Homework 4: Due Friday, December 10 at 11:59pm

For this assignment, you will be analyzing the **`GlobalAncestry.csv`** dataset on Canvas, which contains information on the ancestry and 8916 genetic variants of 242 individuals.

The first column in the dataset, labeled **`ancestry`**, provides the ancestry of each individual:

`African`	San and Yoruban individuals from sub-Saharan Africa
`European`	Italian and Russian individuals from Europe
`EastAsian`	Chinese and Japanese individuals from East Asia
`Oceanian`	Melanesian and Papuan individuals from Oceania
`NativeAmerican`	Pima and Mayan individuals from the Americas
`Mexican`	Mexican individuals from the Americas
`Unknown1`	Unknown ancestry
`Unknown2`	Unknown ancestry
`Unknown3`	Unknown ancestry
`Unknown4`	Unknown ancestry
`Unknown5`	Unknown ancestry

As in the example from our introductory lecture in the course, the remaining columns provide the number of copies (**`0`**, **`1`**, or **`2`**) of 8916 genetic variants.

The goal of this assignment is to become more familiar with model selection, feature selection, and regularization. All analyses must be performed in R using the **`tidyverse`** and **`glmnet`** packages discussed in class. Provide your responses in the designated spaces in this Word document, then save it as a pdf and upload it to Canvas.

Brief overview of the assignment:

The objective of this assignment is to train a multinomial regression classifier to predict *K*=5 ancestries (**`African`**, **`European`**, **`EastAsian`**, **`Oceanian`**, and **`NativeAmerican`**) from genetic data. The training dataset will consist of all individuals with known ancestries (**`African`**, **`European`**, **`EastAsian`**, **`Oceanian`**, and **`NativeAmerican`**), and the test dataset will consist of the five individuals with unknown ancestries (**`Unknown1`**, **`Unknown2`**, **`Unknown3`**, **`Unknown4`**, and **`Unknown5`**). The best classifier will be determined by lassopenalized multinomial regression and 10-fold cross-validation applied to the training dataset. As in our lecture on this topic, you will consider 100 tuning parameter values (λ) evenly spaced between 0.001 and 1000 on a base-10 logarithmic scale, and will choose the simplest classifier that is within 1 standard error of the best classifier. You will then use this classifier to predict the ancestries of the five unknown individuals in the test dataset from their genetic data.

Note: When using **glmnet**, *do not* recode **ancestry** values as **1**, **2**, **3**, etc. We only did this in class to illustrate the connection with using linear regression applied to a response with values **0** and **1**, as linear regression requires a quantitative response.

1. [15%] Load the **GlobalAncestry.csv** dataset using the approach outlined for the **Advertising.csv** dataset in our linear regression lecture, and then create the following two data frames:

   1. Training data frame called **train**, which only includes observations with **ancestry** values **African**, **European**, **EastAsian**, **Oceanian**, and **NativeAmerican**.

   2. Test data frame called **test**, which only includes observations with **ancestry** values **Unknown1**, **Unknown2**, **Unknown3**, **Unknown4**, and **Unknown5**.

Provide code below:

```
# Load dataset library
GlobalAncestry <- read_csv("Homework #4/GlobalAncestry.csv")

# Training Set
train <- GlobalAncestry %>%
  filter(ancestry %in% c("African", "EastAsian","European",
"NativeAmerican", "Oceanian"))

# Test Set
test <- GlobalAncestry %>%
  filter(ancestry %in% c("Unknown1", "Unknown2", "Unknown3", "Unknown4",
"Unknown5"))

# Training Set of X & Y
Y<-train %>% select(ancestry) %>% as.matrix()
X<-train %>% select(pos1:pos8916) %>% as.matrix()
```

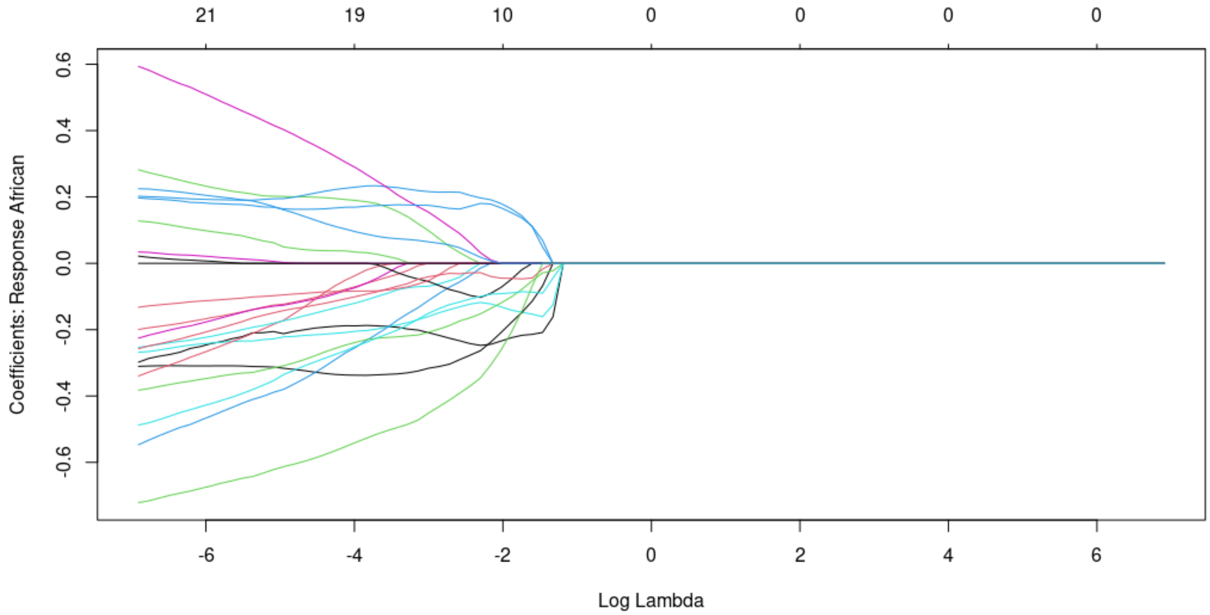
2. **[25%]** Apply **`glmnet`** to the training dataset **`train`** from question 1 to train a lasso penalized multinomial regression classifier to predict **`ancestry`** from the 8916 genetic variants. Consider 100 tuning parameter (λ) values evenly spaced between 0.001 and 1000 on a base-10 logarithmic scale. Plot the regression parameter estimates (coefficients) for each of the *K*=5 classes as a function of log(λ). Based on these results, does it appear that regularization and feature selection are both working? Briefly explain your answer.

   Note: There will be a distinct set of regression coefficients for each of the *K*=5 classes, and so you must provide five graphs. You can access each graph with the back and forward arrows under the "Plots" subpanel in RStudio. You also do not need to plot a legend on each graph, as there are too many potential lines (up to 8917) to make a legend feasible.

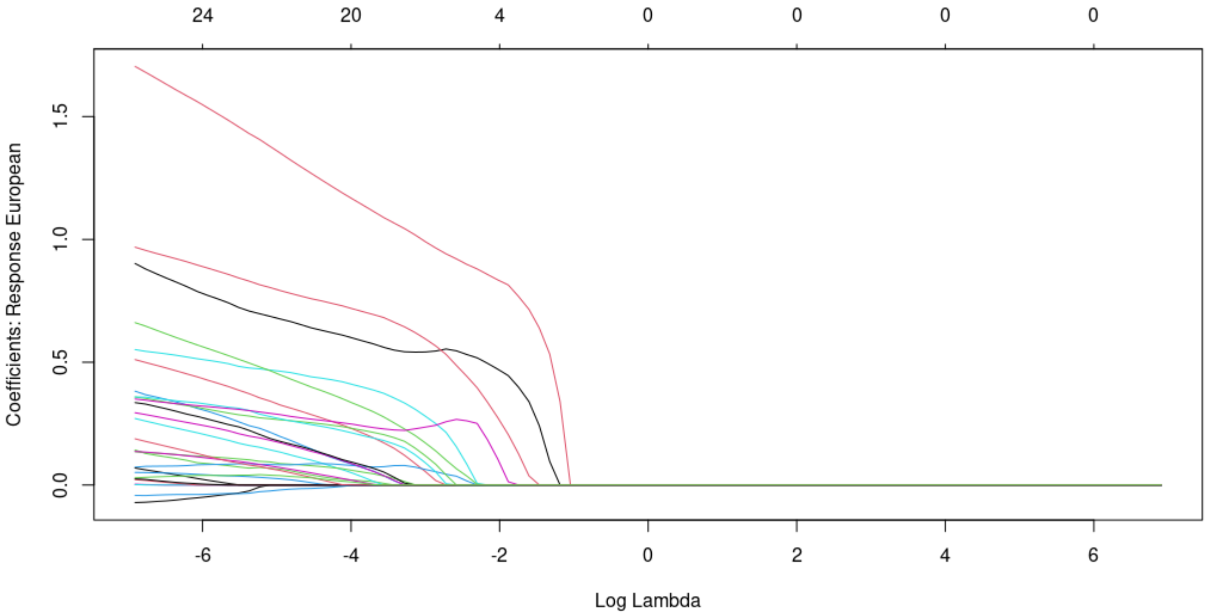
   <u>**Provide code below**</u>**:**

```
# Tuning Parameter
lambdas<- 10^seq(-3,3, length.out=100)

# Training a Lasso-Penalized Multinonmial Regression Classifier
lasso.fit <- glmnet(X,Y, family = "multinomial", alpha=1, lambda=lambdas)

# Plot Lasso.fit
plot(lasso.fit, xvar = "lambda")
```

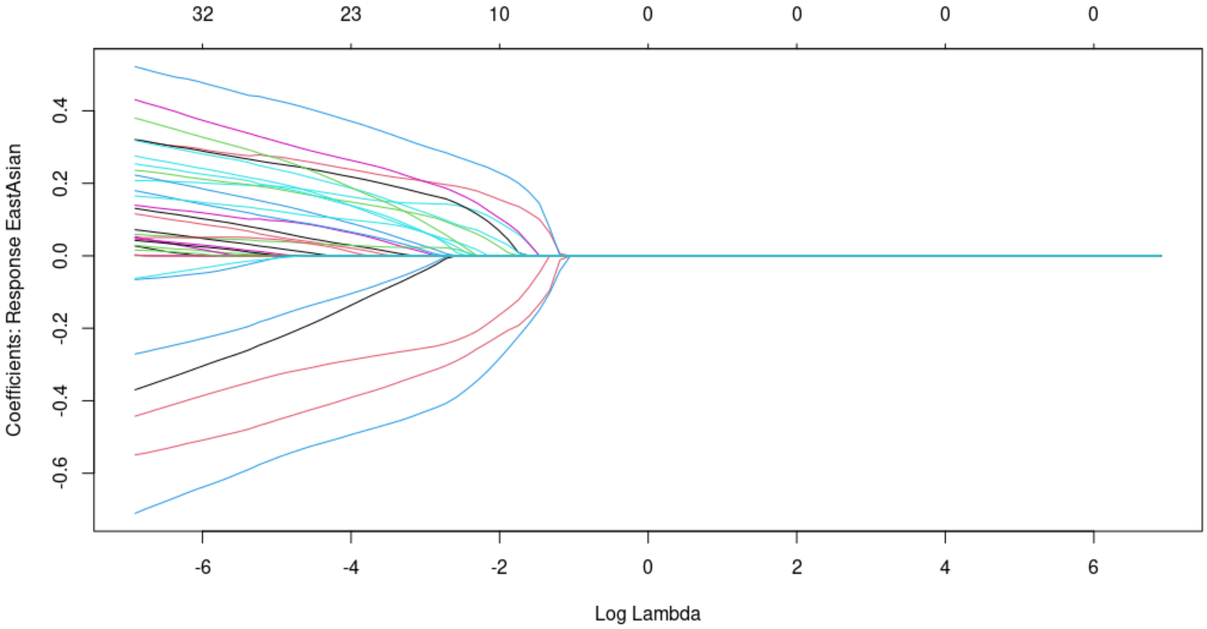
   <u>**Provide figure for African regression coefficients below**</u>**:**



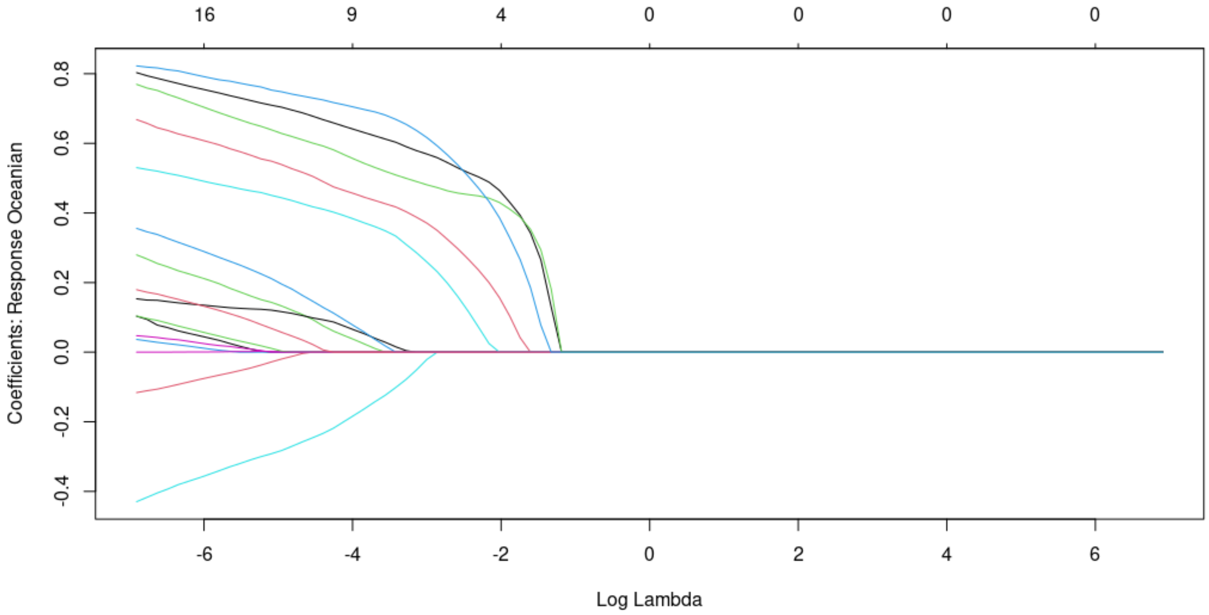
Provide figure for European regression coefficients below:



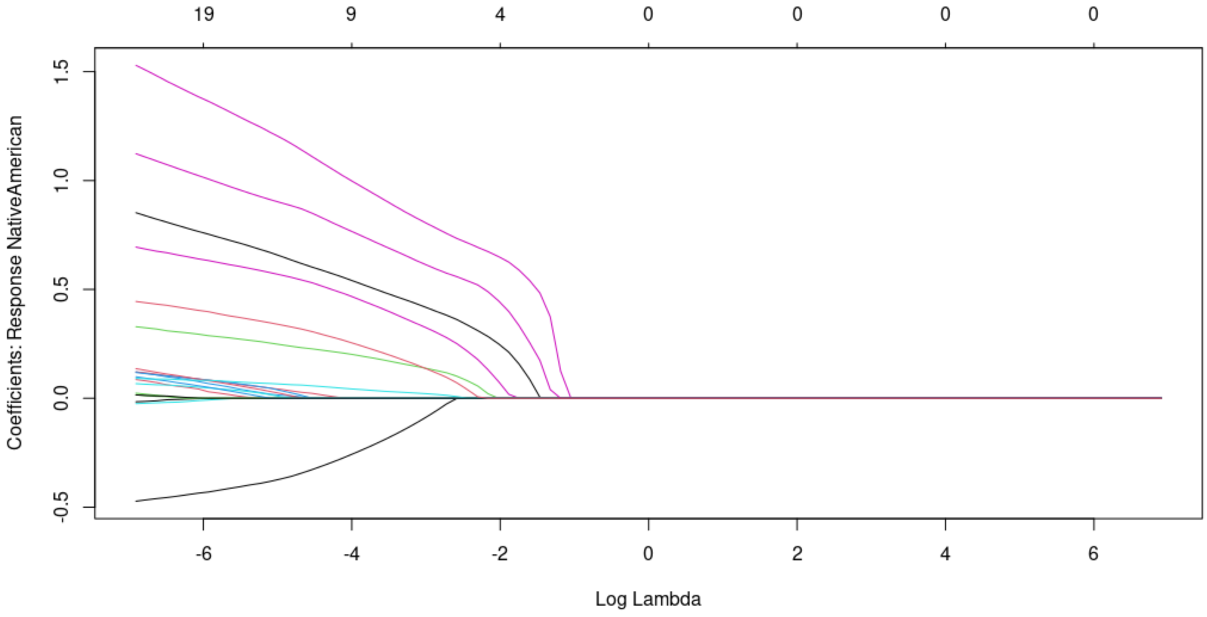
Provide figure for East Asian regression coefficients below:



Provide figure for Oceanian regression coefficients below:



Provide figure for Native American regression coefficients below:



Provide answers to questions below:

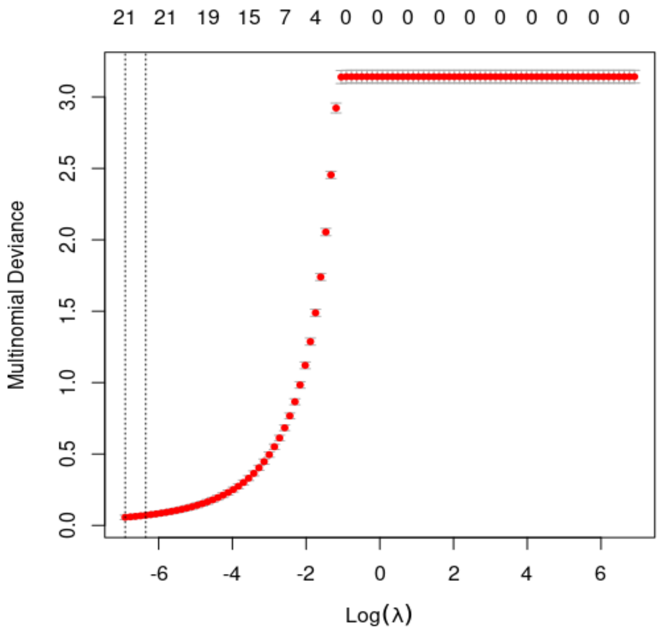
Yes, it does appear regularization and feature selection is working. We used lasso, and lasso performs well when the response is a function of few features. We can see how parameter estimates shrink as lambda increases.

3. **[20%]** Apply **`glmnet`** to the training dataset **`train`** from question 1 to perform 10-fold cross-validation for a lasso-penalized multinomial regression classifier to predict **`ancestry`** from the 8916 genetic variants, again considering 100 tuning parameter (λ) values evenly spaced between 0.001 and 1000 on a base-10 logarithmic scale. Plot the cross-validation error as a function of log(λ). What is the best λ value, and what λ value is associated with the simplest model that is within 1 standard error of the best model?

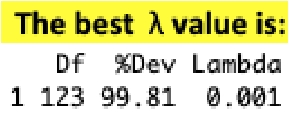
Provide code below:

```
# Determining the cross-validation error as a function of log(lambda)
lasso.cv <- cv.glmnet(X, Y, family = "multinomial", alpha = 1, lambda =
lambdas, nfolds = 10)
plot(lasso.cv)

#Determining the best lambda value
lasso.best <- glmnet(X, Y, family = "multinomial", alpha = 1,lambda =
lasso.cv$lambda.min)
lasso.best # Best Lambda

# Determining the Simplest model within 1 SE
lasso.1se <- glmnet(X, Y, family = "multinomial", alpha = 1,lambda =
lasso.cv$lambda.1se)
lasso.1se # Simplest model within 1 SE
```

Provide figure below:

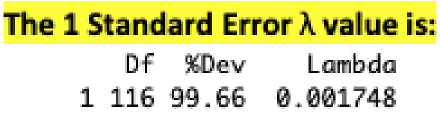


Provide answers to questions below:



The best λ value is:

```
    Df  %Dev Lambda
1 123 99.81  0.001
```



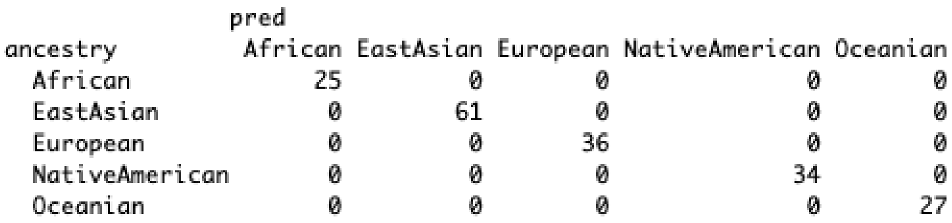
The 1 Standard Error λ value is:

```
   Df  %Dev    Lambda
1 116 99.66  0.001748
```

4. **[20%]** Apply **`glmnet`** to the training dataset **`train`** from question 1 to train a lasso penalized multinomial regression classifier to predict **`ancestry`** from the 8916 genetic variants, using the tuning parameter (λ) value that is associated with the simplest model within 1 standard error of the best model from question 3. Next, apply this fitted model to the training data to predict **`ancestry`**, and create a new data frame that contains the training data along with these predictions. Last, print a confusion matrix and an estimate of classification training accuracy to the console.

Provide code and console output below:

```
# Training a Lasso-Penalized Regression Classifier on lambda 1se
lasso.1se <- glmnet(X, Y, family = "multinomial", alpha = 1,lambda =
lasso.cv$lambda.1se)

# Prediction and new data
estClass <- predict(lasso.1se, X, type = "class", s = lasso.cv$lambda.1se)
train.withPreds <- train %>%
  mutate(pred = c(estClass))

# Confusion Matrix
train.withPreds %>%
  select(ancestry, pred) %>%
  table()
```



```
                pred
ancestry         African EastAsian European NativeAmerican Oceanian
  African             25         0        0              0        0
  EastAsian            0        61        0              0        0
  European             0         0       36              0        0
  NativeAmerican       0         0        0             34        0
  Oceanian             0         0        0              0       27
```

```
#Training Accuracy
train.withPreds %>%
summarize(accuracy = mean(pred == ancestry))
```

```
# A tibble: 1 × 1
 accuracy
   <dbl>
     1
```

5. **[20%]** Apply **`glmnet`** to the test dataset **`test`** from question 1 to predict **`ancestry`** for each of the five individuals with your trained model from question 4. Report the estimated ancestries for each of the five individuals.

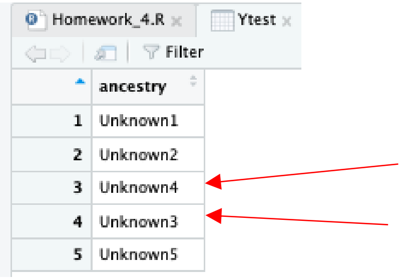
Provide code below:

```
# Test Set X & Y
Ytest<-test %>% select(ancestry) %>% as.matrix()
Xtest<-test %>% select(pos1:pos8916) %>% as.matrix()

# Prediction and new data
estClassTest <- predict(lasso.1se, Xtest, type = "class", s =
lasso.cv$lambda.1se)
test.withPreds <- test %>%
  mutate(pred = c(estClassTest))
head(estClass1)
```

Provide Output:

```
[1,] "EastAsian"
[2,] "African"
[3,] "European"
[4,] "NativeAmerican"
[5,] "Oceanian"
```

**When printing Ytest I noticed that the Unknown feature 3 and 4 is flipped:



	ancestry
1	Unknown1
2	Unknown2
3	Unknown4
4	Unknown3
5	Unknown5

Fill in the predicted ancestries of the five individuals below:

Ancestry	Predicted ancestry
`Unknown1`	EastAsian
`Unknown2`	African
`Unknown3`	Native American
`Unknown4`	European
`Unknown5`	Oceanian