ChronicKidney

April 6, 2019

```
In [1]: library(tidyverse)
        library(repr)
        library(caret)
```

```
Loading tidyverse: ggplot2
Loading tidyverse: tibble
Loading tidyverse: tidyr
Loading tidyverse: readr
Loading tidyverse: purrr
Loading tidyverse: dplyr
Conflicts with tidy packages ----------------------------------------------------
filter(): dplyr, stats
lag():    dplyr, stats
Loading required package: lattice

Attaching package: caret

The following object is masked from package:purrr:

    lift
```

1 Description:

Chronic kidney disease (CKD) is the presence of kidney damage, or a decreased level of kidney function, for three months or more (The Kidney Foundation of Canada). To accurately diagnose CKD, a wide variety of blood and urine tests can be performed, and risk factors such as age, diabetes, and coronary heart disease can be useful for determining the progression of disease (Mayo Clinic). **Our goal in this research project is to determine of the data variables collected on CKD and non-CKD patients, which variable is the most important in categorizing a CKD vs. non-CKD patient.** Chronic Kidney Disease Data Set was collected from Apollo Hospital for a two months ending in July 2015. There are 25 attributes where 11 are numerical variables, and 14 are characteristic variables. (UCI Machine Learning Repository)

2 Reading and tidying data

After loading tidyverse, repr, and caret, we needed to first load our datasets in via the git clone command in our terminal of juptyer:

git clone https://github.com/UBC-DSCI/datasets.git

```
In [2]: install.packages('e1071')
        library(e1071)
```

```
Updating HTML index of packages in '.Library'
Making 'packages.html' ... done
```

We use read_csv() to take in the dataset once it is cloned into our Jupyter hub. Let's first take a look at the dataset:

```
In [3]: kidney_rough <- read_csv('datasets/chronic_kidney_disease/chronic_kidney_disease_full.
        head(kidney_rough)
```

```
Parsed with column specification:
cols(
  .default = col_character(),
  age = col_integer(),
  bp = col_integer(),
  sg = col_double(),
  al = col_integer(),
  su = col_integer(),
  bgr = col_integer(),
  bu = col_double(),
  sc = col_double(),
  sod = col_double(),
  pot = col_double(),
  hemo = col_double(),
  pcv = col_integer(),
  wbcc = col_double(),
  rbcc = col_double()
)
See spec(...) for full column specifications.
```

age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	pcv	wbcc	rbcc	ht
48	80	1.020	1	0	NA	normal	notpresent	notpresent	121	44	7800	5.2	ye
7	50	1.020	4	0	NA	normal	notpresent	notpresent	NA	38	6000	NA	no
62	80	1.010	2	3	normal	normal	notpresent	notpresent	423	31	7500	NA	no
48	70	1.005	4	0	normal	abnormal	present	notpresent	117	32	6700	3.9	ye
51	80	1.010	2	0	normal	normal	notpresent	notpresent	106	35	7300	4.6	no
60	90	1.015	3	0	NA	NA	notpresent	notpresent	74	39	7800	4.4	ye

2.0.1 Problems:

1) We have NA values in our class column which are not useful to us when we are attempting to train our classifier. We need to remove these first before beginning our analysis.

2) In our wbcc column, we need to convert values that are in scientific notation (10e3) to a more readable form (integer).

3) We have 11 numerical variables and 14 characteristic variables. Our statistical analysis will only use the numerical variables. As such, we need to separate our data into numerical and characteristic variables. It's possible that we still use the characteristic variables in the training of our dataset downstream.

4) Various format changes: we need to scale our data so that our distance calculations are not weighted towards any specific column, we need to convert our class variable to a factor type, and we need to create an NA free data set for our ggpair() analysis

In [4]:
```
#Our first step is to read our data through the read_csv() function, and

kidney <- read_csv('datasets/chronic_kidney_disease/chronic_kidney_disease_full.csv') %
    mutate(class = as.factor(class)) %>%
    #Removed NA values in our class column only
    filter(!is.na(class)) %>%
    mutate(wbcc = as.integer(wbcc))  #changed all scientific notation to integer

kidney_num <- kidney %>% #Select all of the columns that are numerical data, we will a
    select(-sg, -su, -rbc, -pc, -pcc, -ba, -htn, -dm, -cad, -appet, -pe, -ane)

kidney_scaled <- kidney_num %>% #We need to now scale the data
    select(-c(age, class)) %>% #Remove the columns that are not numerical data, but co
    scale(center = FALSE)

kidney_scaled <- data.frame(age = kidney$age, kidney_scaled, class = kidney$class)

# kidney_nona will be used with ggpairs
kidney_nona <- kidney_scaled %>% drop_na()

#is.factor(kidney$class)

head(kidney_scaled)
```

```
Parsed with column specification:
cols(
  .default = col_character(),
  age = col_integer(),
  bp = col_integer(),
  sg = col_double(),
  al = col_integer(),
  su = col_integer(),
  bgr = col_integer(),
```

```
  bu = col_double(),
  sc = col_double(),
  sod = col_double(),
  pot = col_double(),
  hemo = col_double(),
  pcv = col_integer(),
  wbcc = col_double(),
  rbcc = col_double()
)
See spec(...) for full column specifications.
```

age	bp	al	bgr	bu	sc	sod	pot	hemo	pcv
48	1.0278113	0.5900968	0.7191124	0.4692584	0.1835944	NA	NA	1.1952734	1.100
7	0.6423821	2.3603874	NA	0.2346292	0.1223963	NA	NA	0.8770512	0.950
62	1.0278113	1.1801937	2.5139220	0.6908526	0.2753916	NA	NA	0.7451055	0.775
48	0.8993349	2.3603874	0.6953401	0.7299575	0.5813823	0.8035411	0.4432017	0.8692897	0.800
51	1.0278113	1.1801937	0.6299663	0.3389088	0.2141935	NA	NA	0.9003358	0.875
60	1.1562878	1.7702905	0.4397878	0.3258739	0.1682949	1.0279535	0.5672982	0.9469049	0.975

3 Choosing variables for classifiers

Now that we have cleaned our data, it is time to provide summary statistics to explore our dataset. Our goal is to narrow our focus on five variables that we believe have an impact on CKD classification. To do this, we will calculate the mean of each numerical variable grouped on CKD classification to compare the difference between CKD and non-CKD patients. The columns that contain the top five differences in our variable group will be used downstream to build our classifiers.

In [5]:
```
#  typeof(kidney_scaled$bu)
```

```
kidney_means <- kidney_scaled %>%
    group_by(class) %>% #We are interested in the differences between ckd and non ckd
    summarize_all(mean, na.rm = TRUE) %>% #This returns a row that contains the means
                                          #it is easier to comcpare if these are displ
    gather(key = 'variable', value = 'value', -class) %>% #transpose elements by gathe
    spread(class, value) %>%
    mutate(difference = abs(ckd - notckd)) %>% #Create a column that contains the diff
    arrange(desc(difference)) #arrange from highest to lowest differences.


kidney_means

# t.test(kidney_scaled$hemo~kidney_scaled$class)
# is.factor(kidney_means$age)
```

variable	ckd	notckd	difference
age	54.4250000	46.3243243	8.10067568
al	1.0156475	0.0000000	1.01564745
sc	0.6778795	0.1330209	0.54485858
bu	0.9470699	0.4261427	0.52092713
bgr	1.0431517	0.6402316	0.40292011
hemo	0.8267734	1.1796961	0.35292262
pcv	0.8234158	1.1593293	0.33591348
rbcc	0.8186862	1.1137961	0.29510993
wbcc	1.0197419	0.8609232	0.15881871
bp	1.0240326	0.9168147	0.10721791
pot	0.8656670	0.7700630	0.09560398
sod	0.9691903	1.0258924	0.05670212

3.0.1 Redirection

We originally chose to find the differences of the means between CKD and non-CKD patients in all of our numerical variables as a means to narrow down our top predictors. However, this method does not take into effect the spread of the data, which could complicate our classifiers if we choose from this chart. Thus, we use ggpairs function to get the graphs and the correlations between the variables and our kidney disease class.

```
In [6]: install.packages('GGally')
        library(GGally)
```

```
also installing the dependencies progress, reshape

Updating HTML index of packages in '.Library'
Making 'packages.html' ... done

Attaching package: GGally

The following object is masked from package:dplyr:

    nasa
```

4 Figure 1

GGpair Analysis of numerical variables

```
In [7]: options(repr.plot.height = 14, repr.plot.width = 12)
        kidney_total <- ggpairs(data = kidney_nona, mapping=ggplot2::aes(colour = class))
        kidney_total
```

```
Warning message in cor(x, y, method = method, use = use):
the standard deviation is zeroWarning message in cor(x, y, method = method, use = use):
```

```
the standard deviation is zeroWarning message in cor(x, y, method = method, use = use):
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the standard deviation is zeroWarning message in cor(x, y, method = method, use = use):
the standard deviation is zeroWarning message in cor(x, y, method = method, use = use):
the standard deviation is zeroWarning message in cor(x, y, method = method, use = use):
the standard deviation is zero`stat_bin()` using `bins = 30`. Pick better value with `binwidth
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`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```
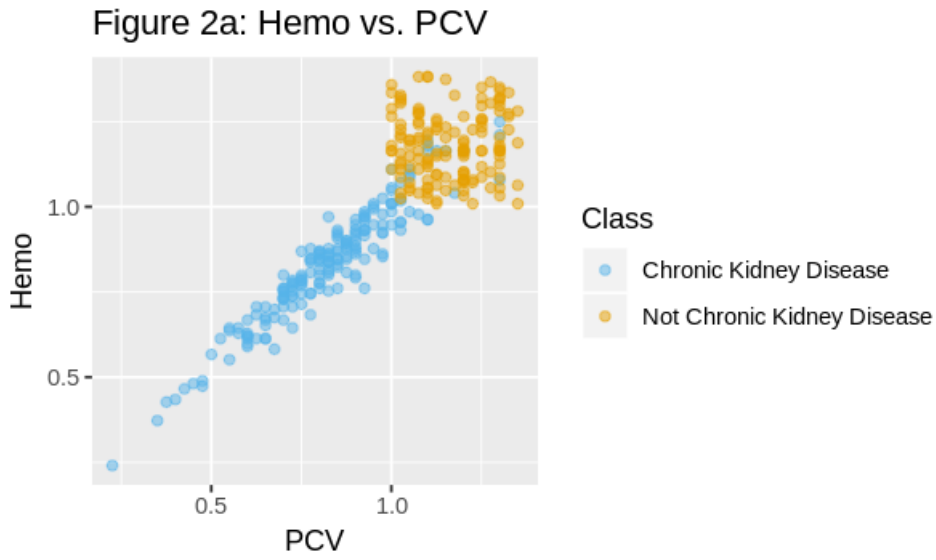

From the box plot we ranked the differences of the means between CKD and other variables and also considered the distribution of the data by looking at the first and the third quartiles. We compared the distributions to find which pair has the most significant difference to roughly get the top three effective variables: hemo, pcv, rbcc, sod and sc.

The three graphs below is a scale of the graphs between the variables we have chosen. From the graphs, we find that hemo, pcv and rbcc have obvious relationships with class, but sod and sc may not have strong relationship with class as we expected.

```
In [22]: #hemo, pcv, rbcc, sod, sc
```

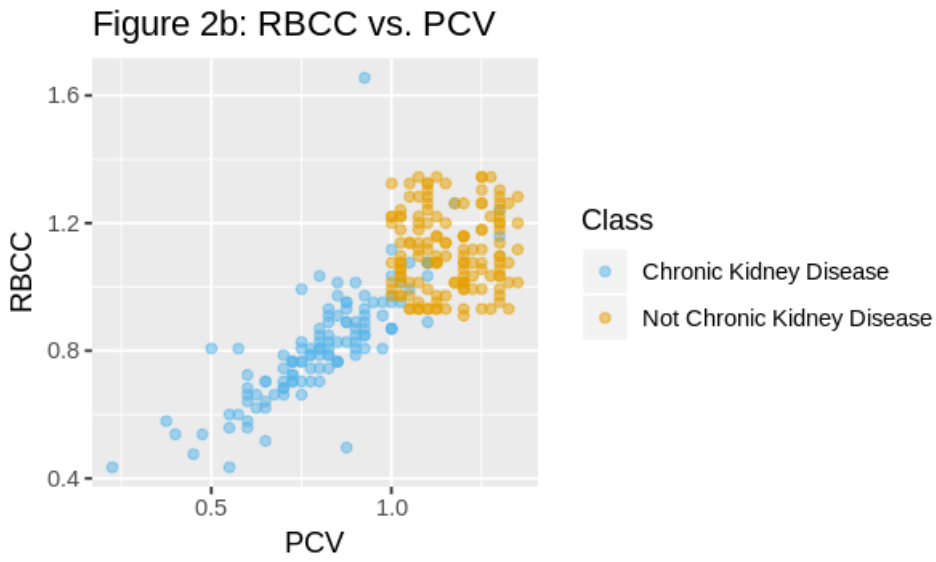
```
cbPalette <- c("#56B4E9", "#E69F00","#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79

options(repr.plot.height = 3, repr.plot.width = 5)

pcv_homo_plot <- kidney_scaled %>%
    ggplot(aes(x = pcv, y = hemo, colour = class)) +
    geom_point(alpha = 0.5) +
    scale_color_manual(name = "Class", labels = c("Chronic Kidney Disease", "Not Chron
    xlab("PCV")+
    ylab("Hemo") +
    ggtitle("Figure 2a: Hemo vs. PCV")

pcv_homo_plot
```

```
Warning message:
Removed 73 rows containing missing values (geom_point).
```



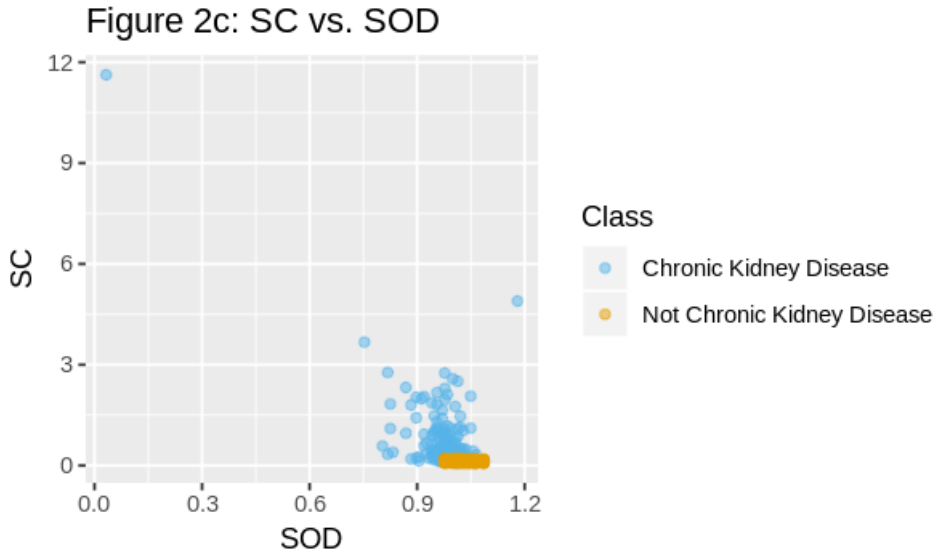
In [23]:
```
pcv_rbcc_plot <- kidney_scaled %>%
    ggplot(aes(x = pcv, y = rbcc, colour = class)) +
    geom_point(alpha = 0.5) +
    scale_color_manual(name = "Class", labels = c("Chronic Kidney Disease", "Not Chron
    xlab("PCV")+
    ylab("RBCC") +
    ggtitle("Figure 2b: RBCC vs. PCV")

pcv_rbcc_plot
```

```
Warning message:
Removed 135 rows containing missing values (geom_point).
```




```
In [24]: sod_sc_plot <- kidney_scaled %>%
             ggplot(aes(x = sod, y = sc, colour = class)) +
             geom_point(alpha = 0.5) +
             scale_color_manual(name = "Class", labels = c("Chronic Kidney Disease", "Not Chro
             xlab("SOD")+
             ylab("SC") +
             ggtitle("Figure 2c: SC vs. SOD")

         sod_sc_plot
```

```
Warning message:
Removed 90 rows containing missing values (geom_point).
```



4.0.1 Adding 'albumin'

We chose the nominal variable 'albumin' to use in a classifier as a negative control for numerical variables. From the ggPairs data visualization, we also chose to continue with hemoglobin (hemo), packed cell volume (pcv), and rbcc (red blood cell count (rbcc) in our downstream classification. We also decided to continue with the nominal and numerical variables that shows our top differences in means; Albumin (al) and sc (serum creatine) respectively. Finally, we chose sodium (sod) as a negative control, since it was the variable that had the least difference in means in kidney class.

5 Creating data partitions, training and validation sets, and classifiers

The following cell contains the code for selecting the training rows that will be used to train the classifiers and validation rows against which the classifiers will be tested.

In [11]:
```
set.seed(1234)

set_rows <- kidney_scaled %>%
    select(class) %>%
    unlist() %>%
    createDataPartition(p = 0.75, list = FALSE) #CHECK TO SEE IF THIS IS RANDOMIZED

#head(set_rows)

training_kidney <- kidney_scaled %>% slice(set_rows)
validation_kidney <- kidney_scaled %>% slice(-set_rows)

tail(validation_kidney)
head(training_kidney)
```

	age	bp	al	bgr	bu	sc	sod	pot	hemo	pcv
94	30	1.0278113	0	0.4873324	0.5474681	0.1070967	1.056910	0.8864035	1.156466	1.125856
95	79	1.0278113	0	0.6596817	0.5735380	0.1835944	1.056910	0.6382105	1.265127	1.000760
96	64	0.8993349	0	0.5764786	0.3519438	0.1070967	1.049671	0.8509473	1.071089	1.225932
97	48	1.0278113	0	0.4457309	0.2867690	0.1223963	0.991758	0.8864035	1.303935	1.275970
98	41	1.0278113	0	0.6656247	0.6256778	0.1070967	1.013475	0.8864035	1.319458	1.300989
99	57	1.0278113	0	0.7904294	0.6256778	0.1835944	1.064149	0.7623070	1.148704	1.150875

age	bp	al	bgr	bu	sc	sod	pot	hemo	pcv
7	0.6423821	2.360387	NA	0.2346292	0.1223963	NA	NA	0.8770512	0.95072
62	1.0278113	1.180194	2.5139220	0.6908526	0.2753916	NA	NA	0.7451055	0.77558
51	1.0278113	1.180194	0.6299663	0.3389088	0.2141935	NA	NA	0.9003358	0.87566
60	1.1562878	1.770291	0.4397878	0.3258739	0.1682949	1.027954	0.5672982	0.9469049	0.97574
24	NA	1.180194	2.4366620	0.4040836	0.1682949	NA	NA	0.9624279	1.10083
52	1.2847642	1.770291	0.8201448	0.7820973	0.2906911	NA	NA	0.8382437	0.82562

The cell below contains the code for the training and validation sets for the Hemo variable. Note that the na.omit() is added after the selection of the columns to preserve the columns that have values for the intended variable and class but miss values for other variables.

In [12]:
```
set.seed(1234)

ks = data.frame(k = seq(1, 49))

training_hemo_nona <- training_kidney %>%
    select(hemo, class) %>%
    na.omit()

training_hemo_X <- training_hemo_nona %>%
    select(hemo) %>%
    data.frame()

training_hemo_Y <- training_hemo_nona %>%
    select(class) %>%
    unlist()

val_hemo <-  validation_kidney %>%
    select(hemo, class) %>%
    na.omit()

val_hemo_X <- val_hemo %>%
    select(hemo) %>%
    data.frame()

val_hemo_Y <- val_hemo %>%
    select(class) %>%
    unlist()

train_control <- trainControl(method = 'cv', number = 3)

hemo_train <- train(x = training_hemo_X, y = training_hemo_Y, method = 'knn', tuneGri
# hemo_train

k <- data.frame(k = 9)

hemo_final <- train(x = training_hemo_X, y = training_hemo_Y, method = 'knn', tuneGri
# hemo_final
```

The following cell contains the code for the RBCC variable classifier. Note that the same strategy for removing missing values is used.

In [13]:
```
set.seed(1234)

ks = data.frame(k = seq(1, 49))
```

```
training_rm_na <- training_kidney %>%
    select(rbcc, class) %>%
    na.omit()%>%
    data.frame()

X_rbcc <- training_rm_na %>%
    select(rbcc)%>%
    data.frame()
Y_rbcc <- training_rm_na %>%
    select(class)%>%
    unlist()

val_rbcc <- validation_kidney %>%
    select(rbcc, class)%>%
    na.omit()%>%
    data.frame()

X_val_rbcc <- val_rbcc %>%
    select(rbcc)%>%
    data.frame()

Y_val_rbcc <- val_rbcc %>%
    select(class)%>%
    unlist()

rbcc_train <- train(x = X_rbcc, y = Y_rbcc, method = "knn", tuneGrid = ks, trControl =
# rbcc_train
k <- data.frame(k = 6)

rbcc_final <- train(x = X_rbcc, y = Y_rbcc, method = "knn", tuneGrid = k)
# rbcc_final
```

Now the classifier using the PCV variable will be trained.

```
In [14]: set.seed(1234)
         #pcv sod, sc
         ks = data.frame(k = seq(1, 49))


         val_pcv <- validation_kidney %>%
             select(pcv, class) %>%
             na.omit()

         val_pcv_X <- val_pcv %>%
             select(pcv) %>%
             na.omit()
```

```
val_pcv_Y <- val_pcv %>%
    select(class) %>%
    unlist()

training_pcv <- training_kidney %>%
    select(pcv, class) %>%
    na.omit()

training_pcv_X <- training_pcv %>%
    select(pcv) %>%
    data.frame()
training_pcv_Y <- training_pcv %>%
    select(class) %>%
    unlist()

pcv_train <- train(x = training_pcv_X, y = training_pcv_Y, method = "knn", tuneGrid =
# pcv_cross
k <- data.frame(k = 45)
pcv_final <- train(x = training_pcv_X, y = training_pcv_Y, method = "knn", tuneGrid =
# pcv_train
```

The following cell will contain the code to train the SOD variable.

```
In [15]: set.seed(1234)
         #pcv sod, sc
         ks = data.frame(k = seq(1, 49))

         training_sod <- training_kidney %>%
             select(sod, class) %>%
             na.omit()

         training_sod_X <- training_sod %>%
             select(sod) %>%
             data.frame()
         training_sod_Y <- training_sod %>%
             select(class) %>%
             unlist()

         val_sod <- validation_kidney %>%
             select(sod, class) %>%
             na.omit()

         val_sod_X <- val_sod %>%
             select(sod) %>%
             na.omit()

         val_sod_Y <- val_sod %>%
             select(class) %>%
```

```
    unlist()

sod_train <- train(x = training_sod_X, y = training_sod_Y, method = "knn", tuneGrid =
# sod_train
k <- data.frame(k = 6)
sod_final <- train(x = training_sod_X, y = training_sod_Y, method = "knn", tuneGrid =
# sod_final
```

Lastly, a classifier using the SC variable is trained.

In [16]:
```
set.seed(1234)
#sc
ks = data.frame(k = seq(1, 49))

training_sc <- training_kidney %>%
    select(sc, class) %>%
    na.omit()

training_sc_X <- training_sc %>%
    select(sc) %>%
    data.frame()
training_sc_Y <- training_sc %>%
    select(class) %>%
    unlist()

val_sc <- validation_kidney %>%
    select(sc, class) %>%
    na.omit()

val_sc_X <- val_sc %>%
    select(sc) %>%
    na.omit()

val_sc_Y <- val_sc %>%
    select(class) %>%
    unlist()

sc_train <- train(x = training_sc_X, y = training_sc_Y, method = "knn", tuneGrid = ks
# sc_train
k <- data.frame(k = 8)
sc_final <- train(x = training_sc_X, y = training_sc_Y, method = "knn", tuneGrid = k)
# sc_final
```

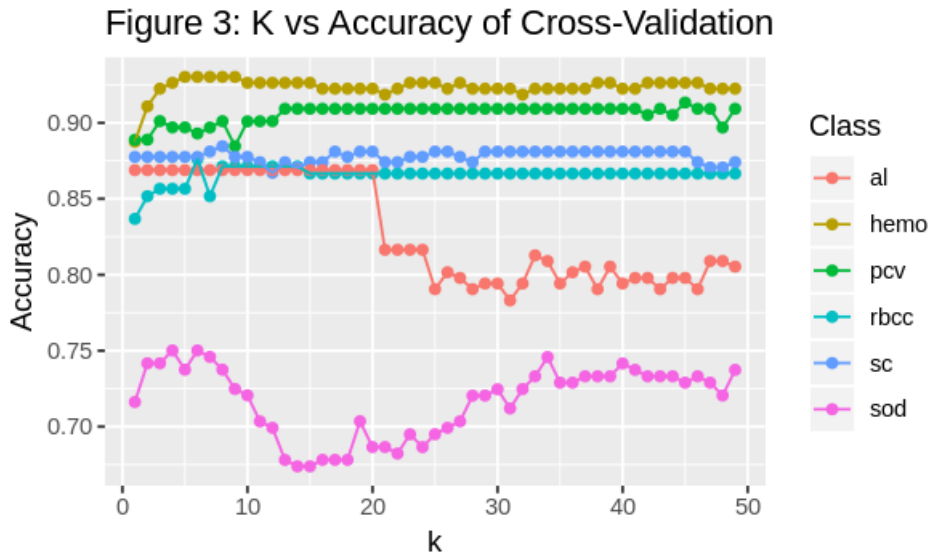
In [17]:
```
set.seed(1234)
#sc
ks = data.frame(k = seq(1, 49))

training_al <- training_kidney %>%
```

```
    select(al, class) %>%
    na.omit()

training_al_X <- training_al %>%
    select(al) %>%
    data.frame()
training_al_Y <- training_al %>%
    select(class) %>%
    unlist()

val_al <- validation_kidney %>%
    select(al, class) %>%
    na.omit()

val_al_X <- val_al %>%
    select(al) %>%
    na.omit()

val_al_Y <- val_al %>%
    select(class) %>%
    unlist()

al_train <- train(x = training_al_X, y = training_al_Y, method = "knn", tuneGrid = ks
# sc_train
k <- data.frame(k = 8)
al_final <- train(x = training_al_X, y = training_al_Y, method = "knn", tuneGrid = k)
# sc_final
```

For choosing the correct k value for each classifier, we extracted the results of each cross validation, gathered around our k column, and plotted k vs accuracy in a joint graph. In doing so, we can also get a good idea of the relative accuracies from each variable. Each variable was assigned a k value that maximized accuracy, while keeping k as low as possible.

In [25]:
```
# graphs of K
# Results of Each train model:
hemo_cv <- hemo_train$results %>%
    select(k,Accuracy)

pcv_cv <- pcv_train$results %>%
    select(k,Accuracy)

rbcc_cv <- rbcc_train$results %>%
    select(k,Accuracy)

sc_cv <- sc_train$results %>%
    select(k,Accuracy)

sod_cv <- sod_train$results %>%
```

```
    select(k,Accuracy)

al_cv <- al_train$results %>%
    select(k,Accuracy)

k_acc <- data.frame(k = seq(1,49),
                    hemo = hemo_cv$Accuracy,
                    pcv = pcv_cv$Accuracy,
                    rbcc = rbcc_cv$Accuracy,
                    sc = sc_cv$Accuracy,
                    sod = sod_cv$Accuracy,
                    al = al_cv$Accuracy)
k_acc <- k_acc %>%
    gather(key = Class, value = Accuracy, -k)

k_acc_plot <- k_acc %>%
    ggplot(aes(x = k, y = Accuracy, color = Class)) +
    geom_point() +
    geom_line() +
    ggtitle('Figure 3: K vs Accuracy of Cross-Validation')

k_acc_plot
```



6 Assessing accuracy of each classifier

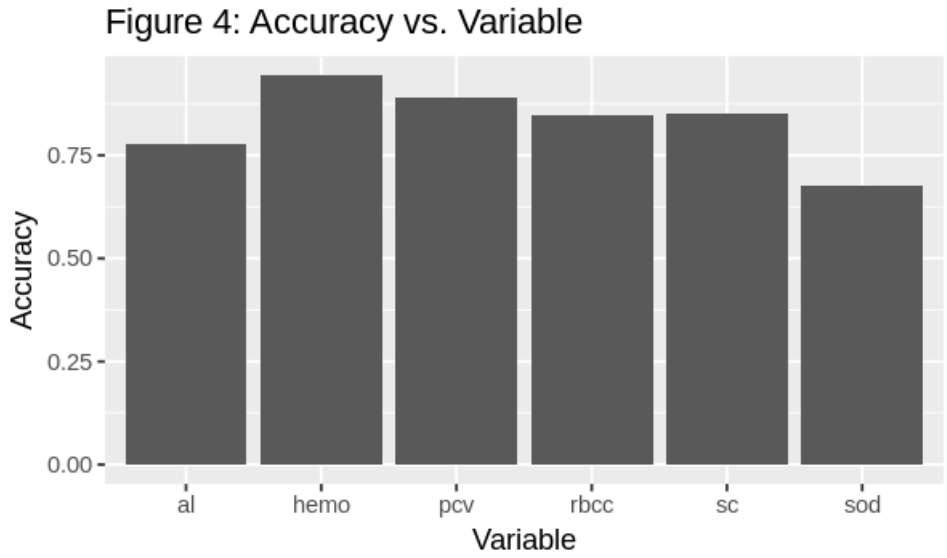
Now that all classifiers have been trained, each classifier's accuracy will be evaluated against the validation set and a measure of accuracy will be given using confusionMatrix.

```
In [19]: set.seed(1234)
         predictions_hemo <- predict(hemo_final, val_hemo_X)
         results_hemo <- confusionMatrix(predictions_hemo, val_hemo_Y)
         # results_hemo

         pred_rbcc <- predict(rbcc_final, X_val_rbcc)
         results_rbcc <- confusionMatrix(pred_rbcc, Y_val_rbcc)
         # results_rbcc

         predictions_pcv <- predict(pcv_final, val_pcv_X)
         results_pcv <- confusionMatrix(predictions_pcv, val_pcv_Y)
         # results_pcv

         predictions_sod <- predict(sod_final, val_sod_X)
         results_sod <- confusionMatrix(predictions_sod, val_sod_Y)
         # results_sod

         predictions_sc <- predict(sc_final, val_sc_X)
         results_sc <- confusionMatrix(predictions_sc, val_sc_Y)
         # results_sc

         predictions_al <- predict(al_final, val_al_X)
         results_al <- confusionMatrix(predictions_al, val_al_Y)
```

Using the results of the confusionMatrix, a bar plot of the accuracies of the variables is plotted to demonstrate their relative accuracy.

```
In [26]: accuracy <- data.frame(hemo = results_hemo$overall, rbcc = results_rbcc$overall, pcv =
             head(n = 1) %>%
             gather(key = variable, value = accuracy) %>%
             arrange(desc(accuracy))
         #     gather(key = type, value = value)
         head(accuracy)

         accuracy_plot <- accuracy %>%
             ggplot(aes(x = variable, y = accuracy)) +
             geom_bar(stat = 'identity') +
             xlab("Variable") +
             ylab("Accuracy") +
             ggtitle("Figure 4: Accuracy vs. Variable")

         accuracy_plot
```

variable	accuracy
hemo	0.9431818
pcv	0.8915663
sc	0.8510638
rbcc	0.8461538
al	0.7764706
sod	0.6756757



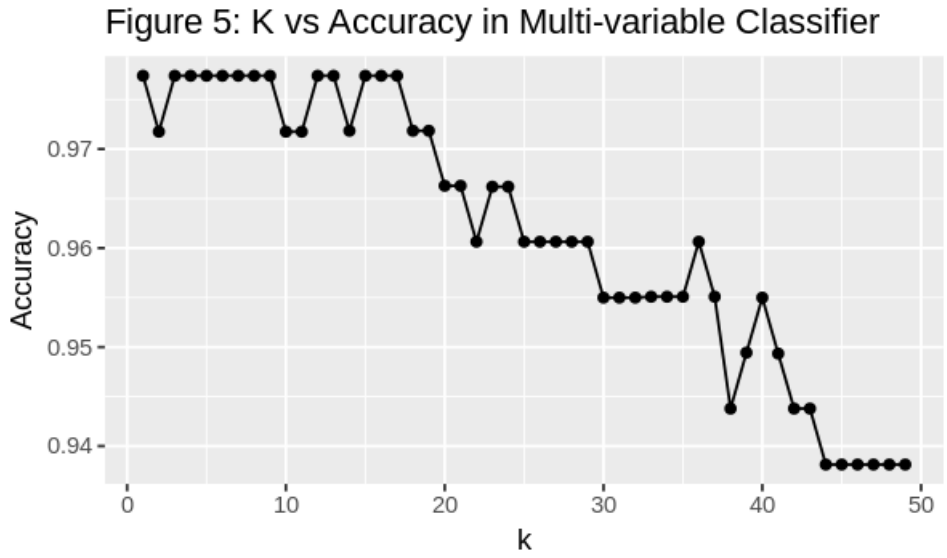
As a comparison, we were interested in the potential accuracy of a classifier that uses all of our top variables (pcv, rbcc, sc, sod, hemo) to predict the class of kidney disease. We created training, and validation data sets, and performed 3-fold cross validation. After deciding that 17 was our optimal k value, we created the classifer, and tested against the validation set. The accuracy was 100% with no errors in predicting.

```
In [27]: # multivariable classifier using the pcv, rbcc, sc, sod, hemo
         set.seed(1234)
         train_multi <- training_kidney %>%
             select(pcv, rbcc, sc, sod, hemo, class) %>%
             na.omit()

         X_train_multi <- train_multi %>%
             select(pcv, rbcc, sc, sod, hemo) %>%
             data.frame()

         Y_train_multi <- train_multi %>%
             select(class) %>%
             unlist()

         val_multi <- validation_kidney %>%
```

```
        select(pcv, rbcc, sc, sod, hemo, class) %>%
        na.omit()

    X_val_multi <- val_multi %>%
        select(pcv, rbcc, sc, sod, hemo) %>%
        data.frame()

    Y_val_multi <- val_multi %>%
        select(class) %>%
        unlist()

    train_control <- trainControl(method = "cv", number = 3)
    k <- data.frame(k = seq(1, 49))
    multi_train <- train(x = X_train_multi, y = Y_train_multi, method = "knn", tuneGrid =

    multi_train_k_plot <- multi_train$results %>%
        ggplot(aes(x = k, y = Accuracy)) +
        geom_point() +
        geom_line() +
        ggtitle('Figure 5: K vs Accuracy in Multi-variable Classifier')

    multi_train_k_plot

    k <- data.frame(k = 17)

    multi_final <- train(x = X_train_multi, y = Y_train_multi, method = "knn", tuneGrid =

    predictions_multi <- predict(multi_final, X_val_multi)
    results_multi <- confusionMatrix(predictions_multi, Y_val_multi)
    results_multi
```

```
Confusion Matrix and Statistics

          Reference
Prediction ckd notckd
    ckd     20      0
    notckd   0     32

               Accuracy : 1
                 95% CI : (0.9315, 1)
    No Information Rate : 0.6154
    P-Value [Acc > NIR] : 1.085e-11

                  Kappa : 1
 Mcnemar's Test P-Value : NA

            Sensitivity : 1.0000
            Specificity : 1.0000
```

```
       Pos Pred Value : 1.0000
       Neg Pred Value : 1.0000
           Prevalence : 0.3846
       Detection Rate : 0.3846
 Detection Prevalence : 0.3846
    Balanced Accuracy : 1.0000

     'Positive' Class : ckd
```



7 Discussion

7.1 Results

Our top performing classifiers were our ggPair picked variables, hemo and pcv, with classifier accuracies of 94.3% and 89.1%. Next came our variable with the highest difference in mean, sc, with a classifier accuracy of 85.1%. Rbcc, al, and sod were our lowest performing classifiers with classifier accuracies of 84.6%, 77.6%, and 67.5% respectively. The initial analysis of the ggpairs plot indicated these variables to have a relatively higher correlation to the classification of non-CKD and CKD. The al variable, a categorical variable that was initially ignored, proved to have very good accuracy overall after a classifier was trained on it. The expected accuracy of these classifiers proved to be slightly lower than the actual ones that were measured using the validation sets. Hence these variables did fulfill the expected accuracy. Interestingly, our lone nominal variable (al) was surprisingly effective in classifying chronic kidney disease. We were surprised, considering that albumin can only be one of 4 values, and was initially dismissed as not being an effective variable to train a classifier. Nevertheless, albumin was more effective than sodium in classifying. Our multi-variable classifer performed the best with a 100% validation accuracy. It is unlikely that

it would perform as well as 100% for larger datasets, and the high accuracy can likely be explained by the relatively small dataset.

7.2 Impact

It is well known that characteristics such as hemoglobin, packed cell volume, and rbcc are related to anemia in patients - a hallmark of chronic kidney disease (NIDDK). Albumin and creatine levels are markers of severe kidney failure, and are related to a hypersecretion of these proteins into the serum (kidney.org). Our findings show that certain blood markers such as hemoglobin and packed cell volume should be a higher priority of measuring from potential CKD patients as opposed to variables such as sodium levels and albumin. Ideally, the best case scenario would be to take blood tests for all 25 attributes; however, considering the sparseness of our chronic kidney disease dataset, it appears that different health care professionals prioritize different blood markers. As our world continues to become more data oriented in predicting and diagnosing disease, our findings are an attempt to prioritize and simplify which characteristics are most valuable to have in diagnosing chronic kidney disease.

7.3 Future Questions

Since in this project we did not choose the top five influential variables by ranking the differences of means between CKD and non-CKD patients in all of our numerical variables, we would like to know whether performing a Welch two sample T test be an effective measure of predicting whether variables are important in our classification. Doing so, and arranging the top variables in this manner is a more methodical way of choosing variables to use downstream, as opposed to selecting them by hand. In addition, we know that we can achieve 100% accuracy by training on all six variables; however, it would be still useful to know what combinations of variables are most important in classifying chronic kidney disease. Finally, it would be important to have a larger dataset for testing and validation, as we can properly see whether the classifiers that we built scale well.

7.3.1 REFERENCES

1) What is kidney disease? The kidney Foundation of Canada (n.d.). Retrieved March 1, 2019, from https://www.kidney.ca/kidney-disease

2) Chronic kidney disease. (2018, March 08). Mayo Clinic. Retrieved March 1, 2019, from https://www.mayoclinic.org/diseases-conditions/chronic-kidney-disease/diagnosis-treatment/drc-20354527

3) L.Jerlin Rubini (2015). UCI Machine Learning Repository [https://archive.ics.uci.edu/ml/machine-learning-databases/00336/]. Irvine, CA: University of California, School of Information and Computer Science.

4) https://www.niddk.nih.gov/health-information/kidney-disease/anemia

5) https://www.kidney.org/kidneydisease/siemens_hcp_acr