1 Praktikum 4

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https://github.com/rizalarfiyan/big-data

1.1 Simple Linear Regression

[18]:
```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import seaborn as sns
from sklearn.datasets import load_diabetes

%matplotlib inline
```

Load data yang sudah disediakan oleh sklearn datasets

[19]:
```
# load dataset diabetes
data_diabetes = load_diabetes(as_frame=True)

# membuat dataframe
df = pd.DataFrame(data_diabetes["frame"])
df.head()
```

[19]:
```
        age       sex       bmi        bp        s1        s2        s3  \
0  0.038076  0.050680  0.061696  0.021872 -0.044223 -0.034821 -0.043401
1 -0.001882 -0.044642 -0.051474 -0.026328 -0.008449 -0.019163  0.074412
2  0.085299  0.050680  0.044451 -0.005670 -0.045599 -0.034194 -0.032356
3 -0.089063 -0.044642 -0.011595 -0.036656  0.012191  0.024991 -0.036038
4  0.005383 -0.044642 -0.036385  0.021872  0.003935  0.015596  0.008142

         s4        s5        s6  target
0 -0.002592  0.019907 -0.017646   151.0
1 -0.039493 -0.068332 -0.092204    75.0
2 -0.002592  0.002861 -0.025930   141.0
3  0.034309  0.022688 -0.009362   206.0
4 -0.002592 -0.031988 -0.046641   135.0
```

Melihat deskripsi dari datasets

[17]:
```
print(data_diabetes["DESCR"])
```

```
.. _diabetes_dataset:

Diabetes dataset
----------------
```

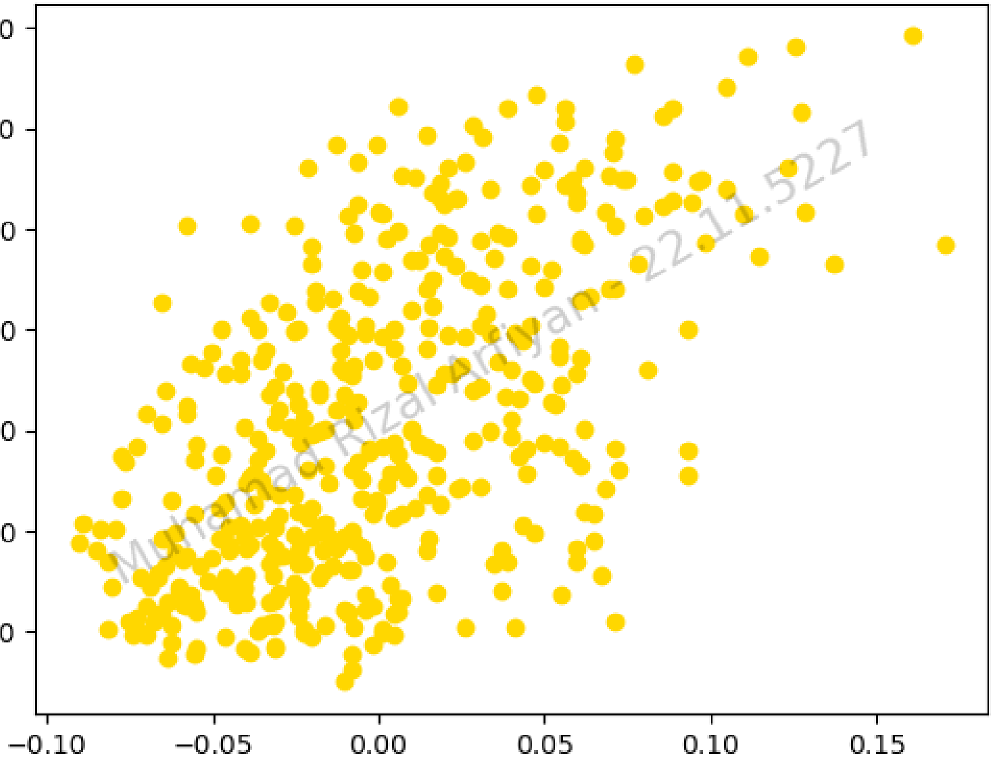
```
Ten baseline variables, age, sex, body mass index, average blood
pressure, and six blood serum measurements were obtained for each of n =
442 diabetes patients, as well as the response of interest, a
quantitative measure of disease progression one year after baseline.

**Data Set Characteristics:**

  :Number of Instances: 442

  :Number of Attributes: First 10 columns are numeric predictive values

  :Target: Column 11 is a quantitative measure of disease progression one year
after baseline

  :Attribute Information:
      - age     age in years
      - sex
      - bmi     body mass index
      - bp      average blood pressure
      - s1      tc, total serum cholesterol
      - s2      ldl, low-density lipoproteins
      - s3      hdl, high-density lipoproteins
      - s4      tch, total cholesterol / HDL
      - s5      ltg, possibly log of serum triglycerides level
      - s6      glu, blood sugar level

Note: Each of these 10 feature variables have been mean centered and scaled by
the standard deviation times the square root of `n_samples` (i.e. the sum of
squares of each column totals 1).

Source URL:
https://www4.stat.ncsu.edu/~boos/var.select/diabetes.html

For more information see:
Bradley Efron, Trevor Hastie, Iain Johnstone and Robert Tibshirani (2004) "Least
Angle Regression," Annals of Statistics (with discussion), 407-499.
(https://web.stanford.edu/~hastie/Papers/LARS/LeastAngle_2002.pdf)
```

1.1.1 Analisis dan visualisasi data

Membuat scatter plot antara kolom bmi dan target.

[41]:

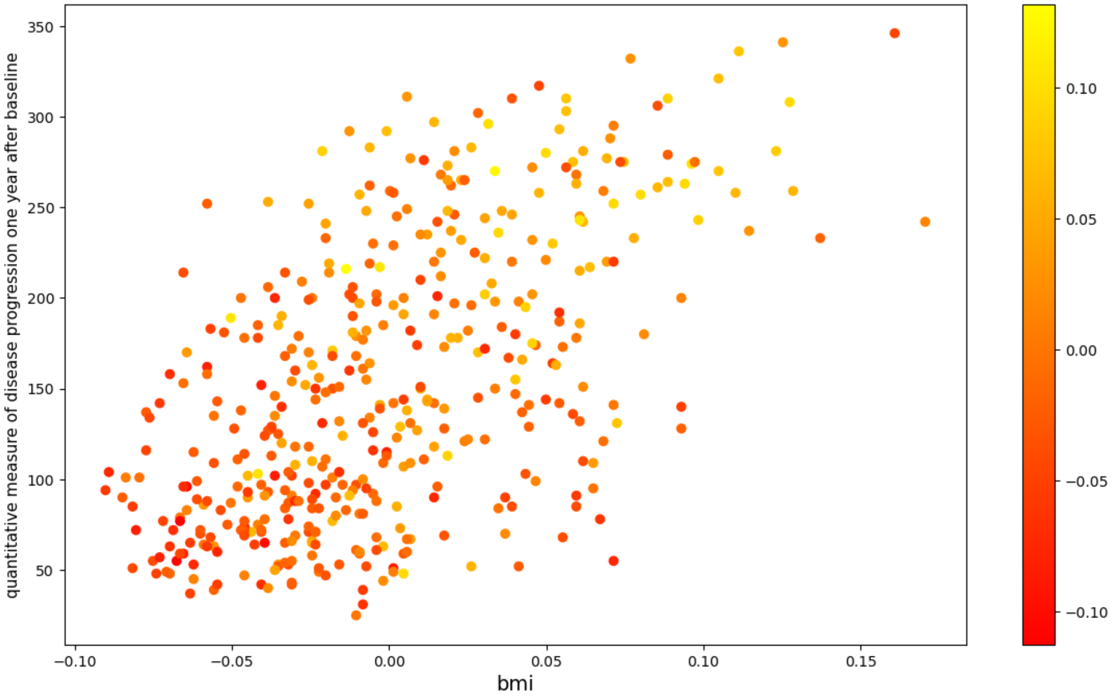
```python
# Scatter plot kolom 'bmi' dan 'target'
plt.text(
    0.5,
    0.5,
    "Muhamad Rizal Arfiyan - 22.11.5227",
    fontsize=18,
    color="black",
    ha="center",
    va="center",
    alpha=0.2,
    transform=plt.gcf().transFigure,
    rotation=30,
)
plt.scatter(df["bmi"], df["target"], color="gold")
plt.show()
```



[42]:

```
# Mengatur warna scatter plot dengan color map
fig, ax = plt.subplots(figsize=(14, 8))
x = ax.scatter(df["bmi"], df["target"], c=df["bp"], cmap="autumn")

ax.set_xlabel("bmi", size=14)
ax.set_ylabel(
    "quantitative measure of disease progression one year after baseline",␣
  ↪size=11
)

# Menambakan color bar
```

```
fig.colorbar(x)

plt.show()
```

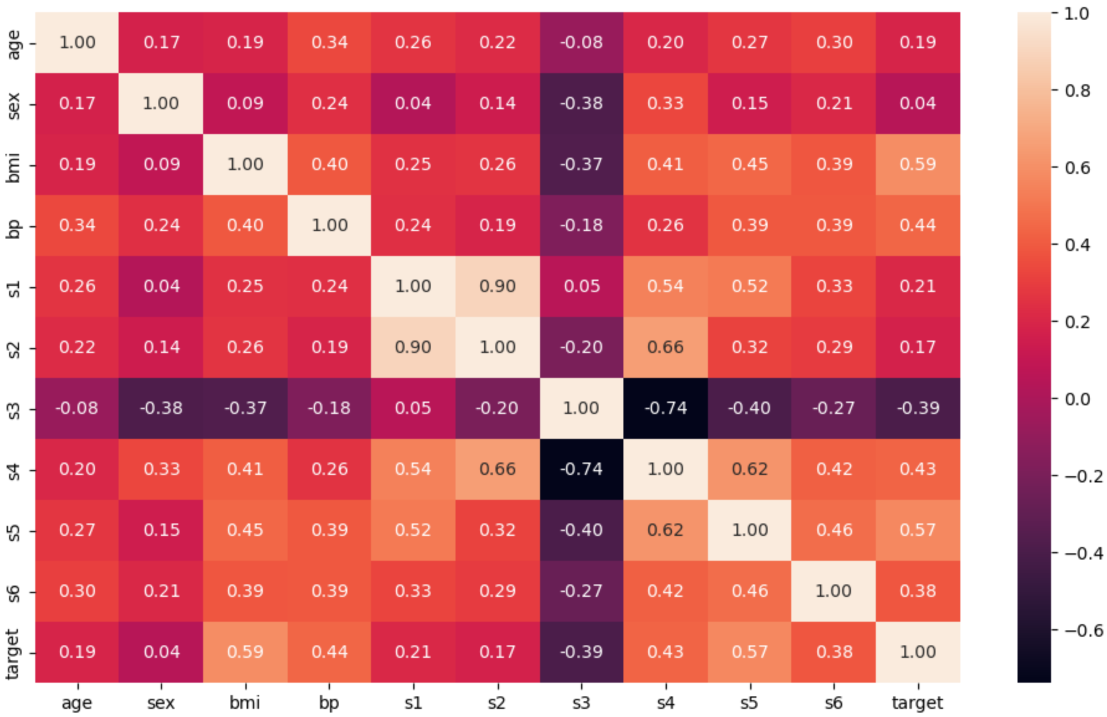


[22]:

```
# Menampilkan korelasi antarkolom

plt.figure(figsize=(12, 7))

corr = df.corr()
sns.heatmap(corr, annot=True, fmt=".2f")
```

[22]:

```
<Axes: >
```



1.2 Data Preparation

1.2.1 Membagi data train dan test

[34]:
```
# Membagi data train dan test

np.random.seed(42)
split = np.random.rand(len(df)) < 0.8
train = df[split]
test = df[~split]
```

[38]:
```
# Mendefinisikan X_train, y_train, X_test, dan y_test

X_train = np.asanyarray(train[["bmi"]])
y_train = np.asanyarray(train[["target"]])

X_test = np.asanyarray(test[["bmi"]])
y_test = np.asanyarray(test[["target"]])
```

1.3 Modeling

1.3.1 Linear regression dengan satu variabel bebas

[25]:

```
from sklearn.linear_model import LinearRegression

# Membuat dan melatih model
lr_model = LinearRegression()
lr_model.fit(X_train, y_train)
```

[25]:

```
LinearRegression()
```

[26]:

```
# Coefficient dan Intercept
print("Coefficients: ", lr_model.coef_)
print("Intercept: ", lr_model.intercept_)
```

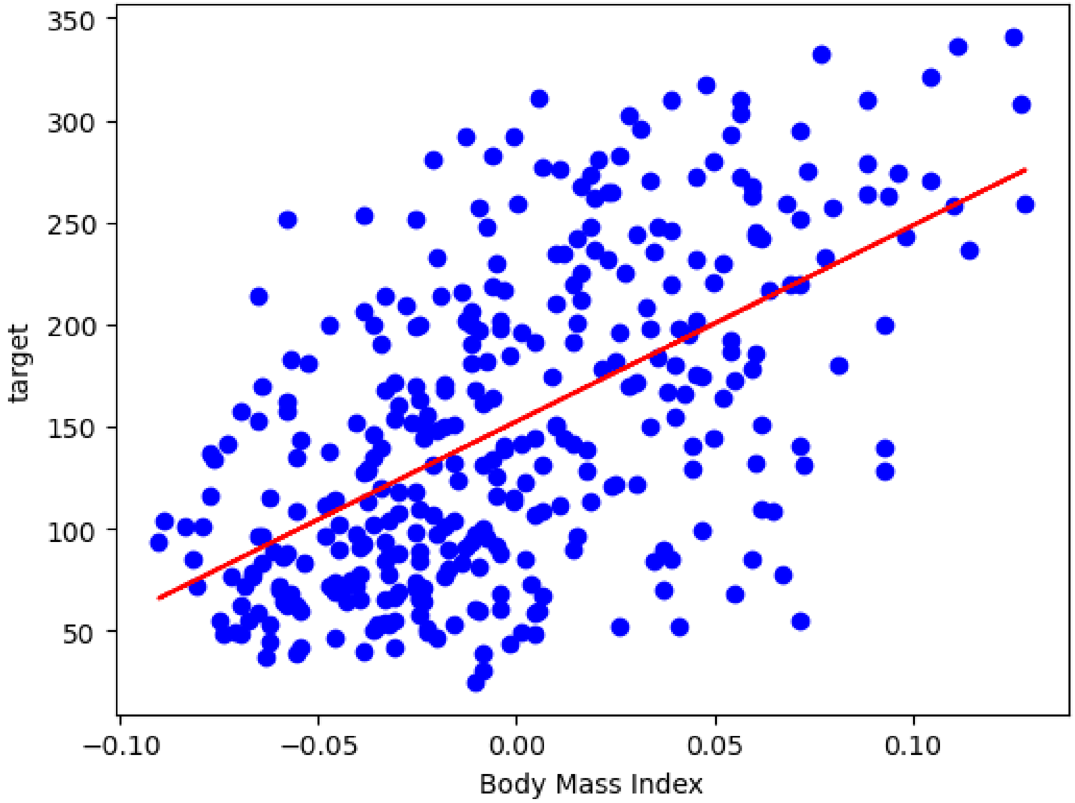
```
Coefficients:  [[958.28967126]]
Intercept:  [152.46395235]
```

[27]:

```
# Visualisasi dengan scatter plot

plt.scatter(X_train, y_train, color="blue")
plt.plot(X_train, lr_model.coef_[0][0] * X_train + lr_model.intercept_[0], "-r")
plt.xlabel("Body Mass Index")
plt.ylabel("target")
```

[27]:

```
Text(0, 0.5, 'target')
```



[28]:
```
# Menguji model dengan X_test

y_pred = lr_model.predict(X_test)

print("Data asli: \n", y_test[0:10])
print("\n")
print("Hasil prediksi: \n", y_pred[0:10])
```

```
Data asli:
 [[ 75.]
 [ 63.]
 [ 69.]
 [179.]
 [ 87.]
 [ 65.]
 [102.]
 [ 92.]
 [155.]
 [ 59.]]
```

```
Hasil prediksi:
 [[103.13689113]
 [150.64827531]
 [169.23968652]
 [124.82687086]
 [104.1697473 ]
 [ 91.77547317]
 [122.76115851]
 [129.99115175]
 [145.48399442]
 [143.41828207]]
```

[30]:

```python
from sklearn.metrics import mean_absolute_error, mean_squared_error

# Menampilkan MAE dan MSE
print("Mean Absolute Error (MAE): %.2f" % mean_absolute_error(y_pred, y_test))
print("Mean Squared Error (MSE): %.2f" % mean_squared_error(y_pred, y_test))
```

```
Mean Absolute Error (MAE): 51.84
Mean Squared Error (MSE): 3694.70
```