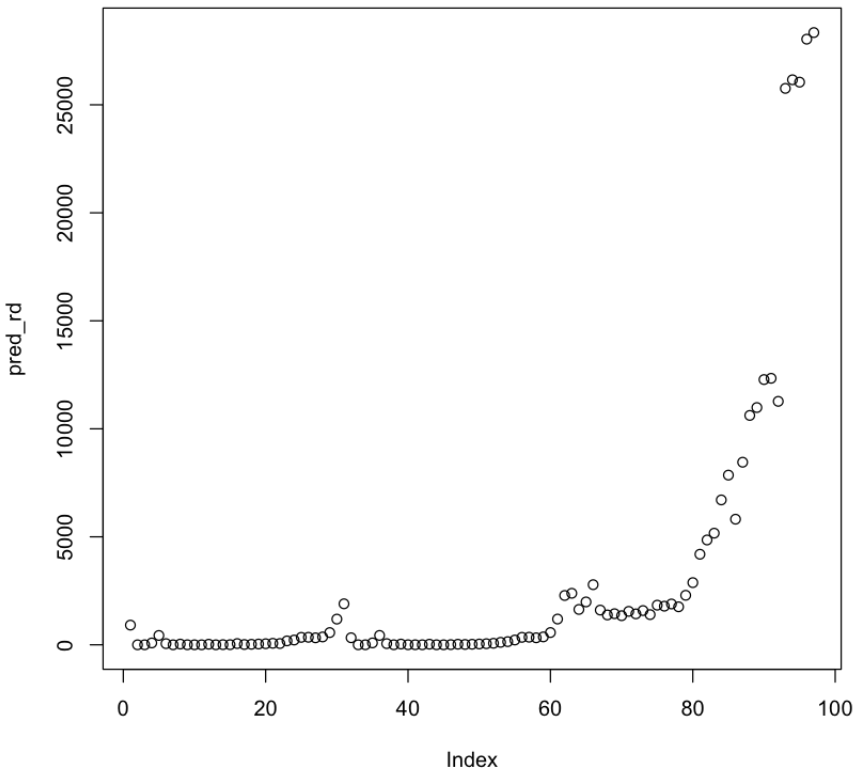
Now, I will make the actual random forest model and preform feature ranking.

In [135]:
```
rf_mod <- randomForest(cases~., data=spreadinus[,-1], ntree=100,
mtry=3, importance=TRUE)
varImpPlot(rf_mod, main="Variable Importance")
#IncMSE: Mean Square Error: important when youre regressing
#IncNodePurity: important when you're classifying
```



Let's predict the current data

In [136]:
```
pred_rd <- predict(rf_mod, spreadinus[,-c(1,5)])
plot(pred_rd)
```



How would the forecasting look for 10 days? Let's create a list of dates to test.

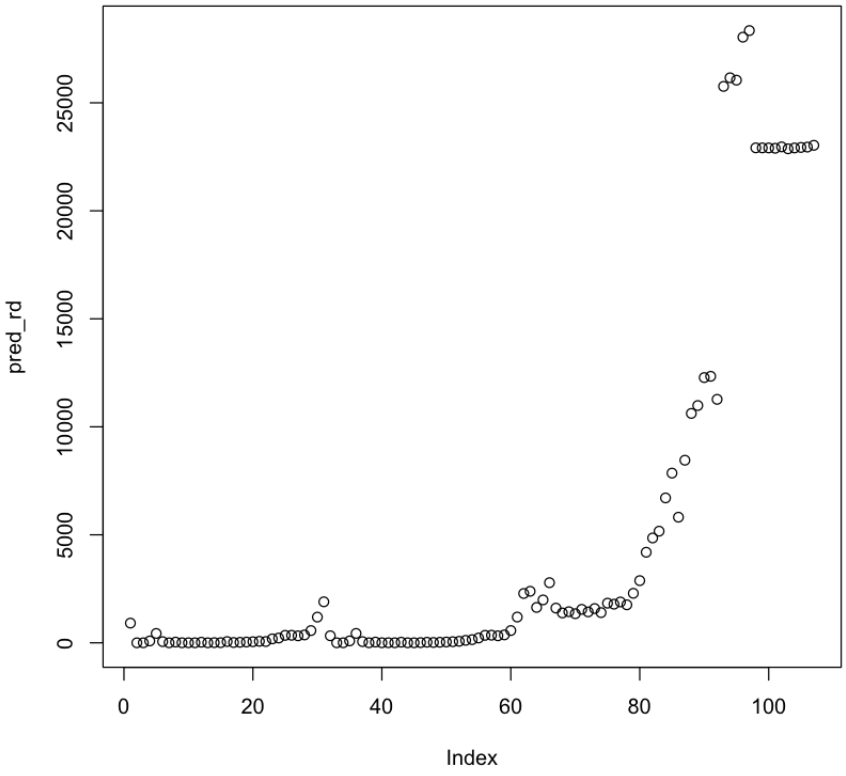
In [137]:
```
install.packages('lubridate')
```

```
The downloaded binary packages are in
        /var/folders/hb/6zq315r16hn_lj34r4s5cqhh0000gn/T//RtmpAGtdO
M/downloaded_packages
```

In [139]:
```
library(lubridate)
dates <- data.frame(daterep=seq(as.Date('2020-04-06'), by='days',
length=10))
dates$day <- factor(day(dates$daterep))
dates$month <- factor(month(dates$daterep))
dates$year <- factor(year(dates$daterep))
dates$popdata2018 <- rep(327167434, times=10)
dates$popdata2018 <- as.integer(dates$popdata2018)
```

Merge the data in a new dataframe called combined. Then, have the model predict on the new data.

In [140]:
```
combined <- rbind(spreadinus[,-5], dates)
pred_rd <- predict(rf_mod, combined[,-1])
plot(pred_rd)
```



The main take away here is that Random Forest does not understand time series trends well. When there is a pattern of seasonality there are methods available to help Random Forest understand the trend. Because there is no real pattern of seasonality in our dataset, lets compare Random Forests forecasting ability to ARIMA and SMA's ability.

First, I would like to show the ARIMA Method:

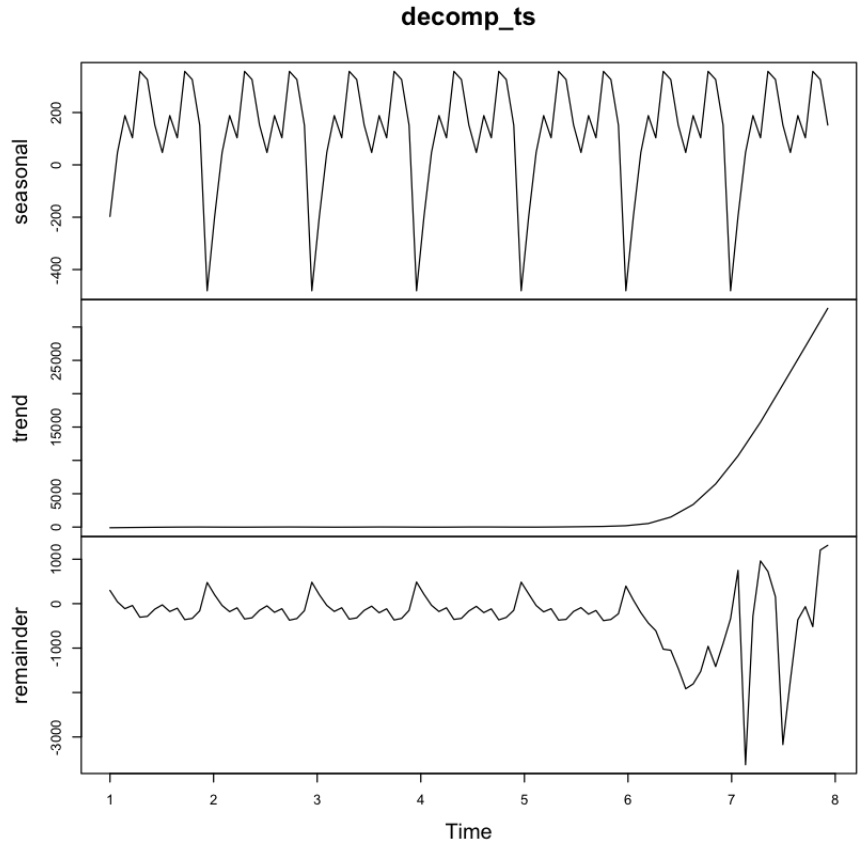
In [147]:
```
install.packages('forecast')
install.packages('rpart')
```

```
The downloaded binary packages are in
        /var/folders/hb/6zq315r16hn_lj34r4s5cqhh0000gn/T//RtmpAGtdO
M/downloaded_packages

The downloaded binary packages are in
        /var/folders/hb/6zq315r16hn_lj34r4s5cqhh0000gn/T//RtmpAGtdO
M/downloaded_packages
```

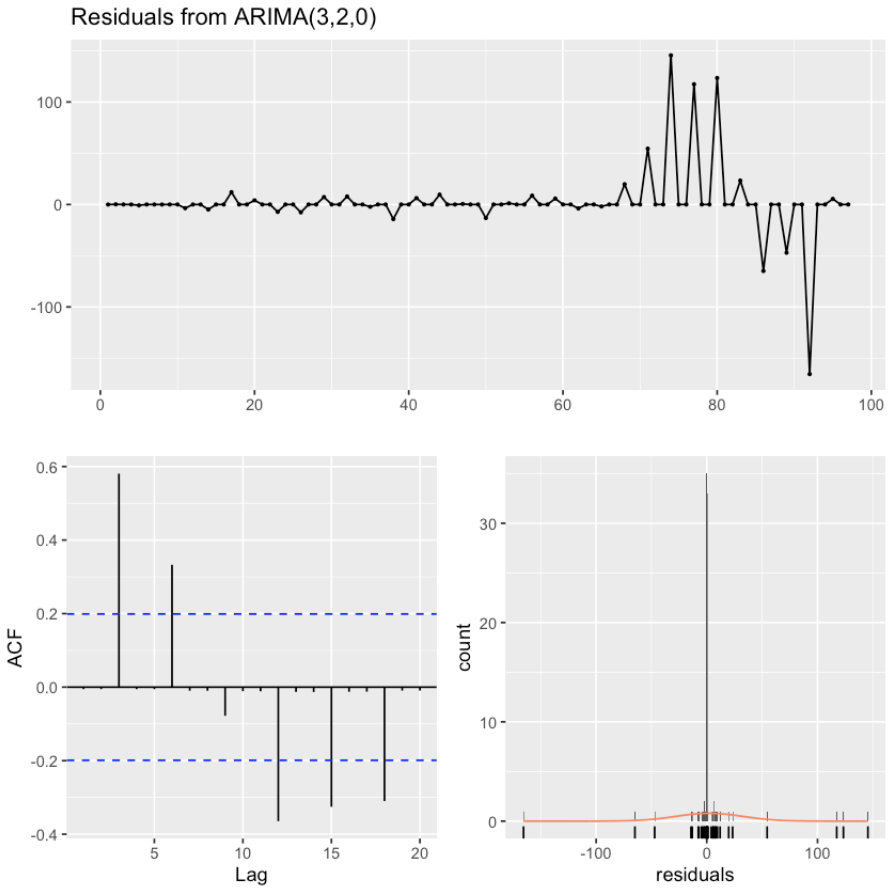
In [151]:
```
library(forecast)
library(rpart)
period <- 97
data_ts <- ts(spreadinus$cases, freq=period/7)
decomp_ts <- stl(data_ts, s.window = "periodic", robust=FALSE)$time
.series
plot(decomp_ts)
trend_part <- ts(decomp_ts[,2])
trend_fit <- auto.arima(trend_part, approximation=FALSE, stepwise=F
ALSE, trace=2)
print(summary(trend_fit))
checkresiduals(trend_fit)
```

```
 ARIMA(0,2,0)                    : 1097.315
 ARIMA(0,2,1)                    : 1099.402
 ARIMA(0,2,2)                    : 1101.536
 ARIMA(0,2,3)                    : Inf
 ARIMA(0,2,4)                    : Inf
 ARIMA(0,2,5)                    : Inf
 ARIMA(1,2,0)                    : 1099.402
 ARIMA(1,2,1)                    : 1101.536
 ARIMA(1,2,2)                    : 1103.716
 ARIMA(1,2,3)                    : Inf
 ARIMA(1,2,4)                    : Inf
 ARIMA(2,2,0)                    : 1101.536
 ARIMA(2,2,1)                    : 1103.716
 ARIMA(2,2,2)                    : 1105.946
 ARIMA(2,2,3)                    : Inf
 ARIMA(3,2,0)                    : 932.9565
 ARIMA(3,2,1)                    : 935.1862
 ARIMA(3,2,2)                    : 937.4666
 ARIMA(4,2,0)                    : 935.1862
 ARIMA(4,2,1)                    : 937.4666
 ARIMA(5,2,0)                    : 937.4666



 Best model: ARIMA(3,2,0)

Series: trend_part
ARIMA(3,2,0)

Coefficients:
         ar1     ar2     ar3
      0.0000  0.0000  0.8959
s.e.  0.0388  0.0387  0.0368

sigma^2 estimated as 967.5:  log likelihood=-462.26
AIC=932.51   AICc=932.96   BIC=942.73
```

```
Training set error measures:
                    ME     RMSE      MAE        MPE      MAPE        MAS
E
Training set 2.214436 30.29191 9.17264 -2.481956 31.72753 0.0266011
5
                     ACF1
Training set -0.005429263
                    ME     RMSE      MAE        MPE      MAPE        MAS
E
Training set 2.214436 30.29191 9.17264 -2.481956 31.72753 0.0266011
5
                     ACF1
Training set -0.005429263
```

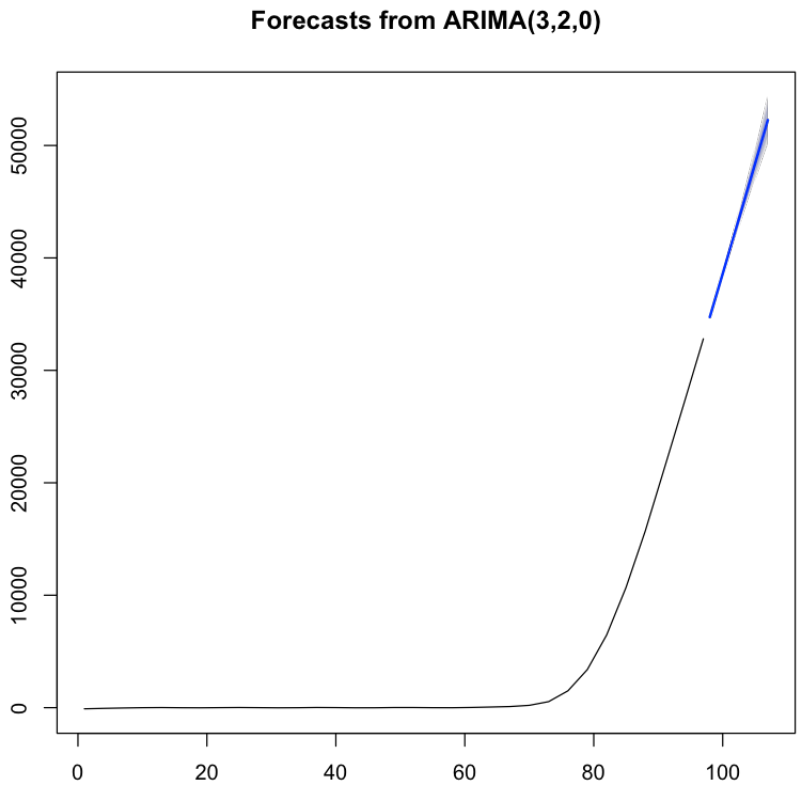



```
        Ljung-Box test

data:  Residuals from ARIMA(3,2,0)
Q* = 46.842, df = 7, p-value = 5.992e-08

Model df: 3.   Total lags used: 10
```



In [152]:
```
plt_arima <- plot(forecast(trend_fit)) #Arima forcast prediction
trend_for <- as.vector(forecast(trend_fit, period)$mean) #Saving th
is trend to apply to random forest prediction
mean(trend_for)
```

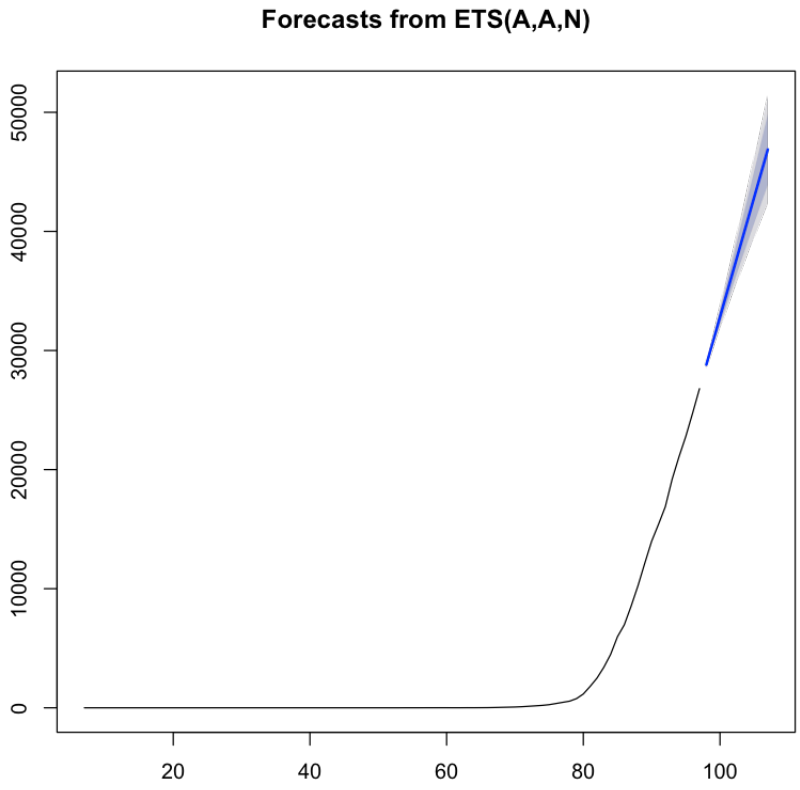
131109.930580171



Next, Let's use SMA (Simple Moving Averages)

In [155]:
```
sma <- SMA(spreadinus$cases, n=7, interval=TRUE)
print(summary(sma))
plot(forecast(sma))
```

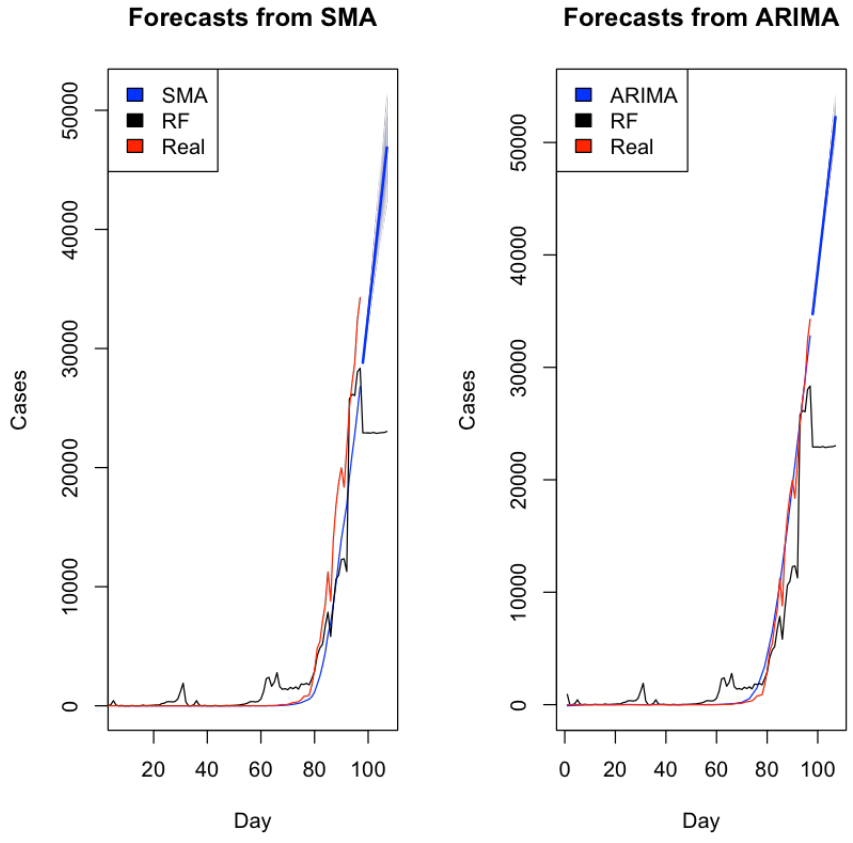
```
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.      NA
's
    0.000     0.286     0.857  2432.851   233.286 26796.000
6
Warning message in ets(object, lambda = lambda, biasadj = biasadj,
allow.multiplicative.trend = allow.multiplicative.trend, :
“Missing values encountered. Using longest contiguous portion of ti
me series”
```



Here is a side by side comparison of SMA and ARIMA Forcasts compared to Random Forest

In [156]:
```
par(mfrow=c(1,2))
plot(forecast(sma), main="Forecasts from SMA", xlab="Day",
     ylab="Cases", col="Blue")
lines(pred_rd, col="Black")
lines(spreadinus$cases, col="Red")
legend("topleft", c("SMA", "RF", "Real"), fill=c("Blue", "Black", "
Red"))
plot(forecast(trend_fit), main="Forecasts from ARIMA", xlab="Day",
     ylab="Cases", col="Blue")  #arima
lines(pred_rd, col="Black") #random forest
lines(spreadinus$cases, col="Red")
legend("topleft", c("ARIMA", "RF", "Real"), fill=c("Blue", "Black",
"Red"))
```

```
Warning message in ets(object, lambda = lambda, biasadj = biasadj,
allow.multiplicative.trend = allow.multiplicative.trend, :
“Missing values encountered. Using longest contiguous portion of ti
me series”
```



Conclusion: As you can see, Random Forest was the weakest in making predictions. This has to do with it's innability to recognize the pattern. Altogether, It looks like the ARIMA method was able to get closest to the real data from the original csv file.

In [ ]: