

easyMF User Manual

(version 1.0)

easyMF is a user-friendly web platform that aims to facilitate biological discovery from large-scale transcriptome data through matrix factorization (MF). It offers several functional tools for gene expression matrix generation, expression matrix factorization, and metagene-based exploratory analysis including sample clustering, signature gene identification, functional gene discovery, subtype cell detection, and pathway activity inference.

- easyMF project is hosted on <https://github.com/cma2015/easyMF>.
- easyMF docker image is available in <https://hub.docker.com/r/malab/easymf>.
- easyMF demo server can be accessed via <http://easymf.omicstudio.cloud>.
- The following part shows installation of easyMF docker image and detailed documentation for each function in easyMF.

easyMF 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.

- Once Docker is installed successfully, you will see the following message:

```
$ docker run hello-world
Unable to find image 'hello-world:latest' locally
latest: Pulling from library/hello-world
1b930d010525: Pull complete
Digest: sha256:4fe721ccc2e8dc7362278a29dc660d833570ec2682f4e4194f4ee23e415e1064
Status: Downloaded newer image for hello-world:latest
```

Hello from Docker!

This message shows that your installation appears to be working correctly.

To generate this message, Docker took the following steps:

1. The Docker client contacted the Docker daemon.
2. The Docker daemon pulled the "hello-world" image from the Docker Hub. (amd64)
3. The Docker daemon created a new container from that image which runs the executable that produces the output you are currently reading.
4. The Docker daemon streamed that output to the Docker client, which sent it to your terminal.

To try something more ambitious, you can run an Ubuntu container with:

```
$ docker run -it ubuntu bash
```

Share images, automate workflows, and more with a free Docker ID:

<https://hub.docker.com/>

For more examples and ideas, visit:

<https://docs.docker.com/get-started/>

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

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

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

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

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

Galaxy

Tools

search tools

Get Data

easyMF

I) MATRIX PREPARATION

Data Retrieval

Expression Matrix Generation

Expression Quality Control

II) MATRIX FACTORIZATION

Matrix Factorization

III) METAGENE-BASED DEEP MINING USING AM

Functional Gene Discovery

Pathway Activity Inference

IV) METAGENE-BASED DEEP MINING USING PM

Sample Clustering Analysis

Temporal-spatial Analysis

Subtype Cell Detection

Workflows

All workflows

Analyze Data

Workflow

Shared Data

Visualization

Admin

Help

User

Using 78.8 GB

Welcome to easyMF

Matrix Factorization-based Transcriptome Analysis

Tutorial

Test Data

Docker

GitHub

History

search datasets

Unnamed history

(empty)

历史已空。You can load your own data or not data from an external source

1

Matrix Preparation

Upload

User Fetch

Data preprocess

Gene expression

Samples

Genes

2

Matrix Factorization

PCA: $F = AX$

• Orthogonal decomposition

ICA: $X = SM + E$

• Independent decomposition

NMF: $V = WH + E$

• Dependent decomposition

Pattern matrix (PM)

Amplitude matrix (AM)

Metagene-based analysis using PM

Clustering analysis

Single-cell analysis

Spatial-course analysis

Time-course analysis

Metagene-based analysis using AM