easyMF User Mannual

(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, and functional gene discovery.It should be noted that the metagenes in PCA can be ranked by the extent to which they explain the variation in the data, the features in both ICA and NMF are assumed to have equal weight. Therefore, we noticed the user that the choice of MF techniques should be based on the purpose of one study with a preferred choice: PCA finds sources of separation in the data, which resulting in identification of dominated variation; ICA learns variation that are statically independent, which resulting in more accurate literature-derived association; NMF is well suited to transcriptional data, which is typically non-negative itself.

- 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.

0. Matrix Factorization

Matrix Factorization can be used to decompose a gene expression matrix into an amplitude matrix (AM) and a pattern matrix (PM) using three different algorithms, i.e., principal component analysis (PCA), independent component analysis (ICA), and non-negative matrix factorization (NMF).

Functions/Tools	Description	Inputs	Outputs	Time (test data)	Program	References
Matrix Factorization	Decompose a gene expression matrix into a product of an amplitude matrix (AM) and pattern matrix (PM)	Gene expression matrix	Amplitude matrix; Pattern matrix	~ 1 mins	prcomp (PCA)	This study
					ica (ICA)	Helwig, 2015
					bignmf (NMF)	Pan *et al.*, 2012

Inputs

- **Decomposition options**: Different algorithms used for gene expression matrix decomposition including PCA, ICA, and NMF.

- **Gene expression matrix**: A gene expression matrix (genes in rows and individual samples in columns).
- **Metagene number**: The number of metagenes decomposed from the gene expression matrix. In current version, easyMF provides three options for users to set this number:

1) **Scan an optimal metagene number automatically by easyMF**: easyMF can automatically chosen an appropriate number using two methods: internal consistency of Cronbach's α value for **PCA** and inflection point of the rate of the mean residual decline for **ICA** and **NMF**;

2) **Set each sample as a metagene**: Setting the number of samples in the gene expression matrix as the number of metagenes;

3) **Specify metagene number by users**: A specified metagene number user provided.

Outputs

- **Statistics analysis of the decomposition**: If users need easyMF automatically chosen an optimal metagene number, easyMF would provide a comprehensive report statistics analysis of the decomposition.
- **Amplitude matrix**: Amplitude matrix decomposed from gene expression matrix (genes in rows and metagenes in columns).

	Metagene 1	**Metagene 2**	**...**	**Metagene n**
Zm00001d053636	0.080	-0.889	...	2.029
Zm00001d053632	1.338	0.729	...	-0.049
...	...	...	...	...
Zm00001d053635	-1.674	0.036	...	-0.494

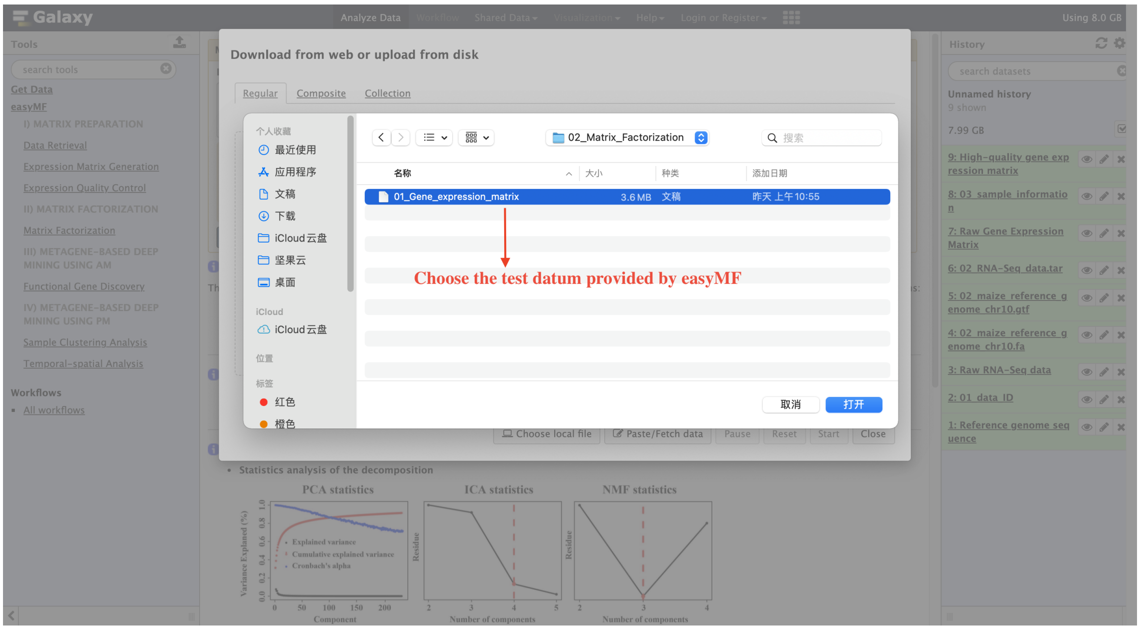
- **Pattern matrix**: Pattern matrix decomposed from gene expression matrix (samples in rows and metagenes in columns).

	Metagene 1	**Metagene 2**	**...**	**Metagene n**
Sample 1	-2.081	0.663	...	-0.711
Sample 2	-2.114	0.711	...	-0.757
...	...	...	...	...
Sample 4	-2.185	0.671	...	-0.719

How to use this function

- Test datum for this function is `01_Gene_expression_matrix` in directory `Test_data/02_Matrix_Factorization`.
- The following screenshots show us how to decompose the gene expression matrix using easyMF.

  Step 1: upload test data in directory `Test_data/02_Matrix_Factorization` to history panel;



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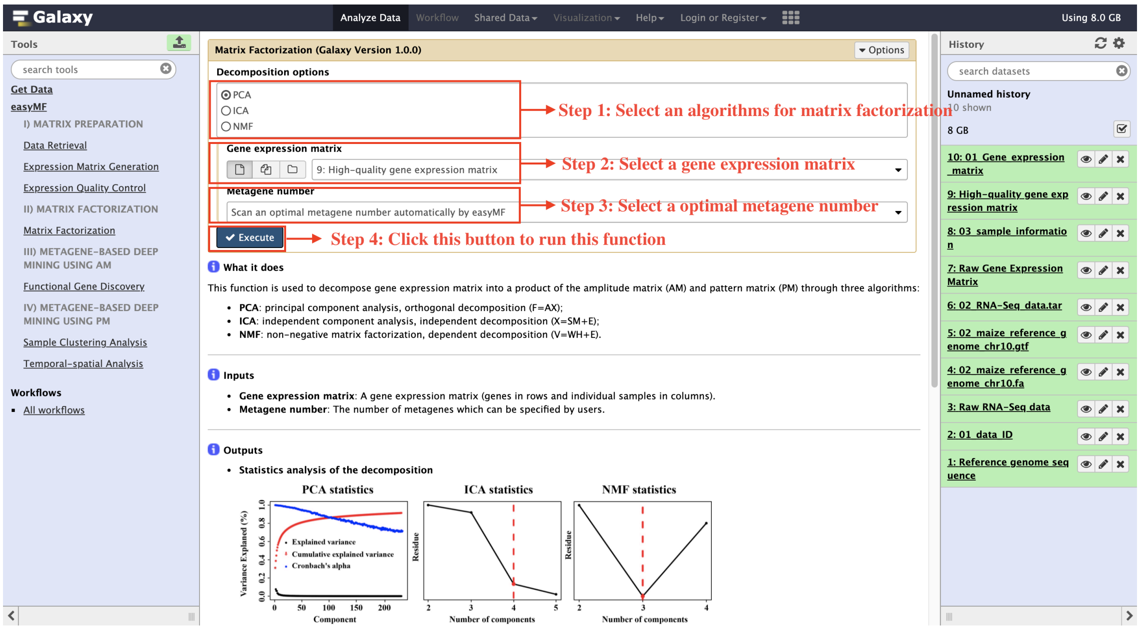
01_Gene_expression_matrix 3.6 MB 文稿 昨天 上午10:55

Choose the test datum provided by easyMF

Step 2: input the corresponding files and appropriate parameters, then run the function.



Matrix Factorization (Galaxy Version 1.0.0)

Decomposition options

● PCA
○ ICA
○ NMF

Step 1: Select an algorithms for matrix factorization

Gene expression matrix: 9: High-quality gene expression matrix

Step 2: Select a gene expression matrix

Metagene number: Scan an optimal metagene number automatically by easyMF

Step 3: Select a optimal metagene number

✔ Execute

Step 4: Click this button to run this function

What it does

This function is used to decompose gene expression matrix into a product of the amplitude matrix (AM) and pattern matrix (PM) through three algorithms:

- **PCA**: principal component analysis, orthogonal decomposition (F=AX);
- **ICA**: independent component analysis, independent decomposition (X=SM+E);
- **NMF**: non-negative matrix factorization, dependent decomposition (V=WH+E).

Inputs

- **Gene expression matrix**: A gene expression matrix (genes in rows and individual samples in columns).
- **Metagene number**: The number of metagenes which can be specified by users.

Outputs

- **Statistics analysis of the decomposition**

Running time

This step will cost ~ 1 mins for the test data.