INTERACTIVE SINGLE-CELL UMAP VIEWER WITH SHINY FOR PYTHON

Overview:

This application permits the user to load .zip files containing .h5ad files including Cell types and other attributes and creates an UMAP plot.

Features:

- Unzips the .zip file uploaded by the user.
- Processes the data.
- Renders the plot created using scanpy.

Requirements:

1. Python 3x
2. **Libraries:**

```
from shiny import App,ui, Inputs,Outputs, Session, reactive, render
import scanpy as sc
import zipfile
import matplotlib
import matplotlib.pyplot
import os
import scipy
import time
t0start = time.time()
import pandas
import numpy
import os
import sys
import matplotlib.pyplot as plt
import matplotlib as mpl
mpl.rcParams['figure.dpi'] = 70
import seaborn as sns
from sklearn.decomposition import PCA
from zipfile import ZipFile
from shiny.types import FileInfo
import umapcodes as uc
from umapcodes import plot
from umapcodes import cluster
from umapcodes import filter
from umapcodes import unzip_file
import io
```

Usage:

1. **Copy the repository:**
   https://github.com/serayyucetin/shiny.git
2. **Library installation:**

By using the code “pip install -r requirement.txt” make sure you install the libraries. Otherwise the app is not going to work.

3. Run the App:

Run the codes and click on the Run Shiny App button.

Then add your zip file.The process can be observed on the terminal while you wait for the clustering and other operations to be concluded.

4. Preview(Before-After):