NYCU Pattern Recognition, Homework 1

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Part. 1, Coding (70%):

1. (0%) Show the learning rate and epoch you choose

2. (5%) Show the weights and intercepts of your linear model.

weights: __1382.536816__ intercepts: __380.13465625__

Intercepts: [1382.536816]
Weights: [380.13465625]

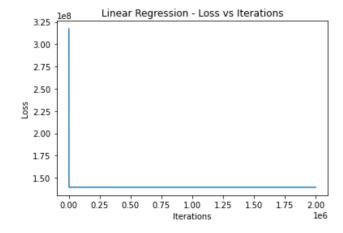
3. (5%) What's your final training loss (MSE)? training loss (MSE): 139562065.48342776

training loss: 139562065.48342776

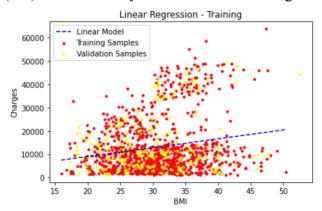
4. (5%) What's the MSE of your validation prediction and validation ground truth? validation loss (MSE): __136920284.33792174__

validation loss: 136920284.33792174

5. (5%) Plot the training curve. (x-axis=epoch, y-axis=loss)



6. (5%) Plot the line you find with the training and validation data.



7. (0%) Show the learning rate and epoch you choose.

learning rate: __5e-4__ epoch: __2500000__

8. (10%) Show the weights and intercepts of your linear model.

weights:

[[259.85086355] [-383.54525304] [333.33251186] [442.55747612] [24032.22098955] [-416.01438888]] intercepts: __-11857.05721739__

Intercepts: [-11857.05721739]
Weights:
 [[259.85086355]
 [-383.54525304]
 [333.33251186]
 [442.55747612]
 [24032.22098955]

[-416.01438888]]

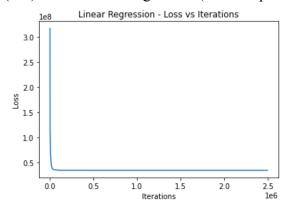
9. (5%) What's your final training loss? training loss (MSE): 34697170.25351918

training loss: 34697170.25351918

10. (5%) What's the MSE of your validation prediction and validation ground truth? validation loss (MSE): __41958565.746851996__

validation loss: 41958565.746851996

11. (5%) Plot the training curve. (x-axis=epoch, y-axis=loss)



12. (20%) Train your own model and fill the testing CSV file as your final predictions.

learning rate: 5e-4 epoch: 1000000

batch size: x train.shape[0]

Used features: age, bmi, children, female, male, smoker_no, smoker_yes, northeast,

northwest, southeast, southwest, age*smoker yes, bmi*smoker yes,

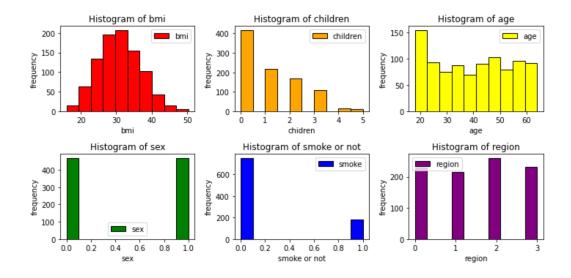
bmi bins smoker yes

(1) Data Analysis

a. Histogram Plot

After doing the Label_Encoding(), I plotted the histograms to see the distributions of each feature. We can observe that:

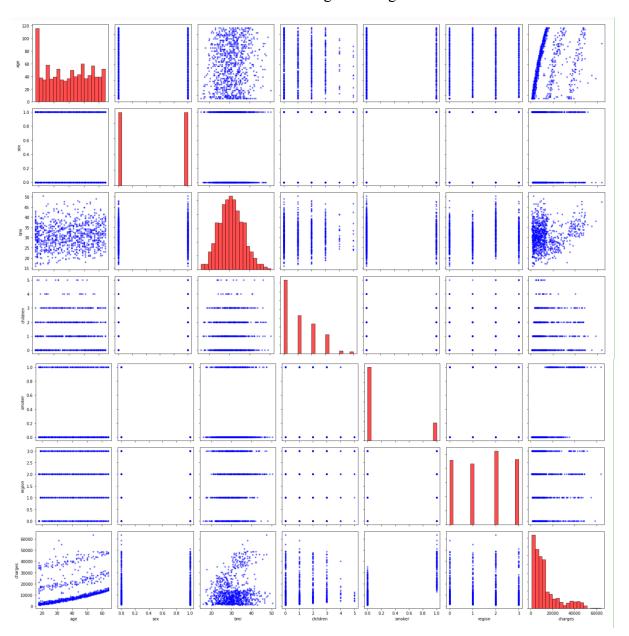
- The bmi distribution is nearly normal distributed.
- There is little difference between the percentage of male and female.
- There is little difference between the percentage of each region.
- Most people in the training dataset do not smoke.



b. Pair_Plot

After doing the Label_Encoding(), I plotted the pair correlation between each feature. We can observe that:

- The higher the age, the higher the insurance value.
- The higher the bmi, the higher the insurance value.
- A non-smoker has less insurance than a smoker.
- The amount of insurance according to gender is similar.
- The value of the insurance according to the region is also similar.



c. Correlation Analysis

After doing the Dummy_Encoding(), I printed the correlation coefficient between each feature by calling df.corr(). We can observe that **charges** has positive correlation with **age**, **bmi**, and especially high positive correlation with **smoker_yes**. Therefore, I considered these features to do the feature engineering.

```
bmi children
                                         charges
                                                   female
                age
                                                               male
age
           1.000000 0.105642 0.033802
                                        0.324213
                                                 0.053253 -0.053253
hmi
           0.105642 1.000000 0.025009
                                        0.189973 -0.015213 0.015213
children 0.033802 0.025009 1.000000 0.048509 0.023992 0.023992
          charges
female
           0.053253 -0.015213 -0.023992 -0.025908
                                                 1.000000 -1.000000
          -0.053253 0.015213 0.023992 0.025908 -1.000000 1.000000
male
smoker_no 0.004509 0.005701 0.012050 -0.789616 0.068751 -0.068751
smoker yes -0.004509 -0.005701 -0.012050 0.789616 -0.068751 0.068751
northeast 0.018921 -0.118775 0.013761 0.031987 -0.001270 0.001270
northwest 0.002003 -0.139207 -0.009561 -0.045389 -0.019092 0.019092
southeast -0.041123 0.252034 -0.022976
                                        0.060100
                                                 0.032250 -0.032250
southwest 0.021920 -0.007685 0.019493 -0.049981 -0.013603 0.013603
           smoker_no smoker_yes northeast northwest southeast southwest
           0.004509 -0.004509 0.018921 0.002003 -0.041123
                                                                0.021920
age
bmi
           0.005701
                      -0.005701 -0.118775 -0.139207
                                                      0.252034 -0.007685
                     -0.012050 0.013761 -0.009561 -0.022976 0.019493
children
           0.012050
           -0.789616   0.789616   0.031987   -0.045389   0.060100   -0.049981
charges
           0.068751 -0.068751 -0.001270 -0.019092 0.032250 -0.013603
female
male
           -0.068751 0.068751 0.001270 0.019092 -0.032250 0.013603

      smoker_no
      1.000000
      -1.000000
      -0.012993
      0.040628
      -0.070703
      0.046728

      smoker_yes
      -1.000000
      1.000000
      0.012993
      -0.040628
      0.070703
      -0.046728

northwest 0.040628 -0.040628 -0.310851 1.000000 -0.339613 -0.313545
southeast -0.070703 0.070703 -0.352875 -0.339613 1.000000 -0.355932
southwest 0.046728 -0.046728 -0.325789 -0.313545 -0.355932 1.000000
```

(2) Feature Engineering

I have added three features. For **age*smoker_yes** and **bmi*smoker_yes**, I multiplied the two specific features, since they are all positively correlated with **charges**. For **bmi_bins_smoker_yes**, I used discretization of the feature to split it into multiple new features which can compile significant interactions to our feature matrix.

```
def Dummy_Encoding(df):
    sex_dummy = pd.get_dummies(df['sex'])
    smoker_dummy = pd.get_dummies(df['region'])
    region_dummy = pd.get_dummies(df['region'])
    df = pd.concat([df,sex_dummy,smoker_dummy,region_dummy], axis=1)
    df.rename(columns={'no': 'smoker_no', 'yes': 'smoker_yes'}, inplace=True)
    df = df.drop(['sex','smoker','region'], axis=1)
    return df

def Feature_Generating(df):
    df['age*smoker_yes'] = df.age * df.smoker_yes
    df['bmi*smoker_yes'] = df.bmi * df.smoker_yes
    df['bmis_smoker_yes'] = pd.cut(x=df['bmi']*df.smoker_yes, bins=df['bmi'].quantile([0, .25, .5, .75, 1.]))
    df = pd.get_dummies(df)
    return df
```

(3) Parameter Tuning

Part. 2, Questions (30%):

(7%) 1. What's the difference between Gradient Descent, Mini-Batch Gradient Descent, and Stochastic Gradient Descent?

• Gradient Descent:

When doing every gradient descent process, all the training data is taken into consideration to compute the gradient and take a single step.

• Mini-Batch Gradient Descent:

When doing every gradient descent process, a batch of a fixed number of training examples is taken into consideration to compute the gradient and take a single step.

• Stochastic Gradient Descent:

When doing every gradient descent process, **only one example** is taken into consideration to compute the gradient and take a single step.

(7%) 2. Will different values of learning rate affect the convergence of optimization? Please explain in detail.

Yes, the value of learning rate can affect the convergence of optimization greatly. If the learning rate is **too small**, the optimization process may take a long time to converge or even get stuck in local minimum. If the learning rate is **too large**, the optimization may oscillate around the minimum or diverge. A proper learning rate should be chosen based on the problem specification and the optimization algorithm which is being used. If the convergence is too slow, the learning rate can be increased; if the optimization diverges, the learning rate should be decreased.

(8%) 3. Suppose you are given a dataset with two variables, X and Y, and you want to perform linear regression to determine the relationship between these variables. You plot the data and notice that there is a strong nonlinear relationship between X and Y. Can you still use linear regression to analyze this data? Why or why not? Please explain in detail.

If there is a strong **nonlinear relationship** between X and Y, linear regression may not be the best method to analyze the data since linear regression assumes that there is a linear relationship between the X and Y. However, if the nonlinearity is not severe, it may still be possible to use linear regression by transforming the variables or by adding polynomial terms to the model. If the nonlinearity is too strong, it may be necessary to use nonlinear regression techniques or other methods which can model more complex relationships between variables.

(8%) 4. In the coding part of this homework, we can notice that when we use more features in the data, we can usually achieve a lower training loss. Consider two sets of features, A and B, where B is a subset of A. (1) Prove that we can achieve a non-greater training loss when we use the features of set A rather than the features of set B. (2) In what situation will the two training losses be equal?

- 1) For linear regression, we are solving the problem by minimizing MSE = (1/n) * sum[(Wx+b) t]^2. Since B is a subset of A, using the features of set A can cover the case of using the features of set B. Therefore, the model trained with the features of set A can achieve the same or lower training loss than the model trained with the features of set B, since set A has provided more information while training.
- 2) When the features in set A and set B have exactly the same fitting ability to the training data (ex: set B contains all the features in feature set A and no additional features) or when the weights of features in set(A-B) is zero, then the training losses of the models trained with feature set A and feature set B will be equal.

It is possible that using all the features in set A may lead to a lower training loss rather than set B. However, using additional features can also add more noise and overfitting to the model.