Full name of software: A preprocessing approach for metabolic confounding effect elimination

Software abbreviated: **MCEE**

Software version: **V3.0**

User Guide

Contents

| 1 Survey | | | 1 | |
|--|------------------------------|---|---|--|
| | 1.1 | Hardware environment | 1 | |
| | 1.2 | Software environment | 1 | |
| | 1.3 | Programming language and its version | 1 | |
| | 1.4 | The number of source code | 1 | |
| | 1.5 | Main functions and technical features | 1 | |
| | 1.6 | Purpose | 2 | |
| 2 Software introduction | | | 2 | |
| | 2.1 | Overview | 2 | |
| | 2.2 | Software features | 2 | |
| | 2.3 | Interface design | 2 | |
| | 2.4 | Introduction of main functions | 2 | |
| 3 | 3 Installation instructions2 | | | |
| 4 Software function and operation steps2 | | | 2 | |
| | 4.1 | Software startup | 2 | |
| | 4.2 | The operation process and interface of software | 3 | |
| | 4.3 | Summary | 7 | |

1 Survey

1.1 Hardware environment

Personal computer, internal storage 512Mb or above, CPU main frequency 1.66GHz or above

1.2 Software environment

Windows XP or higher operating system, Matlab2014a or above, Office Excel 2003 or above.

1.3 Programming language and its version

Matlab language, Matlab 2014a.

1.4 The number of source code

701

1.5 Main functions and technical features

Metabolomics is an important part of systems biology and translational medicine. It refers to a discipline that studies the metabolic network of organisms by analyzing the structure and change of the metabolites produced by stimuli or disturbances. It is now widely used in a variety of studies, such as disease diagnosis, new drug development, drug effect and toxic mechanism. The development and improvement of metabolomics technology is related to the collation, correction and analysis of metabolomics based on high-throughput instruments and / or biological samples. The software for the metabolomics data correction software, can eliminate and reduce the effects of confounding factors for metabolomics data, to help people find the potential confounding factors which affected by confounding factors.

technical features:

- a) The elimination of confounding factors in metabolomics;
- b) Applicable to multi-platform data, such as gas phase mass spectrometry or liquid phase mass spectrometry data.
- c) Provide two methods based on generalized linear regression model and canonical correlation discrimination for users to choose.
- d) More effects of confounding factors can be eliminated at one time.
- e) Add the adjustable parameter.
- f) It does not affect the number of metabolites or samples.
- g) PCA scores plots are provided to user to understand the data and adjust the data in time.
- h) Input and output is excel document, convenient and quick operation.

1.6 Purpose

This tool is a special software for metabolomics. It is suitable for researchers

in medical, biological, chemical, or related fields who have the basis of data analysis and software operation.

2 Software introduction

2.1 Overview

The software is based on MATLAB language. It has simple operation, less resources and friendly interface. It can be used to eliminate the influence of all kinds of confounding factors.

2.2 Software features

In the case of no influence on the number of metabolites, the metabolites related to the confounding factor are filtered through the algorithm and then they are corrected one by one.

2.3 Interface design

The interface is simple and easy to operate.

2.4 Introduction of main functions

It is used to adjust the metabolites in the metabolomics data in order to eliminate the influence of confounding factors.

3 Installation instructions

This software does not need to be installed, and can be used directly in Matlab

4 Software function and operation steps

4.1 Software startup

- 1.1 Start Matlab.
- 1.2 Set up the work path.
- 1.3 In the Current Folder window, find MCEE.m, click right, and select run (Figure 1).

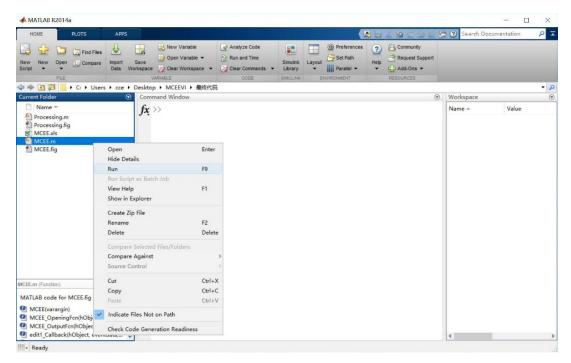


Figure 1. Start MCEE in Matlab

4.2 The operation process and interface of software

4.2.1 Import data

The initial interface of MCEE is shown in figure 2.

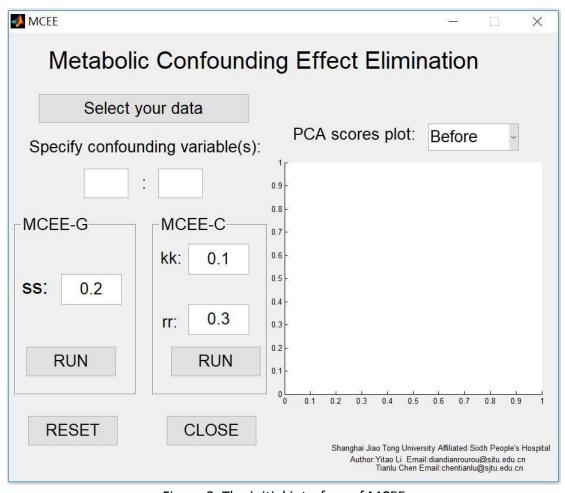


Figure 2. The initial interface of MCEE

Click "Select your data" and select the data file in the pop-up window and open it.

Input data format (Figure 3)

- a) Acceptable file format: .xls.
- b) The first row of the table is the name of the metabolite
- c) In the sheet, each row represents a sample, and each column (except the first two columns) represents a metabolite.
- d) The first column of the data represents groups, such as the normal group and the disease group, which are expressed in 1 and 2 respectively.
- e) The second or more columns represent the confounding factor(s).

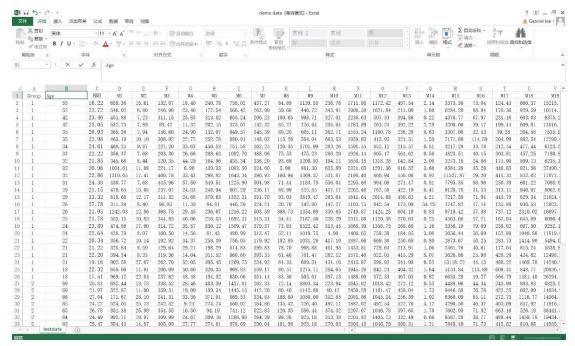


Figure 3. Input data format

4.2.2 Specify the range of confounding factor(s)

The user inputs the range of start and end columns of confounding factor(s), specifying the scope of confounding variables.

4.2.3 Parameter setting

According to the user's needs, select the appropriate method. If the user selects the MCEE -G method, the value of the adjustable parameter ss (0-1) (the initial value is 0.2) shall be specified, and the ss value (0-1) shall be entered in the input box. If the user selects the MCEE –C method, it is necessary to specify the values of the adjustable parameter kk (0-1) (initial value is 0.1) and the adjustable parameter rr(0-1) (initial value is 0.3), and enter the values of kk and rr in the input box.

4.2.4 Program running

Click "RUN" to start the software, this time will pop up a Processing interface to display the running schedule. When the program is finished, the window will prompt" The result has been saved to the folder where the software is located." (Figure 4). The corrected data named MCEE.xls and saved to the folder. Then click "CLOSE" to close the interface.

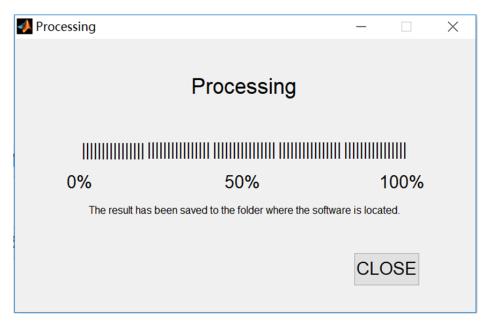


Figure 4. The interface of Processing

4.2.5 Drawing the PCA scores plots

When the program has finished, the PCA scores plots of before that can be selected by the drop-down menu (Figure 5).

4.2.6 Restore default parameters

Click the "RESET" button to restore the default parameters.

4.2.7 Close the software

Click the "CLOSE" button to close the software.

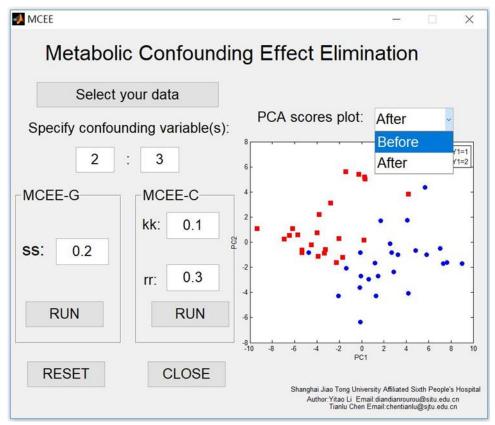


Figure 5. Drawing the PCA scores plots

4.3 Summary

This software is suitable for eliminating the bias caused by confounding factors.