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1. Comparison of loading matrix in Python and R Programming

For the comparison Python and R are figure bellow.

1.1 Python

1.1.1 Code,

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

from matplotlib.pyplot import figure

cell = pd.read_csv('cell_num.csv', index_col=0)

from sklearn.preprocessing import StandardScaler

x = StandardScaler().fit_transform(cell)
x = pd.DataFrame(x, columns=cell.columns)

from sklearn.decomposition import PCA

pcm = PCA()
pcal = pcm.fit_transform(x)

loading = pcm.components_
```

1.1.2 Explanation,

Standard Scaler

```
class sklearn.preprocessing.StandardScaler(*, copy=True, with_mean=True, with_std=True)
```

Standardize features by removing the mean and scaling to unit variance. The standard score of a sample \mathbf{x} is calculated as:

$$z = (x - u) / s$$

where **u** is the mean of the training samples or zero if **with_mean=False**, and **s** is the standard deviation of the training samples or one if **with_std=False**.

PCA

```
class skleann.decomposition.PCA(n\_components=None, *, copy=True, whiten=False, svd\_solver='auto', tol=0.0, iterated\_power='auto', n\_oversamples=10, power\_iteration\_normalizer='auto', random\_state=None)
```

Linear dimensionality reduction using Singular Value Decomposition of the data to project it to a lower dimensional space. The input data is centered but not scaled for each feature before applying the SVD. It uses the LAPACK implementation of the full SVD or a randomized truncated SVD by the method of Halko et al. 2009, depending on the shape of the input data and the number of components to extract. It can also use the *scipy.sparse.linalg* ARPACK implementation of the truncated SVD.

1.1.3 Result

Loading

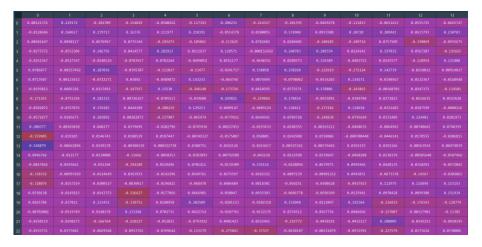


Figure 1. result of loading matrix in Python

Transpose the loading

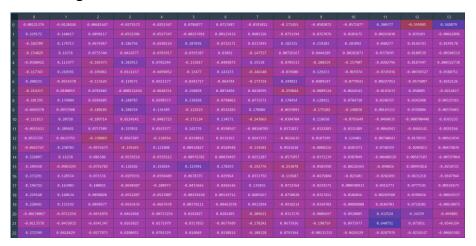


Figure 2. result of loading matrix after Transpose

1.2 R

1.2.1 Code,

```
cell <- read.csv('cell_num.csv')[-1]
cell.pca <- prcomp(cell, center = TRUE, scale. =TRUE)
cell.pca
rotation <- cell.pca$rotation # loading matrix</pre>
```

```
cell.pca2 <- princomp(cell, cor = FALSE, scores = TRUE)
score2 <- cell.pca2$scores # score matrix</pre>
```

1.2.2 Explanation,

Prcomp(data, Center=True, Scale.=True)

Performs a principal components analysis on the given data matrix and returns the results as an object of class prcomp.

Center=True

a logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of x can be supplied. The value is passed to scale.

Scale.=True

a logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is FALSE for consistency with S, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of x can be supplied. The value is passed to scale.

Princomp(data, Cor = False, Score = True)

princomp performs a principal components analysis on the given numeric data matrix and returns the results as an object of class princomp.

Cor = False

a logical value indicating whether the calculation should use the correlation matrix or the covariance matrix. (The correlation matrix can only be used if there are no constant variables.)

Score = True

a logical value indicating whether the score on each principal component should be calculated.

1.2.3 Result

Loading

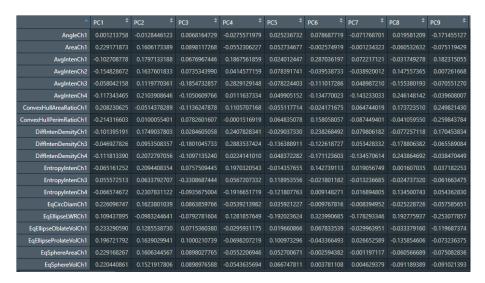


Figure 3. result of loading matrix in R

1.3 Analysis

So for loading result both in Python and R are have similar result but in the python you need to do transpose if you want have same result as in the R result.