

Using MetaboAnalyst 5.0 Part III: Multi-omics integration

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Method Article

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Abstract

Liquid-chromatography coupled with high-resolution mass spectrometry (LC-HRMS) has become a workhorse in global metabolomics studies with growing applications across biomedical and environmental sciences. However, outstanding bioinformatics challenges in terms of data processing, statistical analysis and functional interpretation remain critical barriers to the wider adoption of this technology. To help the user community overcome these barriers, we have made major updates to the well-established MetaboAnalyst platform (www.metaboanalyst.ca). This protocol is part three of four and provides stepwise instructions on how to use MetaboAnalyst to integrate metabolomics data with transcriptomics data or to combine multiple metabolomics datasets.

Introduction

Please see the “Using MetaboAnalyst 5.0 Part I: Optimizing parameters for LC-HRMS spectra processing” protocol for more general background information.

Multi-omics integration

Integrating multiple omics datasets from the same study or integrating the same type of omics datasets across multiple studies can help reduce false positives and derive a more holistic understanding. Data integration approaches have been relatively well-established in other omics fields, including targeted metabolomics where the same compound IDs can be mapped consistently across different datasets^{46,47}. However, this is not the case in global metabolomics where features are generally not comparable across different studies. This is because LC-MS peaks, characterized by their mass-to-charge ratio (m/z) and retention time (rt), are highly susceptible to experimental and analytical batch effects. Since we can compute functional activities from such data, integrating data at a higher level (i.e., pathways) becomes conceptually clear and practical. As the same set of metabolic pathways are defined for both transcriptomics and metabolomics, such an approach permits integrative analysis with transcriptomics data as well as across multiple global metabolomics datasets. Given the exploratory nature of such analysis, statistical integration should always be combined with intuitive data visualization to gain a more comprehensive data understanding.

Reagents

Equipment

Computer requirements

- Browser requirements: MetaboAnalyst 5.0 runs on all modern web browsers. For the best results, we recommend Google Chrome 92+, Firefox 92+, Safari 12+, and Microsoft Edge v93+. JavaScript must be enabled in your browser.
- Internet connection requirements: A fast connection is highly recommended.
- Hardware requirements: >4 GB of RAM and a screen resolution of at least 1200 x 800 is preferred. At least 8 GB hard drive space is needed to store the raw spectra files.

Data files

- *Input Files.* MetaboAnalyst accepts multiple data formats for different modules. For raw spectral processing, the supported data formats include mzML, mzXML, mzData and NetCDF, while other modules usually require comma-separated values (.csv) or tab delimited (.txt) file format.

- *Example Datasets.* Multiple built-in example datasets are offered in each MetaboAnalyst module. Users can simply choose an example dataset and click the 'Submit' button to start exploring the tool. Six datasets are used in this protocol:

- 1) A raw spectra data (*malaria_raw.zip*) consisting of 12 plasma samples from healthy and malaria semi-immune subjects along with 3 Quality Controls (QC) ⁵³.
- 2) A feature table (*malaria_feature_table.csv*) generated from processing the above raw spectra for functional analysis.
- 3) A gene list (*integ_genes_1.txt*) and a compound list (*integ_cmpds.txt*) to demonstrate the integration of targeted metabolomics data with transcriptomics data.
- 4) A gene list (*integ_genes_2.txt*) and a peak list (*integ_peaks.txt*) to demonstrate the integration of global metabolomics data with transcriptomics data.
- 5) Three peak intensity tables (*A1_pos.csv*, *B1_pos.csv*, *C1_pos.csv*) from global metabolomics studies of serum samples from COVID-19 patients to demonstrate the integration of multiple global metabolomics datasets⁵⁴.
- 6) A feature table (*TCE_feature_table.csv*) and its associated metadata table (*TCE_metadata.csv*) from an exposomics study on metabolic changes associated with occupational exposure to trichloroethylene (TCE) ⁵⁵.

Equipment Setup

(Optional) *Download the example datasets.* Go to the MetaboAnalyst home page and click 'Data Formats' link from the left panel. Users can download all the example datasets used in the protocol. These datasets are also available as built-in examples in each corresponding module. Users can directly select those datasets and follow the protocols without downloading and uploading them.

Procedure

Stage 3: Pathway-level integration of multiple datasets (Timing 20 ~ 35min)

MetaboAnalyst provides two approaches to integrate multiple datasets. The first one is the integration of datasets from different omics layers, and the other method is the integration of multiple metabolomic datasets. These two approaches are introduced sequentially in this section.

32. *Starting up.* From the MetaboAnalyst home page, select "Click here to start" to access the module selection page and click the '*Joint-Pathway Analysis*' to enter the module.

33. *Set species.* A total of 25 species are currently supported for integration. Select 'Homo sapiens (Human)' because the data we are going to use is from a study on humans.

34. *Data uploading:* The joint-pathway analysis accepts two lists from transcriptomics/proteomics (genes) and metabolomics (metabolites or peaks). Open the data (*integ_genes_1.txt*) with a text editor and copy-paste the columns into the gene list box and set the ID type as 'Official Gene Symbol'. For metabolomics data, users need to first specify 'Metabolomics Type' - targeted (compound list) or untargeted (peak list). The compound list (*integ_cmpds.txt*) can be uploaded in the same way as uploading a gene list. For demonstration purpose, we will use an example dataset to demonstrate the integration of transcriptomics data with targeted metabolomics data. Click the "Try our example" link at the bottom of the page, select the first example. Click 'Submit' button.

35. *Data integrity check.* The genes and compounds uploaded from the previous step are matched to the MetaboAnalyst knowledgebase. The unrecognized genes or compounds will be highlighted. User could delete or correct these unmatched items. Click 'Proceed' when finish.

Troubleshooting

36. *Parameter setting 1.* The 'Parameter Selection' page allows users to choose a pathway library and an algorithm to perform enrichment analysis. Different pathway libraries are offered to allow users to compare results from integrative analysis with those obtained based on genes or metabolites alone. Users need to configure the algorithms options, which include enrichment analysis algorithms, topology measurement and integration methods. Here we use the default option for the pathway database. Click 'Submit' to perform integration analysis.

Critical Step: *In general, directly combine queries will give more weight to genes which tend to be larger, while combine p values will give similar weight to both, disregarding the much smaller pathway coverage by metabolites (i.e., less reliable). The last two options aim to mitigate these issues by introducing weights to genes / metabolites calculated based on their proportions at the global level or individual pathway level. See **Figure 1** for more guidance on the different integration methods.*

37. *Results from pathway view.* The results from the pathway analysis are summarized as an interactive scatter plot on the left, with topology analysis as the x-axis and Enrichment analysis results as the y-axis (**Figure 2A**). Click a data point on the scatter plot and the corresponding pathway will be displayed on the right panel. The genes/compounds with positive values of log(FC) are shown as red, while the negative ones are shown as green. If the log(FC) column is missing from the input, the matched nodes will be highlighted as yellow. All pathway results are summarized in the table on the bottom of the page. Click the 'Results Table' button to download the statistics of all pathways. Click the 'Matched Features Table' button to download the matched genes and/or compounds of all pathways.

38. *(Optional) Results from network view.* Click the 'Network Explorer' button from the middle of the pathway view page to explore the integration results from a network view (Figure S2). All pathways in the left panel can be highlighted on the network. The network view can be exported as PNG or SVG images.

39. *Integration of genes and peaks.* Return the data upload page and select the 2nd example for integration. This example utilizes the original data sets of the study⁵³. Click 'Submit' to submit your data. Alternatively, users can upload the downloaded gene lists (*integ_genes_2.txt*) similar as described in Step 34. For the metabolomics data (*integ_peaks.txt*), choose the untargeted (peak list) option, an interface similar to the data upload page in Step 20 will appear. Specify the parameters and then click the File Chooser to upload the peak list file.

40. *Data integrity check*. Similarly, the sanity check page summarizes the results of uploaded genes and peaks. Click 'Proceed' to continue.

41. *Parameter Setting 2*. This parameter page provides an introduction on the mechanism of integration as well as a parameter setting panel. Users can choose between two pathway libraries - metabolic pathways or all pathways. The later option also includes regulatory pathways containing only genes. There are two options to merge p values (Fisher and Stouffer). The difference between them is that Stouffer attributes different weights to the p-values when combining two p values, and as a result, it is not as sensitive as Fisher is to very small values.

42. *Results display*. The results are shown in **Figure 2B**. Users could interactively explore the pathways using the scatter plot on the left. Significant pathways supported by both genes and peaks will be located on the top right areas; while those supported mainly by one type of omics data will be distributed along their corresponding axes. The potential compounds predicted based on matched peaks are highlighted in dark blue. User can also optionally explore the pathway from the KEGG network view as described in Step 38.

43. *Integration of multiple global metabolomics datasets*. Go to MetaboAnalyst module selection page, click 'Functional Meta-analysis' to enter the module for integrating multiple metabolomics datasets. Users need to upload and process each dataset (*A1_pos.csv*, *B1_pos.csv*, *C1_pos.csv*) separately using the table provided. The meaning of all parameters here are consistent with the 'Functional Analysis'. For demonstration purpose, we will click the 'Try Example' button to use the first COVID-19 example dataset. Then, click the 'Proceed' button to go the parameter setting page for functional analysis. There are two options for integrating multiple metabolomics datasets. The first one is used to integrate the functional results at the pathway level, while the second one predicts perturbed pathways by pooling all peaks together. Since the datasets are from different studies, click the 'Submit' button in the 'Pathway-level Integration' parameter box to continue.

Critical Step: *Pooling peaks should only be used when the peaks are generated from identical or very similar instruments. A typical use case is to combine peaks generated from both positive and negative modes by the same LC-HRMS to increase the metabolome coverage.*

44. *Integration at pathway level.* The integration results are shown as a bubble plot (**Figure 3A**). Pathways from all datasets are organized based on merged p values. The bubble size is correlated with the enrichment ratio. The intersection of significant pathways identified from different datasets can be explored through an interactive UpSet plot (**Figure 3B**). Optionally, the integration results can also be displayed in network view.

45. *Result Downloading.* Click the 'Download' node from the navigation tree to finalize the analysis and download the results above.

Troubleshooting

Time Taken

Anticipated Results

Joint pathway analysis of transcriptomics and targeted metabolomics data (the first example) reports 17 significant pathways (p values < 0.05). The topological impact values of them are over 0.5. For joint analysis of transcriptomics and untargeted metabolomics data (the second example), there are 23 significant pathways reported (merged p values < 0.05). The gene/compounds matching results and mummichog prediction results are available from the download page. Functional meta-analysis integrates three untargeted metabolomics data tables. Two amino acid metabolism associated pathways are reported as significant (merged p values < 0.05).

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Author Contributions

Z.P., J.E., N.B. and J.X. prepared the manuscript. Z.P., G.Z., J.E., L.C., O.H. and J.X. contributed to the development and testing of the MetaboAnalyst. All authors read and approved the final manuscript.

Competing Financial Interests

The authors declare no competing financial interests.

Data Availability Statement

All example datasets used in the protocol are integrated as example datasets in their respective modules and are also available for download from the “Format” page of MetaboAnalyst (<https://www.metaboanalyst.ca/MetaboAnalyst/docs/Format.xhtml>). There are no restrictions on their use.

Code Availability Statement

MetaboAnalyst is freely accessible as a web-based application. The underlying R code is freely available at GitHub as the MetaboAnalystR (<https://github.com/xia-lab/MetaboAnalystR>) and OptiLCMS (<https://github.com/xia-lab/OptiLCMS>) packages under the GNU General Public License version 2 or later.

Figures

Figure 1

Figure 2

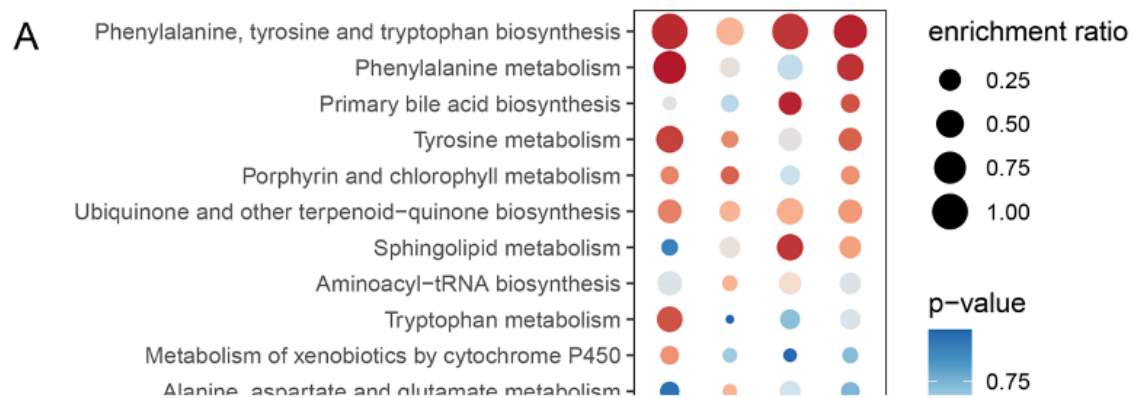


Figure 3