User Guide

Barley 4D Spatial Transcriptomics Pipeline

This pipeline processes Visium SpaceRanger output to generate clustering as well as transcript abundance plots. It requires the *.h5 file and filtered_feature_bc_matrix/features.tsv from SpaceRanger.

Download the pipeline

To access the pipeline, download it from this repository

After downloading, you will find the following directories:

- **pipeline**: Contains the R scripts and notebook that form the pipeline.
- **container**: Includes the Dockerfile, script to run the notebook's container (runJupyterDocker.sh), and R package version file (renv.lock).
- **utils**: Contains the necessary scripts to ensure the visualization application displays all required plots.

Install Docker

To run the pipeline, you'll need Docker. You can either install Docker Desktop cor just the Docker CLI.

Docker Desktop includes both the CLI and a graphical user interface, while the CLI version provides only the command-line tools.

Once installed, you'll be able to build and run the container for the pipeline.

Build the Docker container

Before using the Docker container, you need to build it. Follow the steps below:

```
# Navigate to the directory containing the Dockerfile
cd JupyterNotebook/container

# Build the Docker container
sudo docker build .  -t analysis-pipeline:1.1.0
```

This will build the container based on Dockerfile and tag it as analysis-pipeline:1.1.0.

How to run the pipeline:

1. Navigate to the JupyterNotebook/container directory

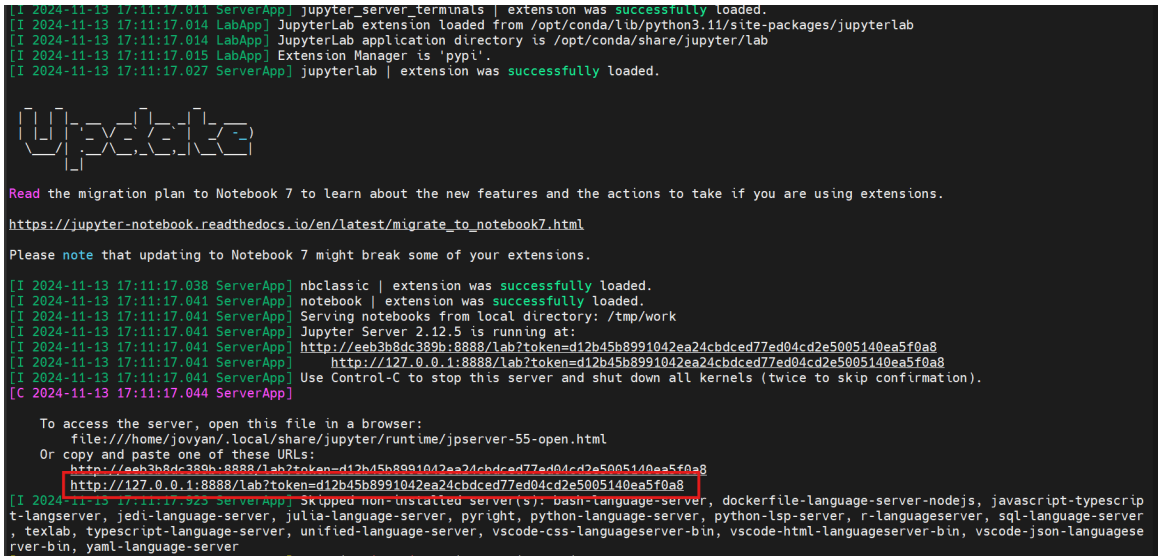
2. Edit the runJupyterDocker.sh script by updating the following variables:

- DATA_DIR: Directory containing your input data
- PIPELINE_DIR: Directory where the pipeline is stored
- UTILS_DIR: Directory containing the necessary scripts for the visualization application

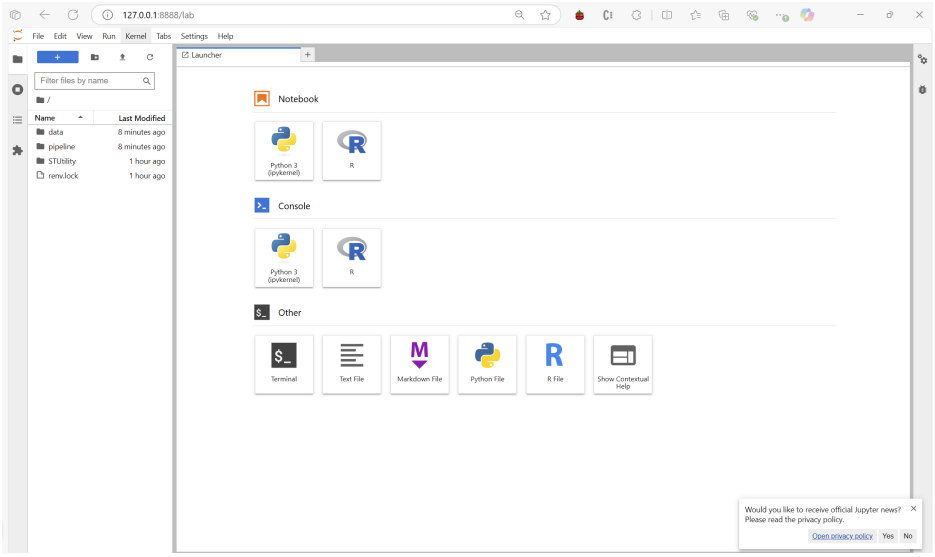
3. Run the Docker container: `sudo bash runJupyterDocker.sh`
4. If you're running the pipeline on a remote Virtual Machine, set up SSH tunneling:

```
# Run the following command to forward the required port:
bash
ssh -L 888:localhost:8888 user@remote_server.com
```

5. Access the Jupyter Notebook: Copy the URL that appears when the container starts and paste it into your browser.



You should now see the landing page:



6. Navigate to the baseNotebook.ipynb:

Inside the pipeline directory, you will find the baseNotebook.ipynb file. This notebook contains detailed instructions and descriptions for each step of the pipeline.