

mlPEA User Manual

(version 1.0)

- mlPEA is a user-friendly and multi-functionality platform specifically tailored to the needs of streamlined processing of m⁶A-Seq data in a reference genome-free manner. By taking advantage of machine learning (ML) algorithms, mlPEA enhanced the m⁶A-Seq data analysis by constructing robust computational models for identifying high-quality transcripts and high-confidence m⁶A-modified regions.
- mlPEA comprises four functional modules: **Data Preprocessing, Transcriptome Construction, m⁶A Calling, and Functional Exploration.**
- mlPEA was powered with an advanced packaging technology, which enables compatibility and portability.
- mlPEA project is hosted on <http://github.com/cma2015/mlPEA>
- mlPEA docker image is available at <http://hub.docker.com/r/malab/mlpea>

mlPEA installation

- **Step 1:** Docker installation

i) Docker installation and start ([Official installation tutorial](#))

For **Windows (Only available for Windows 10 Professional and Enterprise version):**

- Download [Docker](#) for windows;
- Double click the EXE file to open it;
- Follow the wizard instruction and complete installation;
- Search docker, select **Docker for Windows** in the search results and click it.

For **Mac OS X (Test on macOS Sierra version 10.12.6 and macOS High Sierra version 10.13.3):**

- Download [Docker](#) for Mac OS;
- Double click the DMG file to open it;
- Drag the docker into Applications and complete installation;
- Start docker from Launchpad by click it.

For **Ubuntu (Test on Ubuntu 18.04 LTS):**

- Go to [Docker](#), choose your Ubuntu version, browse to **pool/stable** and choose **amd64, armhf, ppc64el or s390x**. Download the **DEB** file for the Docker version you want to install;
- Install Docker, supposing that the DEB file is download into following path: **"/home/docker-ce~ubuntu_amd64.deb"**

```
$ sudo dpkg -i /home/docker-ce<version-XXX>-ubuntu_amd64.deb
$ sudo apt-get install -f
```

ii) Verify if Docker is installed correctly

Once Docker installation is completed, we can run `hello-world` image to verify if Docker is installed correctly. Open terminal in Mac OS X and Linux operating system and open CMD for Windows operating system, then type the following command:

```
$ docker run hello-world
```

Note: root permission is required for Linux operating system.

- **Step 2:** mlPEA installation from Docker Hub

```
# pull latest mlpea Docker image from docker hub
$ docker pull malab/mlpea
```

- **Step 3:** Launch mlPEA local server

```
$ docker run -it -p 880:8080 malab/mlpea bash
$ bash /home/galaxy/run.sh
```

Then, mlPEA local server can be accessed via <http://localhost:8080>

The screenshot displays the mlPEA web application interface. The main content area features a large heading "Welcome to mlPEA" followed by the tagline "a user-friendly and multi-functionality platform for reference genome-free m⁶A-Seq data analysis". Below this, there is an "About" section with bullet points describing the platform's capabilities and a "Tutorial" section. The left sidebar contains a "Tools" menu with categories like "DATA PREPROCESSING", "TRANSCRIPTOME CONSTRUCTION", "FUNCTIONAL EXPLORATION", and "WORKFLOWS". The right sidebar shows a "History" panel with a list of recent analyses, each with a name, a date, and a status icon.