HW10

March 26, 2019

1 HW 10 - KELLY "SCOTT" SIMS

```
In [457]: import pandas as pd
          import numpy as np
          import matplotlib.pyplot as plt
          import seaborn as sns
          from IPython.display import display
          import warnings
          warnings.filterwarnings("ignore")
```

Question 14.1

The breast cancer data set breast-cancer-wisconsin.data.txt from http://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer-wisconsin/ (description at http://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+%28Original%29) has missing values. 1. Use the mean/mode imputation method to impute values for the missing data. 2. Use regression to impute values for the missing data. 3. Use regression with perturbation to impute values for the missing data. 4. (Optional) Compare the results and quality of classification models (e.g., SVM, KNN) build using (1) the data sets from questions 1,2,3; (2) the data that remains after data points with missing values are removed; and (3) the data set when a binary variable is introduced to indicate missing values.

```
In [340]: columns = ['id_number', 'clump_thick', 'cell_size' , 'cell_shape' , 'marginal_adhesi
                      'single_epithelial_size','bare_nuclei','bland_chromatin', 'normal_nucleoli
          df = pd.read_csv('breast-cancer-wisconsin.data.txt', header=None, names=columns)
          df.head()
```

```
Out[340]:    id_number  clump_thick  cell_size  cell_shape  marginal_adhesion  \
          0    1000025            5          1           1                  1
          1    1002945            5          4           4                  5
          2    1015425            3          1           1                  1
          3    1016277            6          8           8                  1
          4    1017023            4          1           1                  3

             single_epithelial_size bare_nuclei  bland_chromatin  normal_nucleoli  \
          0                       2           1                3                1
          1                       7          10                3                2
          2                       2           2                3                1
          3                       3           4                3                7
```

```
4                        2            1                 3                 1

   mitoses  class
0        1      2
1        1      2
2        1      2
3        1      2
4        1      2
```

```
In [341]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 699 entries, 0 to 698
Data columns (total 11 columns):
id_number                   699 non-null int64
clump_thick                 699 non-null int64
cell_size                   699 non-null int64
cell_shape                  699 non-null int64
marginal_adhesion           699 non-null int64
single_epithelial_size      699 non-null int64
bare_nuclei                 699 non-null object
bland_chromatin             699 non-null int64
normal_nucleoli             699 non-null int64
mitoses                     699 non-null int64
class                       699 non-null int64
dtypes: int64(10), object(1)
memory usage: 60.1+ KB
```

It appears that all columns are of type integer except **bare_nuclei**. Since it is of type "object", it must have some values other than integers representative of missing values. Let's inspect a little further

```
In [342]: df['bare_nuclei'].unique()
```

```
Out[342]: array(['1', '10', '2', '4', '3', '9', '7', '?', '5', '8', '6'],
                dtype=object)
```

There is a question mark used as a placeholder for missing values. Let's see all instances of these missing values.

```
In [343]: print(len(df[df.bare_nuclei == '?']))
          df[df.bare_nuclei == '?']
```

```
16
```

```
Out[343]:      id_number  clump_thick  cell_size  cell_shape  marginal_adhesion  \
          23     1057013            8          4           5                  1
```

```
40     1096800            6          6           6                 9
139    1183246            1          1           1                 1
145    1184840            1          1           3                 1
158    1193683            1          1           2                 1
164    1197510            5          1           1                 1
235    1241232            3          1           4                 1
249     169356            3          1           1                 1
275     432809            3          1           3                 1
292     563649            8          8           8                 1
294     606140            1          1           1                 1
297      61634            5          4           3                 1
315     704168            4          6           5                 6
321     733639            3          1           1                 1
411    1238464            1          1           1                 1
617    1057067            1          1           1                 1

     single_epithelial_size bare_nuclei  bland_chromatin  normal_nucleoli  \
23                        2           ?                7                3
40                        6           ?                7                8
139                       1           ?                2                1
145                       2           ?                2                1
158                       3           ?                1                1
164                       2           ?                3                1
235                       2           ?                3                1
249                       2           ?                3                1
275                       2           ?                2                1
292                       2           ?                6               10
294                       2           ?                2                1
297                       2           ?                2                3
315                       7           ?                4                9
321                       2           ?                3                1
411                       1           ?                2                1
617                       1           ?                1                1

     mitoses  class
23         1      4
40         1      2
139        1      2
145        1      2
158        1      2
164        1      2
235        1      2
249        1      2
275        1      2
292        1      4
294        1      2
297        1      2
315        1      2
```

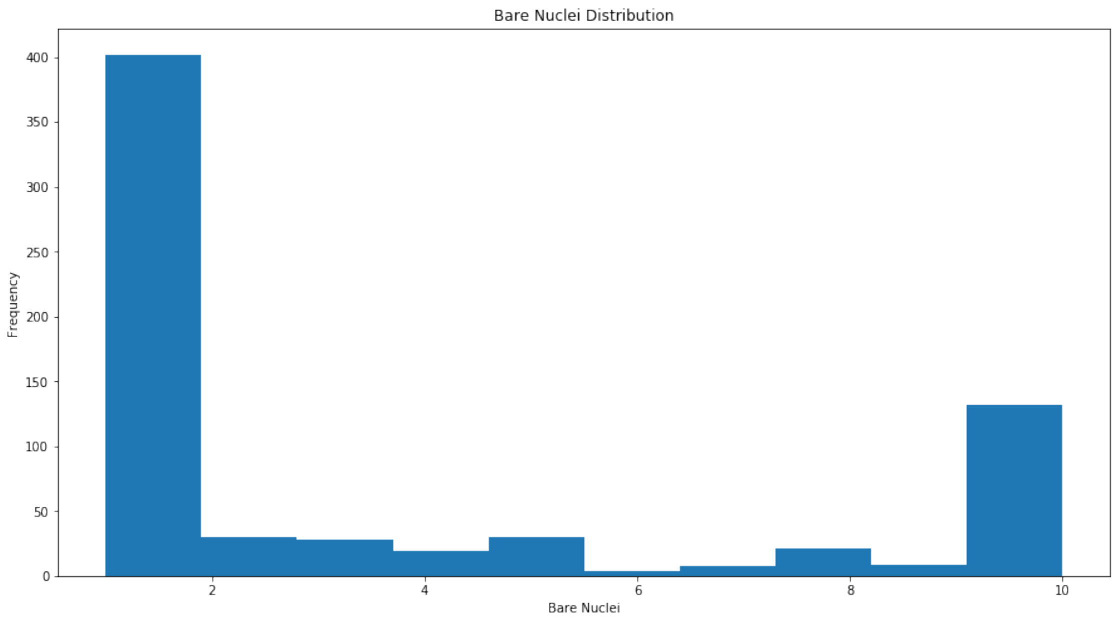
```
321          1        2
411          1        2
617          1        2
```

There are 16 missing values in the bare_nuclei column. We impute using mean/mode method first

1.1 # 1. Mean/Mode Imputation

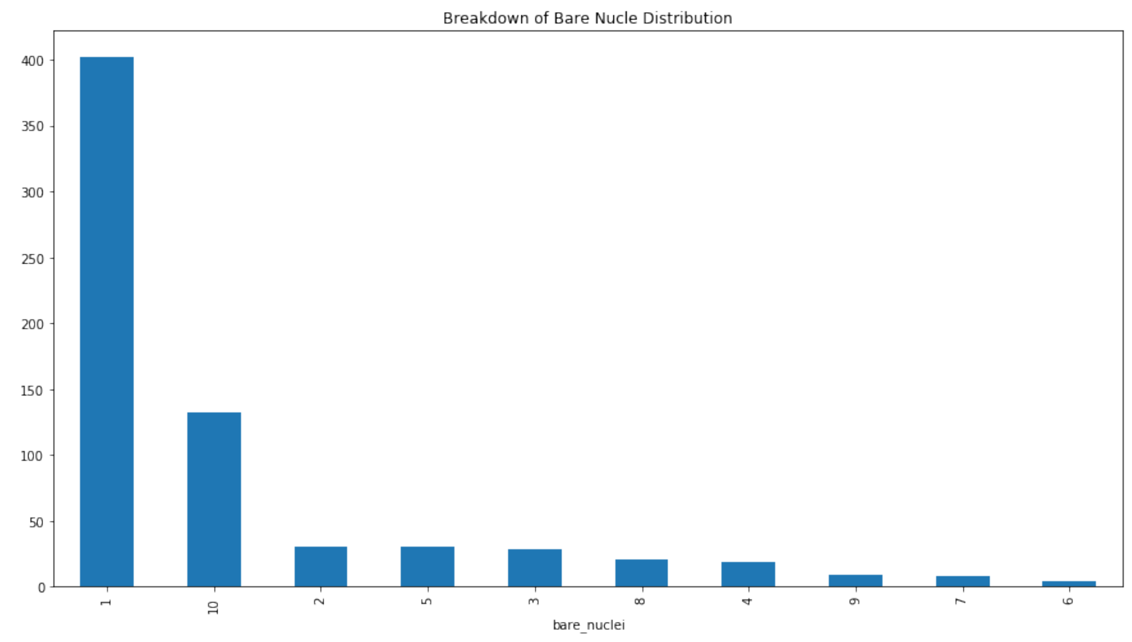
The reason why it is the "mean/mode" imputation is because the method you use is dependent on the distribution of values for that feature. Mean is very sensitive to skew and outlier. Because of this, it should only be used when the distribution is normal. Anything but normal, then we should use the mode. Let's check the distribution of bare_nuclei

```
In [344]: df[df.bare_nuclei != '?'].bare_nuclei.astype('int').plot(kind = 'hist', figsize = (1
          plt.xlabel('Bare Nuclei')
          plt.show()
```



It's very clear that Bare Nuclei is not normally distributed. Therefore, we will use the mode

```
In [345]: df[df.bare_nuclei !='?'].groupby('bare_nuclei', as_index = False)['class']\
                                       .count().sort_values('class',ascending =False)\
                                       .set_index('bare_nuclei')\
                                       .plot(kind = 'bar',
                                            title = 'Breakdown of Bare Nucle Distribution',
                                            figsize=(15,8),
                                            legend=False)
          plt.show()
```



It's clear that 1 is the mode. This is the value we will use for the imputation

```
In [563]: mode_df = df.copy()
          mode_df['bare_nuclei'] = df.bare_nuclei.replace('?', 1).astype('int')
```

```
In [564]: mode_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 699 entries, 0 to 698
Data columns (total 11 columns):
id_number                 699 non-null int64
clump_thick               699 non-null int64
cell_size                 699 non-null int64
cell_shape                699 non-null int64
marginal_adhesion         699 non-null int64
single_epithelial_size    699 non-null int64
bare_nuclei               699 non-null int64
bland_chromatin           699 non-null int64
normal_nucleoli           699 non-null int64
mitoses                   699 non-null int64
class                     699 non-null int64
dtypes: int64(11)
memory usage: 60.1 KB
```

We have imputed all the missing values and now all of our columns are integers as well

2 2. Use Regression to Impute

```
In [348]: from sklearn.model_selection import train_test_split
          from sklearn.preprocessing import MinMaxScaler
```

First we need to remove those observations where data is missing

```
In [512]: train_df = df.copy()
          unknown_df = df.copy()

          train_df = df[df.bare_nuclei !='?']
          unknown_df = df[df.bare_nuclei == '?']
```

```
In [507]: unknown_df.head()
```

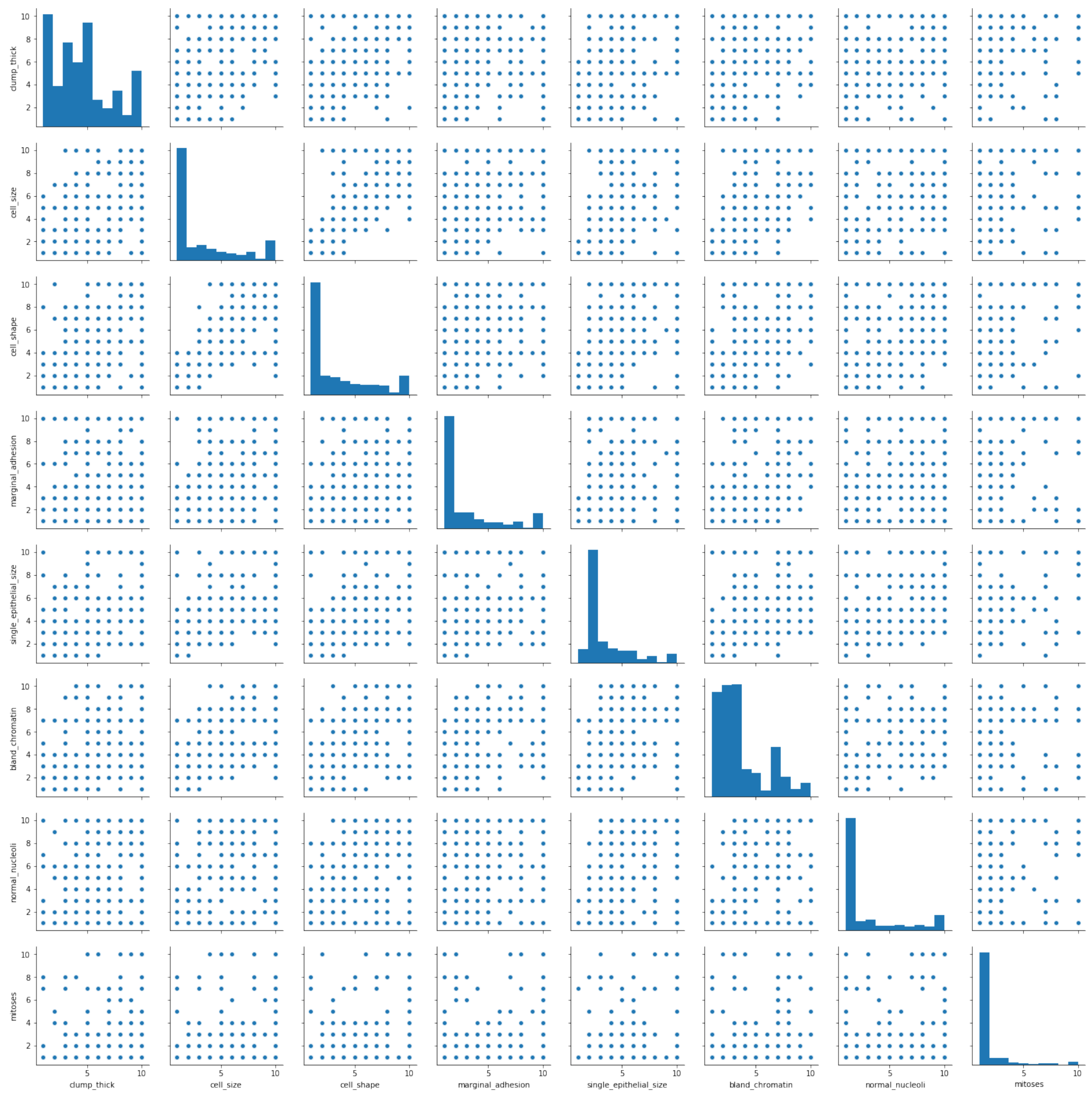
```
Out[507]:      id_number  clump_thick  cell_size  cell_shape  marginal_adhesion  \
          23     1057013            8          4           5                  1
          40     1096800            6          6           6                  9
          139    1183246            1          1           1                  1
          145    1184840            1          1           3                  1
          158    1193683            1          1           2                  1

               single_epithelial_size bare_nuclei  bland_chromatin  normal_nucleoli  \
          23                        2           ?                7                3
          40                        6           ?                7                8
          139                       1           ?                2                1
          145                       2           ?                2                1
          158                       3           ?                1                1

               mitoses  class
          23         1      4
          40         1      2
          139        1      2
          145        1      2
          158        1      2
```

We have our train data and our test data. Next we need separate the training data into train and validation sets while removing the target variable **bare_nuclei** and the ultimate variable being predicted **class**. We need to remove class because training a model with knowledge of what the ultimate variable interest is, is known as **Data Leakage**, and we don't want to train such a model. Finally, we can remove id_number since the identification of a patient should bear no weight on the classification of a tumor. Conversely, depending on the data, it could also be a form of data leakage. If a particular ID number is represented more than once in a data set, it might lead to bias if that particular ID is ever predicted upon again.

```
In [513]: #Remove the target class and ultimate class to avoid data leakage
          X_train = train_df[[x for x in df.columns if x not in ['class', 'bare_nuclei', 'id_nu
          y_train = train_df['bare_nuclei']
```

```
        #Perform the same procedure for the data that needs to be predicted upon
        X_unknown = unknown_df[[x for x in unknown_df.columns if x not in ['class', 'bare_nuc
```

```
In [463]: sns.pairplot(X_train)
          plt.show()
```



There appears to be strong correlation betweel **cell_shape** and **cell_size**. Let's see how strong of a correlation it is

```
In [464]: print('Pearson Correlation factor between cell shape and size: {}'.format(X_train.co
```

```
Pearson Correlation factor between cell shape and size: 0.9072282331914379
```

just as anticipated, there is a high correlation between **cell_shape** and **cell_size**. As a sanity check, let's see all correlation values

```
In [465]: X_train.corr()
```

```
Out[465]:                         clump_thick  cell_size  cell_shape  marginal_adhesion  \
          clump_thick                1.000000   0.642481    0.653470           0.487829
          cell_size                  0.642481   1.000000    0.907228           0.706977
          cell_shape                 0.653470   0.907228    1.000000           0.685948
          marginal_adhesion          0.487829   0.706977    0.685948           1.000000
          single_epithelial_size     0.523596   0.753544    0.722462           0.594548
          bland_chromatin            0.553742   0.755559    0.735344           0.668567
          normal_nucleoli            0.534066   0.719346    0.717963           0.603121
          mitoses                    0.350957   0.460755    0.441258           0.418898

                                  single_epithelial_size  bland_chromatin  \
          clump_thick                           0.523596         0.553742
          cell_size                             0.753544         0.755559
          cell_shape                            0.722462         0.735344
          marginal_adhesion                     0.594548         0.668567
          single_epithelial_size                1.000000         0.618128
          bland_chromatin                       0.618128         1.000000
          normal_nucleoli                       0.628926         0.665602
          mitoses                               0.480583         0.346011

                                  normal_nucleoli   mitoses
          clump_thick                    0.534066  0.350957
          cell_size                      0.719346  0.460755
          cell_shape                     0.717963  0.441258
          marginal_adhesion              0.603121  0.418898
          single_epithelial_size         0.628926  0.480583
          bland_chromatin                0.665602  0.346011
          normal_nucleoli                1.000000  0.433757
          mitoses                        0.433757  1.000000
```

There's relatively high correlation between **cell_size** and **single_epithelial_size** as well as **bland_chromatin** and **normal_nucleoli**. Conversely, with **cell_shape**, there's relatively high correlation wih **single_epithelial_size**, **bland_chromatin** and **normal_nucleoli**. Let's progress by dropping **cell_shape** since it had 90% correlation with **cell_size**. By dropping that feature, that automatically drops the corresponding high correlations with the other features.

```
In [509]: X_train = X_train[[x for x in X_train.columns if x not in ['cell_shape']]]
          X_unknown = X_unknown[[x for x in X_unknown.columns if x not in ['cell_shape']]]
```

```
In [510]: X_train.head()
```

```
Out[510]:    clump_thick  cell_size  marginal_adhesion  single_epithelial_size  \
          0            5          1                  1                       2
          1            5          4                  5                       7
```

```
2            3          1                  1                       2
3            6          8                  1                       3
4            4          1                  3                       2

   bland_chromatin  normal_nucleoli  mitoses
0                3                1        1
1                3                2        1
2                3                1        1
3                3                7        1
4                3                1        1
```

```
In [511]: X_unknown.head()
```

```
Out[511]:      clump_thick  cell_size  marginal_adhesion  single_epithelial_size  \
          23             8          4                  1                       2
          40             6          6                  9                       6
          139            1          1                  1                       1
          145            1          1                  1                       2
          158            1          1                  1                       3

               bland_chromatin  normal_nucleoli  mitoses
          23                 7                3        1
          40                 7                8        1
          139                2                1        1
          145                2                1        1
          158                1                1        1
```

```
In [469]: #Perform a 70/30 train - validate split
          train, val, y_train, y_val = train_test_split(X_train, y_train, test_size=0.30, rand
```

Now that we have prepared our data by removing the target variable from the training data, scaling the data, and splitting the training data into 60% training set and 40% validation set, we can now tune a regression model

```
In [447]: from sklearn.linear_model import LinearRegression, Ridge, Lasso
```

```
In [448]: lm = LinearRegression()
          lr = Ridge(alpha = 0.1)
          ls = Lasso(alpha = 0.1)
```

```
In [449]: lm.fit(train, y_train)
          lr.fit(train, y_train)
          ls.fit(train, y_train)
```

```
Out[449]: Lasso(alpha=0.1, copy_X=True, fit_intercept=True, max_iter=1000,
             normalize=False, positive=False, precompute=False, random_state=None,
             selection='cyclic', tol=0.0001, warm_start=False)
```

```
In [450]: print('TRAINING DATA R^2 SCORE')
          print('------------------------')
          print('Linear Regression Model: {} R^2'.format(lm.score(train,y_train)))
          print('Ridge Linear Regression: {} R^2'.format(lr.score(train,y_train)))
          print('Lasso Linear Regression: {} R^2'.format(ls.score(train,y_train)))
```

```
TRAINING DATA R^2 SCORE
-----------------------
Linear Regression Model: 0.5930626354976749 R^2
Ridge Linear Regression: 0.593062635341173 R^2
Lasso Linear Regression: 0.5926503963396388 R^2
```

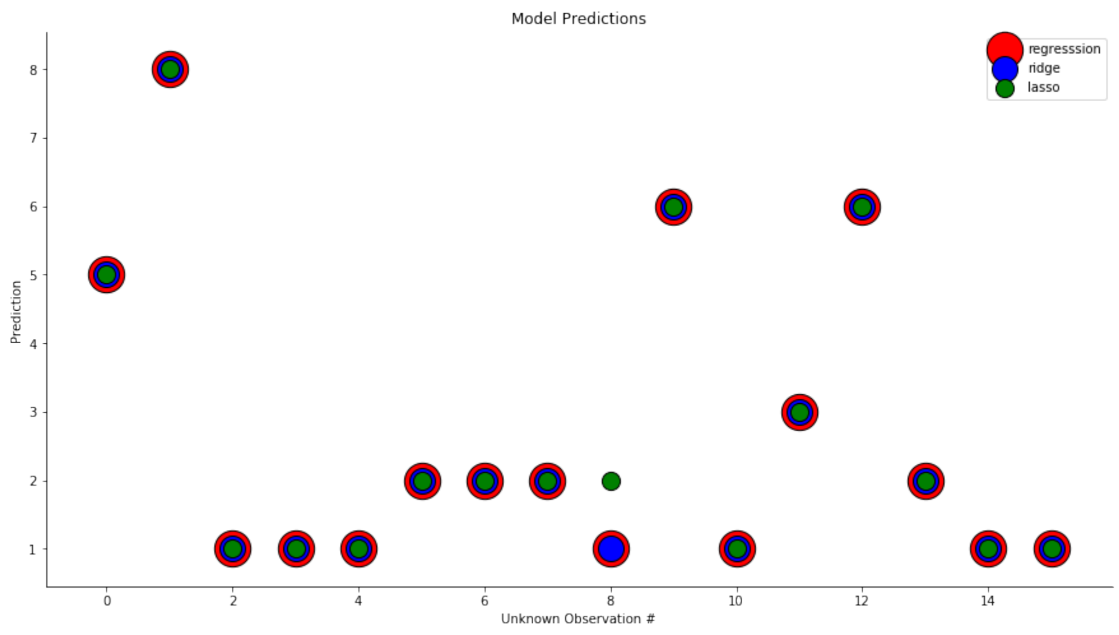
```
In [451]: print('VALIDATION DATA R^2 SCORE')
          print('-------------------')
          print('Linear Regression Model: {} R^2'.format(lm.score(val, y_val)))
          print('Ridge Linear Regression: {} R^2'.format(lr.score(val,y_val)))
          print('Lasso Linear Regression: {} R^2'.format(ls.score(val,y_val)))
```

```
VALIDATION DATA R^2 SCORE
-------------------
Linear Regression Model: 0.6208451201327663 R^2
Ridge Linear Regression: 0.6208448338570569 R^2
Lasso Linear Regression: 0.6193526481579414 R^2
```

Ridge regression and normal linear regression appear to be performing the best intially. Let's predict on the unknown data and compare predicitons amongst all 3 models

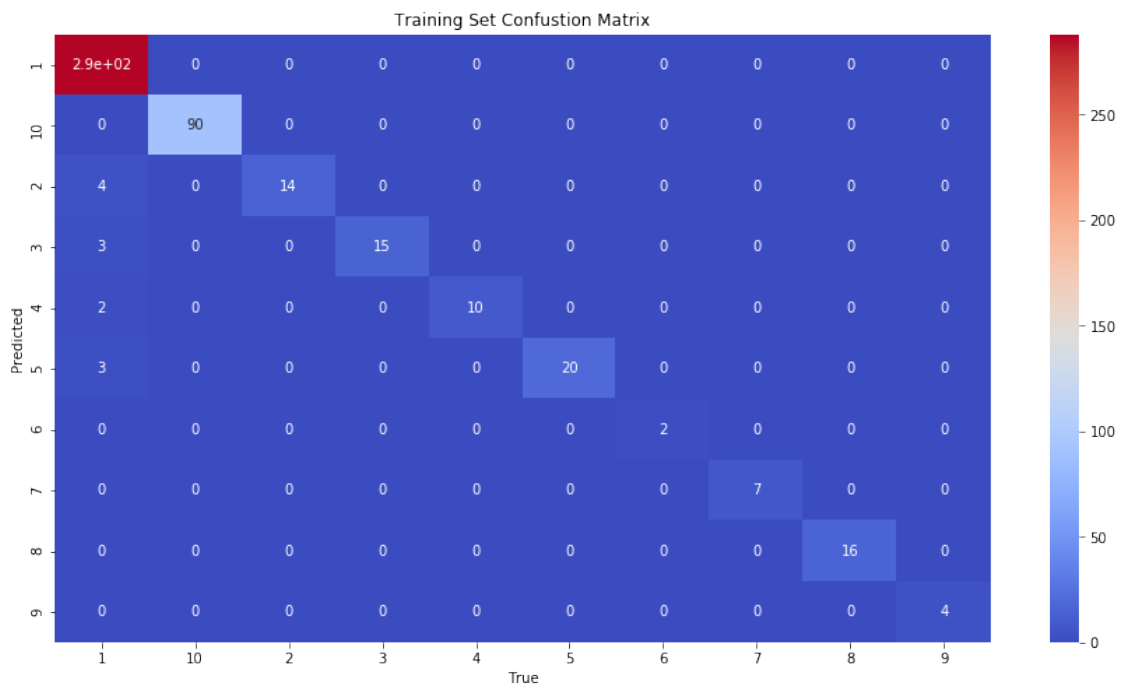
```
In [452]: regression_predictions = [round(x) for x in lm.predict(X_unknown)]
          ridge_predictions = [round(x) for x in lr.predict(X_unknown)]
          lasso_predictions = [round(x) for x in ls.predict(X_unknown)]
```

```
In [453]: plt.subplots(nrows=1, ncols =1, figsize = (15,8))
          ax = plt.subplot(111)
          ax.scatter(range(len(regression_predictions)), regression_predictions, color = 'r', 
          ax.scatter(range(len(regression_predictions)), ridge_predictions, color = 'b', label
          ax.scatter(range(len(regression_predictions)), lasso_predictions, color = 'g', label
          plt.legend()
          plt.title('Model Predictions')
          plt.xlabel('Unknown Observation #')
          plt.ylabel('Prediction')
          ax.spines['right'].set_visible(False)
          ax.spines['top'].set_visible(False)
          plt.show()
```



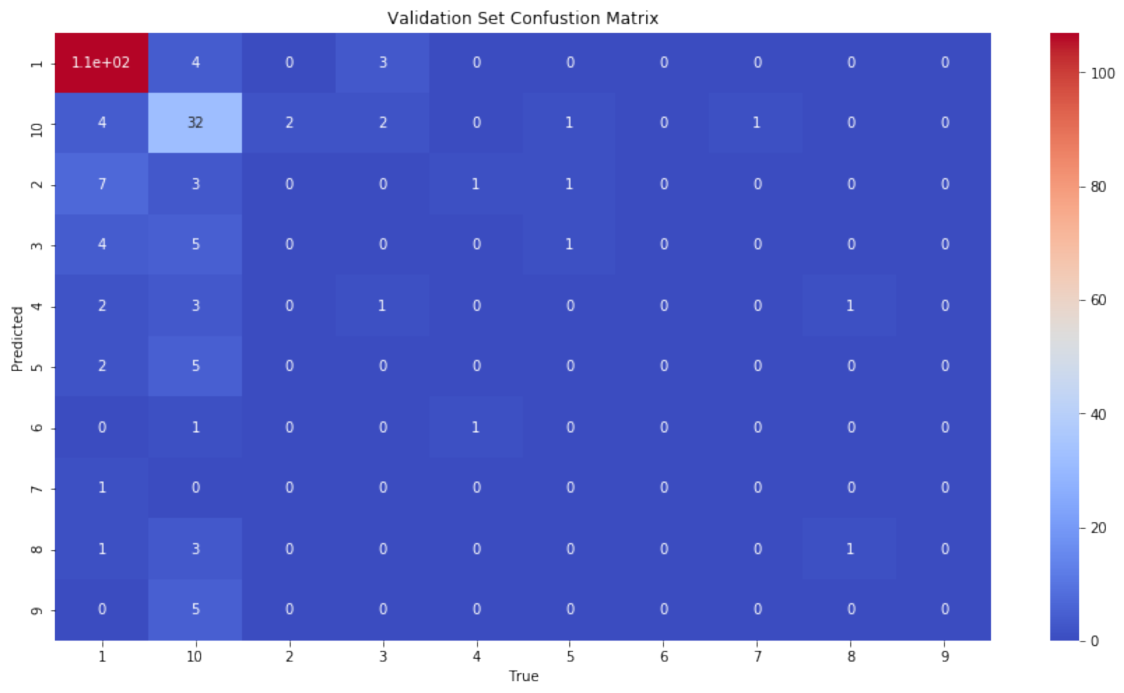
For the most part, it appears that all 3 models agree on predictions for the missing values. Only the LASSO model dissagress with the other two models on 4 instances of the 16 observations. Since the predictions being made are values between 1 and ten, this is could be treated as a multiclass classifcation problem. Real quick, let's just fit a random forest model and see what results it gives us

```
In [387]: from sklearn.ensemble import RandomForestClassifier

In [388]: clf = RandomForestClassifier(n_estimators=500, max_features=3)

In [389]: clf.fit(train, y_train)

Out[389]: RandomForestClassifier(bootstrap=True, class_weight=None, criterion='gini',
                      max_depth=None, max_features=3, max_leaf_nodes=None,
                      min_impurity_decrease=0.0, min_impurity_split=None,
                      min_samples_leaf=1, min_samples_split=2,
                      min_weight_fraction_leaf=0.0, n_estimators=500, n_jobs=1,
                      oob_score=False, random_state=None, verbose=0,
                      warm_start=False)

In [390]: from sklearn.metrics import confusion_matrix, classification_report

In [391]: plt.figure(figsize = (15,8))
          sns.heatmap(confusion_matrix(y_train, clf.predict(train)), annot = True, cmap = 'coo
          plt.xticks(np.arange(10) + 0.5, [1,10,2,3,4,5,6,7,8,9])
          plt.yticks(np.arange(10) + 0.5, [1,10,2,3,4,5,6,7,8,9])
          plt.title('Training Set Confustion Matrix')
          plt.xlabel('True')
          plt.ylabel('Predicted')
          plt.show()
```



```
In [392]: print(classification_report(y_train, clf.predict(train)))

             precision    recall  f1-score   support

          1       0.96      1.00      0.98       288
         10       1.00      1.00      1.00        90
          2       1.00      0.78      0.88        18
          3       1.00      0.83      0.91        18
          4       1.00      0.83      0.91        12
          5       1.00      0.87      0.93        23
          6       1.00      1.00      1.00         2
          7       1.00      1.00      1.00         7
          8       1.00      1.00      1.00        16
          9       1.00      1.00      1.00         4

avg / total       0.98      0.97      0.97       478
```

```
In [393]: plt.figure(figsize = (15,8))
          sns.heatmap(confusion_matrix(y_val, clf.predict(val)), annot = True, cmap = 'coolwarr
          plt.xticks(np.arange(10) + 0.5, [1,10,2,3,4,5,6,7,8,9])
          plt.yticks(np.arange(10) + 0.5, [1,10,2,3,4,5,6,7,8,9])
          plt.title('Validation Set Confustion Matrix')
          plt.xlabel('True')
          plt.ylabel('Predicted')
          plt.show()
```



```
In [458]: print(classification_report(y_val, clf.predict(val)))

             precision    recall  f1-score   support

          1       0.84      0.94      0.88       114
         10       0.52      0.76      0.62        42
          2       0.00      0.00      0.00        12
          3       0.00      0.00      0.00        10
          4       0.00      0.00      0.00         7
          5       0.00      0.00      0.00         7
          6       0.00      0.00      0.00         2
          7       0.00      0.00      0.00         1
          8       0.50      0.20      0.29         5
          9       0.00      0.00      0.00         5

avg / total       0.58      0.68      0.63       205
```

The Random Forest Classifier unfortunately severely overfit the training data. When the model was optimized to reduce high variance, the performance for both the training and validation set greatly attenuated. Let's continue using only our ridge regression model. We will use the original dataframe, filter it by the rows that have the ? symbol, and feed those rows into our trained model to make a prediction. We will then update the original dataframe with those predicted rows

```
In [459]: predicted = df[df.bare_nuclei == '?']
          display(predicted.bare_nuclei)
          predicted['bare_nuclei'] = predicted.loc[:, [x for x in df.columns if x not in ['clas
                                                                                          'bare
                                                                                          'id_n
                                                                                          'cell
          apply(lambda x: int(round(lr.predict(np.array(x).reshape(1,-1))[0])), axis = 1)
          display(predicted.bare_nuclei)
```

```
23     ?
40     ?
139    ?
145    ?
158    ?
164    ?
235    ?
249    ?
275    ?
292    ?
294    ?
297    ?
315    ?
321    ?
411    ?
617    ?
Name: bare_nuclei, dtype: object


23     5
40     8
139    1
145    1
158    1
164    2
235    2
249    2
275    1
292    6
294    1
297    3
315    6
321    2
411    1
617    1
Name: bare_nuclei, dtype: int64
```

```
In [460]: regression_df = predicted.combine_first(df)
```

3 REGRESSION WITH PERTURBATION

For regression with Perturbation, we could perturb the dependent variable and train a model to fit the perturbed labeled classes, or we could perturb one to all of the features in the training set. Let's perform the latter and perturb all the training features by using numpy's **random** module

```
In [482]: from numpy import random
```

Create a function that when passed a value will perturb that value by a value chosen from the random uniform distribution. The uniform function will be bound from a minimum of 0.01 and a maximum of 0.5

```
In [483]: def perturb_data(x):
              random_perturbation_value = random.uniform(0.01, 0.5)
              return x + random_perturbation_value

In [514]: X_perturbed = X_train.applymap(perturb_data).drop('cell_shape', axis = 1)
          X_unknown = X_unknown.drop('cell_shape', axis =1)

In [515]: X_perturbed.head()

Out[515]:    clump_thick  cell_size  marginal_adhesion  single_epithelial_size  \
          0     5.150864   1.081866           1.060537                2.433456
          1     5.415497   4.190781           5.368362                7.276969
          2     3.290998   1.269518           1.453180                2.356982
          3     6.277502   8.389768           1.459068                3.488128
          4     4.260226   1.444531           3.241891                2.207681

             bland_chromatin  normal_nucleoli   mitoses
          0         3.069821         1.063825  1.174128
          1         3.403928         2.045791  1.377286
          2         3.294174         1.468491  1.020592
          3         3.239609         7.453250  1.473643
          4         3.392368         1.197347  1.463228
```

Create the train and validation sets

```
In [516]: #Perform a 70/30 train - validate split
          train, val, y_train, y_val = train_test_split(X_perturbed, y_train, test_size=0.30, 

In [517]: lm = LinearRegression()
          lr = Ridge(alpha = 0.1)
          ls = Lasso(alpha = 0.1)

In [518]: lm.fit(train, y_train)
          lr.fit(train, y_train)
          ls.fit(train, y_train)
```

```
Out[518]: Lasso(alpha=0.1, copy_X=True, fit_intercept=True, max_iter=1000,
             normalize=False, positive=False, precompute=False, random_state=None,
             selection='cyclic', tol=0.0001, warm_start=False)
```

```
In [519]: print('TRAINING DATA R^2 SCORE')
          print('-----------------------')
          print('Linear Regression Model: {} R^2'.format(lm.score(train,y_train)))
          print('Ridge Linear Regression: {} R^2'.format(lr.score(train,y_train)))
          print('Lasso Linear Regression: {} R^2'.format(ls.score(train,y_train)))
```

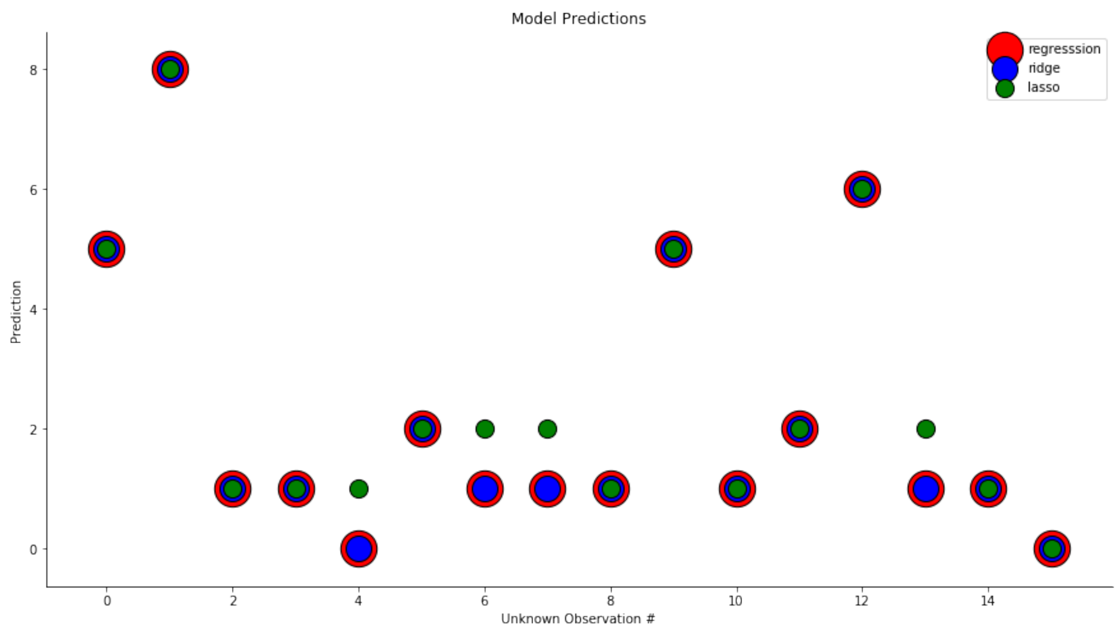
```
TRAINING DATA R^2 SCORE
-----------------------
Linear Regression Model: 0.5934230664771337 R^2
Ridge Linear Regression: 0.5934230663131856 R^2
Lasso Linear Regression: 0.5929464766716372 R^2
```

```
In [520]: print('VALIDATION DATA R^2 SCORE')
          print('-------------------')
          print('Linear Regression Model: {} R^2'.format(lm.score(val, y_val)))
          print('Ridge Linear Regression: {} R^2'.format(lr.score(val,y_val)))
          print('Lasso Linear Regression: {} R^2'.format(ls.score(val,y_val)))
```

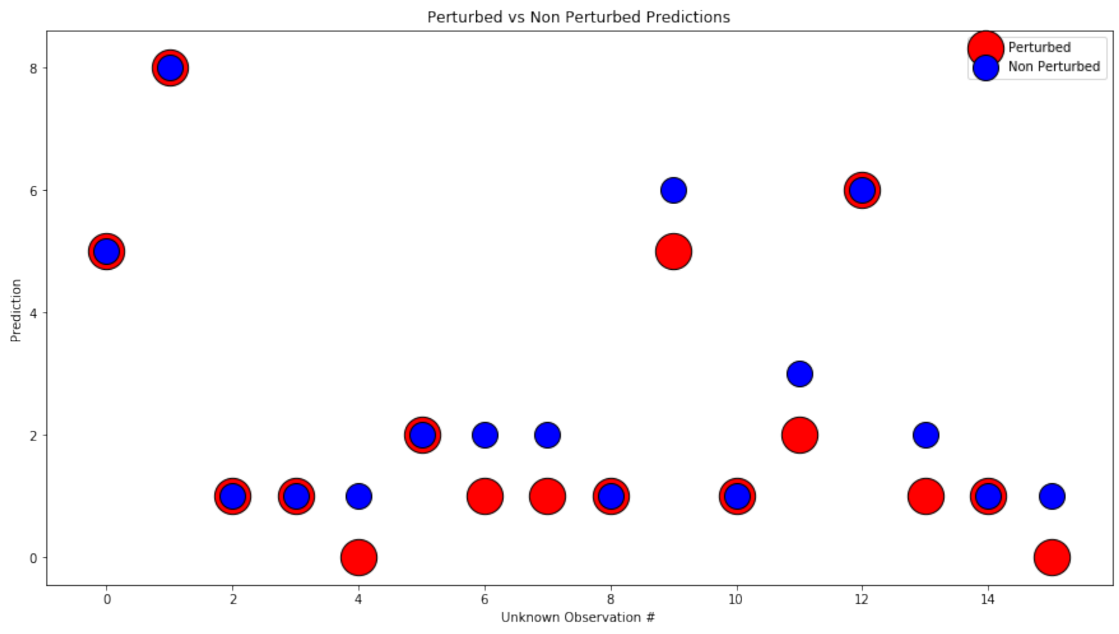
```
VALIDATION DATA R^2 SCORE
-------------------
Linear Regression Model: 0.6181635785395408 R^2
Ridge Linear Regression: 0.6181634698420793 R^2
Lasso Linear Regression: 0.6167314019153769 R^2
```

```
In [521]: perturbed_regression_predictions = [round(x) for x in lm.predict(X_unknown)]
          perturbed_ridge_predictions = [round(x) for x in lr.predict(X_unknown)]
          perturbed_lasso_predictions = [round(x) for x in ls.predict(X_unknown)]
```

```
In [522]: plt.subplots(nrows=1, ncols =1, figsize = (15,8))
          ax = plt.subplot(111)
          ax.scatter(range(len(regression_predictions)), perturbed_regression_predictions, colo
          ax.scatter(range(len(regression_predictions)), perturbed_ridge_predictions, color =
          ax.scatter(range(len(regression_predictions)), perturbed_lasso_predictions, color =
          plt.legend()
          plt.title('Model Predictions')
          plt.xlabel('Unknown Observation #')
          plt.ylabel('Prediction')
          ax.spines['right'].set_visible(False)
          ax.spines['top'].set_visible(False)
          plt.show()
```



```
In [523]: plt.figure(figsize = (15,8))
          plt.scatter(range(len(regression_predictions)), perturbed_regression_predictions, col
          plt.scatter(range(len(regression_predictions)), regression_predictions, color = 'b',
          plt.title('Perturbed vs Non Perturbed Predictions')
          plt.xlabel('Unknown Observation #')
          plt.ylabel('Prediction')
          plt.legend()
          plt.show()
```



The perturbed vs non perturbed models are relatively similar. Where they disagree is, the difference is only by 1.

```
In [526]: perturbed = df[df.bare_nuclei == '?']
          display(perturbed.bare_nuclei)
          perturbed['bare_nuclei'] = perturbed.loc[:, [x for x in df.columns if x not in ['cla
                                                                                          'bar
                                                                                          'id_
                                                                                          'cel
          apply(lambda x: int(round(lr.predict(np.array(x).reshape(1,-1))[0])), axis = 1)
          display(perturbed.bare_nuclei)
```

```
23      ?
40      ?
139     ?
145     ?
158     ?
164     ?
235     ?
249     ?
275     ?
292     ?
294     ?
297     ?
315     ?
321     ?
411     ?
617     ?
Name: bare_nuclei, dtype: object


23      5
40      8
139     1
145     1
158     0
164     2
235     1
249     1
275     1
292     5
294     1
297     2
315     6
321     1
411     1
```

```
617    0
Name: bare_nuclei, dtype: int64
```

```
In [527]: perturbed_df = perturbed.combine_first(df)
```

4 KNN MODEL USING VALUES FROM 1, 2, AND 3

```
In [540]: def prep_df(df):
              df['class'] = df['class'].replace(2,0).replace(4,1)
              y = df['class']
              df = df.drop(['class', 'cell_shape', 'id_number'], axis = 1)
              return df, y

In [528]: from sklearn.neighbors import KNeighborsClassifier

In [558]: models = {}

In [544]: clf = KNeighborsClassifier(n_neighbors = 4)

In [565]: mode_df , y = prep_df(mode_df)
          regression_df , y = prep_df(regression_df)
          perturbed_df, y = prep_df(perturbed_df)

In [566]: def neighbor_model(df, y, clf, impute_type):

              X_train, X_test, y_train, y_test = train_test_split(df, y, test_size=0.33, rando

              clf.fit(X_train, y_train)

              train_score = clf.score(X_train, y_train)

              test_score = clf.score( X_test, y_test)

              models[impute_type] = {'Train Score': train_score, 'Test Score': test_score}
              print('******************** IMPUTATION METHOD: "{}" ********************'.format

              print('TRAINING SET METRICS\n')
              print(classification_report(y_train, clf.predict(X_train)))

              print('\nTEST SET METRICS\n')
              print(classification_report(y_test, clf.predict(X_test)))

In [567]: neighbor_model(mode_df, y, clf, 'MODE')
```

```
******************** IMPUTATION METHOD: "MODE" ********************
TRAINING SET METRICS

             precision    recall  f1-score   support
```

```
         0.0       0.96      0.99      0.98       304
         1.0       0.97      0.93      0.95       164

avg / total       0.97      0.97      0.97       468


TEST SET METRICS

             precision    recall  f1-score   support

         0.0       0.96      0.99      0.97       154
         1.0       0.97      0.92      0.95        77

avg / total       0.97      0.97      0.97       231
```

```
In [569]: neighbor_model(regression_df, y, clf, 'REGRESSION')
```

```
******************** IMPUTATION METHOD: "REGRESSION" ********************
TRAINING SET METRICS

             precision    recall  f1-score   support

         0.0       0.96      0.98      0.97       304
         1.0       0.96      0.93      0.95       164

avg / total       0.96      0.96      0.96       468


TEST SET METRICS

             precision    recall  f1-score   support

         0.0       0.96      0.99      0.97       154
         1.0       0.97      0.92      0.95        77

avg / total       0.97      0.97      0.97       231
```

```
In [570]: neighbor_model(perturbed_df, y, clf, 'PERTUBATION')
```

```
******************** IMPUTATION METHOD: "PERTUBATION" ********************
TRAINING SET METRICS

             precision    recall  f1-score   support
```

```
        0.0       0.96      0.98      0.97       304
        1.0       0.96      0.93      0.95       164

avg / total       0.96      0.96      0.96       468


TEST SET METRICS

             precision    recall  f1-score   support

        0.0       0.96      0.99      0.97       154
        1.0       0.97      0.92      0.95        77

avg / total       0.97      0.97      0.97       231
```

```
In [571]: models

Out[571]: {'MODE': {'Train Score': 0.967948717948718, 'Test Score': 0.9653679653679653},
           'REGRESSION': {'Train Score': 0.9636752136752137,
            'Test Score': 0.9653679653679653},
           'PERTUBATION': {'Train Score': 0.9636752136752137,
            'Test Score': 0.9653679653679653}}

In [573]: pd.DataFrame(models).T

Out[573]:              Test Score  Train Score
          MODE           0.965368     0.967949
          REGRESSION     0.965368     0.963675
          PERTUBATION    0.965368     0.963675
```

4.1 ### CONCLUSION

It appears that all three models are performing very well for both the training and test set. The Mode imputation method however is providing just a little better accuracy on the Train set.

4.2 # Question 15.1

Describe a situation or problem from your job, everyday life, current events, etc., for which optimization would be appropriate. What data would you need?

With Amazon taking over the world in online retail, it is undoubtedly in their best interest to optimize their shipping business model. A good optimization problem could be determining how many products to ship from factory to each warehouse, or from each factory to each warehouse and direct to each end customer, to minimize shipping cost while meeting warehouse demands and not exceeding factory supplies. Data would be:

- Shipping Cost per distance from warehouse
- Shipping Cost per distance from factory

- Factory supply churn rate
- Warehouse capacity
- Factory Supplies Cost

```
In [ ]:
```