

GHARDA INSTITUTE OF TECHNOLOGY



Department of Computer Engineering

Machine Learning Lab BE Computer (Semester-VII)

Experiment No.8: Importance of feature scaling

Aim- To study, understand and test the importance of feature scaling.

Theory-

Feature scaling through standardization (or Z-score normalization) can be an important preprocessing step for many machine learning algorithms. Standardization involves rescaling the features such that they have the properties of a standard normal distribution with a mean of zero and a standard deviation of one.

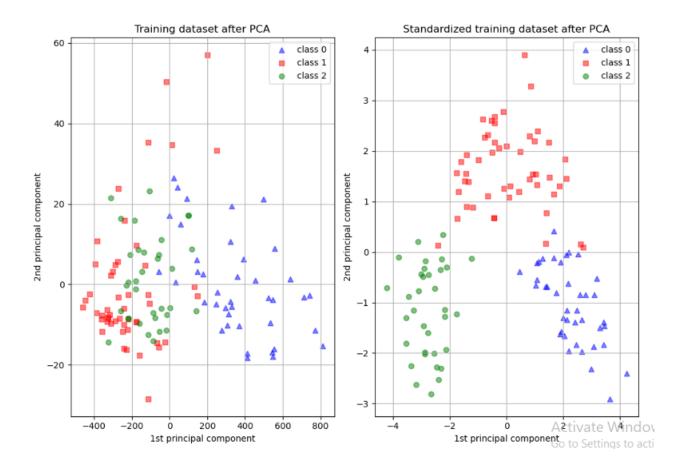
While many algorithms (such as SVM, K-nearest neighbors, and logistic regression) require features to be normalized, intuitively we can think of Principle Component Analysis (PCA) as being a prime example of when normalization is important. In PCA we are interested in the components that maximize the variance. If one component (e.g. human height) varies less than another (e.g. weight) because of their respective scales (meters vs. kilos), PCA might determine that the direction of maximal variance more closely corresponds with the 'weight' axis, if those features are not scaled. As a change in height of one meter can be considered much more important than the change in weight of one kilogram, this is clearly incorrect.

To illustrate this, PCA is performed comparing the use of data with StandardScaler applied to unscaled data. The results are visualized and a clear difference noted. The 1st principal component in the unscaled set can be seen. It can be seen that feature #13 dominates the direction, being a whole two orders of magnitude above the other features. This is contrasted when observing the principal component for the scaled version of the data. In the scaled version, the orders of magnitude are roughly the same across all the features.

The transformed data is then used to train a naive Bayes classifier, and a clear difference in prediction accuracies is observed wherein the dataset which is scaled before PCA vastly outperforms the unscaled version.

** About Dataset- Title: Wine Data Set

The dataset used is the Wine Dataset available at UCI. This dataset has continuous features that are heterogeneous in scale due to differing properties that they measure (i.e. alcohol content and malic acid).



Code -

import matplotlib.pyplot as plt from sklearn.model_selection import train_test_split from sklearn.preprocessing import StandardScaler from sklearn.decomposition import PCA

```
from sklearn.naive bayes import GaussianNB
from sklearn.metrics import accuracy score
from sklearn.datasets import load wine
from sklearn.pipeline import make pipeline
RANDOM STATE = 42
FIG SIZE = (10, 7)
features, target = load wine(return X y=True)
# Make a train/test split using 30% test size
X train, X test, y train, y test = train test split(features, target, test size=0.30,
random state=RANDOM STATE)
# Fit to data and predict using pipelined GNB and PCA
unscaled clf = make pipeline(PCA(n components=2), GaussianNB())
unscaled clf.fit(X train, y train)
pred test = unscaled clf.predict(X test)
# Fit to data and predict using pipelined scaling, GNB and PCA
std_clf = make_pipeline(StandardScaler(), PCA(n_components=2), GaussianNB())
std clf.fit(X train, y train)
pred test std = std clf.predict(X test)
# Show prediction accuracies in scaled and unscaled data.
print("\nPrediction accuracy for the normal test dataset with PCA")
print(f"{accuracy score(y test, pred test):.2%}\n")
print("\nPrediction accuracy for the standardized test dataset with PCA")
print(f"{accuracy score(y test, pred test std):.2%}\n")
# Extract PCA from pipeline
pca = unscaled clf.named steps["pca"]
pca std = std clf.named steps["pca"]
# Show first principal components
print(f"\nPC 1 without scaling:\n{pca.components [0]}")
print(f"\nPC 1 with scaling:\n{pca std.components [0]}")
# Use PCA without and with scale on X_train data for visualization.
X train transformed = pca.transform(X train)
scaler = std clf.named steps["standardscaler"]
scaled X train = scaler.transform(X train)
X train std transformed = pca std.transform(scaled X train)
```

```
# visualize standardized vs. untouched dataset with PCA performed
fig, (ax1, ax2) = plt.subplots(ncols=2, figsize=FIG_SIZE)
target classes = range(0, 3)
colors = ("blue", "red", "green")
markers = ("^", "s", "o")
for target class, color, marker in zip(target classes, colors, markers):
  ax1.scatter(
     x=X train transformed[y train == target class, 0],
     y=X train transformed[y train == target class, 1],
     color=color.
     label=f"class {target class}",
     alpha=0.5,
     marker=marker,
  ax2.scatter(
     x=X train std transformed[y train == target class, 0],
     y=X train std transformed[y train == target class, 1],
     color=color.
     label=f"class {target_class}",
     alpha=0.5,
     marker=marker,
  )
ax1.set title("Training dataset after PCA")
ax2.set title("Standardized training dataset after PCA")
for ax in (ax1, ax2):
  ax.set xlabel("1st principal component")
  ax.set ylabel("2nd principal component")
  ax.legend(loc="upper right")
  ax.grid()
plt.tight_layout()
plt.show()
```

Results -

```
import matplotlib.pyplot as plt
 from sklearn.model selection import train test split
 from sklearn.preprocessing import StandardScaler
 from sklearn.decomposition import PCA
 from sklearn.naive_bayes import GaussianNB
 from sklearn.metrics import accuracy_score
 from sklearn.datasets import load_wine
from sklearn.pipeline import make_pipeline
 RANDOM STATE = 42
FIG SIZE = (10, 7)
features, target = load_wine(return_X_y=True)
# Make a train/test split using 30% test size
X_train, X_test, y_train, y_test = train_test_split(features, target, test_size=0.30, random_state=RANDOM_STATE)
 # Fit to data and predict using pipelined GNB and PCA
unscaled_clf = make_pipeline(PCA(n_components=2), GaussianNB())
unscaled_clf.fit(X_train, y_train)
pred_test = unscaled_clf.predict(X_test)
 # Fit to data and predict using pipelined scaling, GNB and PCA
std_clf = make_pipeline(StandardScaler(), PCA(n_components=2), GaussianNB())
std_clf.fit(X_train, y_train)
pred_test_std = std_clf.predict(X_test)
```

```
# Show prediction accuracies in scaled and unscaled data.
print("\nPrediction accuracy for the normal test dataset with PCA")
print(f"{accuracy_score(y_test, pred_test):.2%}\n")
print("\nPrediction accuracy for the standardized test dataset with PCA")
print(f"{accuracy_score(y_test, pred_test_std):.2%}\n")
# Extract PCA from pipeline
pca = unscaled_clf.named_steps["pca"]
pca_std = std_clf.named_steps["pca"]
# Show first principal components
print(f"\nPC 1 without scaling:\n{pca.components_[0]}")
print(f"\nPC 1 with scaling:\n{pca_std.components_[0]}")
# Use PCA without and with scale on X_train data for visualization.
X train transformed = pca.transform(X train)
scaler = std_clf.named_steps["standardscaler"]
scaled X train = scaler.transform(X train)
X_train_std_transformed = pca_std.transform(scaled_X_train)
# visualize standardized vs. untouched dataset with PCA performed
fig, (ax1, ax2) = plt.subplots(ncols=2, figsize=FIG_SIZE)
target classes = range(0, 3)
colors = ("blue", "red", "green")
markers = ("^", "s", "o")
```

```
for target_class, color, marker in zip(target_classes, colors, markers):
   ax1.scatter(
       x=X_train_transformed[y_train == target_class, 0],
       y=X_train_transformed[y_train == target_class, 1],
       color=color,
       label=f"class {target_class}",
       alpha=0.5,
       marker=marker,
   ax2.scatter(
       x=X_train_std_transformed[y_train == target_class, 0],
       y=X_train_std_transformed[y_train == target_class, 1],
       color=color,
       label=f"class {target_class}",
       alpha=0.5,
       marker=marker.
ax1.set_title("Training dataset after PCA")
ax2.set_title("Standardized training dataset after PCA")
for ax in (ax1, ax2):
   ax.set_xlabel("1st principal component")
   ax.set_ylabel("2nd principal component")
    ax.legend(loc="upper right")
    ax.grid()
```

```
for ax in (ax1, ax2):
    ax.set_xlabel("1st principal component")
    ax.set_ylabel("2nd principal component")
    ax.legend(loc="upper right")
    ax.grid()

plt.tight_layout()

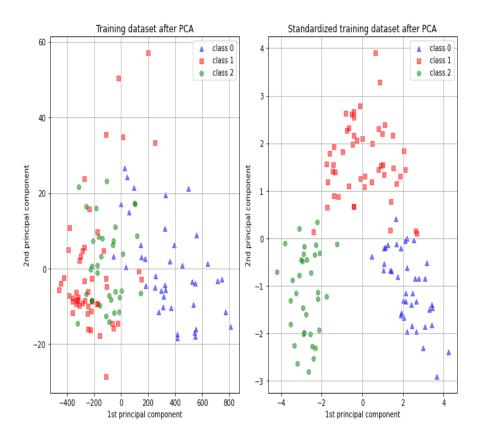
plt.show()
```

```
Prediction accuracy for the normal test dataset with PCA 81.48%

Prediction accuracy for the standardized test dataset with PCA 98.15%

PC 1 without scaling:
[ 1.76342917e-03 -8.35544737e-04 1.54623496e-04 -5.31136096e-03 2.01663336e-02 1.02440667e-03 1.53155502e-03 -1.11663562e-04 6.31071580e-04 2.32645551e-03 1.53606718e-04 7.43176482e-04 9.99775716e-01]

PC 1 with scaling:
[ 0.13443023 -0.25680248 -0.0113463 -0.23405337 0.15840049 0.39194918 0.41607649 -0.27871336 0.33129255 -0.11383282 0.29726413 0.38054255 0.27507157]
```



Discussion -