Homework #2

Build a logistic regression model to predict heart disease

Import data and preview

```
data1 = readtable("../cleveland_data_revised.xlsx");
head(data1,5)
```

```
ans = 5×14 table
```

...

	Age	SEX	chestPain	restingBP	cholest	highBloodSugar	ECG
1	63	1	1	145	233	1	2
2	67	1	4	160	286	0	2
3	67	1	4	120	229	0	2
4	37	1	3	130	250	0	0
5	41	0	2	130	204	0	2

Build model that predicts whether individual has heart disease, and model that predicts disease severity. Evaluate using 3-fold cross validation.

```
X = data1{:,1:13};
Y = double(data1.diseaseSeverity > 0);   % convert logical to double

Y2 = data1.diseaseSeverity;
s = rng;
```

```
indices = crossvalind('kfold',size(data1,1),3);

accuracy = zeros(1,3);
precision = zeros(1,3);
recall = zeros(1,3);

rank = zeros(1,3);
avg_error = zeros(1,3);
accuracy2 = zeros(1,3);

for i = 1:3
    rng(s)
    test = indices == i;
    train = ~test;

    Xtrain = X(train,:);
    Ytrain = categorical(Y(train,:));
    Ytrain2 = categorical(Y2(train,:));

    Xtest = X(test,:);
```

```
    Ytest = Y(test,:);
    Ytest2 = Y2(test,:);

    % Model 1
    [mdl1,~,stats1] = mnrfit(Xtrain,Ytrain);
    probability = mnrval(mdl1,Xtest);
    Ypred = round(probability(:,2));

    accuracy(i) = sum(Ypred==Ytest)/length(Ypred);
    precision(i) = sum(Ypred==1 & Ytest==1)/sum(Ypred==1);
    recall(i) = sum(Ypred==1 & Ytest==1)/sum(Ytest==1);

    % Model 2
    [mdl2,~,stats2] = mnrfit(Xtrain,Ytrain2);
    probability2 = mnrval(mdl2,Xtest);
    [max_prob, index] = max(probability2,[],2);  % find highest probability

    Ypred2 = index-1;    % subtract 1 so that index equals disease severity

    rank(i) = corr(Ytest2,Ypred2,"type","Spearman","rows","complete");
    avg_error(i) = nanmean(abs(Ypred2-Ytest2));
    accuracy2(i) = sum(Ypred2==Ytest2)/length(Ypred2);
end
```

Model 1 Performance

```
mean(accuracy)
```

```
ans = 0.8086
```

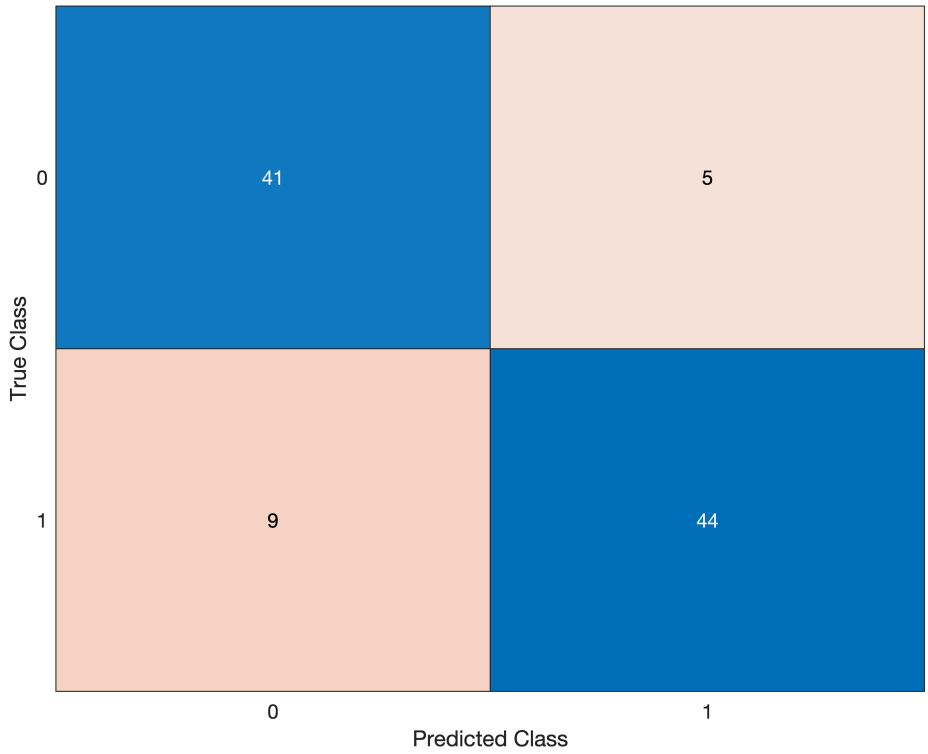
```
mean(precision)
```

```
ans = 0.8042
```

```
mean(recall)
```

```
ans = 0.7962
```

```
confusionchart(Ytest,Ypred);   % uses last cross-validation iteration
```



Model 2 Performance

```
mean(rank)
```

```
ans = 0.6776
```

```
mean(avg_error)
```

```
ans = 0.6436
```

```
mean(accuracy2)
```

```
ans = 0.5710
```

Compare models to distribution of 100 random guesses using a t-test

```
guess_accuracy1 = zeros(100,1);
guess_accuracy2 = zeros(100,1);
for i = 1:100
    mdl1_guess = Y(randperm(length(Ytest)));
    mdl2_guess = Y2(randperm(length(Ytest2)));

    guess_accuracy1(i,1) = sum(mdl1_guess == Ytest)/length(Ytest);
    guess_accuracy2(i,1) = sum(mdl2_guess == Ytest2)/length(Ytest2);

end
```

```
mean(guess_accuracy1)
```

```
ans = 0.4939
```

```
mean(guess_accuracy2)
```

```
ans = 0.3407
```

```
[h_mdl1, p_mdl1] = ttest2(accuracy,guess_accuracy1)
```

```
h_mdl1 = 1
p_mdl1 = 1.7905e-18
```

```
[h_mdl2, p_mdl2] = ttest2(accuracy2,guess_accuracy2)
```

```
h_mdl2 = 1
p_mdl2 = 2.6424e-18
```

Most important features from each model, based on p-value

Model 1

```
[p1,m1] = mink(stats1.p,5)
```

```
p1 = 5×1
    0.0000
    0.0054
    0.0111
    0.0111
    0.0368
m1 = 5×1
    13
    14
     1
     4
    11
```

```
% Must subtract 1 from index to account for intercept term
data1.Properties.VariableNames([12, 13, 3, 10])
```

```
ans = 1×4 cell array
    {'fluoroscopy'}    {'thalliumTest'}    {'chestPain'}    {'ECGDepression'}
```

Model 2

```
mdl2_pvalues = mean(stats2.p,2);   % take mean p-value for each features
[p2,m2] = mink(mdl2_pvalues,5)
```

```
p2 = 5×1
    0.0277
    0.0509
    0.1221
    0.2007
    0.2198
m2 = 5×1
     1
    13
```

```
    12
    14
     9
```

```
data1.Properties.VariableNames([12,11,13,8])
```

```
ans = 1×4 cell array
    {'fluoroscopy'}    {'slopeST'}    {'thalliumTest'}    {'maxHR'}
```

Brain cancer survival data set

Import and inspect data

```
data2 = readtable("Top 100 Genes.xlsx");
tail(data2,5)
```

ans = 5×104 table

...

	PATIENT_ID	SurvivalDaysOS	SurvivalDaysPF	Test	LIX1L	NEU4
1	'GSM1912975'	313	313	0	0.1122	-1.5424
2	'GSM1912976'	962	277	0	0.8193	0.9344
3	'GSM1912977'	826	826	0	0.3891	1.7826
4	'GSM1912978'	257	257	0	-0.3570	-1.5359
5	'GSM1912979'	593	395	1	0.4702	2.6611

Create train and tests sets X and Y

```
Xtrain = data2{data2.Test==0,5:end};
Xtest = data2{data2.Test==1,5:end};

Ytrain = data2{data2.Test==0,3};
Ytest = data2{data2.Test==1,3};
```

Build lasso model

```
[B1, Fit] = lasso(Xtrain,Ytrain,'CV',10);
B1_coeff = B1(:,Fit.IndexMinMSE);
B1_intercept = Fit.Intercept(Fit.IndexMinMSE)
```

```
B1_intercept = 458.9062
```

Build stepwise model

```
[B2,~,~,inmodel,stats] = stepwisefit(Xtrain,Ytrain,"display","off" );
```

Use models to predict survival (PFS). Calculate correlation and mean absolute error

Lasso

```
Ypred_lasso = Xtest * B1_coeff + B1_intercept;
r_lasso = corr(Ypred_lasso,Ytest)
```

```
r_lasso = 0.2258
```

```
avg_error_lasso = mean(abs(Ypred_lasso-Ytest))
```

```
avg_error_lasso = 284.4510
```

Stepwise

```
Ypred_step = Xtest(:,find(stats.PVAL < 0.05))*B2(find(stats.PVAL < 0.05)) + stats.inter
r_stepwise = corr(Ypred_step,Ytest)
```

```
r_stepwise = 0.4530
```

```
avg_error_stepwise = mean(abs(Ypred_step-Ytest))
```

```
avg_error_stepwise = 275.6031
```

Compare regression methods with linear regession

Build linear regression model with top 15 correlated genes

```
% Find correlation of all 100 genes and then extract data for top 15 genes
r_100 = corr(Xtrain,Ytrain);
[r_15,index_15] = maxk(abs(r_100),15);

% Create new training and test sets with top 15 genes
Xtrain_15 = Xtrain(:,index_15);
Xtest_15 = Xtest(:,index_15);

mdl = fitlm(Xtrain_15,Ytrain)
```

```
mdl =
Linear regression model:
    y ~ 1 + x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x9 + x10 + x11 + x12 + x13 + x14 + x15

Estimated Coefficients:
                   Estimate      SE       tStat       pValue
                   ________    _______    ________    __________

    (Intercept)      457.33     56.354      8.1153    5.9897e-09
    x1               213.75     120.73      1.7704      0.087166
    x2              -160.74     114.06     -1.4093       0.16939
    x3              -33.507     159.69    -0.20982       0.83527
    x4                174.4      195.9     0.89022       0.38068
    x5               31.944     170.59     0.18725       0.85277
    x6               180.64     128.12      1.4099        0.1692
    x7              -80.843        193    -0.41887       0.67839
    x8               215.96     213.79      1.0102       0.32077
    x9                48.88     44.087      1.1087       0.27666
    x10              8.2189     69.133     0.11888       0.90619
    x11             -41.904     167.72    -0.24985       0.80447
    x12              63.079     59.104      1.0673       0.29466
    x13             -120.49     156.75    -0.76867       0.44831
    x14               55.38     60.463     0.91593       0.36726
    x15             -94.028     173.23    -0.54279       0.59142
```

```
Number of observations: 45, Error degrees of freedom: 29
Root Mean Squared Error: 231
R-squared: 0.674,  Adjusted R-Squared: 0.505
F-statistic vs. constant model: 3.99, p-value = 0.000688
```

Predict survival (PFS) in test set and measure model accuracy

```
Ypred_norm = predict(mdl,Xtest_15);

r_norm = corr(Ytest,Ypred_norm)
```

```
r_norm = 0.0677
```

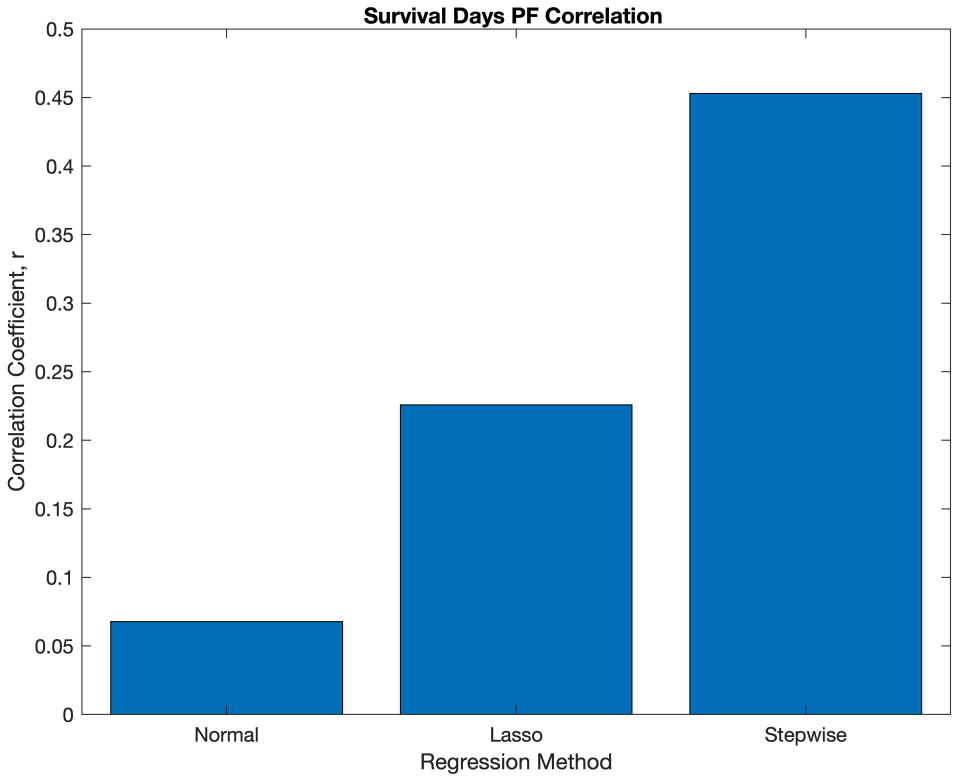
```
avg_error = mean(abs(Ypred_norm-Ytest))
```

```
avg_error = 279.0284
```

Compare correlation and number of features of 3 methods

```
% Create labels for bar graphs
x = categorical({'Normal','Lasso','Stepwise'});
x = reordercats(x,{'Normal','Lasso','Stepwise'});

% Correlation bar graph.
bar(x,[r_norm,r_lasso,r_stepwise])
xlabel("Regression Method")
ylabel("Correlation Coefficient, r")
title("Survival Days PF Correlation ")
```




```
% Find number of features in each model
size_lin_reg = size(mdl.Coefficients,1)-1    % subtract 1 for intercept term
```

```
size_lin_reg = 15
```

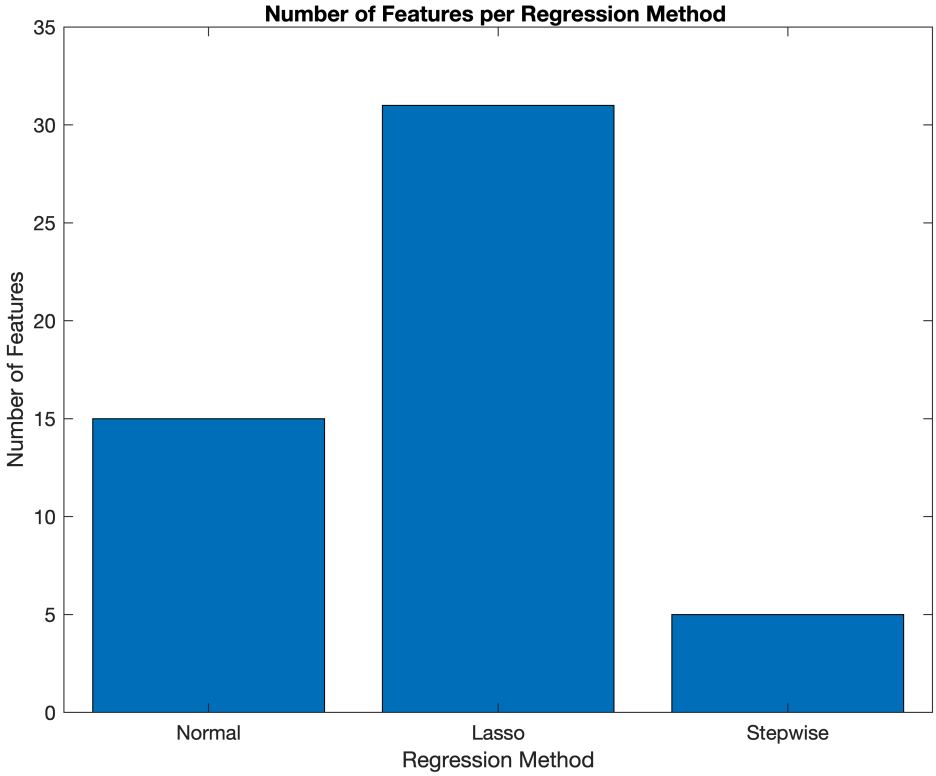
```
size_lasso = sum(B1_coeff ~= 0)
```

```
size_lasso = 31
```

```
size_stepwise = length(find(stats.PVAL < 0.05))
```

```
size_stepwise = 5
```

```
% Number of features bar graph
bar(x,[size_lin_reg,size_lasso,size_stepwise])
xlabel("Regression Method")
ylabel("Number of Features")
title("Number of Features per Regression Method ")
```


Number of Features per Regression Method
35
30
25
20
15
10
5
0
Number of Features
Normal
Lasso
Stepwise
Regression Method