Data Import and Setup

```
data = readtable("HW3_data.xlsx");
```

```
% Transpose data so Observations are rows and Genes are columns
data1 = rows2vars(data,"VariableNamesSource","ID_REF");
```

```
Warning: Table variable names were modified to make them valid MATLAB identifiers.
```

```
% Create X and Y by removing non-numerical rows from data1.
X = cell2mat(data1{3:end,2:end-1});
Xz = zscore(X);
Y = cell2mat(data1{3:end,"SurvivalDays"});
Yz = zscore(Y);
```

Find Top 100 Genes (p-value)

```
% Extract r and p-value data
[r, pval] = corr(X,Y);
```

```
% Identify top 100 correlated genes based on p-value
[gene_pval,gene_index] = mink(abs(pval),100);
var_names = data1.Properties.VariableNames(gene_index+1)
```

```
var_names = 1×100 cell array
    {'A_23_P342744'}    {'A_24_P246891'}    {'A_23_P24535'}    {'A_23_P75362'}    {'A_32_P76399'}    {'A_2
```

```
% Create new data set w/ 100 genes plus Survival Days data
data_rev = data1(:,[gene_index+1;end]);
```

```
% Check that new matrix looks correct
head(data_rev)
```

```
ans = 8×101 table
```

...

	A_23_P342744	A_24_P246891	A_23_P24535	A_23_P75362	A_32_P76399	A_23_P102973
1	'LIX1L'	'NEU4'	'TTC12'	'IFITM10'	'EIF3L'	'DGCR14'
2	'Lix1 homolog...	'sialidase 4'	'tetratricope...	'interferon i...	'eukaryotic t...	'DiGeorge syn...
3	-0.0999	-0.9610	0.2836	-0.3181	-0.2663	0.3688
4	1.0914	1.6402	-1.4203	-0.5402	-0.0894	1.1947
5	-0.3744	1.7162	0.1795	0.7548	0.4971	-0.0330
6	-0.5794	-0.3284	0.0996	-0.6180	-1.4039	-0.9170
7	0.1093	0.9673	1.8210	0.0177	-0.8933	-0.2180
8	0.1558	-0.2542	0.9784	-0.4683	-0.2940	-0.5283

```
% Write new matrix to csv file for future use
writetable(data_rev,"Top 100 Genes.csv")
```

```
% Create new X and Y matrices

X_100 = cell2mat(data_rev{3:end,1:100});
Y_100 = cell2mat(data_rev{3:end,end});
```

Hold Out Validation Model

Using Top 20 Correlated Genes from Training Set

```
% Create X and Y training/test sets from 100 genes
[trainInd,~,testInd] = dividerand(size(X_100,1),0.7,0,0.3);
Xtrain = X_100(trainInd,:);
Xtest = X_100(testInd,:);
Ytrain = Y_100(trainInd,:);
Ytest = Y_100(testInd,:);

% Find top 20 correlated genes with training data
r_100 = corr(Xtrain,Ytrain);
[r_20,index_20] = maxk(abs(r_100),20);

% Create new training and test predictor data sets with top 20 genes
Xtrain_20 = Xtrain(:,index_20);
Xtest_20 = Xtest(:,index_20);

mdl_20 = fitlm(Xtrain_20,Ytrain)
```

```
mdl_20 = 
Linear regression model:
    y ~ 1 + x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x9 + x10 + x11 + x12 + x13 + x14 + x15 + x16 + x17 + x

Estimated Coefficients:
                   Estimate      SE        tStat        pValue  
                   ________    ______    __________    __________

    (Intercept)     536.06      69.11        7.7566    1.3465e-07
    x1             -22.317     63.378      -0.35213       0.72825
    x2              84.066     49.352        1.7034       0.10325
    x3              180.93      89.93        2.0119      0.057239
    x4              38.562     169.01       0.22817       0.82172
    x5             -43.673     51.844       -0.8424       0.40906
    x6              223.31     156.38         1.428         0.168
    x7               91.61     162.47       0.56386       0.57882
    x8              62.336     69.476       0.89723       0.37977
    x9              3.3181     98.448      0.033704       0.97343
    x10            -56.429     143.82      -0.39237       0.69874
    x11             7.2124     98.879      0.072941       0.94254
    x12              30.05     78.329       0.38364        0.7051
    x13             59.653     60.625       0.98397       0.33633
    x14            -128.54     157.77      -0.81476       0.42435
    x15             72.859     123.38       0.59051       0.56115
    x16            -72.814      104.6      -0.69615       0.49397
    x17             18.293      85.73       0.21338       0.83309
    x18            -53.038    143.21       -0.37034       0.71483
    x19            -58.021    69.837        -0.8308       0.41543
    x20          -0.072881    117.67    -0.00061935       0.99951


Number of observations: 42, Error degrees of freedom: 21
Root Mean Squared Error: 205
R-squared: 0.7,  Adjusted R-Squared: 0.414
F-statistic vs. constant model: 2.45, p-value = 0.0238
```

```
Ypred = predict(mdl_20,Xtest_20);
r_mdl = corr(Ytest,Ypred)
```

```
r_mdl = 0.2431
```

```
r2_mdl = r_mdl^2
```

```
r2_mdl = 0.0591
```

```
RMSE = sqrt(mean((Ypred-Ytest).^2))
```

```
RMSE = 418.5823
```

```
avg_error = mean(abs(Ypred-Ytest)./Ytest*100)
```

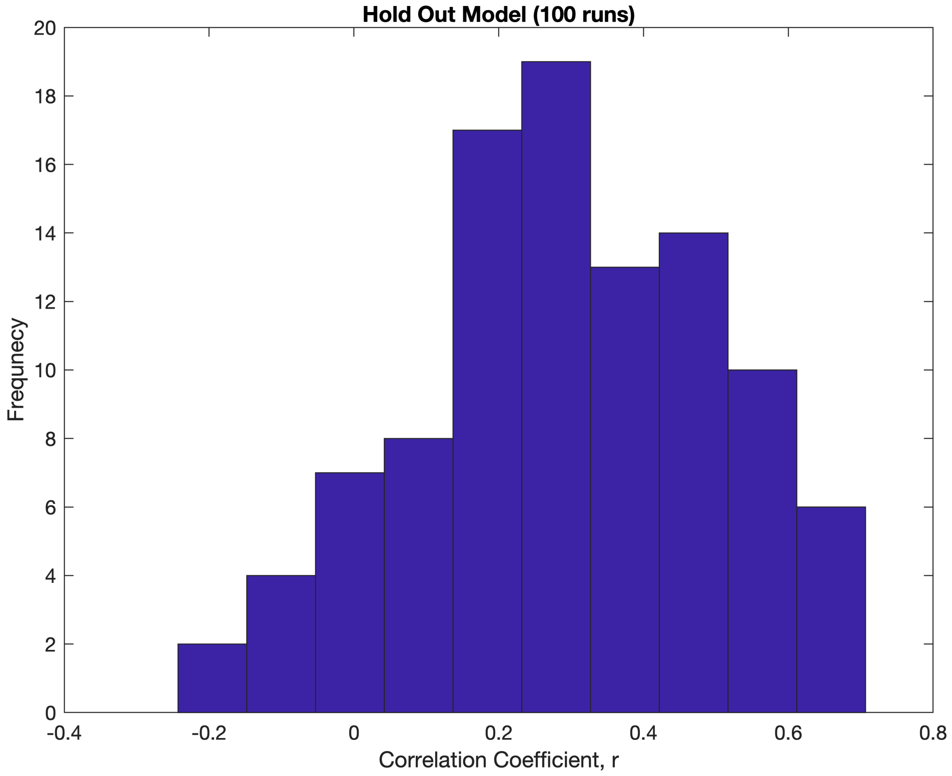
```
avg_error = 143.5671
```

Hold Out Model w/ For Loop

Top 20 Correlated Genes are Reselected Each Iteration

```
r_mdl = zeros(100,1);
for j = 1:100
    % Create X and Y training/test sets from 100 genes
    [trainInd,~,testInd] = dividerand(size(X_100,1),0.7,0,0.3);
    Xtrain = X_100(trainInd,:);
    Xtest = X_100(testInd,:);
    Ytrain = Y_100(trainInd,:);
    Ytest = Y_100(testInd,:);

    % Find top 20 correlated genes with training data
    r_100 = corr(Xtrain,Ytrain);
    [r_20,index_20] = maxk(abs(r_100),20);

    % Create new training and test predictor data sets with top 20 genes
    Xtrain_20 = Xtrain(:,index_20);
    Xtest_20 = Xtest(:,index_20);

    mdl_20 = fitlm(Xtrain_20,Ytrain);

    Ypred = predict(mdl_20,Xtest_20);

    r_mdl(j) = corr(Ytest,Ypred);
    %r2_mdl = r_mdl^2
    %RMSE = sqrt(mean((Ypred-Ytest).^2))
    %avg_error = mean(abs(Ypred-Ytest)./Ytest*100)
```

```
end

hist(r_mdl)
xlabel("Correlation Coefficient, r")
ylabel("Frequnecy")
title("Hold Out Model (100 runs)")
```



K-fold Cross Validation Model

```
% For K-fold model, using top 20 correlated genes from entire data set (not
% just the training set, as the 20 genes would change each iteration)

r_100_kfold = corr(X_100,Y_100);
[r_20_kfold,index_20_kfold] = maxk(abs(r_100_kfold),20);
```

```
indices = crossvalind('kfold',size(X_100,1),5);
RMSE_kfold = zeros(5,1);
corr_kfold = zeros(5,1);
avg_error = zeros(5,1);
X_kfold = X_100(:,index_20_kfold);

% Run through loop 5 times and assign iteration number to i. Identify rows
% in indices equal to i and assign to test; assign remaining rows to train.
for i = 1:5
    test = (indices == i);
    train = ~test;
    % Extract train rows from X and Y. Create linear model with train data.
    Xtrain = X_kfold(train,:);
    Ytrain = Y_100(train,:);
    model = fitlm(Xtrain,Ytrain);

    %Extract test rows from X and Y
    Xtest = X_kfold(test,:);
    Ytest = Y_100(test,:);

    % Predict Y values from model. Calculate stat parameters and assign
    % to index i of variables
    Ypred = predict(model,Xtest);
    corr_kfold(i) = corr(Ytest,Ypred);
    RMSE_kfold(i) = sqrt(mean((Ypred-Ytest).^2));
    avg_error(i) = mean(abs(Ypred-Ytest)./Ytest*100);
end

mean(corr_kfold)
```

```
ans = 0.4558
```

```
mean(RMSE_kfold)
```

```
ans = 338.8842
```

```
mean(abs(avg_error))
```

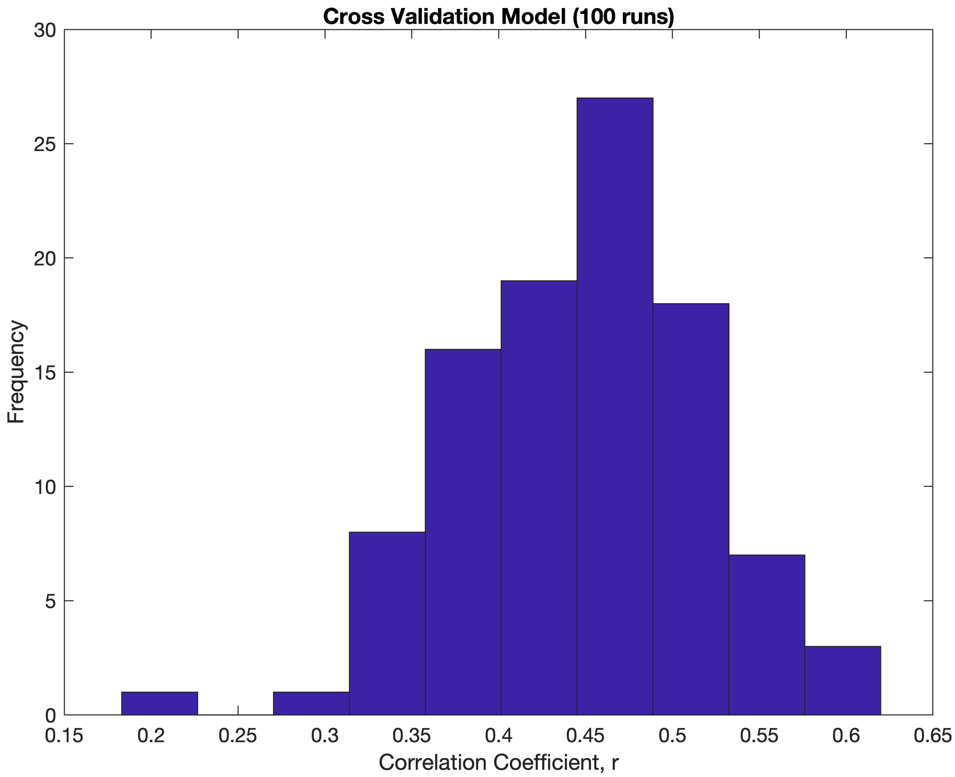
```
ans = 81.9366
```

K-fold Cross Validation w/ For Loop

```
corr_kfold = zeros(5,100);
X_kfold = X_100(:,index_20_kfold);


for j = 1:100
    indices = crossvalind('kfold',size(X_100,1),5);
    %RMSE_kfold = zeros(5,1);
    %corr_kfold = zeros(5,1);
    %avg_error = zeros(5,1);

    % Run through loop 5 times and assign iteration number to i. Identify rows
    % in indices equal to i and assign to test; assign remaining rows to train.
    for i = 1:5
        test = (indices == i);
        train = ~test;

        % Extract train rows from X and Y. Create linear model with train data.
        Xtrain = X_kfold(train,:);
        Ytrain = Y_100(train,:);
        model = fitlm(Xtrain,Ytrain);
        %Extract test rows from X and Y
        Xtest = X_kfold(test,:);
        Ytest = Y_100(test,:);

        % Predict Y values from model. Calculate stat parameters and assign
        % to index i of variables
        Ypred = predict(model,Xtest);
        corr_kfold(i,j) = corr(Ytest,Ypred);
       % RMSE_kfold(i) = sqrt(mean((Ypred-Ytest).^2));
        %avg_error(i) = mean(abs(Ypred-Ytest)./Ytest*100);
    end

end

mean_corr = mean(corr_kfold);
mean(mean_r,"all")
```

```
ans = 0.4067
```

```
hist(mean_corr)
xlabel("Correlation Coefficient, r")
ylabel("Frequency")
title("Cross Validation Model (100 runs)")
```


Cross Validation Model (100 runs)
Frequency
Correlation Coefficient, r