HW - simple ML sklearn

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source: https://www.kaggle.com/datasets/mathchi/diabetes-data-set?datasetId=818300&sortBy=voteCount

Read Data And Clean Data

```
# library
from sklearn.linear_model import LinearRegression
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
from sklearn import tree
import pandas as pd
import numpy as np

# read data
url = 'https://raw.githubusercontent.com/plotly/datasets/master/diabetes.csv'
diabetes = pd.read_csv(url)
```

```
# preview head data
diabetes.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

```
# preview tail data
diabetes.tail()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

```
# info check missing value
diabetes.isna().sum() # non missing value?
```

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

```
# describe
diabetes.describe()

## observe at minimum values, the Pregnancies, Glucose, BloodPresure, SkinThickness, Insulin and BMI are 0 ?
## assume that they filled NaN value with 0
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Ou
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.0
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885	0.3
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.4
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.0
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.0
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.0

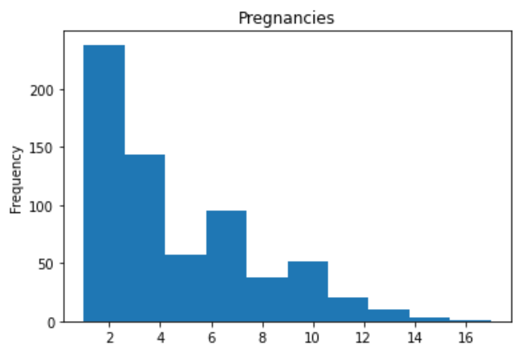
Ideal: We will fill minimum value(0) above with median value

```
diabetes[['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']]\
 = diabetes[['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']].replace(0, np.NaN)
```

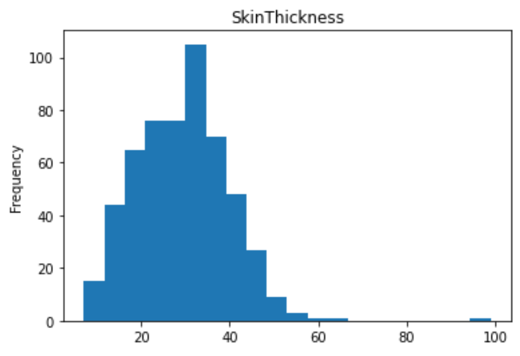
```
diabetes.isna().sum()
```

```
Pregnancies                 111
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
DiabetesPedigreeFunction      0
Age                           0
Outcome                       0
dtype: int64
```

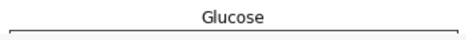
```
diabetes['Pregnancies'].plot(kind='hist').set_title('Pregnancies');
```



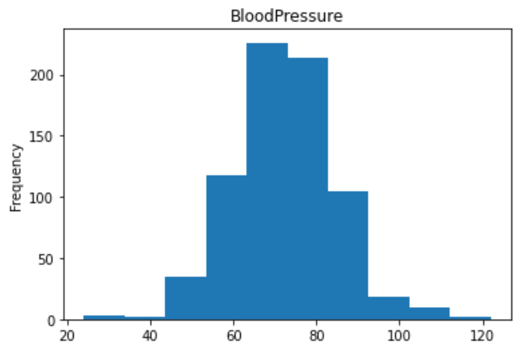
```
diabetes['SkinThickness'].plot(kind='hist', bins = 20).set_title('SkinThickness');
```



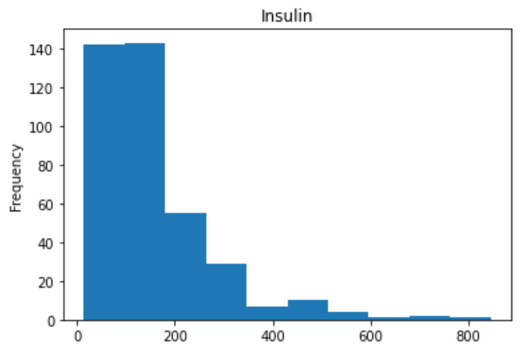
```
diabetes['Glucose'].plot(kind='hist').set_title("Glucose");
```



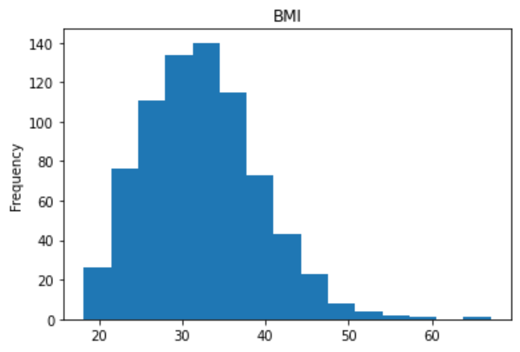
```
diabetes['BloodPressure'].plot(kind='hist').set_title("BloodPressure");
```



```
diabetes['Insulin'].plot(kind='hist').set_title("Insulin");
# use median
```



```
diabetes['BMI'].plot(kind='hist', bins=15).set_title("BMI");
```



```
# The missing values will be filled with the median values of each variable.

def median_target(var):

    temp = diabetes[diabetes[var].notnull()]

    temp = temp[[var, 'Outcome']].groupby(['Outcome'])[[var]].median().reset_index()

    return temp
```

```
columns = diabetes.columns

columns = columns.drop("Outcome")

for col in columns:

    diabetes.loc[(diabetes['Outcome'] == 0 ) & (diabetes[col].isnull()), col] = median_target(col)[col][0]
    diabetes.loc[(diabetes['Outcome'] == 1 ) & (diabetes[col].isnull()), col] = median_target(col)[col][1]
```

```
# check missing value final!
diabetes.isna().sum()
```

```
Pregnancies                 0
Glucose                     0
```

```
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

Split Data

```
# prepare data
X = diabetes.drop(['Outcome'], axis=1)
y = diabetes['Outcome']

# split data
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size = 0.30, random_state = 28 #set.seed()
)
```

```
print(f"X_train: {X_train.shape} \ny_train: {y_train.shape}")
```

```
X_train: (537, 8)
y_train: (537,)
```

Logistic Regression (Classification)

Predicted New Data (Scoring)

```
# train model
gl_model = LogisticRegression()
gl_model.fit(X_train, y_train)

# test model
p = gl_model.predict(X_test)
print(p)
```

```
[0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 1 1 1 1 0 0
 1 0 1 0 1 0 0 1 1 1 0 1 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0
 0 1 0 0 0 0 1 1 0 0 1 1 0 0 0 1 0 0 0 0 0 0 0 0 1 0 0 1 1 0 0 0 0 0 0 0 1
 0 0 0 0 1 0 1 0 1 0 1 1 0 0 0 0 0 0 0 0 0 1 0 1 0 0 1 1 0 1 0 0 1 0 0 0 1
 1 1 0 0 0 0 0 0 0 1 0 1 0 0 0 0 0 0 1 1 0 0 1 1 1 0 0 0 0 1 0 0 0 1 1 0 1
 0 1 0 1 0 0 0 1 1 0 0 0 0 0 0 0 1 0 1 0 0 1 0 0 0 1 0 1 0 1 1 1 0 0 0 0 1
 0 0 1 1 0 0 1 0 1]
/usr/local/lib/python3.8/dist-packages/sklearn/linear_model/_logistic.py:814: ConvergenceWarning: lbfgs failed to converg
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
```

Model Evaluation

```
from sklearn.metrics import accuracy_score
accuracy_score(y_test, p) # accuracy score
```

```
0.8095238095238095
```

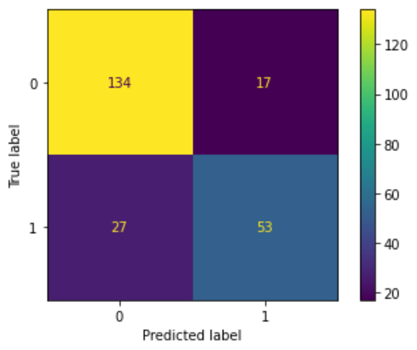
```
from sklearn.metrics import classification_report
tag_names = ['without diabetes', 'diabetes']
print(classification_report(y_test, p, target_names = tag_names))
```

```
                  precision    recall  f1-score   support

without diabetes       0.83      0.89      0.86       151
        diabetes       0.76      0.66      0.71        80

        accuracy                           0.81       231
       macro avg       0.79      0.77      0.78       231
    weighted avg       0.81      0.81      0.81       231
```

```
from sklearn.metrics import confusion_matrix
print(confusion_matrix(y_test, p))
```

```
    [[134  17]
     [ 27  53]]
```

```
from sklearn.metrics._plot.confusion_matrix import ConfusionMatrixDisplay
conf_matrix = confusion_matrix(y_test, p)
disp = ConfusionMatrixDisplay(conf_matrix,)
disp.plot();
```



Linear Regression

Split Data

```
# prepare data
X = diabetes.drop(['BMI'], axis=1)
y = diabetes['BMI']

# split data
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size = 0.30, random_state = 99 #set.seed()
)
```

Predicted New Data (Scoring)

```
from sklearn.tree import DecisionTreeRegressor
from sklearn.ensemble import RandomForestRegressor
# train model
tree_model = RandomForestRegressor()
tree_model.fit(X_train, y_train)

# test model
p_tree = tree_model.predict(X_test)
print(p_tree)
```

```
    [32.477 27.705 25.815 28.285 35.179 34.192 28.957 26.434 29.747 33.028
     32.085 39.614 27.743 31.593 31.252 39.552 25.739 36.68  37.605 30.488
     29.945 27.782 28.645 29.009 30.338 30.934 40.65  35.264 26.626 29.443
     40.292 30.376 36.201 31.552 31.442 34.695 35.141 24.642 36.167 33.616
     32.596 26.935 32.889 31.122 26.545 23.421 37.24  38.129 35.286 28.808
     32.299 23.383 32.286 38.515 31.511 31.73  33.279 28.182 25.508 34.285
     32.002 34.111 38.805 36.876 27.834 28.315 26.732 35.16  32.219 31.608
     31.387 34.924 36.109 33.174 28.24  31.781 33.099 33.38  36.996 35.684
     36.91  31.199 25.335 25.316 32.884 28.519 32.864 40.592 37.994 25.507
     28.492 33.722 31.672 28.806 25.603 26.125 34.134 34.415 34.59  28.892
     36.592 29.382 32.939 32.236 29.483 29.325 30.213 25.485 35.005 32.63
     36.338 29.844 37.347 28.081 35.215 33.548 34.091 25.861 25.766 35.41
     26.292 36.313 26.533 28.299 34.327 26.365 31.048 37.644 41.144 41.293
     26.38  35.952 36.627 39.51  24.949 29.556 34.261 30.006 32.274 37.595
     39.365 25.494 34.908 32.279 32.993 31.187 28.786 29.816 27.676 25.168
     26.805 28.88  30.251 28.973 36.708 27.29  25.44  33.511 28.911 34.547
     35.575 31.642 36.653 25.761 37.868 25.985 33.715 28.577 28.743 30.793
     35.064 33.225 35.769 30.124 32.55  39.962 28.693 27.838 36.664 31.345
     27.616 40.527 31.549 42.11  27.102 29.505 38.123 39.447 45.723 30.585
     37.116 33.48  30.291 31.644 38.441 27.213 37.316 34.668 26.754 27.788
     30.419 26.253 37.66  38.483 30.578 35.823 39.525 28.498 26.985 32.147
     36.42  28.297 31.119 30.806 27.39  34.196 28.995 32.54  41.523 32.424
     27.912 35.082 35.028 30.575 37.662 32.133 39.864 40.488 32.769 30.961
     29.448]
```

Model Evaluation

```
tree_model.score(X_test, y_test) # R2
```

```
0.43531492102461167
```