④主成分分析 実装演習

In [1]:

```
import pandas as pd
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
import matplotlib.pyplot as plt
%matplotlib inline
```

・ガンのデータを使用

In [3]:

```
cancer_df = pd. read_csv('C:/Users/Kadoya Toshiki/Desktop/2. 機械学習/機械学習_実習演習用コード/study_ai_ml_google/data/cancer.csv')
print('cancer df shape: {}'.format(cancer_df.shape))
```

cancer df shape: (569, 33)

In [4]:

cancer_df

Out[4]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothn
0	842302	М	17.99	10.38	122.80	1001.0	
1	842517	М	20.57	17.77	132.90	1326.0	
2	84300903	М	19.69	21.25	130.00	1203.0	
3	84348301	М	11.42	20.38	77.58	386.1	
4	84358402	М	20.29	14.34	135.10	1297.0	
564	926424	М	21.56	22.39	142.00	1479.0	
565	926682	М	20.13	28.25	131.20	1261.0	
566	926954	М	16.60	28.08	108.30	858.1	
567	927241	М	20.60	29.33	140.10	1265.0	
568	92751	В	7.76	24.54	47.92	181.0	

569 rows × 33 columns

In [5]:

#不要なデータ削除

cancer_df.drop('Unnamed: 32', axis=1, inplace=True)

cancer_df

Out[5]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothn
0	842302	М	17.99	10.38	122.80	1001.0	
1	842517	М	20.57	17.77	132.90	1326.0	
2	84300903	М	19.69	21.25	130.00	1203.0	
3	84348301	М	11.42	20.38	77.58	386.1	
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569 rows × 32 columns

[・]diagnosis: 診断結果 (良性がB / 悪性がM)・説明変数は3列以降、目的変数を2列目としロジスティック回帰で分類

In [6]:

```
# 目的変数の抽出
y = cancer_df. diagnosis. apply(lambda d: 1 if d == 'M' else 0)
# 説明変数の抽出
X = cancer_df.loc[:, 'radius_mean':]
# 学習用とテスト用でデータを分離
X_train, X_test, y_train, y_test = train_test_split(X, y, random_state=0)
#標準化
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
# ロジスティック回帰で学習
logistic = LogisticRegressionCV(cv=10, random_state=0)
logistic.fit(X_train_scaled, y_train)
# 検証
print('Train score: {:.3f}'.format(logistic.score(X_train_scaled, y_train)))
print('Test score: {:.3f}'.format(logistic.score(X_test_scaled, y_test)))
print('Confustion matrix:\frac{\pmatrix}{\pmatrix}\frac{\pmatrix}{\pmatrix}'. format(confusion_matrix(y_true=y_test, y_pred=logistic.predict(X))
_test_scaled))))
```

```
④主成分分析 実装演習
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Train score: 0.988 Test score: 0.972 Confustion matrix:

[[89 1] [3 50]] C:\Users\Users\Kadoya Toshiki\Uperanaconda3\Uperaconda3\Up

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・検証スコア(Test score):97%で分類できることを確認

========

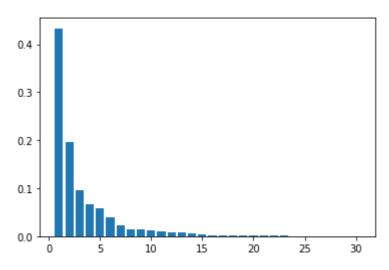
1.主成分分析

In [7]:

```
pca = PCA(n_components=30)
pca.fit(X_train_scaled)
plt.bar([n for n in range(1, len(pca.explained_variance_ratio_)+1)], pca.explained_variance_ratio_)
```

Out[7]:

<BarContainer object of 30 artists>



・第1主成分から第m主成分までの寄与率(m=30)

In [8]:

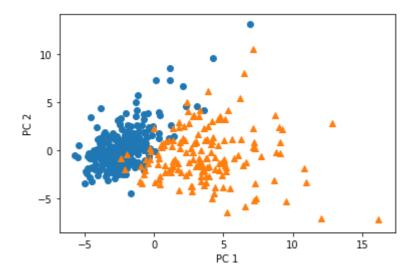
```
# PCA
# 次元数2まで圧縮
pca = PCA (n_components=2)
X_train_pca = pca.fit_transform(X_train_scaled)
print('X_train_pca shape: {}'.format(X_train_pca.shape))
# X_train_pca shape: (426, 2)
# 寄与率
print('explained variance ratio: {}'.format(pca.explained_variance_ratio_))
# explained variance ratio: [ 0.43315126  0.19586506]
# 散布図にプロット
temp = pd. DataFrame(X_train_pca)
temp['Outcome'] = y_train.values
b = temp[temp['Outcome'] == 0]
m = temp[temp['Outcome'] == 1]
plt. scatter(x=b[0], y=b[1], marker='o') # 良性は〇でマーク
plt.scatter(x=m[0], y=m[1], marker='^') # 悪性は△でマーク
plt. xlabel('PC 1') # 第1主成分をx軸
plt.ylabel('PC 2') # 第2主成分をy軸
```

X_train_pca shape: (426, 2)

explained variance ratio: [0.43315126 0.19586506]

Out[8]:

Text (0, 0.5, 'PC 2')



=======

・主成分分析により次元圧縮を実施。(使用する特徴量:30個→2個)・複数の説明変数(特徴量)から新しい合成変数を生み出している・主成分の数はパラメータとして調整できる・各成分の寄与率も確認可能・学習に使用する特徴量が少ない状態で、精度の高い予測結果を達成することが可能

In []: