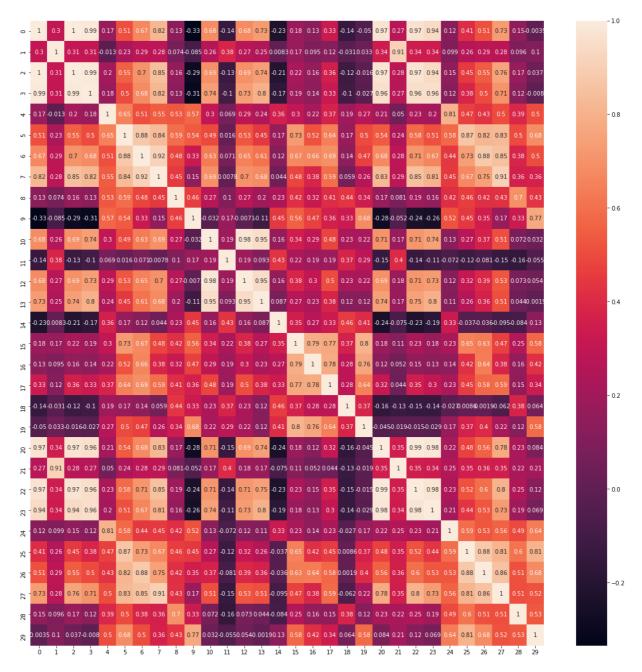
主成分分析

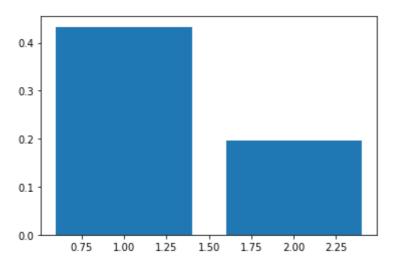
```
In [1]:
         import warnings
         import pandas as pd
         import matplotlib.pyplot as plt
         import numpy as np
         from sklearn.model_selection import train_test_split
         from sklearn.preprocessing import StandardScaler
         from sklearn.linear_model import LogisticRegressionCV
         from sklearn.metrics import confusion_matrix
         from sklearn. decomposition import PCA
         from sklearn.datasets import load_breast_cancer
         import seaborn
         warnings. simplefilter('ignore')
In [2]:
         data_breast_cancer = load_breast_cancer()
         X = pd. DataFrame (data_breast_cancer["data"], columns=data_breast_cancer["feature_names"
         y = pd. DataFrame(data_breast_cancer["target"], columns=["target"])
         X_train, X_test, y_train, y_test = train_test_split(X, y, random_state=0)
         sc = StandardScaler()
         X_train_std = sc. fit_transform(X_train)
         X_{\text{test\_std}} = \text{sc.transform}(X_{\text{test}})
In [3]:
         Ir = LogisticRegressionCV(cv=10, random_state=0)
         Ir. fit(X_train_std, y_train)
         print('train score:', Ir. score(X_train_std, y_train))
         print('test score:', Ir. score(X_test_std, y_test))
         train score: 0.9882629107981221
         test score: 0.972027972027972
In [4]:
         plt.figure(figsize=(20, 20))
         seaborn. heatmap(pd. DataFrame(X_train_std).corr(), annot=True)
```

Out[4]: <matplotlib.axes._subplots.AxesSubplot at Ox26207f29908>



```
pca = PCA(n_components=2)
pca. fit(X_train_std)
plt. bar([n for n in range(1, len(pca.explained_variance_ratio_)+1)], pca.explained_variance_ratio_)+1)], pca.explained_variance_ratio_)+1)]
```

Out[9]: <BarContainer object of 2 artists>

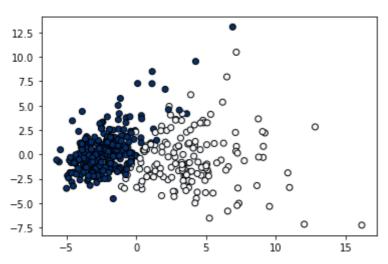


```
In [10]: X_train_pca = pca.fit_transform(X_train_std)
X_test_pca = pca.fit_transform(X_test_std)

Ir = LogisticRegressionCV(cv=10, random_state=0)
Ir.fit(X_train_pca, y_train)
print('train score:', Ir.score(X_train_pca, y_train))
print('test score:', Ir.score(X_test_pca, y_test))
plt.scatter(X_train_pca[:, 0], X_train_pca[:, 1], c = y_train.values.flatten(), edgecol
```

train score: 0.9647887323943662 test score: 0.916083916083916

Out[10]: <matplotlib.collections.PathCollection at 0x26208d13408>



乳がんデータを主成分分析を行って次元削減したデータを、ロジスティック回帰で分類した。 2つの主成分だけで、データの分散の6割近くを担っていたため、すべてのデータを用いて行った場合とほぼ遜色なく学習ができた。

3つに増やした場合も行ったが、それほどスコアに変化はなかった。

欠点としては、より学習の中身がブラックボックス化してしまうため、説明性がひくくなる。