Data Wrangling: Clean, Transform, Merge, Reshape

Much of the programming work in data analysis and modeling is spent on data preparation loading, cleaning, transforming, and rearranging. Sometimes the way that data is stored in files or databases is not the way you need it for a data processing application.

pandas along with the Python standard library provide you with a high-level, flexible, and high-performance set of core manipulations and algorithms to enable you to wrangle data into the right form without much trouble.

```
import pandas as pd
import numpy as np
#Combining and Merging Data Sets
#1. pandas.merge:
    #connects rows in DataFrames based on one or more keys.
df1 = pd.DataFrame({'key': ['b', 'b', 'a', 'c', 'a', 'a', 'b'],
                'data1': range(7)})
df2 = pd.DataFrame({'key': ['a', 'b', 'd'],
                'data2': range(3)})
print("First Dataframe: \n", df1)
print("Second Dataframe: \n", df2)
#This is an example of a many-to-one merge situation; the data in dfl has
multiple rows labeled a and b,
#whereas df2 has only one row for each value in the key column. Calling
merge with these objects we obtain:
print("Many-to-one Merge: \n",pd.merge(df1, df2))
First Dataframe:
   data1 key
Ω
     0 b
      1 b
1
2
      2 a
      3 с
3
4
      4 a
5
      5 a
      6 b
Second Dataframe:
   data2 kev
0
     0 a
1
     1 b
2
     2 d
Many-to-one Merge:
  data1 key data2
0
    0 b
              1
     1 b
                1
1
     6 b
2
                1
      2 a
                0
3
      4 a
                0
4
5
      5
                Ω
          а
##Note that I didn't specify which column to join on. If not specified,
merge uses the
```

```
explicitly, though:
print("Many-to-one Merge: \n",pd.merge(df1, df2, on = 'key'))
Many-to-one Merge:
    data1 key data2
0
      0
         b
                  1
1
       1
          b
2
       6
          b
                 1
3
       2
          а
                 0
4
       4
          а
                 0
       5
          а
#Many-to-many merges
df1 = pd.DataFrame({'key': ['b', 'b', 'a', 'c', 'a', 'b'],
                 'data1': range(6)})
df2 = pd.DataFrame({'key': ['a', 'b', 'a', 'b', 'd'],
                          'data2': range(5)})
print("First Data Frame:\n",df1)
print("First Data Frame:\n",df2)
print("Left Outer Join: \n",pd.merge(df1, df2, on='key',
                                    how='left'))
print("Inner Join: \n",pd.merge(df1, df2, on='key', how='inner'))
First Data Frame:
    data1 key
Ω
      0 b
1
      1 b
2
       2 a
3
       3
          С
4
       4
          а
      5
5
          b
First Data Frame:
    data2 kev
0
      0
         а
1
      1 b
2
       2 a
3
       3
          b
      4
4
          d
Left Outer Join:
     data1 key data2
0
      0 b
                1.0
1
       0
           b
                3.0
2
                1.0
       1
           b
3
                3.0
       1
           b
       2
                0.0
4
           а
5
       2
                2.0
           а
6
       3
                NaN
           С
7
                0.0
       4
           а
                2.0
8
        4
           а
9
        5
           b
                1.0
10
       5
          b
                3.0
Inner Join:
    data1 key data2
0
      0
          b
                 1
1
       0
          b
                  3
2
       1
          b
                 1
3
       1
          b
                 3
4
       5
          b
                 1
```

#overlapping column names as the keys. It's a good practice to specify

```
5 b
5
                   3
        2 a
6
                    0
7
                    2
8
        4
                    Ω
9
        4
            а
                    2
#To merge with multiple keys, pass a list of column names:
left = pd.DataFrame({'key1': ['foo', 'foo', 'bar'],
                     'key2': ['one', 'two', 'one'],
'lval': [1, 2, 3]})
right = pd.DataFrame({'key1': ['foo', 'foo', 'bar', 'bar'],
                      'key2': ['one', 'one', 'one', 'two'], 'rval': [4, 5, 6, 7]})
```

pd.merge(left, right, on=['key1', 'key2'], how='outer')

	key1	key2	lval	rval
0	foo	one	1.0	4.0
1	foo	one	1.0	5.0
2	foo	two	2.0	NaN
3	bar	one	3.0	6.0
4	bar	two	NaN	7.0

#To merge with multiple keys, when column names are not same:

```
left = pd.DataFrame({'key11': ['foo', 'foo', 'bar'],
                  'lval1': [1, 2, 3]})
right = pd.DataFrame({'key22': ['foo', 'foo', 'bar', 'bar'],
                   'rva21': [4, 5, 6, 7]})
```

pd.merge(left, right, left on='key11', right on='key22', how='outer')

	key11	lval1	key22	rva2l
0	foo	1	foo	4
1	foo	1	foo	5
2	foo	2	foo	4
3	foo	2	foo	5
4	bar	3	bar	6
5	bar	3	bar	7

#To merge with multiple keys, when column names are not same:

```
left = pd.DataFrame({'key11': ['foo', 'foo', 'bar'],
                   'key21': ['one', 'two', 'one'],
'lval1': [1, 2, 3]})
right = pd.DataFrame({'key21': ['foo', 'foo', 'bar', 'bar'],
                     'key22': ['one', 'one', 'one', 'two'],
                     'rva21': [4, 5, 6, 7]})
pd.merge(left,right, left on=['key11', 'key21'],
          right on=['key21', 'key22']
          , how='outer')
```

	key11	key21_x	lval1	key21_y	key22	rva2l
0	foo	one	1.0	foo	one	4.0
1	foo	one	1.0	foo	one	5.0
2	foo	two	2.0	NaN	NaN	NaN
3	bar	one	3.0	bar	one	6.0
4	NaN	NaN	NaN	bar	two	7.0

c NaN 2.0 NaN

#2. Concatenating Along an Axis #Another kind of data combination operation is alternatively referred to as concatenation, binding, or stacking. #NumPy has a concatenate function for doing this with raw NumPy arrays: #The concat function in pandas provides you hte same functionality s1 = pd.Series([0, 1], index=['a', 'b']) s2 = pd.Series([2, 3, 4], index=['c', 'd', 'e'])s3 = pd.Series([5, 6], index=['f', 'g'])print("First Series:\n",s1) print("Second Series:\n",s2) print("Third Series:\n",s3) print("Concatinated Series: \n",pd.concat([s1, s2, s3])) First Series: 0 а b 1 dtype: int64 Second Series: c 2 3 d 4 е dtype: int64 Third Series: 5 f 6 dtype: int64 Concatinated Series: Ω 1 b 2 d 3 4 е 5 6 dtype: int64 #By default concat works along axis=0, producing another Series. If you pass axis=1, the #result will instead be a DataFrame (axis=1 is the columns): print("Concatinated Series on axis = 1: \n", pd.concat([s1, s2, s3], axis=1)) Concatinated Series on axis = 1: 0 1 a 0.0 NaN NaN b 1.0 NaN NaN

```
d NaN 3.0 NaN
e NaN 4.0 NaN
f NaN NaN 5.0
  NaN NaN 6.0
g
s1 = pd.Series([0, 1], index=['a', 'b'])
s2 = pd.Series([2, 3, 4], index=['a', 'd', 'e'])
s3 = pd.Series([5, 6], index=['a', 'g'])
print("First Series:\n",s1)
print("Second Series:\n",s2)
print("Third Series:\n",s3)
print("Concatinated Series on axis = 1: \n",
     pd.concat([s1, s2, s3], axis=1))
First Series:
а
b
    1
dtype: int64
Second Series:
a 2
d
    3
    4
dtype: int64
Third Series:
a 5
    6
dtype: int64
Concatinated Series on axis = 1:
   0 1 2
a 0.0 2.0 5.0
b 1.0 NaN NaN
d NaN 3.0 NaN
e NaN 4.0 NaN
q NaN NaN 6.0
#Duplicates
data = pd.DataFrame({'k1': ['one'] * 3 + ['two'] * 4,
                 'k2': [1, 1, 2, 3, 3, 4, 4]})
print("Data Frame with duplicate values: \n", data)
Data Frame with duplicate values:
    k1 k2
0 one
        1
1 one
        1
2 one
        2
3 two
        3
4 two
        3
5 two
        4
6 two
#Identifying the duplicate values:
#The DataFrame method duplicated returns a boolean Series indicating
whether each
#row is a duplicate or not:
print("Identify duplicate values: \n", data.duplicated())
Identify duplicate values:
0
     False
     True
    False
3
    False
```

```
4
     True
5
    False
6
      True
dtype: bool
#drop duplicates returns a DataFrame where the duplicated array is True:
print("Drop Duplicates: \n", data.drop duplicates())
Drop Duplicates:
    k1 k2
0 one
  one
  two
  two
#Both of these methods by default consider all of the columns;
alternatively you can specify
#any subset of them to detect duplicates
print("Drop K1 Duplicate:\n ",data.drop duplicates(['k1']))
Drop K1 Duplicate:
      k1 k2
0 one
3 two
#duplicated and drop duplicates by default keep the first observed value
combination.
#Passing take last=True will return the last one:
data.drop duplicates(['k1', 'k2'], keep='last')
  k1 | k2
1 one 1
2 one 2
4 two 3
6 two 4
#Replacing Values
#Filling in missing data with the fillna method can be thought of as a
special case of more general value replacement.
data = pd.Series([1., -999., 2., -999., -1000., 3.])
print(data)
0
       1.0
    -999.0
1
2
        2.0
    -999.0
3
4
  -1000.0
        3.0
dtype: float64
#The -999 values might be sentinel values for missing data. To replace
these with NA
#values that pandas understands, we can use replace, producing a new
Series:
print("Replace -999 with NA :\n",data.replace(-999, np.nan))
print("Replace -999 and -1000 with NA :\n", data.replace([-999,-1000],
                                                         np.nan))
Replace -999 with NA:
        1.0
```

```
1
       NaN
2
       2.0
3
       NaN
4
    -1000.0
5
       3.0
dtype: float64
Replace -999 and -1000 with NA:
     1.0
1
     NaN
2
     2.0
3
    NaN
4
    NaN
     3.0
dtvpe: float64
#To use a different replacement for each value, pass a list of substitutes:
print("Replace -999 and -1000 with NA :\n", data.replace([-999,-1000],
                                                       [np.nan, 0]))
Replace -999 and -1000 with NA:
0
    1.0
    NaN
1
2
     2.0
3
    NaN
4
    0.0
5
     3.0
dtype: float64
#Detecting and Filtering Outliers
np.random.seed(12345)
data = pd.DataFrame(np.random.randn(1000, 4))
print("Data Frame describe: \n", data.describe())
Data Frame describe:
                             1
count 1000.000000 1000.000000 1000.000000 1000.000000
mean
       -0.067684
                    0.067924
                                 0.025598 -0.002298
                     0.992106
std
        0.998035
                                  1.006835
                                               0.996794
min
        -3.428254
                     -3.548824
                                -3.184377
                                              -3.745356
25%
        -0.774890
                    -0.591841
                                 -0.641675
                                              -0.644144
50%
        -0.116401
                     0.101143
                                  0.002073
                                              -0.013611
75%
         0.616366
                      0.780282
                                  0.680391
                                               0.654328
         3.366626
                      2.653656
                                  3.260383
                                               3.927528
max
#Computing Indicator/Dummy Variables
#Another type of transformation for statistical modeling or machine
learning applications is
#converting a categorical variable into a "dummy" or "indicator" matrix. If
a column in a DataFrame
#has k distinct values, you would derive a matrix or DataFrame containing k
columns containing
#all 1's and 0's. pandas has a get dummies function for doing this.
df = pd.DataFrame({'key': ['b', 'b', 'a', 'c', 'a', 'b'],
                'data1': range(6)})
print("Dummy Encoding: \n", pd.get dummies(df['key']))
Dummy Encoding:
   a b c
0 0 1 0
```

```
1 0 1 0
2 1 0 0
3 0 0 1
4 1 0 0
5 0 1 0
```

GroupBy: Split, Apply, Combine

Simple aggregations can give you a flavor of your dataset, but often we would prefer to aggregate conditionally on some label or index: this is implemented in the so-called groupby operation.

```
import pandas as pd
df = pd.DataFrame({'key': ['A', 'B', 'C', 'A', 'B', 'C'],
                   'data': range(6)}, columns=['key', 'data'])
df
 key data
0 A
1 B
     1
2 C
3 A
     3
4 B
5 C
     5
#he most basic split-apply-combine operation can be computed with the
groupby() method of DataFrames,
```

```
#he most basic split-apply-combine operation can be computed with th
groupby() method of DataFrames,
#passing the name of the desired key column:

df.groupby('key')
<pandas.core.groupby.DataFrameGroupBy object at 0x000002101CCB30B8>
```

It returned a DataFrameGroupBy object. This object is where the magic is: you can think of it as a special view of the DataFrame, which is poised to dig into the groups but does no actual computation until the aggregation is applied. This "lazy evaluation" approach means that common aggregates can be implemented very efficiently in a way that is almost transparent to the user.

To produce a result, we can apply an aggregate to this DataFrameGroupBy object, which will perform the appropriate apply/combine steps to produce the desired result:

```
'data2': rng.randint(0, 10, 6)},
columns = ['key', 'data1', 'data2'])
```

df

	key	data1	data2
0	A	0	5
1	В	1	0
2	C	2	3
3	A	3	3
4	В	4	7
5	C	5	9

df.groupby('key').aggregate(['min', np.median, max])

		data1		data2				
	min	median	max	min	median	max		
key								
A	0	1.5	3	3	4.0	5		
В	1	2.5	4	0	3.5	7		
C	2	3.5	5	3	6.0	9		

#Another useful pattern is to pass a dictionary mapping column names to operations to be applied on that column:

	data1	data2
key		
A	0	5
В	1	7
C	2	9

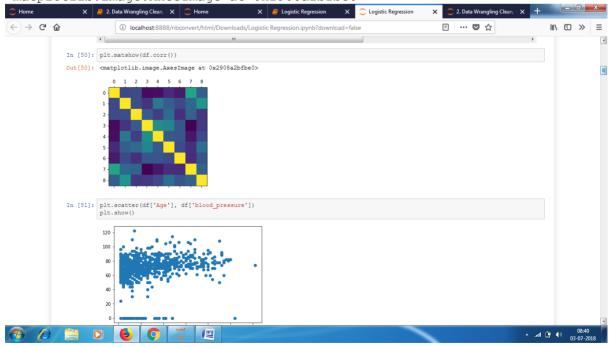
```
import pandas as pd
import pylab as plt
import numpy as np
from sklearn.model selection import train test split
from sklearn.linear model import LogisticRegression
from sklearn import metrics
import os
os.chdir('C:\\Analytics\\Personal\\Machine Learning\\Training\\R\\Dataset')
# read the data in
df = pd.read csv("diabetes.csv")
print(df.columns.values)
['times_pregnant' 'Plasma_glucose_concentration 2 hr' 'blood pressure'
 'Triceps_skin_fold_thickness ' 'Hr2_serum_insulin' 'BOI'
' Diabetes pedigree function' 'Age' 'Class']
print("Summary Statistics :\n", df.describe())
Summary Statistics :
       times pregnant Plasma glucose concentration 2 hr blood pressure
                                            768.000000
          768.000000
                                                          768.000000
count
           3.845052
                                            120.894531
                                                           69.105469
mean
           3.369578
                                                           19.355807
std
                                            31.972618
min
           0.000000
                                             0.000000
                                                            0.000000
25%
           1.000000
                                            99.000000
                                                           62.000000
50%
                                            117.000000
           3.000000
                                                           72.000000
75%
                                            140.250000
           6.000000
                                                           80.000000
           17.000000
                                            199.000000
max
                                                          122.000000
       Triceps skin fold thickness
                                    Hr2 serum insulin
                                                              BOI \
count
                         768.000000
                                           768.000000 768.000000
mean
                         20.536458
                                            79.799479 31.992578
std
                         15.952218
                                           115.244002
                                                        7.884160
min
                          0.000000
                                             0.000000
                                                        0.000000
25%
                          0.000000
                                             0.000000 27.300000
                         23.000000
                                            30.500000 32.000000
50%
75%
                                            127.250000 36.600000
                         32.000000
                                           846.000000 67.100000
max
                         99.000000
       Diabetes_pedigree function
                                        Aae
                                                  Class
                       768.000000 768.000000 768.000000
count
                         0.471876 33.240885 0.348958
mean
                                               0.476951
                         0.331329
                                 11.760232
std
                                 21.000000
                        0.078000
                                              0.000000
min
                                 24.000000
25%
                        0.243750
                                              0.000000
                                 29.000000
                                              0.000000
50%
                        0.372500
75%
                        0.626250 41.000000
                                              1.000000
                        2.420000 81.000000 1.000000
max
df.corr()
```

	times _preg nant	Plasma_gluc ose_concentr ation_2 hr	_pres	in_fold_thi	Hr2_se rum_in sulin	BO I	Diabetes_p edigree_fu nction	Ag e	Cla ss
times_pregn ant	1.000 000	0.129459	0.141 282	-0.081672		0.0 176 83		0.5 443 41	
Plasma_gluc ose_concentr		1.000000	0.152 590	0.057328		0.2 210	0.137337	0.2 635	

ation_2 hr						71		14	81
blood_pressu re	0.141 282	0.152590	1.000	0.207371	0.08893	0.2 818 05	0.041265	0.2 395 28	0.0 650 68
Triceps_skin _fold_thickn ess	-0.081 672	0.057328	0.207 371	1.000000	0.43678	0.3 925 73	0.183928	- 0.1 139 70	0.0 747 52
Hr2_serum_i nsulin	-0.073 535	0.331357	0.088 933	0.436783	1.00000	0.1 978 59	0.185071	- 0.0 421 63	0.1 305 48
воі	0.017 683	0.221071	0.281 805	0.392573	0.19785	1.0 000 00	0.140647	0.0 362 42	0.2 926 95
Diabetes_pe digree_functi on	-0.033 523	0.137337	0.041 265	0.183928	0.18507	0.1 406 47	1.000000	0.0 335 61	0.1 738 44
Age	0.544 341	0.263514	0.239 528	-0.113970	0.04216 3	0.0 362 42	0.033561	1.0 000 00	0.2 383 56
Class	0.221 898	0.466581	0.065 068	0.074752	0.13054	0.2 926 95	0.173844	0.2 383 56	1.0 000 00

plt.matshow(df.corr())

<matplotlib.image.AxesImage at 0x2908a2bfbe0>



plt.scatter(df['Age'], df['blood_pressure'])
plt.show()

	times_p regnant	Plasma_glucose _concentration_ 2 hr	blood_ pressur e	Triceps_skin_ fold_thickness	Hr2_seru m_insuli n	B O I	Diabetes_pedi gree_function		Cl as s
0	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
1	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
3	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
4	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
5	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
6	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
8	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
9	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
1 0	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
1 1	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
1 2	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
1	False	False	False	False	False	Fa	False	Fa	Fa

3						ls e		ls e	lse
1 4	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
1 5	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
1 6	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
1 7	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
1 8	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
19	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2 0	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2 2	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2 3	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2 4	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2 5	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2 6	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2 7	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
2	False	False	False	False	False	Fa	False	Fa	Fa

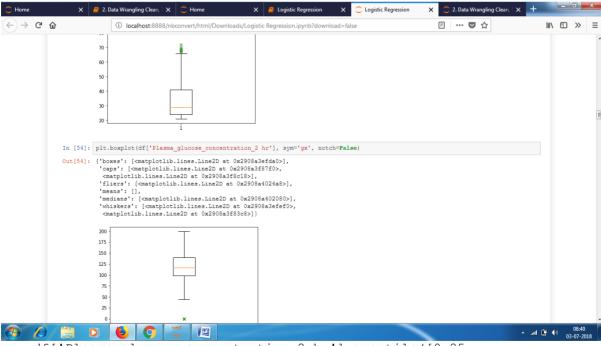
8						ls e		ls e	lse
2	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 3 8	False	False	False	False	False	Fa ls e	False	Fa ls e	
7 3 9	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 0	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 1	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 2	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 3	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 4	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 5	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 6	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 7	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 8	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 4 9	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 5 0	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse

7 5 1	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 5 2	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 5 3	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 5 4	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 5 5	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 5 6	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 5 7	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 5 8	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 5 9	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 6 0	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 6 1	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 6 2	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 6 3	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 6 4	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 6 5	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse

7 6 6	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse
7 6 7	False	False	False	False	False	Fa ls e	False	Fa ls e	Fa lse

768 rows \times 9 columns

```
plt.boxplot(df['Age'], sym='gx', notch=False)
{'boxes': [<matplotlib.lines.Line2D at 0x2908a390a90>],
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 'whiskers': [<matplotlib.lines.Line2D at 0x2908a390be0>,
  <matplotlib.lines.Line2D at 0x2908a3980b8>]}
plt.boxplot(df['Plasma glucose concentration 2 hr'], sym='gx', notch=False)
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  <matplotlib.lines.Line2D at 0x2908a3f83c8>]}
```



```
print(x.values)
print(x.index)
print(x[.25])
print(x[.5])
```

```
print(x[.75])
[ 99.
       117.
              140.25]
Float64Index([0.25, 0.5, 0.75], dtype='float64')
99.0
117.0
140.25
IQR = x[.75] - x[.25]
print(IOR)
IOR15 = 1.5*IOR
IOR15
41.25
61.875
U W = x[.75] + IQR15
LW = x[.25] - IQR15
print("Upper Whisker :", U W)
print("Lower Whisker :", L W)
Upper Whisker: 202.125
Lower Whisker: 37.125
#Identify outliers
print("Upper Outliers")
df['Plasma glucose concentration 2 hr']
[df['Plasma glucose concentration 2 hr'] > U W]
print("Lower Outliers")
df['Plasma glucose concentration 2 hr']
[df['Plasma glucose concentration 2 hr'] < L W]
Upper Outliers
Lower Outliers
75
      0
182
      0
342
      0
349
      0
Name: Plasma glucose concentration 2 hr, dtype: int64
#Calculating 5 nad 95 percentile
cap = df['Plasma glucose concentration 2 hr'].quantile([0.05,0.95])
cap
0.05
        79.0
0.95
        181.0
Name: Plasma glucose concentration 2 hr, dtype: float64
#Treat outlier with capping and flooring
df['Plasma_glucose_concentration 2 hr']
[df['Plasma glucose concentration 2 hr'] < L W] = cap[.05]
C:\Users\manish.khati\AppData\Local\Continuum\anaconda3\lib\site-
packages\ipykernel launcher.py:3: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame
See the caveats in the documentation: http://pandas.pydata.org/pandas-
docs/stable/indexing.html#indexing-view-versus-copy
  This is separate from the ipykernel package so we can avoid doing imports
until
df['Plasma glucose concentration 2 hr']
[df['Plasma glucose concentration 2 hr'] == 0]
Series([], Name: Plasma glucose concentration 2 hr, dtype: int64)
df.iloc[75]
                                      1.00
times pregnant
```

```
Plasma glucose concentration 2 hr
blood pressure
                                    48.00
Triceps skin fold thickness
                                    20.00
Hr2 serum insulin
                                    0.00
BOI
                                    24.70
Diabetes pedigree function
                                    0.14
                                    22.00
Class
                                     0.00
Name: 75, dtype: float64
plt.boxplot(df['Plasma glucose concentration 2 hr'], sym='gx', notch=False)
{'boxes': [<matplotlib.lines.Line2D at 0x2908a2ff160>],
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 'whiskers': [<matplotlib.lines.Line2D at 0x2908a2ff358>,
 <matplotlib.lines.Line2D at 0x2908a2ffc88>]}
# target variable % distribution
print(df['Class'].value counts(normalize=True))
    0.651042
Ω
    0.348958
Name: Class, dtype: float64
#build a quick logistic regression model and check the accuracy
X = df.iloc[:,:8] # independent variables
y = df['Class'] # dependent variables
# evaluate the model by splitting into train and test sets
X train, X test, y train, y_test = train_test_split(X, y,
                                                  test size=0.3,
                                                  random state=0)
# instantiate a logistic regression model, and fit
model = LogisticRegression()
model = model.fit(X_train, y_train)
# predict class labels for the train set. The predict fuction converts
probability values > .5 to 1 else 0
y pred = model.predict(X test)
y_pred
array([1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0,
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      0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 1, 1, 1, 0, 0, 0,
      0], dtype=int64)
# generate class probabilities
# Notice that 2 elements will be returned in probs array,
probs = model.predict proba(X test)
# 1st element is probability for negative class,
# 2nd element gives probability for positive class
array([[ 0.10927859, 0.89072141],
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#probability for positive class
y pred prob = probs[:, 1]
y pred prob
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          0.72309784, 0.68613583, 0.50269205, 0.12177033, 0.30159246,
          0.13038323, 0.20737989, 0.23656378, 0.39163112, 0.2823235,
          0.19434755, 0.26683477, 0.21858776, 0.39183243, 0.18772974,
          0.1385338 , 0.13281591, 0.35707235, 0.34735667, 0.24858914,
          0.33565387, 0.46937929, 0.33707901, 0.53058559, 0.24465829,
          0.18416764, 0.09569746, 0.40767607, 0.58553048, 0.51681912,
          0.65168494, 0.2745515, 0.29844631, 0.10726635, 0.19710395,
          0.442285021)
# generate evaluation metrics
print("Accuracy: ", metrics.accuracy score(y test, y pred))
Accuracy: 0.78354978355
# extract false positive, true positive rate
fpr, tpr, thresholds = metrics.roc curve(y test, y pred prob)
roc auc = metrics.auc(fpr, tpr)
print("Area under the ROC curve : %f" % roc auc)
Area under the ROC curve : 0.838785
i = np.arange(len(tpr)) # index for df
roc = pd.DataFrame({'fpr' : pd.Series(fpr, index=i),'tpr' : pd.Series(tpr,
index = i),'1-fpr' : pd.Series(1-fpr, index = i)})
print(roc)
         1-fpr
                       fpr
     1.000000 0.000000 0.013514
\cap
    1.000000 0.000000 0.054054
1
    0.993631 0.006369 0.054054
    0.993631 0.006369 0.067568
    0.987261 0.012739 0.067568
    0.987261 0.012739 0.094595
5
                0.019108 0.094595
    0.980892
                0.019108 0.243243
7
    0.980892
                0.025478 0.243243
    0.974522
                0.025478 0.310811
    0.974522
                0.031847 0.310811
    0.968153
11
    0.968153 0.031847 0.351351
    0.961783 0.038217 0.351351
13 0.961783 0.038217 0.418919
```

0.18032021, 0.55279025, 0.14351131, 0.85687787, 0.74580731,

```
14 0.949045 0.050955 0.418919
15 0.949045 0.050955 0.432432
16 0.942675 0.057325 0.432432
17 0.942675 0.057325 0.459459
18 0.936306 0.063694 0.459459
19 0.936306 0.063694 0.472973
20 0.929936 0.070064 0.472973
21 0.929936 0.070064 0.513514
             0.082803 0.513514
22 0.917197
23 0.917197 0.082803 0.527027
             0.101911 0.527027
24 0.898089
24 0.898089 0.101911 0.527027
25 0.898089 0.101911 0.540541
26 0.872611 0.127389 0.540541
27 0.872611 0.127389 0.554054
28 0.847134 0.152866 0.554054
29 0.847134 0.152866 0.594595
        . . .
                  . . .
43 0.745223 0.254777 0.756757
44 0.738854 0.261146 0.756757
45 0.738854 0.261146 0.783784
46 0.732484 0.267516 0.783784
47 0.732484 0.267516 0.797297
48 0.675159 0.324841 0.797297
49 0.675159 0.324841 0.810811
50 0.662420 0.337580 0.810811
51 0.662420 0.337580 0.824324
52 0.643312 0.356688 0.824324
53 0.643312 0.356688 0.851351
54 0.636943 0.363057 0.851351
55 0.636943 0.363057 0.878378
56 0.630573 0.369427 0.878378
57 0.630573 0.369427 0.905405
58 0.579618 0.420382 0.905405
59 0.579618 0.420382 0.918919
60 0.573248 0.426752 0.918919
61 0.573248 0.426752 0.932432
62 0.535032 0.464968 0.932432
63 0.535032 0.464968 0.945946
64 0.528662 0.471338 0.945946
65 0.528662 0.471338 0.959459
66 0.401274 0.598726 0.959459
67 0.401274 0.598726 0.972973
68 0.382166 0.617834 0.972973
69 0.382166 0.617834 0.986486
70 0.197452 0.802548 0.986486
71 0.197452 0.802548 1.000000
72 0.000000 1.000000 1.000000
[73 rows x 3 columns]
#Which Error is Costly??
```

Rare Event or Imbalanced Dataset

Providing an equal samples of positive and negative instances to the classification algorithm will result in an optimal result. Datasets that are highly skewed toward one or more classes have proven to be a challenge.

Resampling is a common practice to address the imbalanced dataset issue.

Random under-sampling - Reduce majority class to match minority class count.

Random over-sampling - Increase minority class by randomly picking samples within minority class till counts of both class match.

Synthetic Minority Over-Sampling Technique (SMOTE) - Increase minority class by introducing synthetic examples through connecting all k (default = 5) minority class nearest neighbors using feature space similarity (Euclidean distance).

Bias and Variance

A fundamental problem with supervised learning is the bias variance trade-off. Ideally a model should have two key characteristics.

- 1. Sensitive enough to accurately capture the key patterns in the training dataset.
- 2. It should be generalized enough to work well on any unseen datasets. Unfortunately, while trying to achieve the above-mentioned first point, there is an ample chance of over-fitting to noisy or unrepresentative training data points leading to a failure of generalizing the model. On the other hand, trying to generalize a model may result in failing to capture important regularities.

Bias

If model accuracy is low on a training dataset as well as test dataset the model is said to be under-fitting or that the model has high bias. This means the model is not fitting the training dataset points well in regression or the decision boundary is not separating the classes well in classification; and two key reasons for bias are 1) not including the right features, and 2) not picking the correct order of polynomial degrees for model fitting.

To solve an under-fitting issue or to reduced bias, try including more meaningful features and try to increase the model complexity by trying higher-order polynomial fittings.

Variance

If a model is giving high accuracy on a training dataset, however on a test dataset the accuracy drops drastically, then the model is said to be over-fitting or a model that has high variance. The key reason for over-fitting is using higher-order polynomial degree (may not be required), which will fit decision boundary tools well to all data points including the noise of train dataset, instead of the underlying relationship. This will lead to a high accuracy (actual vs. predicted) in the train dataset and when applied to the test dataset, the prediction error will be high. To solve the over-fitting issue:

Try to reduce the number of features, that is, keep only the meaningful features.

Dimension reduction can eliminate noisy features, in turn, reducing the model variance.

Brining more data points to make training dataset large will also reduce variance.

Choosing right model parameters can help to reduce the bias and variance, for example.

Using right regularization parameters can decrease variance in regression-based models.

For a decision tree reducing the depth of the decision tree will reduce the variance.

K-Fold Cross-Validation

K-folds cross-validation splits the training dataset into k-folds without replacement, that is, any given data point will only be part of one of the subset, where k-1 folds are used for the model training and one fold is used for testing. The procedure is repeated k times so that we obtain k models and performance estimates.

```
from sklearn.cross validation import cross val score
df = pd.read csv("diabetes.csv")
X = df.iloc[:,:8].values # independent variables
y = df['Class'].values # dependent variables
# Normalize Data
from sklearn import preprocessing
sc = preprocessing.StandardScaler()
sc.fit(X)
X = sc.transform(X)
# evaluate the model by splitting into train and test sets
X train, X test, y train, y test = train test split(X, y,
                                                    test size=0.3,
                                                    random state=2017)
# build a decision tree classifier
from sklearn import tree
from sklearn import metrics
from sklearn.cross validation import train test split
clf = tree.DecisionTreeClassifier(random state=2017)
# evaluate the model using 10-fold cross-validation
train scores = cross val score(clf, X train, y train,
                               scoring='accuracy', cv=5)
test_scores = cross_val_score(clf, X_test, y_test,
                              scoring='accuracy', cv=5)
print("Train Fold AUC Scores: ", train scores)
print("Train CV AUC Score: ", train scores.mean())
Train Fold AUC Scores: [ 0.7037037  0.63888889  0.65420561  0.6635514
0.710280371
Train CV AUC Score: 0.674125995154
print("\nTest Fold AUC Scores: ", test scores)
print("Test CV AUC Score: ", test scores.mean())
Test Fold AUC Scores: [ 0.70212766  0.74468085  0.74468085  0.64444444
0.666666671
Test CV AUC Score: 0.700520094563
```

Stratified K-Fold Cross-Validation

An extended cross-validation is the Stratified K-fold cross-validation, where the class proportions are preserved in each fold, leading to better bias and variance estimates

Ensemble Methods

Ensemble methods enable combining multiple model scores into a single score to create a robust generalized model. At a high level there are two types of ensemble methods.

- 1. Combine multiple models of similar type #### Bagging (Bootstrap aggregation)
- 2. Bootstrap aggregation (also known as bagging) was proposed by Leo Breiman in 1994, which is a model aggregation technique to reduce model variance. The training data is split into multiple samples with replacements called bootstrap samples. Bootstrap sample size will be the same as the original sample size, with 3/4th of the original values and replacement result in repetition of values

3.

4. Independent models on each of the bootstrap samples are built, and the average of the predictions for regression or majority vote for classification is used to create the final model.

5.

6. Random Forest

7.

Boosting

The core concept of boosting is that rather than an independent individual hypothesis, combining hypotheses in a sequential order increases the accuracy. Essentially, boosting algorithms convert the weak learners into strong learners. Boosting algorithms are well designed to address the bias problems.

At a high level the AdaBoosting (adaptive boosting) process can be divided into three steps.

- 1. Assign uniform weights for all data points WO(x) = 1 / N, where N is the total number of training data points.
- 2. At each iteration fit a classifier ym(xn) to the training data and update weights to minimize the weighted error function.
 - 3. The final model.