

A tutorial for MataOmics

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1 Introduction

MetaOmics software suite is an interactive software with graphical user interface (GUI) for genomic meta-analysis implemented using R shiny. Many state of art meta-analysis tools are available in this software, including MetaProcess for omics data preprocessing, MetaQC for quality control, MetaDE for differential expression analysis, MetaPath for pathway enrichment analysis, MetaNetwork for differential co-expression network analysis, MetaPredict for classification analysis, MetaClust for sparse clustering analysis, MetaPCA for principal component analysis.

In this tutorial, we will go through installation and usage of MetaOmics step by step using real data examples. The MetaOmics suite software is publicly available at <https://github.com/metaOmics/metaOmics>. The tutorial itself can be found at https://github.com/metaOmics/tutorial/blob/master/metaOmics_tutorial.pdf. Each MetaOmics module will be introduced in later sections and their R packages are also available on GitHub <https://github.com/metaOmics>.

2 Preliminaries

2.1 Citing MetaOmics

MetaOmics software suite implements many meta-analytic methodologies by many different authors. Please cite appropriate papers if you used MeteOmics, by which the authors will receive professional credits for their work.

- MetaOmics software suite itself can be cited as: Ma et al. MetaOmics: Comprehensive Analysis Pipeline and Brower-based Software Suite for Transcriptomic Meta-Analysis.
- MetaQC: Kang, D. D., Sible, E., Kaminski, N., and Tseng, G. C. (2012). Metaqc: objective quality control and inclusion/exclusion criteria for genomic meta-analysis. *Nucleic acids research*, 40(2):e15–e15.
- MetaDE:
 - Fisher, R. A. (1925). *Statistical methods for research workers*. Genesis Publishing Pvt Ltd.
 - Li, J., Tseng, G. C., et al. (2011). An adaptively weighted statistic for detecting differential gene expression when combining multiple transcriptomic studies. *The Annals of Applied Statistics*, 5(2A):994–1019.
 - Choi, J. K., Yu, U., Kim, S., and Yoo, O. J. (2003). Combining multiple microarray studies and modeling interstudy variation. *Bioinformatics*, 19(suppl 1):i84–i90.
 - and many more
- MetaPath:
 - Shen, K. and Tseng, G. C. (2010). Meta-analysis for pathway enrichment analysis when combining multiple genomic studies. *Bioinformatics*, 26(10):1316–1323.
 - Fang, Z., Zeng, X., Lin, C.-W., Ma, T., and Tseng, G. C. (2016). *Comparative Pathway Integrator: a framework of meta-analytic integration of multiple transcriptomic studies for consensual and differential pathway analysis*. PhD thesis, University of Pittsburgh.
- MetaClust: Huo, Z., Ding, Y., Liu, S., Oesterreich, S., and Tseng, G. (2016). Meta-analytic framework for sparse k-means to identify disease subtypes in multiple transcriptomic studies. *Journal of the American Statistical Association*, 111(513):27–42.
- MetaPCA: Kim, S., Kang, D., Huo, Z., Park, Y., and Tseng, G. C. (submitted). Meta-analytic principal component analysis in integrative omics application.
- MetaPredict: Kim, S., Lin, C.-W., and Tseng, G. C. (2016). MetaKTSP: A Meta-Analytic Top Scoring Pair Method for Robust Cross-Study Validation of Omics Prediction Analysis. *Bioinformatics*, 32(March):btw115.

- MetaNetwork: Zhu, L., Ding, Y., Chen, C.-Y., Wang, L., Huo, Z., Kim, S., Sotiriou, C., Oesterreich, S., and Tseng, G. C. (2016). Metadcn: meta-analysis framework for differential co-expression network detection with an application in breast cancer. *Bioinformatics*, page btw788.

2.2 How to start MetaOmics

The full instruction of how to install, start MetaOmics software suite is also available at <https://github.com/metaOmics/metaOmics>.

2.2.1 Requirement

- R >= 3.3.1
- Shiny >= 0.13.2

2.2.2 How to install the metaOmics software

- At MetaOmics home page at <https://github.com/metaOmics/metaOmics>, clone the project by clicking on “Clone or download” and extract to a working directory, or type in the following in command line

```
git clone https://github.com/metaOmics/metaOmics
```

2.2.3 How to start the metaOmics software

- In R (suppose the application directory is metaOmics),
`install.packages('shiny')`
`shiny::runApp('metaOmics', port=9987, launch.browser=T)`

2.3 MetaOmics setting page

After starting MetaOmics, the first page is the MetaOmics setting page as shown in Figure 1. There are 4 tabs on top of the page (at position (1)): Setting, Preprocessing, Saved Data and Toolsets. The welcome page is below the 4 tabs. Further below, the first header is the session information. [Why do we need session information?](#) The second header is Directory for Saving Output Files (at position (2)). By clicking “...”, user can set default working directory, in which all the meta-analysis results will be saved. Users can view their current working directory on the top right corner (at position (3)). The third header is Toolsets (at position (4)), where user can click to install desired modules if the “status” shows “not installed”. If the packages are installed, there is a checked installed status. Otherwise, users can install individual package by clicking install blue button. The installation progress may take a few minutes for each module. There will be a notification icon at the bottom right corner after the installation. After the modules are installed to R, restart the MetaOmics software suit so that the shiny application interface is updated with installed modules. Position (5) shows the current active dataset, which will be introduced in Section 4.1 ??.

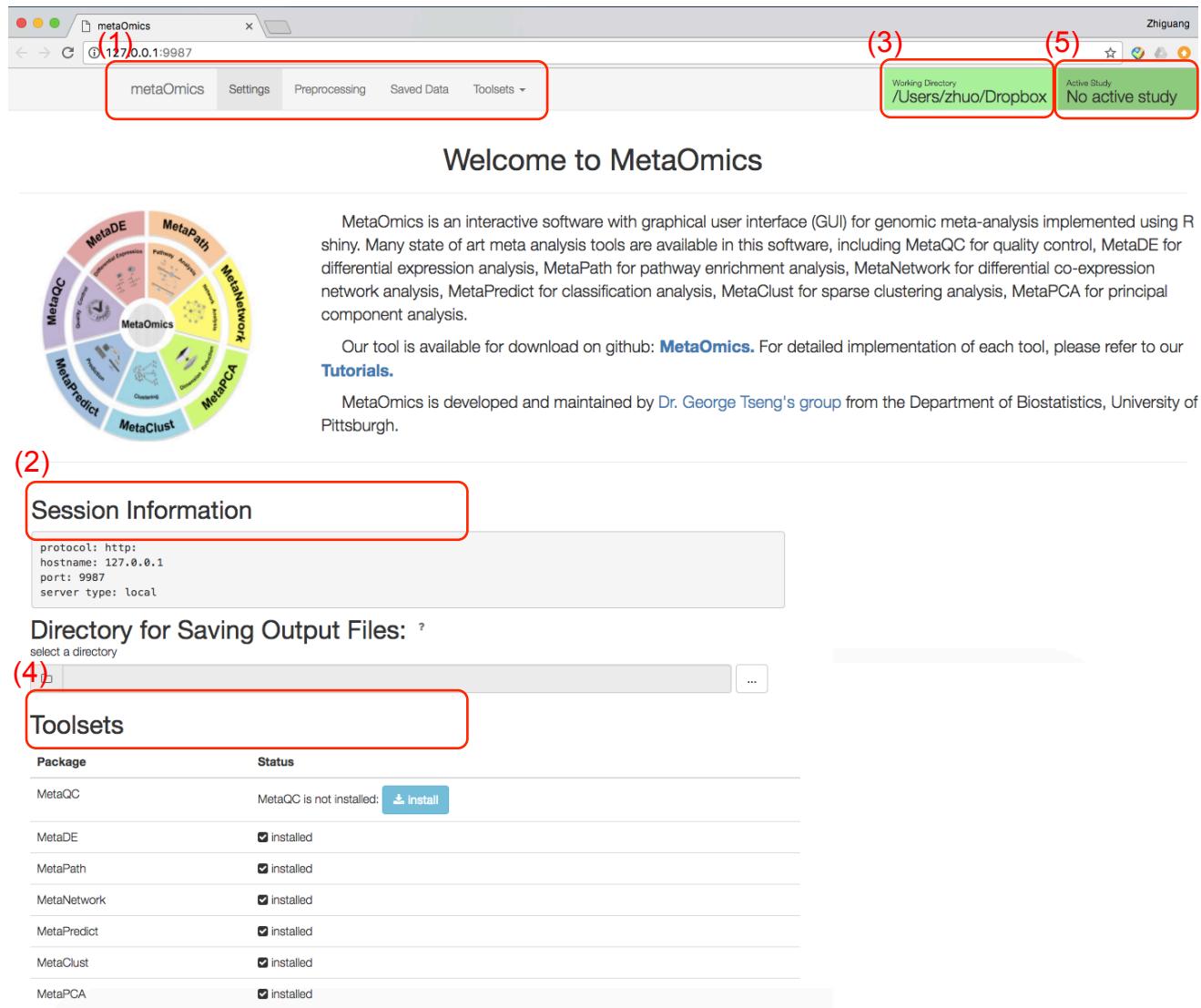


Figure 1: MetaOmics software suite GUI setting page

2.4 Question and bug report

Who should be responsible for maintaining the software?

3 Prepare data

3.1 Raw data

Data should be prepared as the example in Figure 2. First column should be feature ID (e.g. gene symbol) and the rest of the columns are samples. Note that the first column can also be other feature type (i.e. probe id, entrez ID). The first row is sample ID. Valid data type includes continuous data and count data.

	A	B	C	D	E	F	G	H	I	J	K
1	ID	GSM445939	GSM445940	GSM445952	GSM445965	GSM445966	GSM445995	GSM446005	GSM446015	GSM446019	GSM446020
2	COX1	14.1741845	14.5190482	13.8179896	14.1805909	14.7791613	14.3450467	14.68766	14.7869009	14.7574207	14.1582959
3	COX2	13.8544454	14.1854915	13.4474018	13.6646626	14.4244321	13.9044761	14.2370772	13.9931093	14.0432901	13.4166744
4	ND4	13.840222	14.4856644	13.5612402	13.8816752	14.5739527	14.1081131	14.5813899	14.2519264	14.2616291	13.8095574
5	RPL41	14.4218804	13.4484882	14.1035968	14.1046225	14.2929066	13.9955247	14.1029454	14.5718506	14.5623457	14.0077579
6	RPS2	14.1384864	13.3737668	13.8091098	13.8294958	13.897014	13.7186942	13.9696975	14.2643786	14.135146	13.7457779
7	RPL23A	13.9851543	13.0577958	13.807726	13.7652435	13.5068014	13.4619198	13.6286114	14.0471201	13.8060203	13.5260356
8	TPT1	14.2015622	13.4487804	13.8933327	13.9124043	14.197062	14.0453267	14.2141676	14.4791302	14.5081582	13.8800374
9	RPL39	14.1331827	13.1026579	13.6928306	13.8217088	14.1705206	13.8267709	14.069521	14.3923098	14.3014678	13.7313433
10	ND2	11.8044506	14.1266472	12.3268843	13.3365085	14.1230073	13.8853862	14.2394535	13.835649	13.6857053	13.4025025

Figure 2: A example input data format

3.2 Clinical data

Clinical data should be prepared as the example in Figure 3. First column should be sample ID and each row represents a sample. The rest of the columns are clinical information (e.g. case/control labels).

	A	B	C	D	E
1	label				
2	GSM445939	inv(16)			
3	GSM445940	inv(16)			
4	GSM445952	inv(16)			
5	GSM445965	inv(16)			
6	GSM445966	inv(16)			
7	GSM445995	inv(16)			
8	GSM446005	inv(16)			
9	GSM446015	inv(16)			
10	GSM446019	inv(16)			

Figure 3: A example clinical data format

3.3 Example data with the MetaOmics software

We collected three multi-study examples as testing datasets for the MetaOmics software. Table 1 shows three acute myeloid leukemia (AML) gene expression profiles. Table 2 shows four breast cancer gene expression profiles, in which the first study contains both count data and FPKM data. Table 3 shows gene expression profiles from eight prostate cancer datasets. The leukemia datasets are used to demonstrate MetaProcess, MetaDE, MetaPath, MetaNetwork, MetaPredict, MetaClust and MetaPCA. The prostate cancer datasets are used to demonstrate MetaQC.

4 MetaPreprocess

In this subsection, we introduce how to upload your dataset into the MetaOmics suit such that each functional modules can be utilized. The R package for MetaPreprocess module can be found <https://github.com/metaOmics/preproc>.

Table 1: Multi-study acute myeloid leukemia (AML) gene expression profiles. All three studies are from Affymetrix Human Genome U133plus2 with 5,135 genes. Three subtypes of leukemia are defined as the chromosomal translocation, including inversion of chromosome 16 - inv(16), translocation of chromosome 15 and 17 - t(15;17) and translocation of chromosome 8 and 21 - t(8;21).

Study	source	# samples	# samples by subtypes inv(16)/t(15;17)/t(8;21)
Study 1	Verhaak et al. (2009)	89	33/21/35
Study 2	Balgobind et al. (2010)	74	27/19/28
Study 3	Kohlmann et al. (2008)	105	28/37/40

Table 2: Multi-study breast cancer gene expression profiles. Each gene expression profiles of all four studies contain 10,330 genes. Study 1 contains both count data and fpkm (continuous) data so user should **select only one of them**. The other three studies contain only continuous data. The phenotype of interest is estrogen-receptor (comparing ER+ vs ER-).

Study	source	scale	# samples	# samples by ER ER+/ER-
Study 1	Weinstein et al. (2013)	count continuous	406	319/87
Study 2	Desmedt et al. (2007)	continuous	198	134/64
Study 3	Wang et al. (2005)	continuous	286	209/77
Study 4	Ivshina et al. (2006)	continuous	245	211/34

4.1 Procedure

Step 1 Uploading data:

After clicking the Preprocessing tab as in Figure 4, users can click on “Choosing/Upload Expression Data” tab to upload individual expression data files or choose the existing saved data file as in Figure 5 (at position (1)). The data should be prepared according to Section 3. Users may optionally upload Clinical Data (at position (2)), depending on their biological purposes. All MetaOomics modules except for MetaClust require external clinical labels. Three example datasets are available within MetaOomics folder “metaOomics/data/example/”, but we will focus on the leukemia dataset (“metaOomics/data/example/”) throughout this tutorial.

Step 2 Preprocessing:

The MetaOomics suit also provides handlers (at position (3) of Figure 4) for feature annotation, missing value imputation and multiple probe same genes. After the csv file for gene expression profile is specified, users can preview their data on the right hand side of the page as Figure 5. Several expression data parsing options (e.g. header, column separator, etc) are available on the left panel of Figure 5. For preprocessing, click on “Annotate/Impute/Replicate” to

1. annotate the probe ID/reference sequence ID/Entrez ID of individual dataset (choose Gene Symbol if the input data rows are already annotated).
2. impute missing value using knn method.
3. handle the multiple probes matching to the same gene issue.

A complete introduction of these options is available at the end of this subsection. The right hand side of Figure 5 shows the summary statistics of uploaded data and preview of the data matrix. There is a search box such that the users can search their favorite genes.

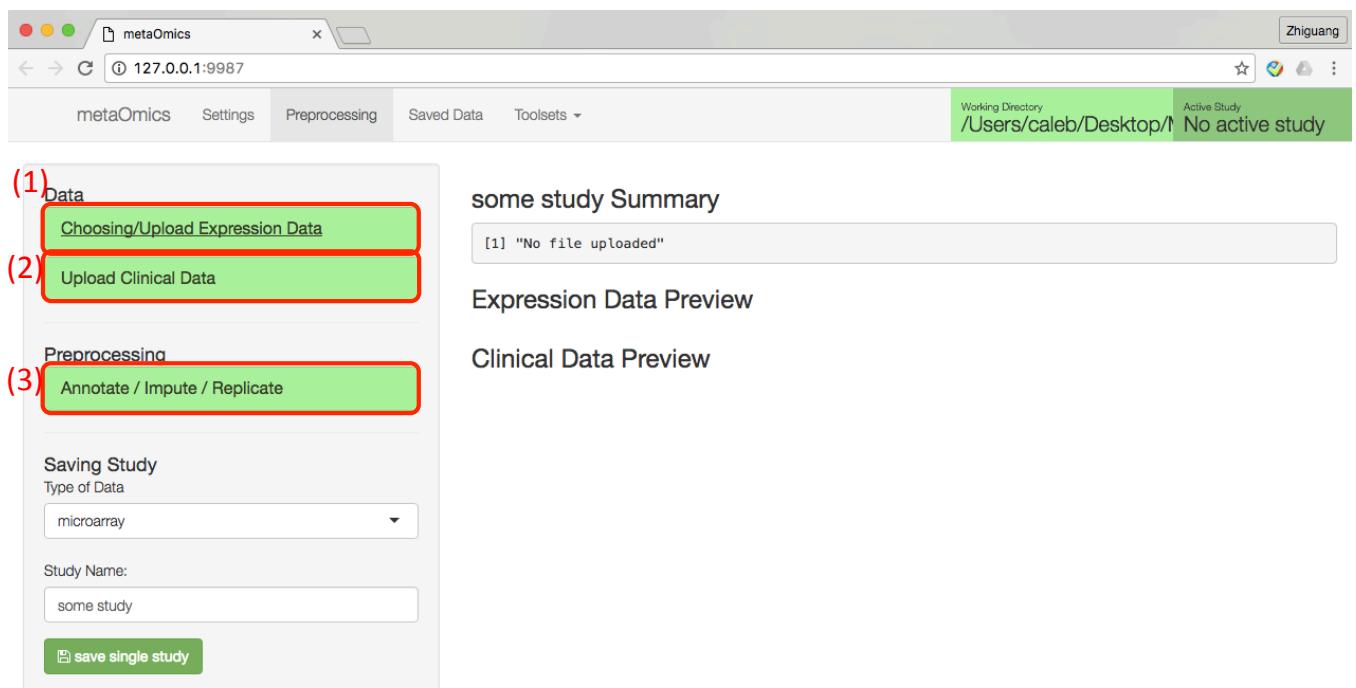


Figure 4: GUI Preprocessing page

Table 3: Multi-study prostate cancer dataset information. Eight prostate cancer gene expression profiles were measured by different microarray platforms.

Study	source	# samples	# samples by label Normal/Primary	# genes
Study 1	Welsh et al. (2001)	34	9/25	8798
Study 2	Yu et al. (2004)	146	81/65	8799
Study 3	Lapointe et al. (2004)	103	41/62	13579
Study 4	Varambally et al. (2005)	13	6/7	19738
Study 5	Singh et al. (2002)	102	50/52	8799
Study 6	Wallace et al. (2008)	89	20/69	12689
Study 7	Nanni et al. (2006)	30	7/23	12689
Study 8	Tomlins et al. (2006)	57	27/30	9703

The screenshot shows the metaOmics software interface. The top navigation bar includes tabs for 'metaOmics', 'Settings', 'Preprocessing', 'Saved Data', and 'Toolsets'. The status bar indicates 'Working Directory /Users/caleb/Desktop/' and 'Active Study No active study'. The main window has a sidebar labeled 'Data' containing sections for 'Choosing/Upload Expression Data' (with a 'Choose CSV File' button and 'Upload complete' message), 'Expression Data Parsing Option' (checkbox for 'Header', radio buttons for 'Separator' (Comma selected), and 'Quote for String' (Double Quote selected)), 'Log transforming data' (radio buttons for 'Yes' (selected) and 'No'), and 'Or use existing datasets' (dropdown menu). Below the sidebar is a green 'Upload Clinical Data' button. The main content area displays a summary for 'Balgobind_internal.csv' with statistics for four samples (GSM445939, GSM445940, GSM445952, GSM445965) and a preview of the expression data for various genes like COX1, COX2, ND4, RPL41, RPS2, RPL23A, and TPT1.

Figure 5: Uploading individual studies

After users upload clinical data (e.g. case control labels) and specify type of data and study name. They can click “save single study” button, single study will be saved.

Step 3 Save single study: In the next step, specify the data type (“microarray” or “RNA-seq”, continuous or discrete) and study name, click “save single study”. To upload RNA-seq data, the count data file and FPKM/TPM data should be uploaded separately and saved using different names.

Step 4 Upload datasets for all studies: Repeat the steps above for all studies for meta-analysis. All uploaded studies are now available in the “Saved Data” tab.

4.2 Saved Data tab

After uploading multiple studies with or without clinical data, users can turn to the Saved Data tab.

(1) Merging and Filtering Datasets

Selected Datasets ?
study1.csv study2.csv study3.csv

Merging and Filtering Datasets ?

mean:
0.3

variance:
0.3

Project Name:
[redacted]

Merge from Selected Datasets

Danger Zone

(2) List of saved data

Show 10 entries

	data type	numeric nature	study type	features	sample size
study1.csv	microarray	continuous	single	5135	89
study2.csv	microarray	continuous	single	5135	74
study3.csv	microarray	continuous	single	5135	105

Showing 1 to 3 of 3 entries

Search: [redacted]

Previous 1 Next

(3) Active Study
No active study

Figure 6: Merge from selected datasets

Step 1 Merging and Filtering: All saved datasets from the previous step will be found in Figure 6 (at position (2)). Users should select multiple datasets for further meta-analysis purpose. Users can filter out genes with low expression level (by default, mean expression lower than 30th percentile) or low variance (by default, variance lower than 30th percentile). Low expression genes can be non-expressed genes and low variance genes can be non-informative genes thus including them may contribute false positives. After specifying filtering criteria, enter Project Name and click on the “Merge from Selected Datasets” (at position (1)). A merged dataset (study type = “multiple”) will appear on the “List of saved data” panel (at position (3)). Creating multiple projects with varying preprocessing criteria is useful. For example, the user can start from a project with harsh filtering criteria (maintain 500-1000 genes) and give a test run through all modules to save time. If successful, a larger project can be created and implemented. If users want to delete any dataset, they can click the red danger zone button and delete selected dataset.

Step 2 Make active dataset:

The last thing to do before using meta-analytic toolsets is to select merged data and click on “Make your dataset Active Dataset” - A big green button in Figure 7. Then the merged data becomes active study and shows up on the top right corner. The active dataset serves as the input for all other MetaOmics modules.

	data type	numeric nature	study type	features	sample size
study1.csv	microarray	continuous	single	5135	89
study2.csv	microarray	continuous	single	5135	74
study3.csv	microarray	continuous	single	5135	105
merge05	continuous	continuous	multiple	1283	268

Figure 7: Make merged Dataset Active

Complete List of Options:

1. Upload expression data:

- Header: should be checked if the input file includes a header.
- Separator: indicates what type of separator is used for the data matrix.
- Quote for String: how is the data matrix quoted.
- Log transforming data: if you want to perform log transformation of your data, check yes.
- Use existing datasets: if you want to load a dataset previously uploaded, you can choose from the checklist.

2. Annotation/impute/Replicate:

- Annotation: possible ID type can be Gene Symbol (default), Probe ID, reference sequence ID, entrez ID.
- Impute: if selected, missing value imputation will be performed by k-nearest neighbor algorithm.
- Replicate Handling: if selected, if the same gene symbol maps to multiple probes, the probe with the largest inner quantile range (IQR) will be selected as a representative for this gene.

3. Saved Data, Merging and Filtering Datasets:

- Mean: the criteria such that how many percent of genes will be filtered out based on sum of mean ranks (e.g. 0.3 represent 30%).
- Variance: after the Mean filtering, the criteria such that how many percent of genes will be filtered out based on sum of variance ranks (e.g. 0.3 represent 30%).
- Study Name: dataset name after merging. This name will appear in the list of saved data table.
- Merge from Selected Datasets: perform filtering and merging.

4. Danger zone:

- Delete Selected Data: the selected data will be delete permanently if clicked, so please be cautious.

5 Toolsets

After the MetaPreprocess, all the preparatory steps are done. It's time to apply seven metaOomics modules by clicking on the "Toolsets" tab and select the tool for your research question. In the next few subsections, we will introduce in details how to run these modules. For each module, a summary table to studies and sample sizes is shown on the top left corner. There is an "about" drop-down menu which contains brief introduction and tutorial associated with the module. The "options" drop-down menu contains common options users can select or tune in the analysis. The "advanced options" section are more technical which we generally do not recommend users to change unless they are familiar with the methods. After applying these metaOomics modules, all result files will be automatically saved in the working directory which is specified in Section 2.3. For computationally demanding methods, the procedure may take minutes or up to hours depending on size of datasets. Users can keep track of the progress by checking the R console.

5.1 MetaQC

MetaQC package provides an objective and quantitative tool to help determine the inclusion/exclusion of studies for meta-analysis. More specifically, MetaQC provides users with six quantitative quality control (QC) measures: including IQC, EQC, AQCg, CQCg, AQCp and CQCp. Details of how each measure is defined and computed can be found in the Manuscript. In addition, visualization plots and summarization tables are generated using principal component analysis (PCA) biplots and standardized mean ranks (SMR) to assist in visualization and decision. Detailed information can be found in the "MetaQC" package in the metaOomics software suite (<https://github.com/metaOomics/MetaQC>). The test data used to demo the "MetaQC" package here is merged from eight prostate cancer studies and 50% mean filtering and 50% variance filtering. Detailed descriptions of these studies can be found in Table 3.

5.1.1 Procedure

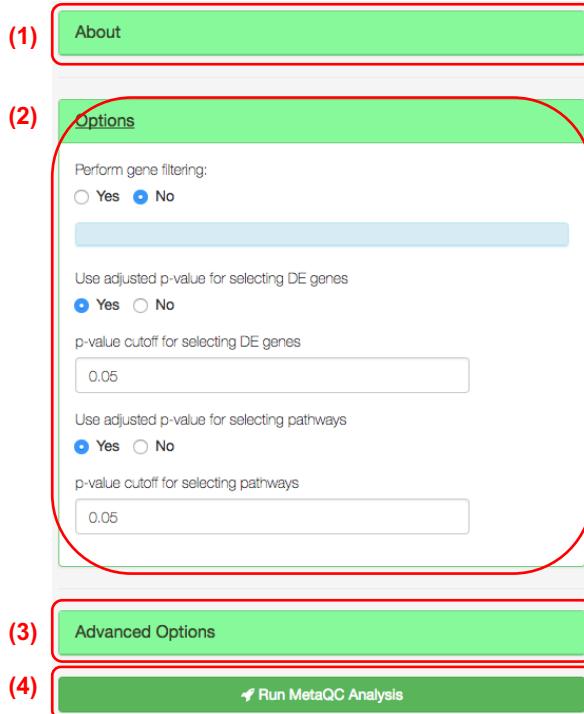


Figure 8: "MetaQC" options

There are three main options available for the "MetaQC" package as shown in Figure 8.

Step 1 Options: Under the drop-down menu "options" ((2) in Figure 8), users can specify whether to

- perform gene filtering. Gene filtering is suggested to reduce computational cost. Once “Yes” is chosen for gene filtering, users are further asked to specify the filtering cutoffs by mean or by variance like in merging step. In the demo example, the merged data have already had gene filtering, no further filtering is performed.
- users need to specify the approach (either by raw p-value or FDR) and cutoff to select potentially DE genes needed in the computation of IQC, EQC, AQCg and CQCg.
- users need to specify the approach (either by raw p-value or FDR) and cutoff to select potentially enriched pathways needed in the computation of AQCp and CQCp.

Step 2 Advanced options:

Under the drop-down menu “Advanced Options” (**(3)** in Figure 8), users are allowed to tune other parameters of MetaQC. In particular, it includes the selection of pathways by pathway size and the number of permutations to run to obtain the six measures. A detailed list of all options available for the package can be found at the end of the section. However, this is optional and users are suggested not to modify the option setting in this section without knowing the method.

Step 3 Run MetaQC Analysis:

Once all the above options are specified, users can click on **(4)** “Run MetaQC Analysis” to implement the tool.

Complete List of Options:

1. Options

- Perform gene filtering: If yes: cut lowest percentile by mean, cut lowest percentile by variance.
- Use adjusted p-value for selecting DE genes
- p-value cutoff for selecting DE genes
- Use adjusted p-value for selecting pathways
- p-value cutoff for selecting pathways

2. Advanced Option (**Optional):

- Pathway min gene size
- Pathway max gene size
- Number of permutations

3. Run MetaQC Analysis

5.1.2 Results

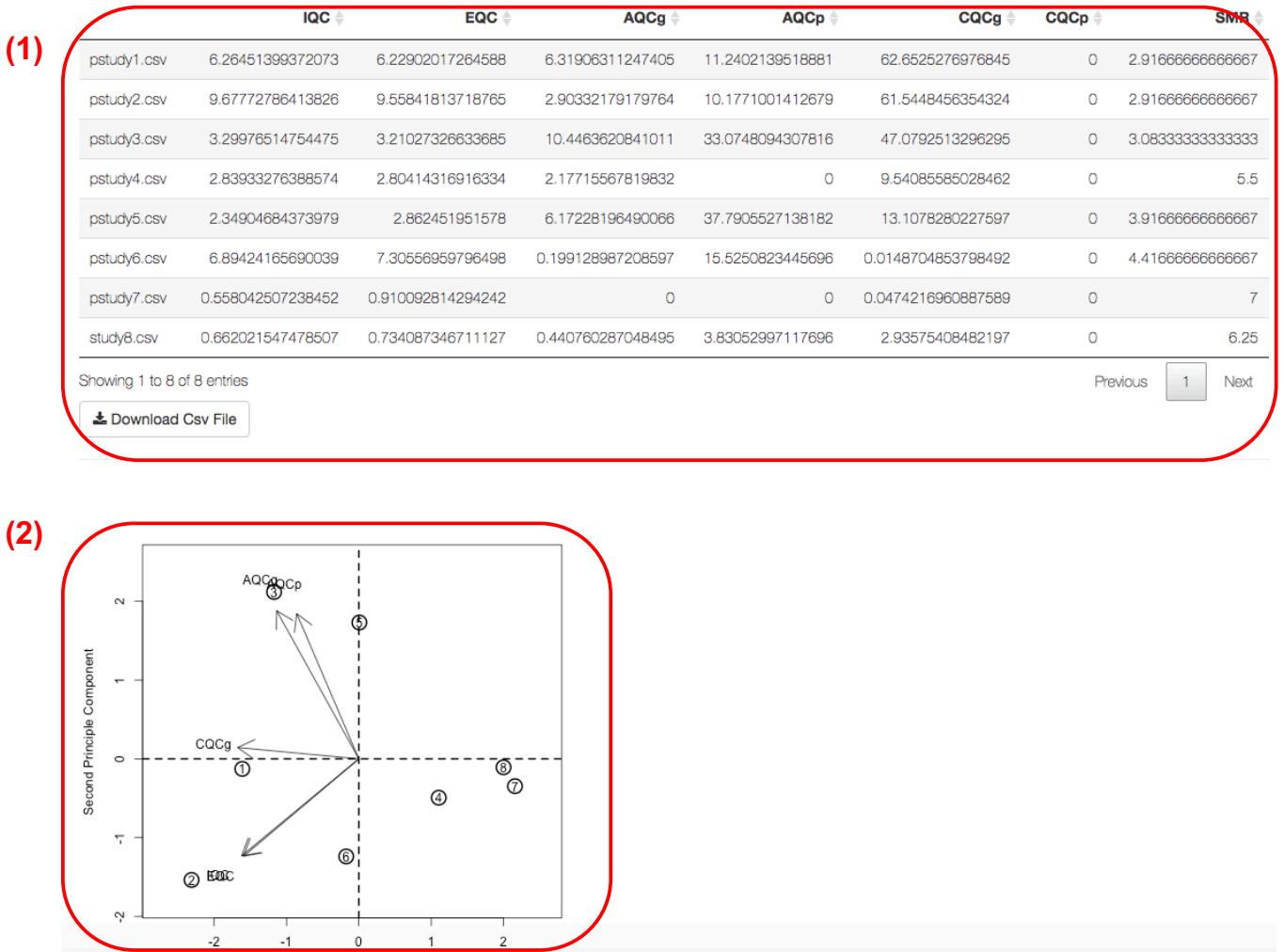


Figure 9: “MetaQC” Results

We applied MetaQC on the eight prostate cancer datasets. After performing merging of the eight datasets and filtering out 50% genes by mean and 50% by variance, 1060 genes remained for the MetaQC analysis. As shown in Figure 9, there are (1) a summary table of MetaQC results as well as (2) a PCA biplot generated. The table includes seven columns, with the first six columns corresponding to the six quantitative quality control measures of all studies (a larger value indicates a better quality) and the seventh column is the rank summary statistics of all the six quality measures (a lower rank indicates a better quality). Users can download the full table as a csv file by clicking on “Download Csv File”. In addition to the tabular results, “MetaQC” also generated a PCA biplot based on the six quality control measures, where the circled number is the study index and arrows indicate different measures. Generally, studies with larger SMR values, and studies more off from the other studies and a majority of the measures are considered lower quality. In this case, the 7th and the 8th studies have relatively poorer quality. Both tabular summary and biplot are automatically saved to the working directory.

5.2 MetaDE

MetaDE package implements 12 major meta-analysis methods for differential expression analysis falling into 3 main categories: combining p-values, combining effect sizes and others (e.g. combining ranks, etc.). De-

pending on the types of outcome, the package can perform two class comparisons, multi-class comparison, association with continuous or survival outcome. The package allows the input of either microarray (continuous intensity) and/or RNA-seq data (count) for individual study analysis. The R package for MetaDE module can be found <https://github.com/metaOmics/MetaDE>. After obtaining DE genes from meta-analysis, users can further perform pathway enrichment analysis based on the declared DE genes. In the two subsections below we will go over how to perform (1) meta-analysis and (2) pathway enrichment analysis based on (1).

5.2.1 Procedure of Meta-analysis for differential expression

The figure shows a software interface for 'MetaDE'. At the top is a green 'About' bar. Below it is a series of red-bordered boxes labeled (1) through (10). Box (1) contains 'Meta Method Type' with a dropdown menu showing 'Combine P-Value'. Box (2) contains 'Meta Method' with a dropdown menu showing 'AW Fisher*'. Box (3) contains 'mixed data types?' with a radio button set to 'No'. Box (4) is a green bar labeled 'Response Type'. Box (5) is a green bar labeled 'Individual Study Option'. Box (6) is a light blue bar labeled 'Advanced Options'. Box (7) is a green bar labeled 'Run' with a checkmark icon. Box (8) contains 'Pathway Databases:' with a dropdown menu showing 'KEGG GO Biological Process GO Cellular Component GO Molecular Function Reactome BioCarta'. Box (9) is a light blue bar labeled 'Pathway Analysis Options'. Box (10) is a green bar labeled 'Run Pathway Analysis' with a checkmark icon.

Figure 10: “MetaDE” options

In Figure 10, Red boxes (1) - (7) are the steps to tuning parameters and run meta-analysis. A detailed list of all options available for the package can be found at the end of this subsection.

Step 1 Choose the type of meta-analysis methods: There are three types of meta-analysis to choose: combining p-values, combining effect size and others.

Step 2 Choose a meta-analysis method:

- For “combining p-values” category, users can choose from “Fisher”, “AW-Fisher”, “maxP”, “minP”, “roP” and “Stouffer”, where some of them have the one-sided corrected versions.
- For “combining effect size” category, users can choose from “FEM” and “REM”, where “REM” has choice of six analytical algorithms for implementation.
- For “others”, there are three rank-based method (PR, SR and rankProd) and minMCC for multi-class meta-analysis. To choose from the overwhelmingly many meta-analysis methods, we follow Chang et al. (2013) and mark * for top performing methods AW-Fisher, REM (HO option) and roP as recommendation for users.

Step 3 Mixed data type: If this option is selected, MetaDE will allow partial studies with count data from RNA-seq and remaining studies with continuous intensities from microarray.

Step 4 Choose the response type: Under the drop-down menu, users can specify types of outcome (response) variable to be two-class, continuous, multi-class or survival. By choosing “two class comparison”, users can specify the group label name for the Label Attribute (from the column names of your clinical data). Then for group label (a factor of at least two levels), specify the name for the “Control Label” and “Experimental Label”, respectively. For the other types, only group label name is needed.

Step 5 Choose Study Design for individual study:

- Individual data type can be either discrete (count) or continuous.
- Under drop-down menu “Setting Individual Study method”, user can specify individual study method according to individual data type. For continuous data (e.g. microarray), available options include LIMMA (default method) and SAM. For discrete data (e.g. RNA-seq count), available options include edgeR, DESeq2 and voom.
- The users can also specify whether each study is paired design or not.

Step 6 Advanced Options

- Use complete options: other uncommonly used options will become available. Again, this is not suggested if you are not familiar with the method.
- Parametric: if No is selected, permutation will be performed instead of parametric closed form solution.
- Covariate: indicate if any covariate will be adjusted.
- Alternative Hypothesis: two-sided or one-sided.

Step 7 Run: Once all the above options are specified, users can click on “Run” button to perform MetaDE analysis

5.2.2 Results of Meta-analysis for differential expression

For the MetaDE model, we used multi-study leukemia gene expression data as example. After performing merging of the three datasets and filter 50% genes by mean and 50% by variance, 1283 genes remained. In this example we only compare two phenotypes: inv(16) and t(15;17). Two main outputs from the first “meta differential analysis” step in the procedure are shown in Figure 11. Heatmap of DE genes is drawn on top after specifying the FDR cutoff for selection of DE genes and clicking on “Plot DE Genes Heatmap”. The “image size” can be adjusted by dragging the scroll bar. In the heatmap, rows refer to DE genes selected, columns refer to samples, solid white lines are used to separate different studies and the dashed white lines are used to separate groups. Colors of the cells correspond to scaled expression level as indicated in the color key below. For the results generated by “AW-Fisher”, there is one additional column of cross-study weight distribution on the left end of the heatmap and the genes in the heatmap are sorted by their weight distribution. Summary of meta analysis results is on bottom, including information of individual test statistics, individual study p-value, meta-analysis p-value, FDR, etc.

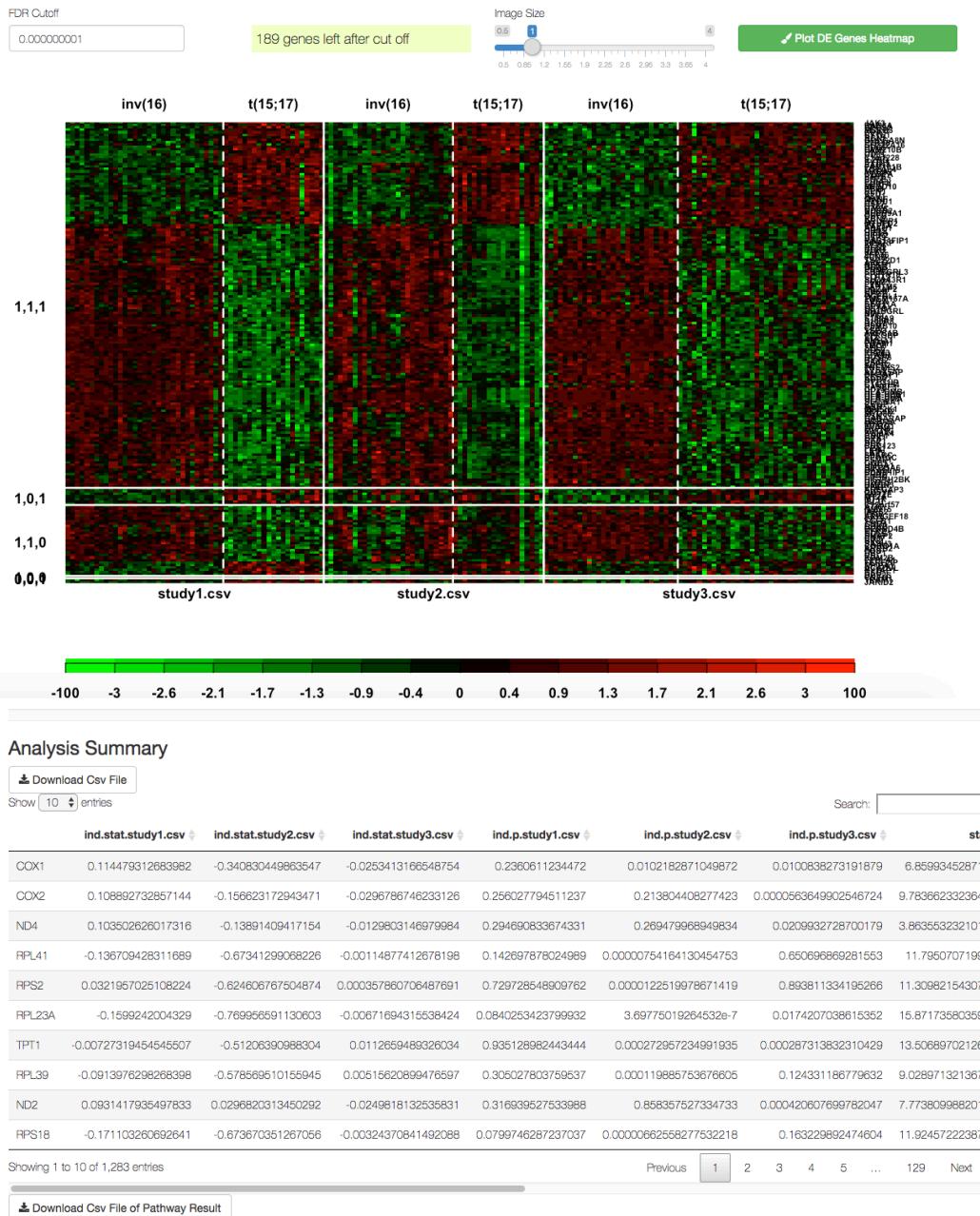


Figure 11: “MetaDE” Results

5.2.3 Procedure of downstream pathway analysis

Users can then perform pathway enrichment analysis on the declared DE genes from the previous step, which can be achieved in **Red boxes (8) - (10)** in Figure 10. Procedure is ruled out as below.

Step 1 Choose the pathway database: Users can select from 25 available pathway databases to perform the pathway enrichment analysis.

Step 2 Choose the pathway enrichment method and the pathway size range: In this step users can choose pathway enrichment options with Kolmogorov-Smirnov (KS) test as default option, or Fisher’s exact test by specifying number of input genes for pathway analysis. For Fisher’s exact test, the input genes can be obtained by either specifying a MetaDE p-value cutoff, or specifying number of top DE

genes. Users can also specify the minimum/maximum gene size of pathways to be included for pathway enrichment analysis.

Step 3 Run: Once all the above options are specified, users can click on “Run Pathway analysis” button to perform pathway enrichment analysis.

5.2.4 Result of downstream pathway analysis

The result for downstream pathway analysis is tabulated in Figure 12. The summary includes the pathway names, the corresponding enrichment p-value and FDR. In addition to the results shown in the Browser, users can download the result by clicking on "Download Csv File" on the top left of the summary table.

	pvalue ▲	qvalue ▲
GO:MF structural molecule activity	1.81847314458884e-7	0.000309867823837939
GO:MF structural constituent of ribosome	5.34434561258283e-7	0.000455338246192057
Reactome 3' -UTR-mediated translational regulation	0.00000131924749561921	0.000749325775117111
Reactome SRP-dependent cotranslational protein targeting to membrane	0.00000647265931113214	0.00230118179349581
Reactome Nonsense Mediated Decay Enhanced by the Exon Junction Complex	0.00000675229399499945	0.00230118179349581
Reactome Translation	0.000009118216981995	0.00258957362288658
Reactome Peptide chain elongation	0.00001184735674493	0.00272268422704801
KEGG Ribosome	0.0000280413574894046	0.00597280914524318
KEGG Leishmania infection	0.0000559715298195024	0.010330830261965
Reactome Influenza Viral RNA Transcription and Replication	0.0000606269381570718	0.010330830261965

Showing 1 to 10 of 1,901 entries

Previous 1 2 3 4 5 ... 191 Next

Figure 12: Downstream pathway analysis based on MetaDE genes

Complete List of Options:

1. Meta Method Type: Combining p-value, Combining effect size, Others.
2. Meta Method: Fisher, AW-Fisher, FEM, REM, Sum of Rank, Produce of Rank, multi-class correlation, Rank product.
3. Mixed data type: selected if both count data and continuous data exist.
4. Response Type:
 - Two class comparison, Multi-class comparison, Continuous outcome, Survival outcome.
 - Label Attribute: select the label name of the outcome.
 - Control Label & Experimental Label: specify the case/control label for two-class comparison.
5. Individual Study Option:
 - Setting individual study method
 - Setting individual study paired option
6. Advanced Option (**Optional):
 - Use complete options
 - Parametric

- Covariate
- Alternative hypothesis

7. Run
8. Pathway Databases
9. Pathway Analysis Option:
 - Pathway enrichment method
 - Pathway min gene size
 - Pathway max gene size
10. Run Pathway Analysis

5.3 MetaPath

In MetaDE package, following the detection of biomarkers, pathway analysis (a.k.a. gene set enrichment analysis) is usually performed for functional annotation and biological interpretation. Beyond that, the MetaPath module provides two advanced meta-analytic pathway analysis tools: Comparative Pathway Integrator (CPI) and Meta-Analysis for Pathway Enrichment (MAPE) (Shen et al., 2010; Fang et al., 2017). Pathway clustering with statistically valid text mining is included in the package to reduce pathway redundancy to condense knowledge and increase interpretability of clustering results. The R package for MetaPath module can be found <https://github.com/metaOmics/MetaPath>.

5.3.1 Procedure

The MetaPath package requires the input of raw expression data as in MetaDE. There are three major steps to implement the package: pathway analysis, pathway clustering diagnostics and pathway clustering with text mining. As shown in Figure 13, there are 9 major options that need to be specified to implement the package. detailed list of all options available for the package can be found at the end of this subsection.

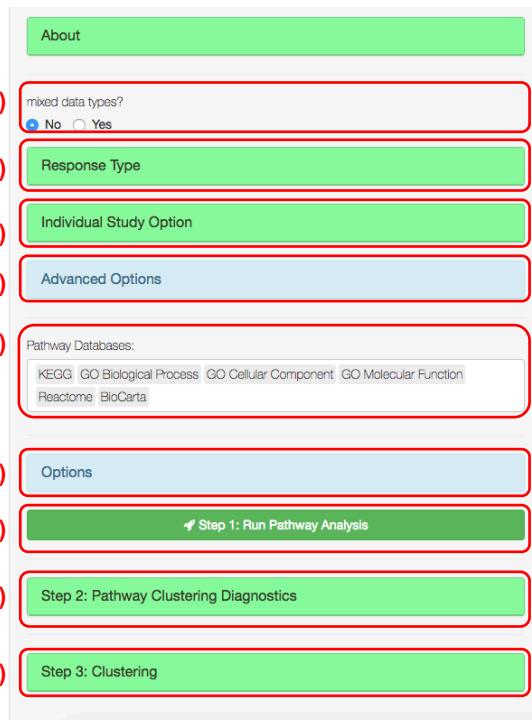


Figure 13: “MetaPath” options

Step 1 Setup pathway analysis parameters: Users need to specify (1) whether the input gene expression profile is mixed of continuous data and discrete data; (2) response type, case/control labels (similar to MetaDE); (3) individual study option (similar to MetaDE); (4) advanced options including whether to adjust for covariates or the direction of hypothesis testing;. In (5), users can select from 25 available pathway databases for the enrichment analysis. In (6), users can select MetaPath method (either CPI or MAPE). By default, the “CPI” approach is used, otherwise “MAPE” approach can also be used. Other options include pathway enrichment method (the Fisher’s exact test or KS test), the minimum as well as the maximum pathway size. If “Fisher’s exact test” is chosen for the enrichment method, users need to further specify the criteria for selection of DE genes, e.g. the number of top ranked genes. On the other hand, if “KS test” is chosen, one needs to further specify whether to use permutation to obtain enrichment p-value.

Step 2 Run Pathway Analysis: Once the above options are specified, users can click on (7), “Run Pathway Analysis”.

Pathway clustering diagnostics: From the previous step (Step **Step 2**), users can choose the top enriched pathways for further clustering. One can expand the drop-down menu and use FDR cutoff to choose top pathways and click on (8), “Pathway clustering diagnostics” to implement the second step.

Pathway clustering with text mining: From the previous step (Step **Step 2**), users can determine the optimal number of clusters in the pool of pathways selected. Now, one can specify the number of clusters and click on (9) “Get clustering result” to implement the third step. Note that you may not want to select too large a K since you wish to have a certain amount of pathways in each cluster for the validity of text mining algorithm. We generally suggest users to specify K no larger than 7 for fewer than 100 pathways.

Complete List of Options:

1. mixed data types:
 - Two class comparison, Multi-class comparison, Continuous outcome, Survival outcome.
 - Label Attribute: select the label name of the outcome.
 - Control Label & Experimental Label: specify the case/control label for two-class comparison.
2. Response Type:
 - Setting individual study method
 - Setting individual study paired option
3. Individual Study Option:
 - Covariate
 - Alternative hypothesis
4. Advanced Option (**Optional):
 - Software
 - Pathway enrichment method
 - Pathway min gene size
 - Pathway max gene size
5. Pathway Databases
6. Pathway Analysis Option:
 - Step1: Run Pathway Analysis
 - Step2: Pathway Clustering Diagnostics
 - Step3: Get Clustering Result

5.3.2 Results

Analysis Summary

Show 10 entries

Search:

	q_value_meta	p_value_meta	study1.csv	study2.csv	study3.csv
KEGG Glycolysis / Gluconeogenesis	0.999952944432397	0.975713730375006	0.716589454064696	0.814873418361965	0.865769906161247
KEGG Citrate cycle (TCA cycle)	0.999952944432397	0.510889688669431	0.211530174577612	0.992916710335908	0.821404141054911
KEGG Pentose phosphate pathway	0.999952944432397	0.85144555453665	0.548102615399992	0.856164955367949	0.471951151317958
KEGG Fructose and mannose metabolism	0.999952944432397	0.433422300367834	0.816463757920819	0.752605531269185	0.170427359195984
KEGG Galactose metabolism	0.999952944432397	0.969760558119967	0.840628669648421	0.963989021054332	0.692998846745079
KEGG Ascorbate and aldarate metabolism	0.999952944432397	0.351690352701752	0.663648742104101	0.176746098320381	0.163240921127113
KEGG Fatty acid metabolism	0.999952944432397	0.785586400080126	0.584204394255307	0.403175881949791	0.750935078799842
KEGG Steroid biosynthesis	0.999952944432397	0.241772080559306	0.151118401862353	0.171251505076894	0.145612810184764
KEGG Primary bile acid biosynthesis	0.999952944432397	0.939258438255731	0.606195296926418	0.617063475433555	0.989348045492025
KEGG Steroid hormone biosynthesis	0.999952944432397	0.731719469083418	0.993283631448111	0.356962695144036	0.993038039433862

Showing 1 to 10 of 1,704 entries

Previous 1 2 3 4 5 ... 171 Next

Figure 14: “MetaPath” Results (1)

The input dataset is same as the input for MetaDE module. We used multi-study leukemia gene expression data as example. After performing merging of the three datasets and filter 50% genes by mean and 50% by variance, 1283 genes remained. In this example we only compare two phenotypes: inv(16) and t(15;17).

After the Step **Step 2** is finished, a summary table was generated as shown in Figure 14 (based on the default CPI method). The “Analysis Summary” includes the analysis results of all pathways, including individual study association analysis p-value, meta pathway analysis p-value/FDR, etc. Users can search the gene name in the “Search” bar, and the full table is automatically saved in the working directory specified before.

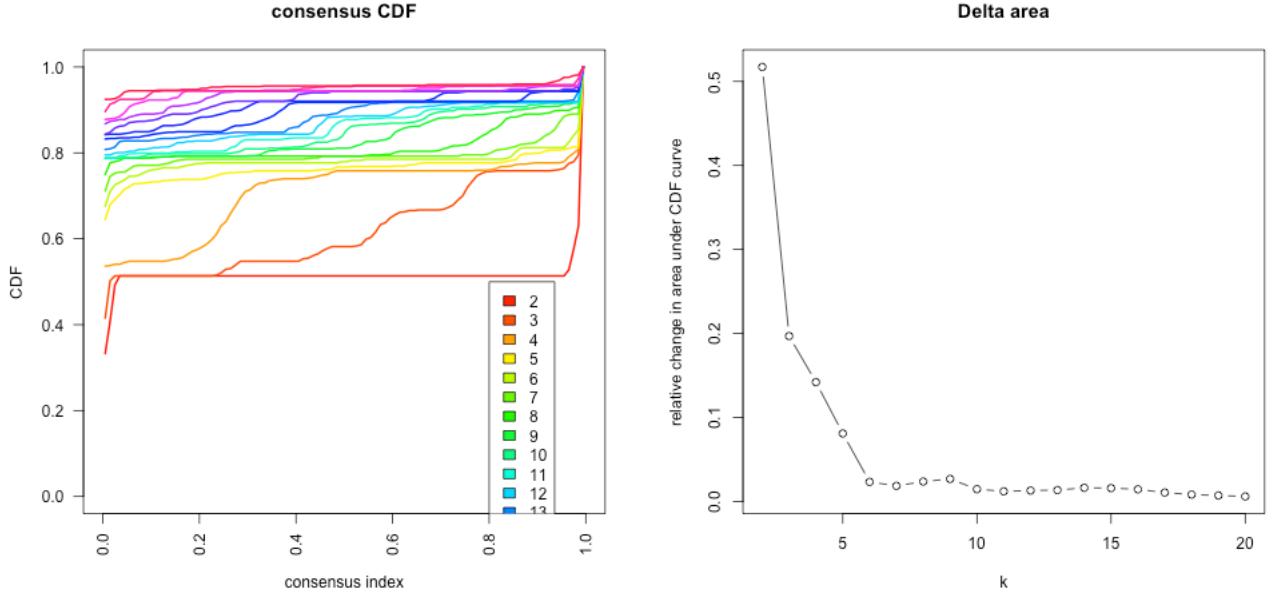


Figure 15: “MetaPath” Results (2)

After the “Pathway Cluster Diagnostics” step is finished, we will see two plots generated on the right panel (Figure 15): consensus CDF and Delta area plots, both from the “ConsensusClusterPlus” package. The CDF of the consensus matrix for each K (indicated by colors) is estimated by a histogram of 100 bins. The CDF reaches an approximate maximum, thus consensus and cluster confidence is at a maximum at this K . The delta area shows the relative change in area under the CDF curve comparing K and $K - 1$, thus allows users to determine the determine K at which there is no appreciable increase in CDF. Both plots assist users in finding the optimal number of clusters “ K ” and you may refer to (Monti et al., 2003) for more detailed interpretation of the two plots. In the demo example, $K = 6$ have large enough CDF, is thus chosen (though $K = 7$ captures more, we only have 38 pathways here).

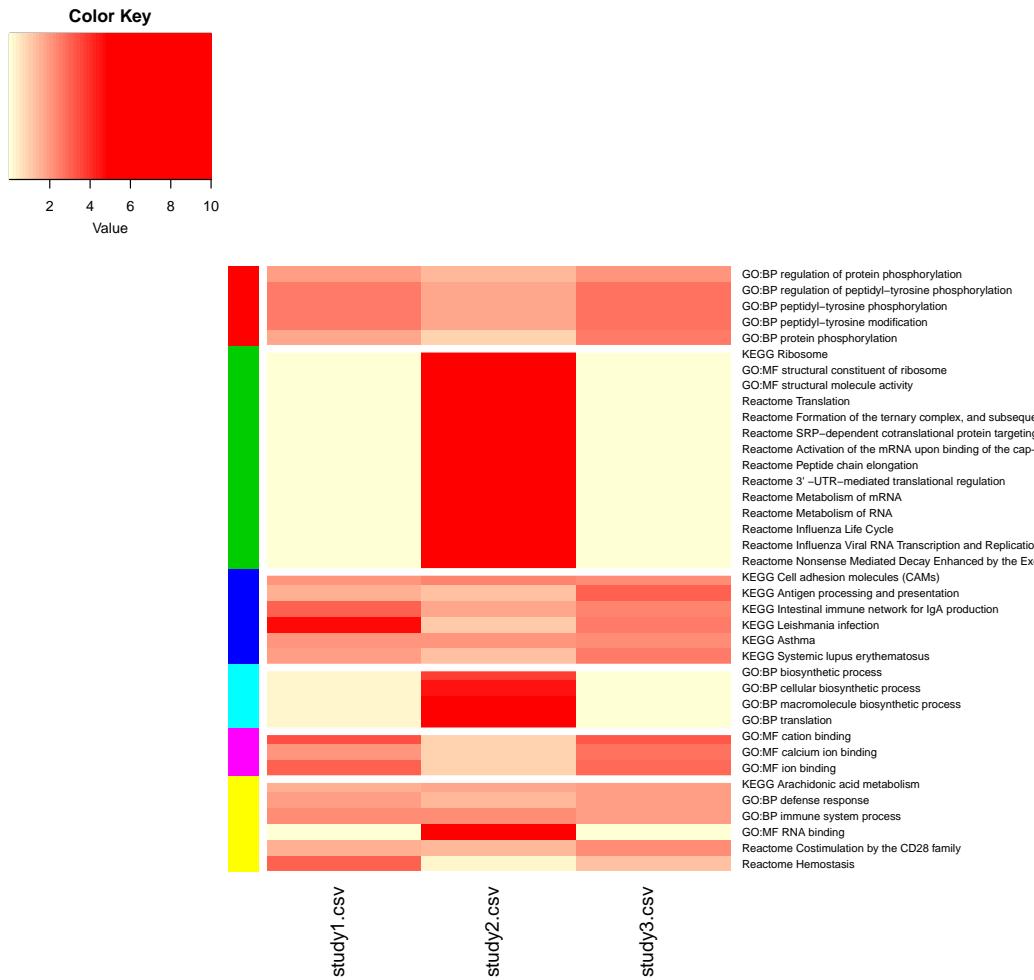


Figure 16: “MetaPath” Results (3)

The heatmap in Figure 16 shows the $-\log_{10}$ transformed p-value of enrichment analysis in each study from **Step 2**. Studies are on columns and the selected pathways are on rows, red means more enriched. The pathways are sorted by the pathway cluster as indicated by the colors on the left side of the heatmap. In addition, the key words of each cluster of pathways are extracted and analyzed by a built-in text mining algorithm and one file named “Clustering_Summary.csv” is saved to the working directory which shows a summary of the text mining result.

5.4 MetaNetwork

By clicking toolsets and then MetaNetwork, users are directed to MetaNetwork home page as Figure 17. The R package for MetaNetwork module can be found <https://github.com/metaOmics/MetaNetwork>.

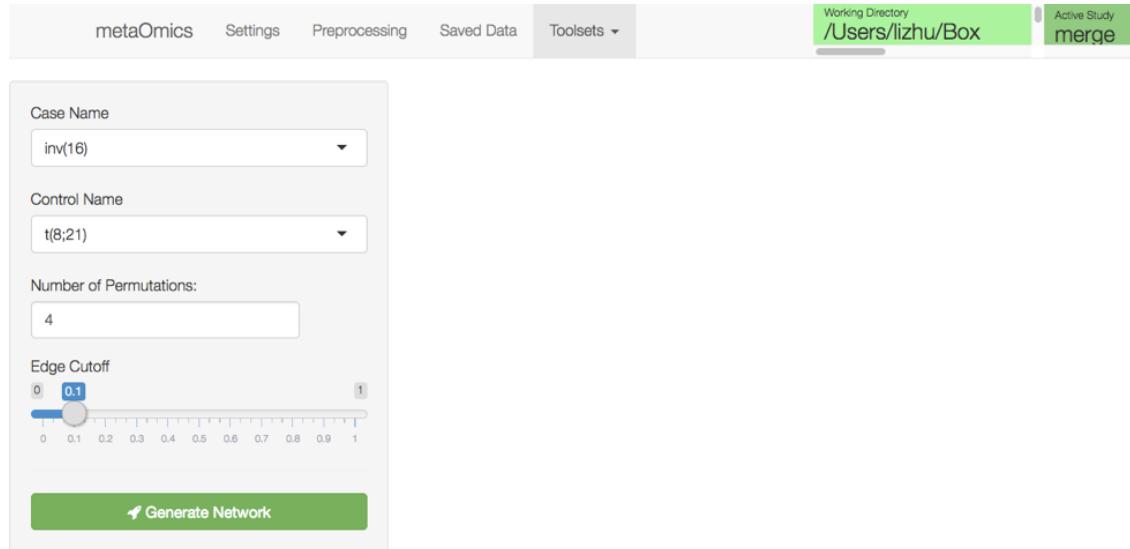


Figure 17: MetaNetwork homepage

MetaNetwork includes three steps to get differentially co-expressed networks: generate network, search for basic modules, and assemble supermodules. The left screen is the control panel of step 1. The control panel for next step will show up after the previous step is done.

5.4.1 Procedure

Step 1 Generate Network The first step of MetaNetwork is to generate co-expression network. In this step, the network for permuted data will also be generated. Users need to select case and control names, the number of permutations, and edge cut-off which determines the proportion of edges to be kept in the network. After clicking **Generate Network** button, screen will show message indicating the algorithm is running to generate network.

Step 2 Search for basic modules

The next step is to search basic modules. Advanced options (recommended not to change) include the number of repeats used for each initial seed modules (“Number of repeat”), the maximum Monte Carlo steps for simulated annealing algorithm (MC Steps), and the maximum pairwise Jaccard index allowed for basic modules (Jaccard Cutoff), as shown in Figure 18. After clicking **Search for basic modules** button, screen will show message indicating the algorithm is running to search for basic modules. This step is computationally demanding depending on gene size. After this step is done, the screen will show a table of basic modules highly connected in cases but lose connections in control and vice versa.

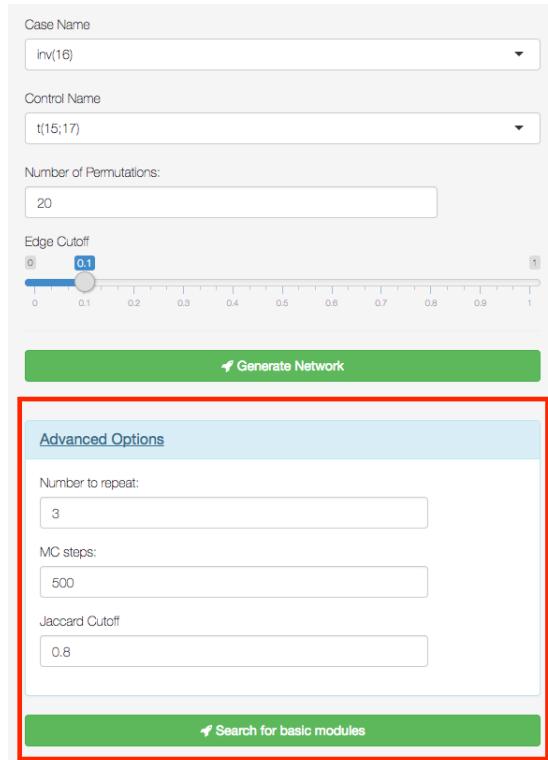


Figure 18: MetaNetwork control panel for search for basic modules

Search for basic modules will take minutes, especially if a large number of genes are used. After this step is done, the screen will show a table of basic modules higher correlated in case and a table of basic modules higher correlated in control as Figure 19.

Basic modules higher correlated in case:

Basic modules higher correlated in case:			
Module.Index	Component.Number	Repeat.Index	Gene.Set
1 H1	2	1	PSAP/CTSS/CECR1/LGALS3/AP1S2/TLR2/HEXB/SMIM24/CTSB/OGFRL1/MYO1F/CPXM1/SERPINA1/MNDA/TNF
2 H2	2	2	SERPINA1/AP1S2/CECR1/SMIM24/PSAP/TRBV27/RGS10/CPXM1/TLR2/CAPN2/OGFRL1/MS4A6A
3 H3	2	3	CTSB/TLR2/RGS10/HEXB/SERPINA1/CECR1/LGALS3/AP1S2/SMIM24/S100A9/CPXM1/MAP2K1/CAPN2
4 H4	6	1	NFIL3/IER3/CD83/CPXM1/EZR/RIPK2/SLC2A3
5 H5	6	2	NFIL3/IER3/LCP1/CDKN1A/TCEAL4/TGFB1
6 H6	6	3	NFIL3/LYN/IER3/LCP1/UCP2/MARCKSL1/RAB11FIP1

Showing 1 to 6 of 6 entries

Previous 1 Next

Basic modules higher correlated in control:

Basic modules higher correlated in control:			
Module.Index	Component.Number	Repeat.Index	Gene.Set
1 L1	2	1	GCA/FABP5/PRR11/PCNA/C1QBP/MAFF/FAM107B/PRDX3/TNFSF13B/PRTN3/PRKACB/CBF/CAT/RAB10/AN
2 L2	2	2	ICAM3/TGFB1/TYROBP/PLP2/BIN2/HCST/MYO1F/TIMP1/LAPTM5/S100A9
3 L3	2	3	PCNA/FAM107B/GCA/PRTN3/C1QBP/KIAA0101/EZR/RAB10/CAT/PRDX3/TNFSF13B/ANP32E/DYNLL1
4 L4	6	1	SLC2A3/JUP/LYN/PPP1R15A/EZR/PCNA/RAB10/FLNA/PIM3/KLF6
5 L5	6	2	STAM/JUP/LYN/PIM3/PDLIM1/HLA-DPA1/ITM2A/TPSAB1/CSTA
6 L6	6	3	SLC2A3/STAM/JUP/LYN/PPP1R15A/PCNA/FLNA/PLP2/HLA-DPA1

Showing 1 to 6 of 6 entries

Previous 1 Next

Figure 19: MetaNetwork output from search for basic modules step

Step 3 Assemble supermodules

After search for basic modules step is done, the control panel will be Figure 20. The last step is to assemble supermodules. Users can decide the FDR cut-off to select basic modules for supermodule assembly. After clicking **Assemble supermodules** button, screen will show message indicating the algorithm is running to assemble supermodules. A table for basic modules, supermodules and their network visualization will be shown on the right panel of screen. MetaNetwork automatically creates files for top supermodules designed to input to a Cytoscape plug-in “MetaDCNExplorer” (<http://tsenglab.biostat.pitt.edu/software.htm>) for improved visualization and dynamic exploration.

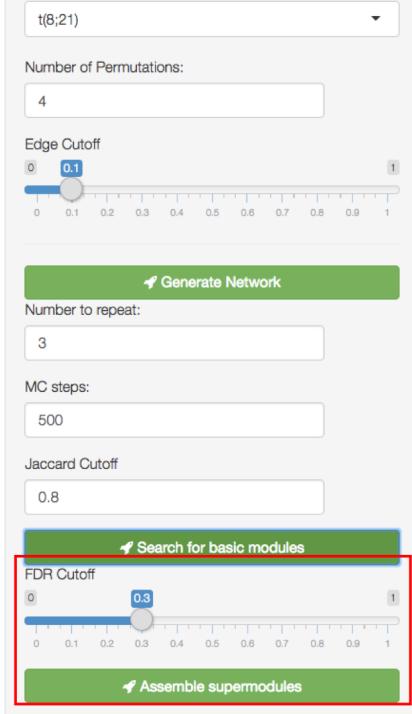


Figure 20: MetaNetwork control panel for assemble supermodules step

Complete List of Options:

1. Generate Network:
 - Case Name: specify case group label.
 - Control Name: specify control group label.
 - Number of Permutations: the number of permutations used for generating network.
 - Edge Cutoff: edge cut-off determines the proportion of edges to be kept in the network.
2. Search for basic modules:
 - Number to repeat: the number of repeats used for each initial seed modules.
 - MC steps: the maximum Monte Carlo steps for simulated annealing algorithm.
 - Jaccard cutoff: maximum pairwise Jaccard index allowed for basic modules.
3. Assemble supermodules:
 - FDR cutoff: FDR cut-off to select basic modules for supermodule assembly.

5.4.2 Results

We used multi-study leukemia gene expression data as example. After performing merging of the three datasets and filter 80% genes by mean and 80% by variance, 206 genes remained. In this example we only compare two phenotypes: inv(16) and t(15;17). In general, the MetaNetwork tool is time consuming for large datasets (for both network generation and search for basic modules steps). We generally suggest users to carefully restrict the number of genes (e.g. less than a thousand) for a test run before implementing large gene set. By default, all outputs and several interim RData files will be automatically saved to the folder named “MetaNetwork” under the working directory specified in Section 2.3.

Generate Network

After the generate network step is done, no output will show up in the screen. Instead, a message box indicating several Rdata files are saved in the MetaNetwork folder, including:

- AdjacencyMatrices.Rdata is a list of adjacency matrices for case and control subjects in each study. The order is study1 case, study2 case, ..., studyS case, study1 control, study2 control, ..., studyS control.
- CorrelationMatrices.Rdata is a list of correlation matrices for case and control subjects in each study.
- AdjacencyMatricesPermutationP.Rdata is a list of adjacency matrices for permuted datasets in permutation P.

Search for basic modules

After this step is done, the screen will show a table of basic modules higher correlated in case and a table of basic modules higher correlated in control as Figure 19. Meanwhile, several files will be saved in the MetaNetwork folder:

- basic_modules_summary_forward_weight_w1.csv is a summary table of basic modules that are higher correlated in case, detected using w1.
- basic_modules_summary_backward_weight_w1.csv is a summary table of basic modules that are higher correlated in control, detected using w1.
- threshold_forward.csv is a table of number of basic modules higher correlated in case, detected under different w1 values and FDR cut-offs.
- threshold_backward.csv is a table of number of basic modules higher correlated in control, detected under different w1 values and FDR cut-offs.
- permutation_energy_forward_P.Rdata is a list of energies for basic modules that higher correlated in case, detected from permutation P.
- permutation_energy_backward_P.Rdata is a list of energies for basic modules that higher correlated in control, detected from permutation P.

Assemble supermodules

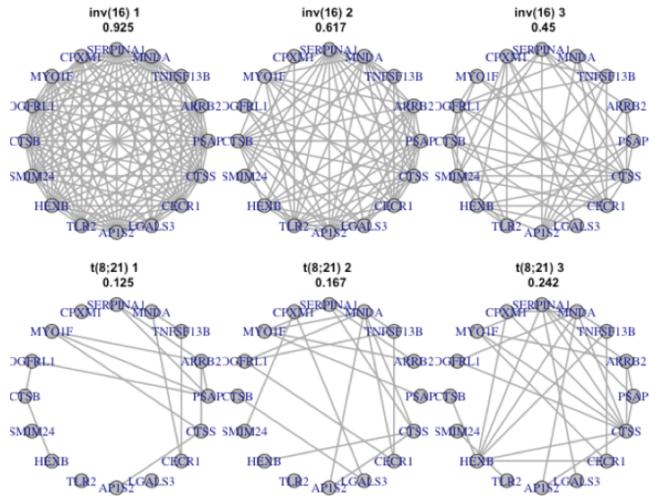
After supermodule assembly is done, screen will show a table of supermodules (Figure 21). Users can also select basic modules to plot (Figure 22). Meanwhile several files will be saved in the folder MetaNetwork:

- module_assembly_summary_weight_w1.csv is summary table of supermodules using w1 weight.
- CytoscapeFiles folder contains the input files for Cytoscape to visualize supermodules.

MetaDCN pathway-guided supermodules				
Show 10 entries	Search: <input type="text"/>			
pathway_name	pathway_size	p_value	q_value	size
KEGG_LYSOSOME	121	9.73e-05	0.01	20
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	91	0.00697	0.0393	20
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	208	0.00495	0.0393	25
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	89	0.00281	0.0393	22
BIOCARTA_MCALPAIN_PATHWAY	25	0.00283	0.0393	30
GO_CYTOSKELETAL_PROTEIN_BINDING	159	0.00185	0.0393	13
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	63	0.00431	0.0393	14
GO_ACTIN_FILAMENT_BINDING	26	0.00369	0.0393	13
BIOCARTA_CFTR_PATHWAY	12	0.00725	0.0393	18
GO_ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	105	0.00697	0.0393	20

Figure 21: MetaNetwork supermodules table

3 modules higher correlated in case under FDR 0.3, select modules to plot:



6 modules higher correlated in control under FDR 0.3, select modules to plot:

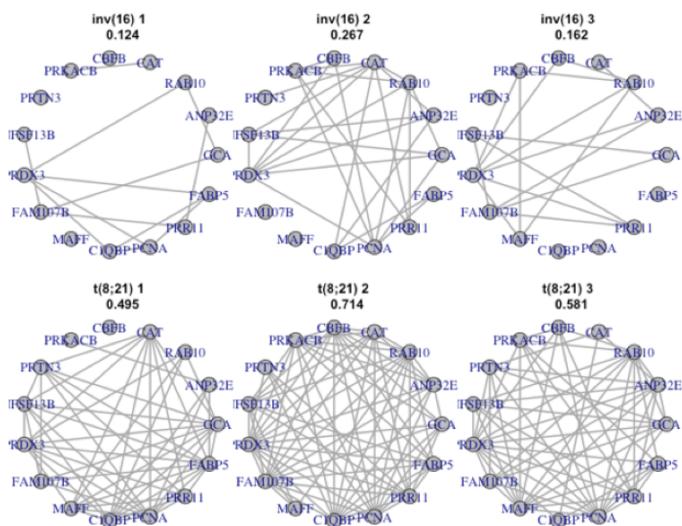


Figure 22: MetaNetwork select basic modules to plot

5.5 MetaPredict

Top scoring pairs is a robust algorithm for predicting gene expression profiles, which adopts nonparametric rank-based prediction rule. The MetaPredict is a meta-analysis version of the TSP algorithm that combines multiple transcriptomic studies to build a prediction model and shows improved prediction accuracy as compared to single study analysis. The R package for MetaPredict module can be found <https://github.com/metaOmic/MetaPredict>.

After opening the MetaPredict page, as shown in Figure 23, there are 1 drop-down menu (“Methods for MetaPredict”) (1), three number entries (“Max number of top scoring pairs (K)” (2), “Number of cores for parallel computing” (3) and “Number of top scoring pairs (K)” (7)), three character entries (“Please select TWO labels to cluster” (4), “Please select studies for training” (5), and “Please select studies for testing” (6), and two executing tabs (“Train model” and “Predict”).

5.5.1 Procedure

The screenshot shows the MetaPredict interface. At the top, there's a navigation bar with tabs for 'metaOmics', 'Settings', 'Preprocessing', 'Saved Data', 'Toolsets', 'Working Directory' set to '/Users/Masaki/Dropbox', and 'Active Study' set to 'Demo'. Below the navigation bar, there are two main sections: 'Summary Table' on the left and 'Gene pair table' on the right. The 'Summary Table' contains a table with three rows:

#Genes	#Samples
2515	89
2515	74
2515	105

The 'Gene pair table' section includes a 'K diagnostic plot' tab. On the left, under 'Train model', there are seven input fields, each labeled with a red number from 1 to 7:

- (1) Methods for Meta KTSP: A dropdown menu currently set to 'Mean score'.
- (2) Max number of top scoring pairs (K): An input field containing the value '9'.
- (3) Number of cores for parallel computing: An input field containing the value '2'.
- (4) Please select TWO labels to cluster: A dropdown menu.
- (5) Please select studies for training: A dropdown menu.
- (6) Please select ONE study for testing: A dropdown menu.
- (7) Number of top scoring pairs (K): An input field containing the value '9'.

Below these input fields are two green buttons: 'Train model' and 'Predict'.

Figure 23: Homepage of MetaPredict

Step 1 Building prediction model based on meta-analysis

First, we need to decide a method to select K top scoring gene pairs from multiple studies (Figure 23). Second, we need to provide the maximum number of top scoring pairs K (algorithm will search from 1 up to K) and the number of cores for parallel computing. Next, we need to select only TWO labels to build the classification model. In other words, if there exists more than two kinds of labels, we need to choose two from them. Our interface will pop up all labels that are available. Then, select the dataset as training data and testing respectively, and click the "Train model" tab to run the MetaPredict program. It may take a while to run the model.

Step 2 MetaPredict prediction

After the model training is finished, on the top right it will show up a "Gene pair table" ((1) in Figure 24) which present the top K gene pairs statistics. A diagnostic plot ((2) in Figure 24) is output to assist users decide which K to use in the final prediction model. The suggested value is shown in the plot as green line, which is decided by VO method we introduced in the original paper. Users may also decide K on their own to predict the class label of testing data. After deciding K , then hit the tab "Predict" (Figure 24). Finally, a confusion matrix is output to show the prediction results ((1) in Figure 24).

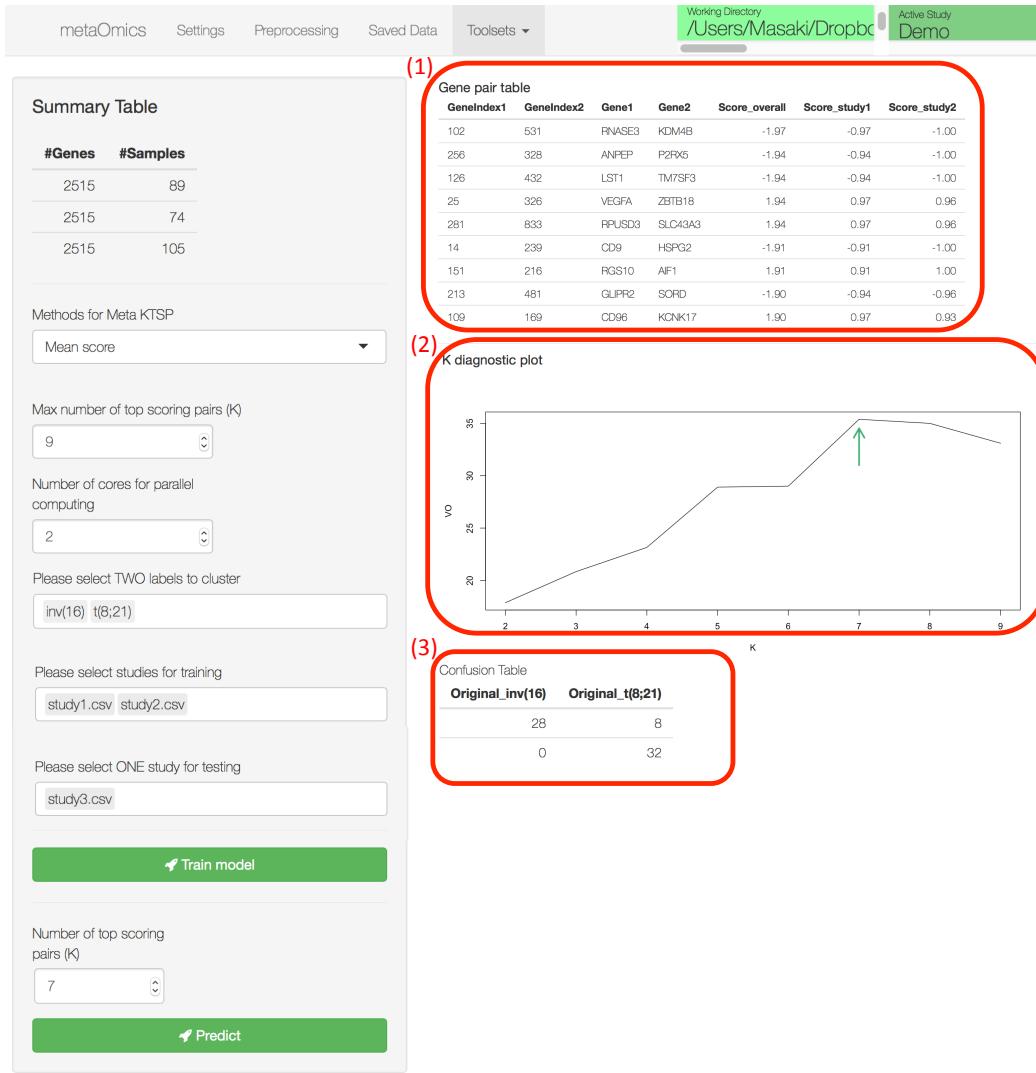


Figure 24: Results for MetaPredict.

Complete List of Options:

1. Model trainings:

- Methods for MetaPredict: include Mean score, Fisher, Stouffer.
- Max number of top scoring pairs (K)
- Number of cores for parallel computing
- TWO labels to cluster: labels for MetaPredict
- Please select studies for training
- Please select studies for testing
- Number of top scoring pairs (K): Number of top scoring pairs (K) for prediction.

5.5.2 Results

A confusion matrix is output to show the prediction results ((1) in Figure 24). The prediction results are also saved in the folder.

5.6 MetaClust

By clicking toolsets and then metaClust, users are directed to metaClust home page as Figure 25. MetaClust (Huo et al., 2016) aims to perform sample clustering analysis combining multiple transcriptomic studies. By integrate information from multiple studies of similar biological purposes, MetaClust can identify an unified intrinsic gene sets among all studies, perform weighted clustering analysis using these common intrinsic gene sets, match the clustering pattern across studies to define disease subtype/cluster type. The resulting clustering from meta-analysis is more robust and accurate than single study analysis. The R package for MetaClust module can be found <https://github.com/metaOmics/MetaSparseKmeans>.

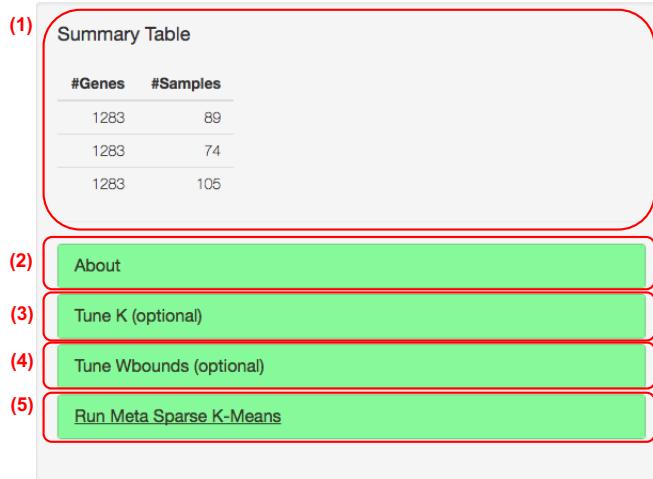


Figure 25: MetaClust home page

5.6.1 Procedure

Figure 25 shows the home page of MetaClust. On the top left panel users can see data summary Table (at position (1)). Below there are 4 tabs. About tab (at position (2)) includes basic introduction of MetaClust. Starting with multiple studies, we could run MetaSparseKmeans (at position (5)) with pre-specified number of clusters (K) and gene selection tuning parameter (Wbounds). If you are not sure about what are good K and Wbounds, please try Tune K (at position (3)) and Tune Wbounds (at position (4)) panel.

Step 1 Tune K:

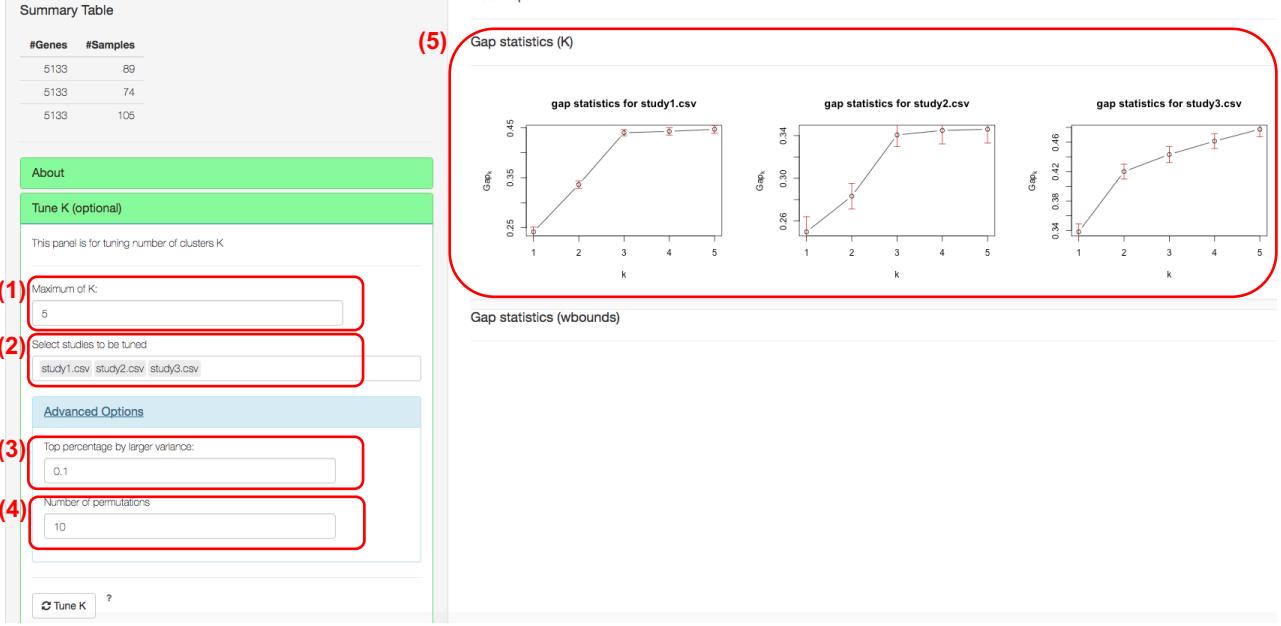


Figure 26: Tuning parameter selection for number of clusters

If the users are not sure what is number of clusters, they can start to use the Tune K panel as in Figure 26. Gap statistics will be used to get optimal K for each individual study. Users need to specify maximum number of K (at position (1)), which the algorithm will search number of studies from 1 to K. Studies to be tuned can be selected (at position (4)). In advanced options, users can further specify number of top variance genes to be included and number of permutations. But if users don't know the algorithm, please leave them as default. Top percentage p% by larger variance means that we will use top p% larger variance genes to perform gap statistics (at position (3)). Number of permutation is number of bootstrap samples for gap statistics (at position (4)). At least 50 bootstrap samples are suggested for a stable result of number of clusters. By clicking button "Tune K", we will obtain gap statistics as in Figure 26. A good K is selected such that the Gap_k is maximized or stabilized across all studies. From the figure, K=3 is preferred since the gap statistics from all three studies become flat (at position (5)).

Step 2 Tune Wbounds:

Wbounds directly control number of features selected by metaClust. If the users are not sure what is a good Wbound, they can start to use the Tune Wbounds panel as in Figure 27.

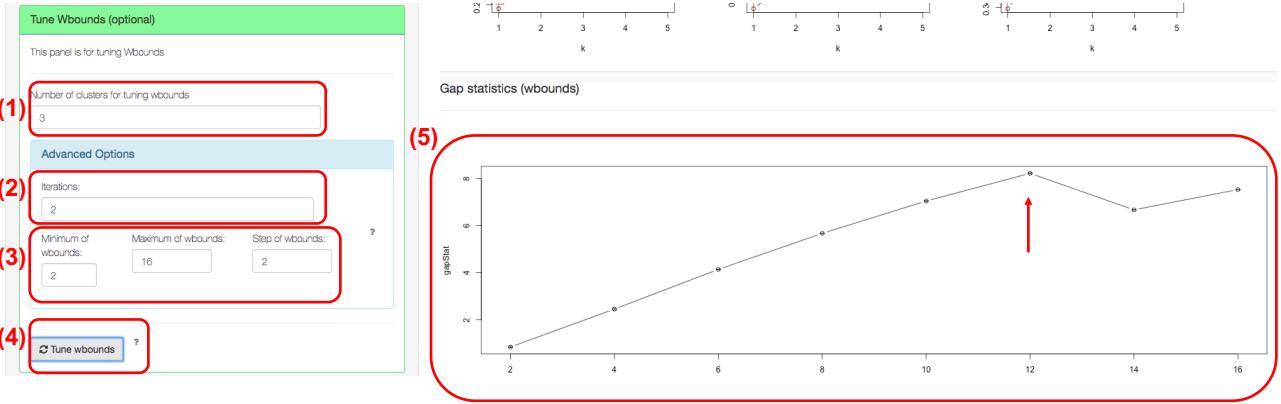


Figure 27: Wbound selection

Again, gap statistics will be used for tuning Wbounds. Users will specify number of clusters for tuning Wbounds (at position (1)), which could be obtained from the previous step. In advanced options, users can further specify number of iterations and the range of candidate Wbounds. But if users don't know the algorithm, please leave them as default. Iterations (at position (2)) is the same thing as number of bootstrap samples for gap statistics. Users also need to specify the searching space of Wbounds by minimum of Wbounds, maximum of Wbounds and Step of Wbounds (at position (3)). After all these steps are set, user can click on "Tune wbounds" button (at position (4)). The results will be shown in Figure 27 position (5). Wbound=12 is preferred since the corresponding gap statistics is maximized (where the red arrow indicates).

Step 3 Run Meta Sparse K-Means:

Under Run Meta Sparse K-Means panel, user can specify number of clusters (at position (1)), Wbounds (at position (2)) and run meta sparse K means (at position (5)), as in Figure 28.

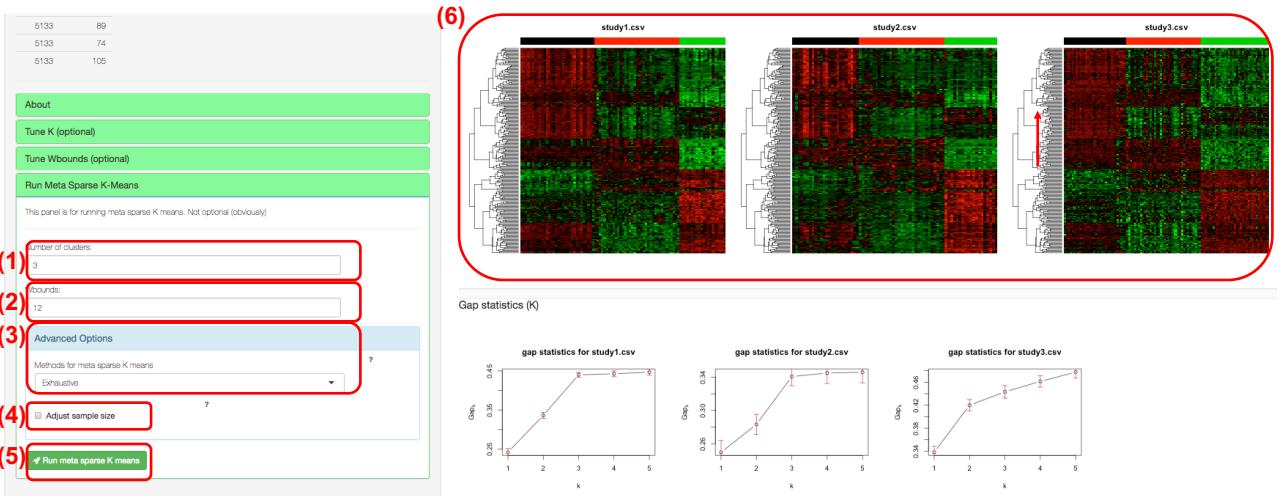


Figure 28: Result for MetaClust

In advanced options (for which users are not suggested to change if they are not familiar with the algorithm), There are three clustering matching methods (at position (3)): Exhaustive, linear, MCMC. Exhaustive is suggested if the data is not large. Linear will perform smart search and get solution much

faster than Exhaustive, but it may yield less accuracy with very low probability. MCMC is suitable if many studies and clusters are provided. Adjust sample size checkbox (at position (5)) allows users to adjust sample size effect. After number of clusters and Wbounds are specified, users can click on Run meta sparse K means and obtain results as Figure 28.

Complete List of Options:

1. Tune K (** optional)
 - Maximum of K: the maximum number of K that gap statistics will step through.
 - Top percentage by larger variance: Top percentage p% by larger variance means that we will use top p% larger variance genes to perform gap statistics.
 - Number of permutations: Number of permutation is number of bootstrap samples for gap statistics.
 - Select studies to be tuned: Studies to be tuned.
 - Tune K: start tuning K.
2. Tune Wbounds (** optional)
 - Number of clusters for tuning wbounds: number of clusters for tuning Wbounds.
 - Iterations: Iterations are number of bootstrap samples for gap statistics.
 - Minimum of wbounds: lower bound of the searching space of Wbounds.
 - Maximum of wbounds: upper bound of the searching space of Wbounds.
 - Step of wbounds: stepsize of the searching space of Wbounds.
 - Tune wbounds: start tuning wbounds.
3. Run Meta Sparse K -means:
 - Number of clusters: number of clusters. Can be tuned from Tune K option.
 - Wbounds: control numbers of selected features. Can be tuned from Tune Wbounds option.
 - Methods for meta sparse Kmeans: Exhaustive is suggested if the data is not large. Linear will perform smart search and get solution much faster than Exhaustive, but it may yield less accuracy. MCMC might be very time consuming.
 - Adjust sample size: adjust sample size effect.
 - Run meta sparse Kmeans: start tuning wbounds.

5.6.2 Results

We used multi-study leukemia gene expression data as example. After performing merging of the three datasets, we didn't filter by mean or variance (filter 0% genes by mean and 0% by variance) and 5133 genes remained. In this example actually do not need extra label information. The result is shown in Figure 28 at position (5). We obtained unified feature selection across all studies. The clusters are well separated in each study and the cluster patterns are consistent across all studies. The clustering heatmaps and labels are saved in the metaOmics folder.

5.7 MetaPCA

Dimension reduction is a popular data mining approach for transcriptomic analysis. MetaPCA aims to combine multiple omics datasets of identical or similar biological hypothesis and perform simultaneous dimensional reduction in all studies. The results show improved accuracy, robustness and better interpretation among all studies. By clicking toolsets and then metaPCA, users are directed to metaPCA home page as Figure 29. The R package for MetaPCA module can be found <https://github.com/metaOmics/metaPCA>.

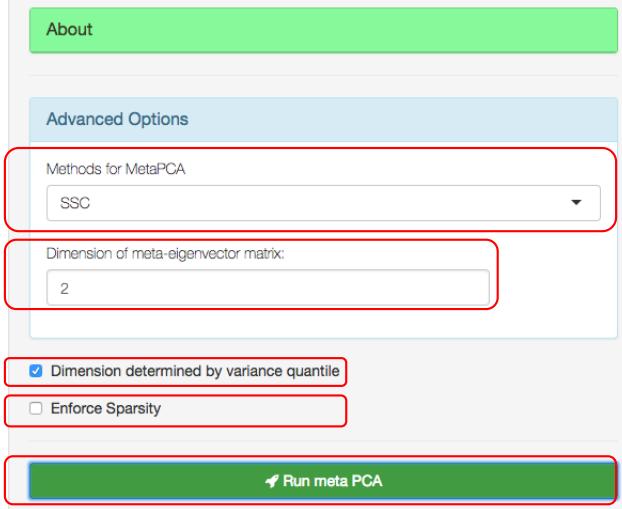


Figure 29: MetaPCA settings

5.7.1 Procedure

Step 1 Specify parameters

There are very few parameter to be specify in metaPCA, as in Figure 29. Advanced options are not suggested to change unless the users are confident. There are two methods for MetaPCA (at position (1)). SSC represent MetaPCA via sum of squared cosine (SSC) maximization. SV represent MetaPCA via sum of variance decomposition (SV). Details of SSC and SV can be found in metaPCA manuscript. SSC has better performance and is suggested. Dimension of meta-eigenvector matrix option (at position (2)) allows user to specify dimension of the output meta-eigenvector matrix. The checkbox of “dimension determined by variance quantile” is suggested to be selected (at position (3)), If it is selected, the dimension size of each study’s eigenvector matrix (SSC) is determined by the pre-defined level of variance quantile 80%. If the checkbox of “sparsity encouraged” is selected (at position (4)), users can perform metaPCA. After clicking on search for optimal tuning parameter button, the optimum tuning parameter will be returned to the box “tuning parameter for sparsity”, which may be time consuming.

Step 2 Perform metaPCA

By clicking the “Run meta PCA” button, MetaPCA will be performed.

Complete List of Options:

1. Common metaPCA parameters:
 - Methods for metaPCA: SSC represent MetaPCA via sum of squared cosine (SSC) maximization. SV represent MetaPCA via sum of variance decomposition (SV).
 - Dimension of meta-eigenvector matrix: dimension of the output meta-eigenvector matrix.
 - Dimension determined by variance quantile: the dimension size of each study’s eigenvector matrix (SSC) is determined by the pre-defined level of variance quantile 80%.
2. If sparsity encouraged is selected, there are extra tuning parameter (λ) that may need to be tuned.
 - Min λ : lower bound of the searching space of λ .
 - Max λ : upper bound of the searching space of λ .
 - Step of λ : stepsize of the searching space of λ .
 - Tuning parameter for sparsity: Tuning parameter for sparsity that will be used for sparse metaPCA.

5.7.2 Results

The input dataset is same as the input for MetaDE module. We used multi-study leukemia gene expression data as example. After performing merging of the three datasets and filter 50% genes by mean and 50% by variance, 1283 genes remained.

The result of metaPCA is shown in Figure 30. For each study, only first two studies are visualized. The results show nice separations between three groups. These figures and eigenvectors from metaPCA are saved.

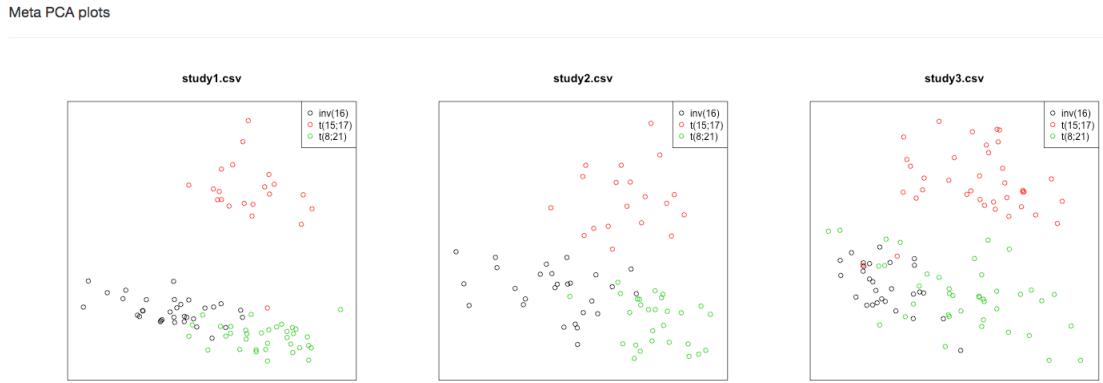


Figure 30: MetaPCA result

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