Cogs 109: Modeling and Data Analysis

Homework 3

1. ISLR chapter 4, exercise 4 (page 168-169)
    a. 0.1 or 10%
    b. 0.1^2 = 0.01 or 1%
    c. 0.1^{100}
    d. For any p, we would use “0.1^p * 100” percent of the points for our prediction. As our number of predictors increases, the number of observations used to make our prediction decreases exponentially.
    e. Some p predictors, our sides of the hypercube will be the pth root of 0.1. Think of the 2D case: If you have a square with an area of 0.1, then the sides are √(0.1). This generalizes to the other dimensions.

2. ISLR chapter 4, exercise 6

$$p(X) = \frac{\exp(\beta_0 + \beta_1 X_1 + \beta_2 X_2)}{1 + \exp(\beta_0 + \beta_1 X_1 + \beta_2 X_2)}$$

$$X_1 = hoursstudied, X_2 = undergradGPA$$

$$\beta_0 = -6, \beta_1 = 0.05, \beta_2 = 1$$

a) (1 point)

$$p(X) = \frac{\exp\left(-6 + 0.05X_1 + X_2\right)}{1 + \exp\left(-6 + 0.05X_1 + X_2\right)}$$

$$= \frac{\exp\left(-6 + 0.05 \times 40 + 3.5\right)}{1 + \exp\left(-6 + 0.05 \times 40 + 3.5\right)} = 0.3775$$

b) (2 points)

$$
\begin{aligned}
X &= [X_1 hours, 3.5GPA] \\
p(X) &= \frac{\exp(-6 + 0.05X_1 + X_2)}{1 + \exp(-6 + 0.05X_1 + X_2)} \\
0.50 &= \frac{\exp(-6 + 0.05X_1 + 3.5)}{1 + \exp(-6 + 0.05X_1 + 3.5)}
\end{aligned}
$$

$$0.50(1 + \exp(-2.5 + 0.05X_1)) = \exp(-2.5 + 0.05X_1)$$

$$0.50 + 0.50\exp(-2.5 + 0.05X_1)) = \exp(-2.5 + 0.05X_1)$$

$$0.50 = 0.50\exp(-2.5 + 0.05X_1)$$

$$\log(1) = -2.5 + 0.05X_1$$

$$X_1 = 2.5/0.05 = 50hours$$

3. ISLR chapter 4, exercise 7

$$p_k(x) = \frac{\pi_k \frac{1}{\sqrt{2\pi\sigma}} \exp(-\frac{1}{2\sigma^2}(x - \mu_k)^2)}{\sum \pi_l \frac{1}{\sqrt{2\pi\sigma}} \exp(-\frac{1}{2\sigma^2}(x - \mu_l)^2)}$$

$$p_{yes}(x) = \frac{\pi_{yes} \exp(-\frac{1}{2\sigma^2}(x - \mu_{yes})^2)}{\sum \pi_l \exp(-\frac{1}{2\sigma^2}(x - \mu_l)^2)}$$

$$= \frac{\pi_{yes} \exp(-\frac{1}{2\sigma^2}(x - \mu_{yes})^2)}{\pi_{yes} \exp(-\frac{1}{2\sigma^2}(x - \mu_{yes})^2) + \pi_{no} \exp(-\frac{1}{2\sigma^2}(x - \mu_{no})^2)}$$

$$= \frac{0.80\exp(-\frac{1}{2*36}(x - 10)^2)}{0.80\exp(-\frac{1}{2*36}(x - 10)^2) + 0.20\exp(-\frac{1}{2*36}x^2)}$$

$$p_{yes}(4) = \frac{0.80\exp(-\frac{1}{2*36}(4 - 10)^2)}{0.80\exp(-\frac{1}{2*36}(4 - 10)^2) + 0.20\exp(-\frac{1}{2*36}4^2)} = 75.2\%$$

hw3_python_code

October 19, 2017

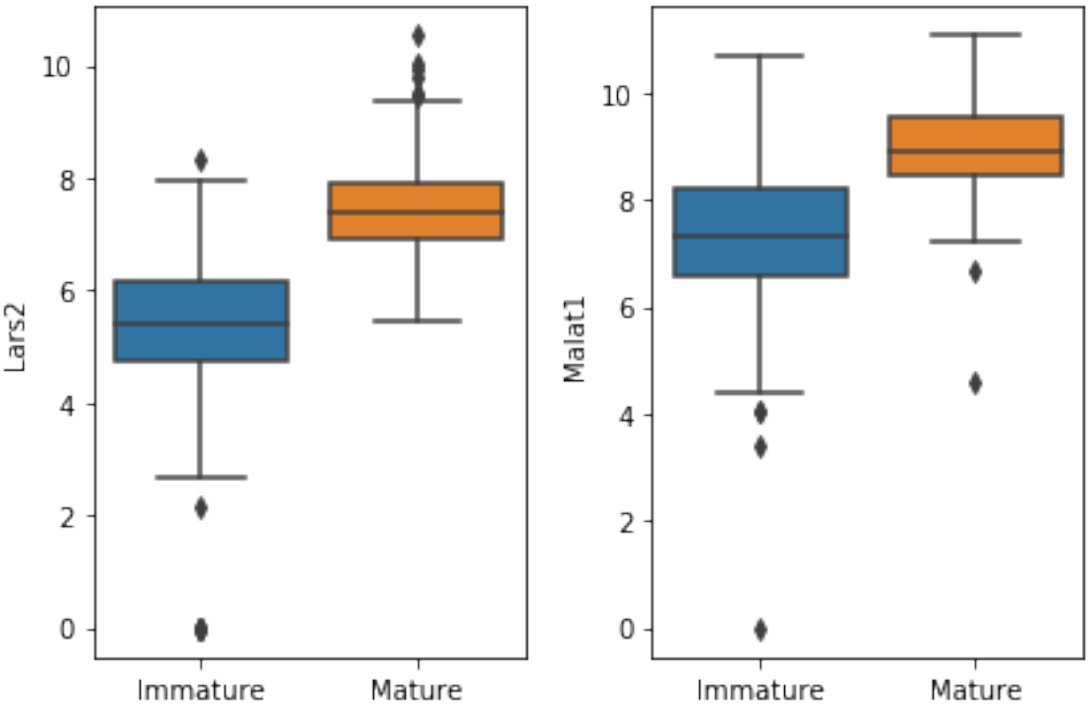
```
In [96]: import pandas as pd
         import numpy as np
         import matplotlib.pyplot as plt
         import seaborn as sns
         import statsmodels.formula.api as smf
```

```
In [97]: df = pd.read_csv('hw3_divseq_data.csv')
         df.head()
         # df.shape
```

```
Out[97]:    Lars2  Malat1  mature
         0   9.95    6.69       1
         1  10.54    8.53       1
         2   6.58    8.74       1
         3   7.49    9.09       1
         4   7.42    9.87       1
```

0.0.1 (a) boxplot

```
In [98]: fig, axs = plt.subplots(1,2)
         sns.boxplot(x='mature', y='Lars2', data=df, ax=axs[0]) # boxplot
         sns.boxplot(x='mature', y='Malat1', data=df, ax=axs[1])
         axs[0].set_xlabel('') # remove x_label
         axs[1].set_xlabel('')
         axs[0].set_xticklabels(['Immature', 'Mature']) # add x_ticklabels
         axs[1].set_xticklabels(['Immature', 'Mature'])

         fig.tight_layout()
         plt.show()
```



0.0.2 (b) comment

A classifier cannot perfectly predict a neuron's maturity based on Lars2, because Lar2 values of the 2 categories overlap with each other.

0.0.3 (c) logistic regression

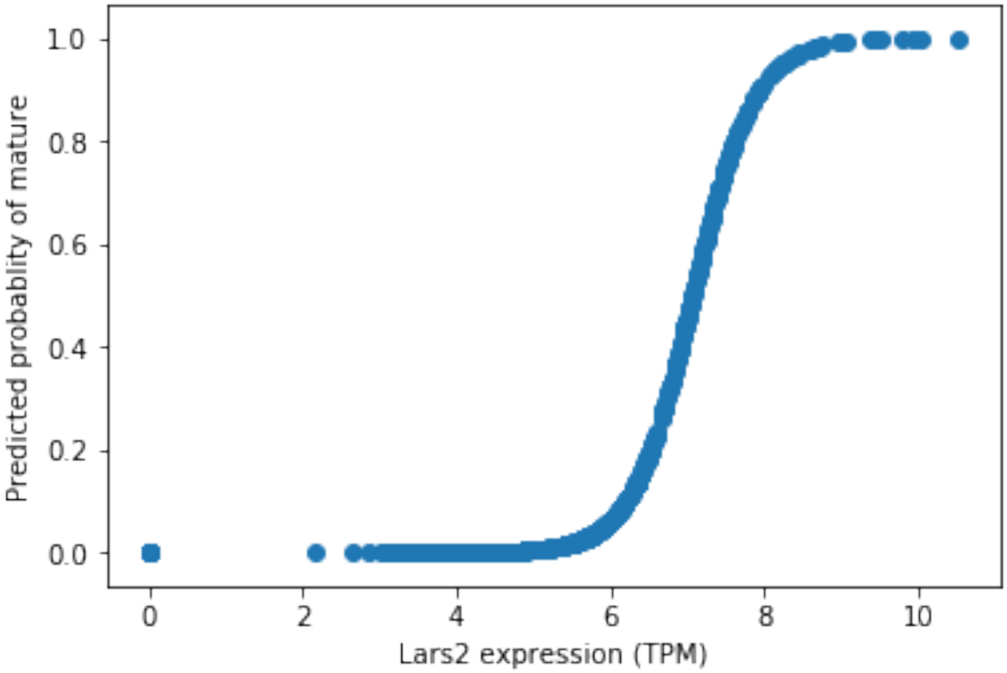
```
In [99]: res = smf.logit(formula='mature ~ Lars2', data=df).fit()
         print(res.summary())
         print(res.pvalues)
```

```
Optimization terminated successfully.
         Current function value: 0.235975
         Iterations 9
                           Logit Regression Results
==============================================================================
Dep. Variable:                 mature   No. Observations:                  817
Model:                          Logit   Df Residuals:                      815
Method:                           MLE   Df Model:                            1
Date:                Thu, 19 Oct 2017   Pseudo R-squ.:                  0.5310
Time:                        00:29:55   Log-Likelihood:                -192.79
converged:                       True   LL-Null:                       -411.04
                                        LLR p-value:                 6.284e-97
==============================================================================
                 coef    std err          z      P>|z|      [0.025      0.975]
------------------------------------------------------------------------------
Intercept    -17.9775      1.432    -12.556      0.000     -20.784     -15.171
Lars2          2.5422      0.209     12.191      0.000       2.134       2.951
==============================================================================
Intercept    3.679364e-36
Lars2        3.455778e-34
dtype: float64
```

P-value is 3.46e-34, which is very small, which indicates Lars2 expression level significantly associates with maturity.

0.0.4 (d)

```
In [100]: p_mature = res.predict(df.Lars2)
          fig, ax = plt.subplots()
          ax.scatter(df.Lars2, p_mature)
          ax.set_xlabel('Lars2 expression (TPM)')
          ax.set_ylabel('Predicted probablity of mature')
          plt.show()
```



Based on the plot, Lars2=8 indicates there is about 80% chance that neuron is mature.

0.0.5 (e) and (f)

```
In [101]: yhat = 1*(res.predict(df.Lars2) > 0.5)
          TP = FP = TN = FN = 0
          for y_i, yhat_i in zip(y, yhat):
              if (y_i, yhat_i) == (0, 0):
                  TN += 1
              elif (y_i, yhat_i) == (0, 1):
                  FP += 1
              elif (y_i, yhat_i) == (1, 0):
                  FN += 1
              elif (y_i, yhat_i) == (1, 1):
                  TP += 1

          print(TP, FP, TN, FN)

          sensitivity = TP/(TP + FN)
          specificity = TN/(TN + FP)
          print('Sensitivity is %f, and specificity is %f' % (sensitivity, specificity))
```

```
108 36 616 57
Sensitivity is 0.654545, and specificity is 0.944785
```

0.0.6 (g)

```
In [102]: yhat_2 = 1*(res.predict(df.Lars2) > 0.2)
          # repeat the previous calculation for yhat_2
          TP = FP = TN = FN = 0
          for y_i, yhat_i in zip(y, yhat_2):
              if (y_i, yhat_i) == (0, 0):
                  TN += 1
              elif (y_i, yhat_i) == (0, 1):
                  FP += 1
              elif (y_i, yhat_i) == (1, 0):
                  FN += 1
              elif (y_i, yhat_i) == (1, 1):
                  TP += 1

          print(TP, FP, TN, FN)

          sensitivity = TP/(TP + FN)
          specificity = TN/(TN + FP)
          print('Sensitivity is %f, and specificity is %f' % (sensitivity, specificity))
```

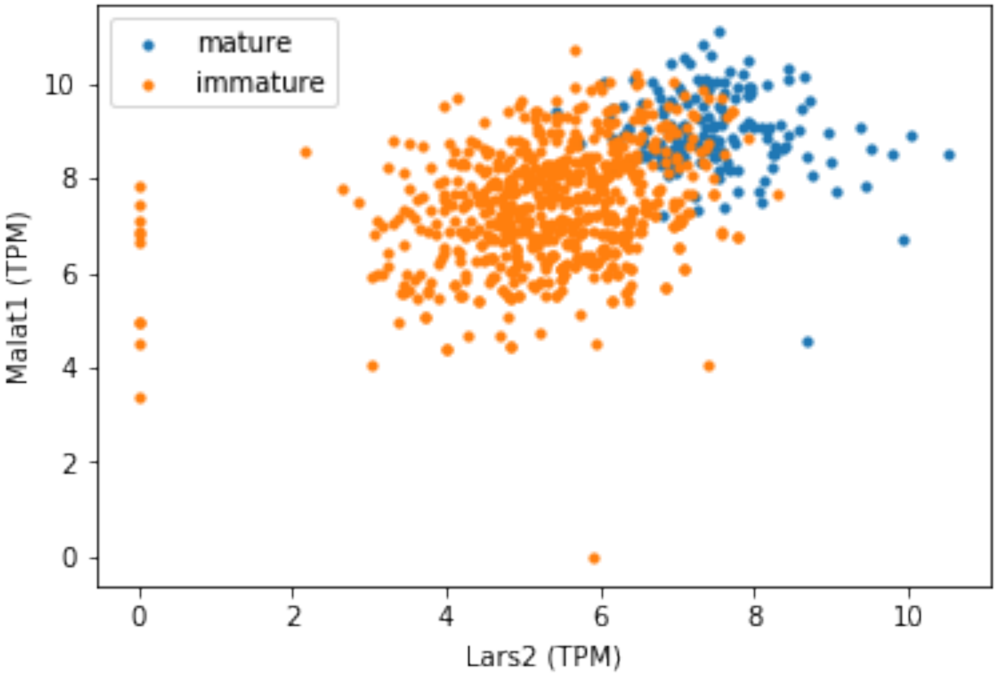
```
150 86 566 15
Sensitivity is 0.909091, and specificity is 0.868098
```

It's easier for a neuron to be classfied as mature for a threshold of 0.2 than for that of 0.5. So a mature cell should more likely to be (correctly) classified as mature, and immature cells are also more likely to be mislabelled as mature for a lower threshold.

Generally, in cases where we care sensitivity more than specificity, we might want to low down threshold. In this case, if we want to pick up neuron maturity in early stage, we could try using a low threshold.

0.0.7 (h)

```
In [103]: df_mature = df[df.mature==1]
          df_immature = df[df.mature==0]
          fig, ax = plt.subplots()
          ax.scatter(df_mature.Lars2, df_mature.Malat1, s=10, label='mature')
          ax.scatter(df_immature.Lars2, df_immature.Malat1, s=10, label='immature')
          ax.set_xlabel('Lars2 (TPM)')
          ax.set_ylabel('Malat1 (TPM)')
          ax.legend()
          plt.show()
```



0.0.8 (i)

```
In [104]: res_2 = smf.logit(formula='mature ~ Lars2 + Malat1', data=df).fit()
          res_2.summary()
```

```
Optimization terminated successfully.
         Current function value: 0.196827
         Iterations 9
```

```
Out[104]: <class 'statsmodels.iolib.summary.Summary'>
          """
                                     Logit Regression Results
          ==============================================================================
          Dep. Variable:                 mature   No. Observations:                  817
          Model:                          Logit   Df Residuals:                      814
          Method:                           MLE   Df Model:                            2
          Date:                Thu, 19 Oct 2017   Pseudo R-squ.:                  0.6088
          Time:                        00:30:01   Log-Likelihood:                -160.81
          converged:                       True   LL-Null:                       -411.04
                                                  LLR p-value:                 2.122e-109
          ==============================================================================
                           coef    std err          z      P>|z|      [0.025      0.975]
          ------------------------------------------------------------------------------
          Intercept    -25.5697      2.177    -11.743      0.000     -29.838     -21.302
          Lars2          2.3119      0.223     10.354      0.000       1.874       2.750
          Malat1         1.0836      0.156      6.941      0.000       0.778       1.390
          ==============================================================================
          """
```

Both predictors have significant effects.

0.0.9 (j)

```
In [105]: yhat_3 = 1*(res_2.predict(df[['Lars2', 'Malat1']]) > 0.5)

          # repeat the previous calculation for yhat_3
          TP = FP = TN = FN = 0
          for y_i, yhat_i in zip(y, yhat_3):
              if (y_i, yhat_i) == (0, 0):
                  TN += 1
              elif (y_i, yhat_i) == (0, 1):
                  FP += 1
              elif (y_i, yhat_i) == (1, 0):
                  FN += 1
              elif (y_i, yhat_i) == (1, 1):
                  TP += 1

          print(TP, FP, TN, FN)

          sensitivity = TP/(TP + FN)
          specificity = TN/(TN + FP)
          print('Sensitivity is %f, and specificity is %f' % (sensitivity, specificity))
```

```
120 34 618 45
Sensitivity is 0.727273, and specificity is 0.947853
```

Compared with the results of part (e), both sensitivity and specificity values here increases, indicating this new classifier with 2 predictors combined outperforms the one using only Lars2 as feature.

Solution to Question 4

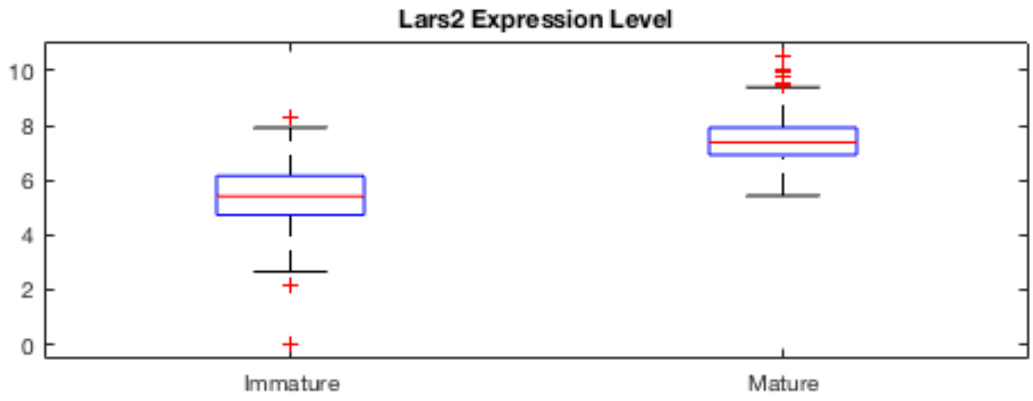
Contents

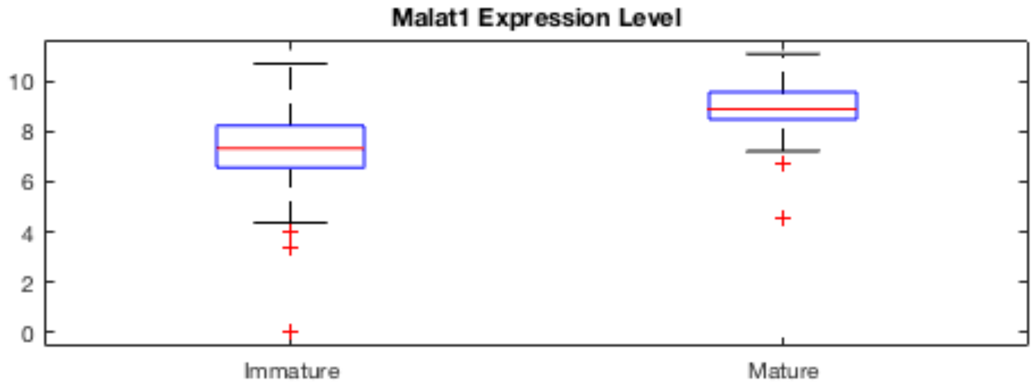
Read in

```
data = readtable('hw3_divseq_data.csv');
```

Part a - Create Boxplot of Mature vs Imature Neurons

```
subplot(2,1,1);
boxplot(data.Lars2, data.mature, 'Labels', {'Immature', 'Mature'});
title('Lars2 Expression Level');
subplot(2,1,2);
boxplot(data.Malat1, data.mature, 'Labels', {'Immature', 'Mature'});
title('Malat1 Expression Level');
```





Part b

Perfect prediction of mature vs non-mature neurons does not look possible for these two gene expression measures seperately, as the distibutions for gene expression are overlapping.

Part c - Fit Logistic Regression Using Lars2

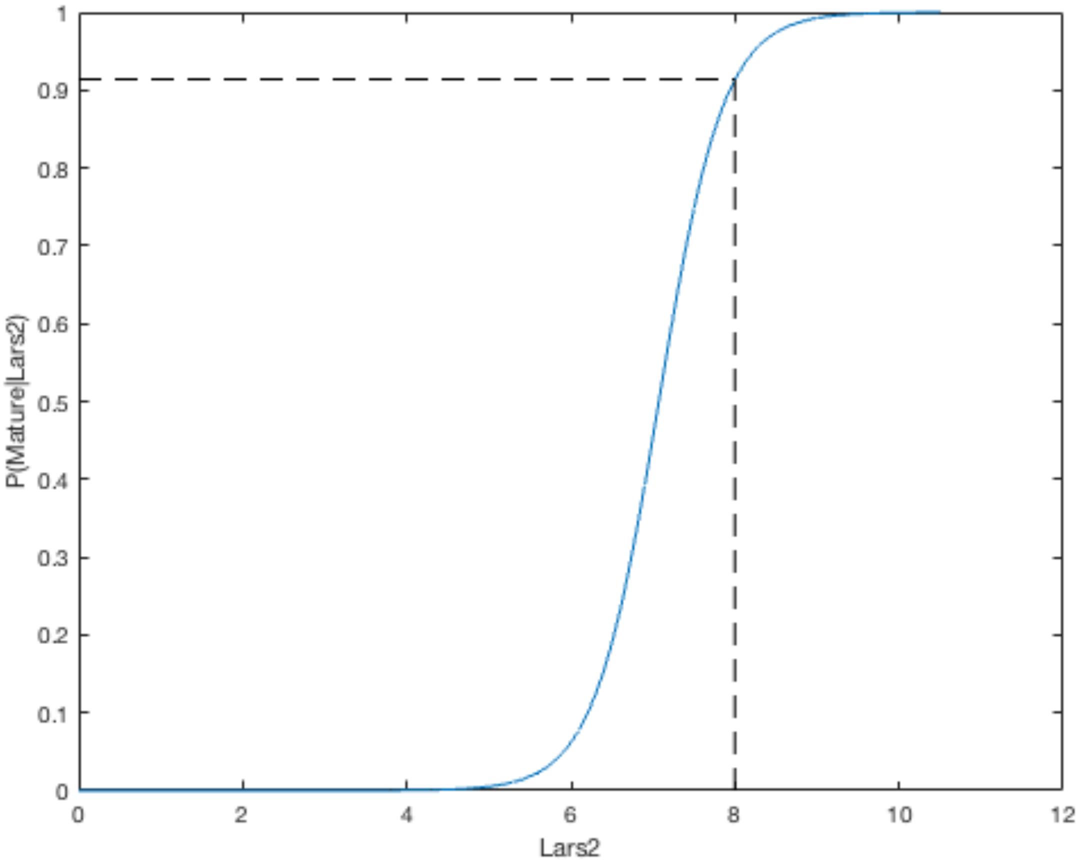
```
model = fitglm(data, 'mature~Lars2', 'distribution', 'binomial')
```

```
model = 


Generalized linear regression model:
    logit(mature) ~ 1 + Lars2
    Distribution = Binomial

Estimated Coefficients:
                   Estimate      SE        tStat       pValue  
                   ________    _______    _______    __________

    (Intercept)    -17.978      1.4318    -12.556    3.6794e-36
    Lars2           2.5422     0.20853     12.191    3.4558e-34


817 observations, 815 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 436, p-value = 6.28e-97
```

P value for slope coefficient is very low indicating that there is a significant effect. The positive slope means that increasing Lars2 expression increases the probability of the neuron being classified as mature.

Part d - Plot Relationship Between Lars2 Expression and Maturity Probability

```
clf
x= array2table([0:0.1:max(data.Lars2)]', 'VariableNames', {'Lars2'});
y_hat = predict(model, x);
plot(x.Lars2, y_hat);
xlabel('Lars2');
ylabel('P(Mature|Lars2)');
hold on
% Predict probability for Lars2 = 8
cell8 = array2table(8, 'VariableNames', {'Lars2'});
prob8 = predict(model, cell8);
% Plot lines on graph
plot([0, 8], [prob8, prob8], 'LineStyle', '--', 'color', 'black');
plot([8, 8], [0, prob8], 'LineStyle', '--', 'color', 'black');
```



Investigating the graph, the predicted probability of a Lars2=8 cell being mature is approximatly 0.9

Part e - Calculate Predicted Probabilities of for each cell

```
data.Predict_Lars2 = predict(model, data);
% Use Bayesian classifier (0.5 threshold)
data.Predict_Lars2_bayes = (data.Predict_Lars2 > 0.5);
% Calculate sensitivity
TP = sum(data.Predict_Lars2_bayes(logical(data.mature)) == 1);
sensitivity = TP/sum(data.mature)
```

```
sensitivity =

    0.6545
```

Part f - Calculate Specificity

```
FP = sum(data.Predict_Lars2_bayes(~data.mature) == 0);
specificity = FP/sum(~data.mature)
```

```
specificity =

    0.9448
```

Part g - Use 20% Threshold Classifier

```
data.Pred_20perc = (data.Predict_Lars2 > 0.2);
% Calculate sensitivity
TP = sum(data.Pred_20perc(logical(data.mature)) == 1);
sensitivity = TP/sum(data.mature)

% Calculate Specificity
FP = sum(data.Pred_20perc(~data.mature) == 0);
specificity = FP/sum(~data.mature)
```

```
sensitivity =

    0.9091


specificity =

    0.8681
```

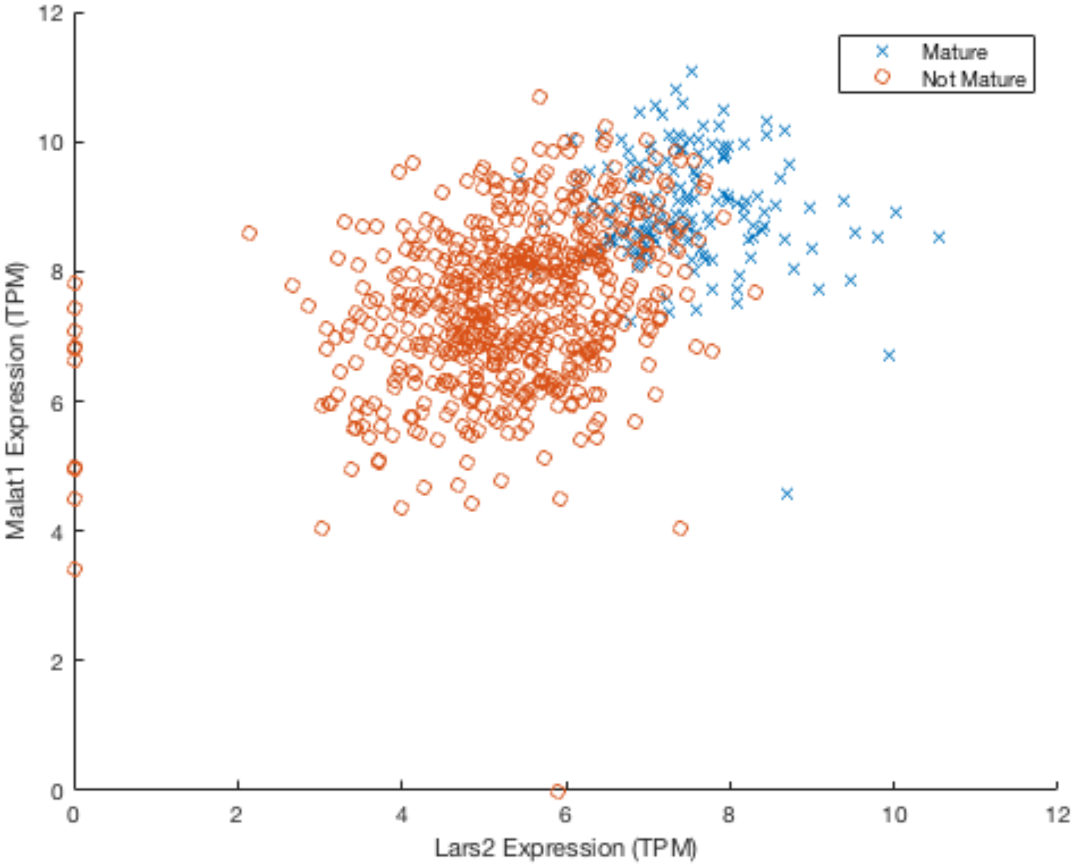
The sensitivity went up because with a lower threshold more cell are being classified as mature. The specificty went down as some of these cell were incorrectly classifed to be mature when in fact they were immature

You may want to use a 20% threshold when you are attempting to classify neurons as mature at an earlier timepoint.

You may also want a threshold of 20% when you care more about specificity than you do about sensitivity.

Part h - Make a 2D Scatter Plot of Expression for the Two Genes

```
clf
mature_ind = logical(data.mature);
scatter(data.Lars2(mature_ind), data.Malat1(mature_ind), 'Marker', 'x', 'DisplayName', 'Mat
ure');
hold on
scatter(data.Lars2(~mature_ind), data.Malat1(~mature_ind), 'Marker', 'o', 'DisplayName', 'N
ot Mature');
xlabel('Lars2 Expression (TPM)');
ylabel('Malat1 Expression (TPM)');
legend('show');
```



Part i - Fit Logistic Regression Using both Lars2 and Malat1 as Predictors

```
model = fitglm(data, 'mature ~ Lars2 + Malat1',  'distribution', 'binomial')
```

```
model = 


Generalized linear regression model:
    logit(mature) ~ 1 + Lars2 + Malat1
    Distribution = Binomial

Estimated Coefficients:
                   Estimate      SE        tStat       pValue  
                   ________    _______    _______    __________

    (Intercept)    -25.57       2.1775    -11.743    7.6914e-32
    Lars2          2.3119      0.22328     10.354    3.9955e-25
    Malat1         1.0836      0.15611     6.9413    3.8856e-12


817 observations, 814 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 500, p-value = 2.12e-109
```

Given the very low P-values both the gene expression variables have a significant effect

Part j - Calculate sensitivity and specificity

```
data.Preict_Larst2_Malat1 = predict(model, data);
% Use Bayesian classifier (0.5 threshold)
```

```
y_hat = (data.Preict_Larst2_Malat1 > 0.5);
% Calculate sensitivity
TP = sum(y_hat(logical(data.mature)) == 1);
sensitivity = TP/sum(data.mature)

% Calculate Specificity
FP = sum(y_hat(~data.mature) == 0);
specificity = FP/sum(~data.mature)
```

```
sensitivity =

    0.7273


specificity =

    0.9479
```

Compared with the results of part (e), both sensitivity and specificity values here increases, indicating this new classifier with 2 predictors combined outperforms the one using only Lars2 as feature.

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