**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>

1. **Library installation:**

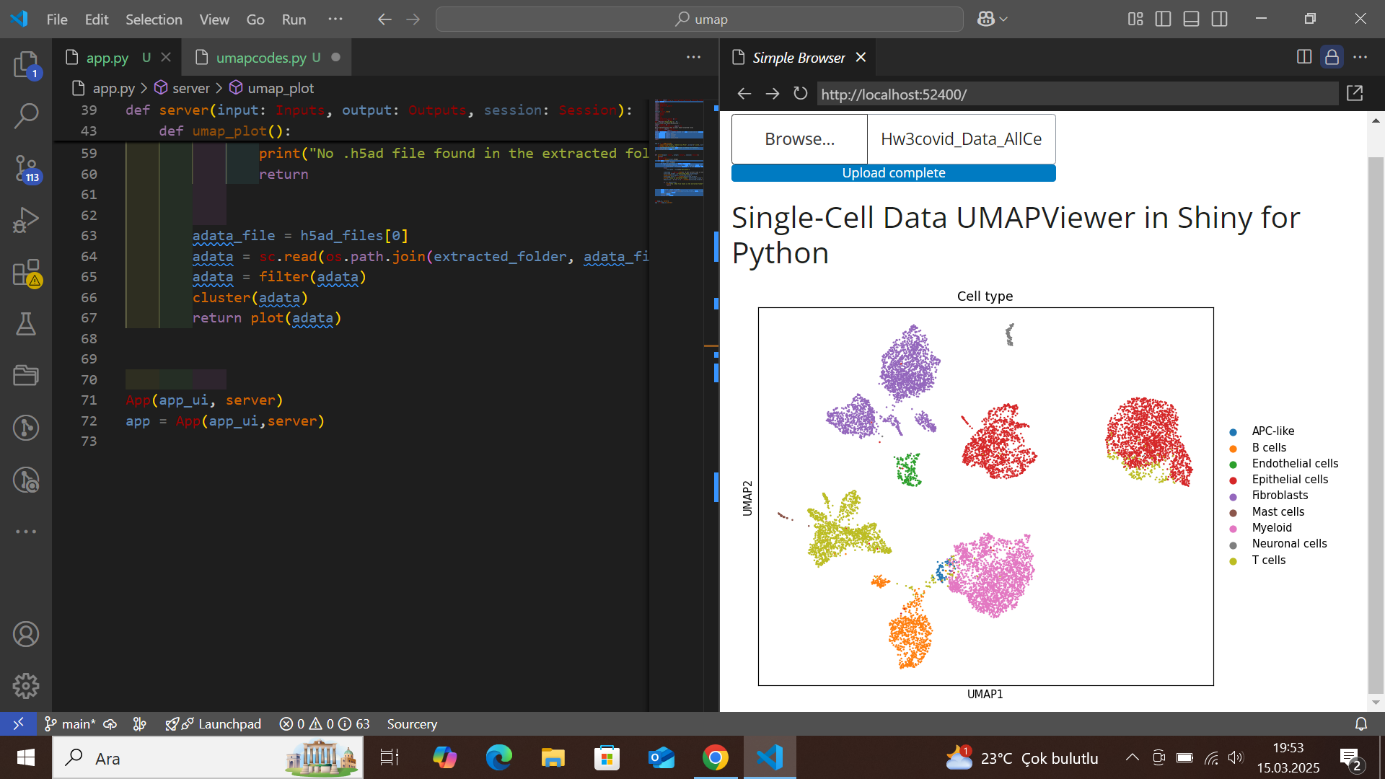
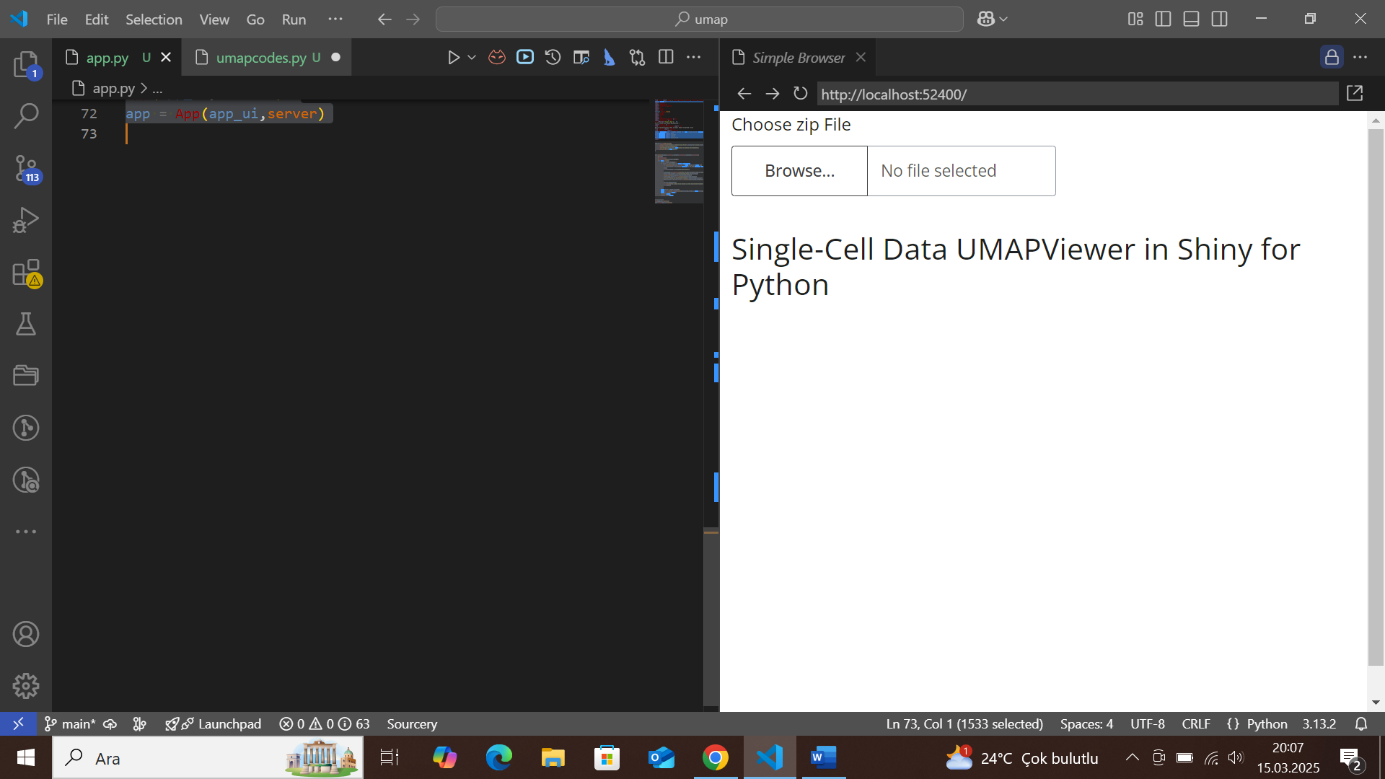
By using the code “pip install -r requirement.txt” make sure you install the libraries. Otherwise the app is not going to work.

1. **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.

1. **Preview(Before-After):**

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