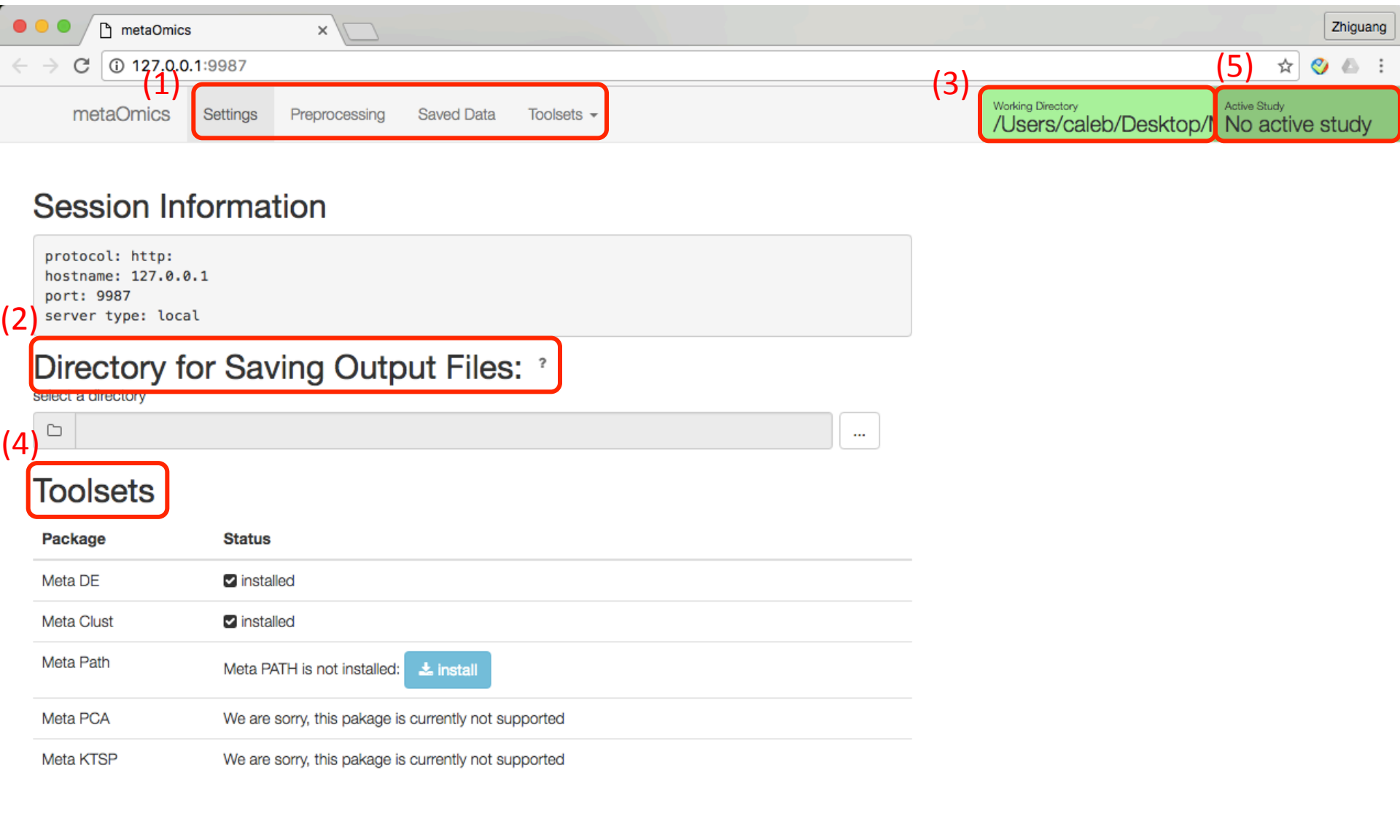
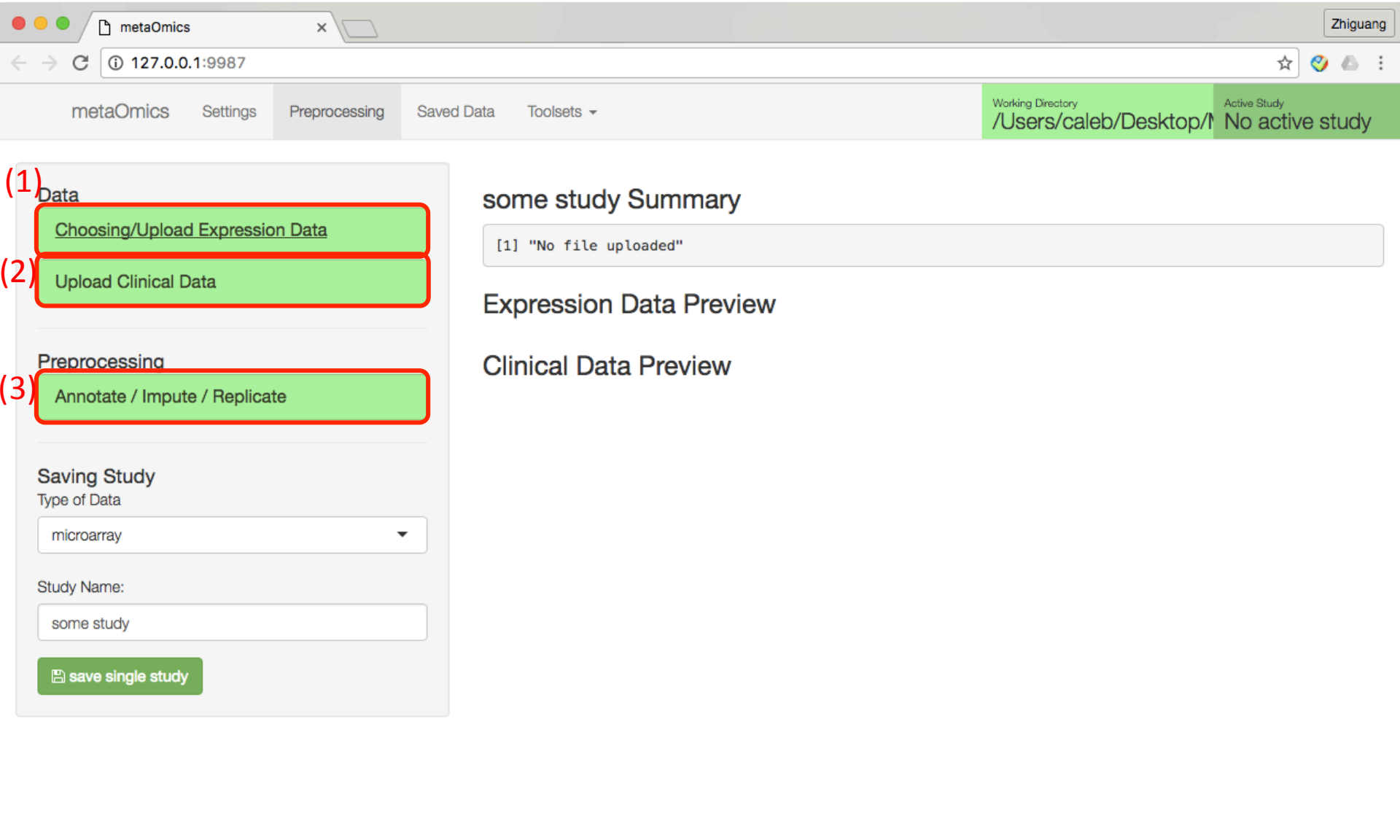

metaOmics
Zhiguang
127.0.0.1:9987
(1)
metaOmics
Settings
Preprocessing
Saved Data
Toolsets
(3)
Working Directory
/Users/caleb/Desktop/
(5)
Active Study
No active study
Session Information
protocol: http:
hostname: 127.0.0.1
port: 9987
server type: local
(2)
Directory for Saving Output Files:
Select a directory
...
(4)
Toolsets
Package
Status
Meta DE
installed
Meta Clust
installed
Meta Path
Meta PATH is not installed:
install
Meta PCA
We are sorry, this pakage is currently not supported
Meta KTSP
We are sorry, this pakage is currently not supported


metaOmics
Zhiguang
127.0.0.1:9987
metaOmics
Settings
Preprocessing
Saved Data
Toolsets
Working Directory
/Users/caleb/Desktop/M
Active Study
No active study
(1)
Data
Choosing/Upload Expression Data
(2)
Upload Clinical Data
Preprocessing
(3)
Annotate / Impute / Replicate
Saving Study
Type of Data
microarray
Study Name:
some study
save single study
some study Summary
[1] "No file uploaded"
Expression Data Preview
Clinical Data Preview

Data

## Choosing/Upload Expression Data

Choose CSV File

Choose File Balgobind_internal.csv

Upload complete

### Expression Data Parsing Option

Header

Separator

Comma Semicolon Tab

Quote for String

None Double Quote Single Quote

Log tranforming data

Yes No

Or use existing datasets

Choose from below

## Upload Clinical Data

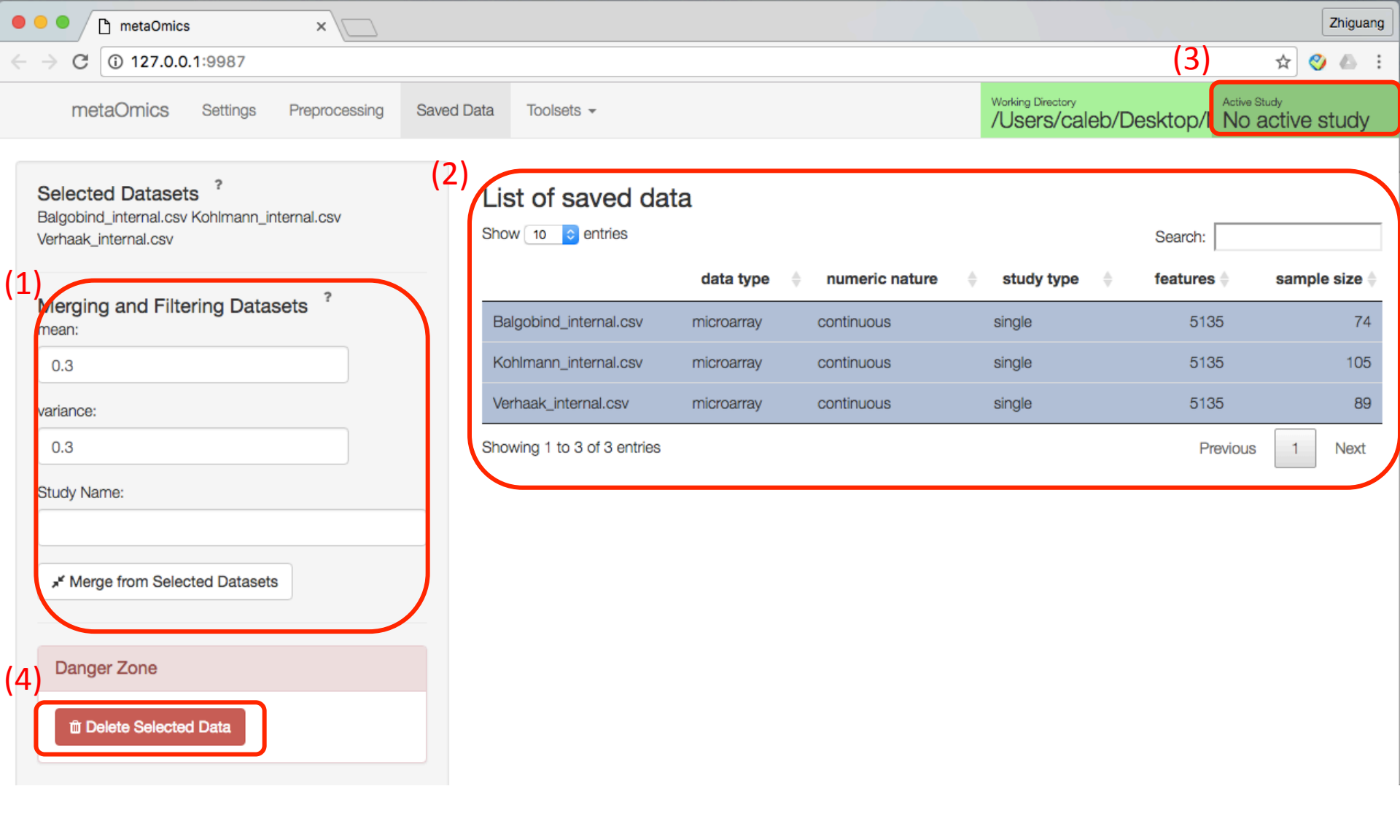
# Balgobind_internal.csv Summary

```
   GSM445939       GSM445940       GSM445952       GSM445965
Min.   :2.258   Min.   :2.157   Min.   :2.367   Min.   :2.110
1st Qu.:2.761   1st Qu.:2.669   1st Qu.:2.808   1st Qu.:2.842
Median :2.890   Median :2.783   Median :2.929   Median :2.962
Mean   :2.921   Mean   :2.807   Mean   :2.958   Mean   :2.992
3rd Qu.:3.049   3rd Qu.:2.920   3rd Qu.:3.080   3rd Qu.:3.109
Max.   :3.850   Max.   :3.860   Max.   :3.818   Max.   :3.826
   GSM445966       GSM445995       GSM446005       GSM446015
```

# Expression Data Preview

Show 10 entries Search:

| | GSM445939 | GSM445940 | GSM445952 | GSM445965 | GSM445966 | |
|---|---|---|---|---|---|---|
| COX1 | 3.82519383224611 | 3.85987497010207 | 3.78847583019565 | 3.82584574935784 | 3.88549249642589 | 3.842 |
| COX2 | 3.79227705926325 | 3.8263442278892 | 3.74925555068105 | 3.77237792982363 | 3.85044260996059 | 3.797 |
| ND4 | 3.79079518125679 | 3.85655395569921 | 3.76141721328021 | 3.79510977041338 | 3.8653203034628 | 3.818 |
| RPL41 | 3.85018737983642 | 3.74937209426887 | 3.81799123492144 | 3.81809615068597 | 3.83722742706631 | 3.806 |
| RPS2 | 3.82155577003902 | 3.74133396216782 | 3.78754841145626 | 3.78967665724583 | 3.79670302562472 | 3.778 |
| RPL23A | 3.805824265197 | 3.70683948384657 | 3.78740383496946 | 3.78295822557168 | 3.75561416064749 | 3.750 |
| TPT1 | 3.82797772961395 | 3.74940343986743 | 3.79632081017041 | 3.79829985958213 | 3.82778917271292 | 3.812 |
| RPL39 | 3.8210144805602 | 3.71178758656832 | 3.77534880813478 | 3.78886408642662 | 3.82482085619493 | 3.786 |


metaOmics
Zhiguang
127.0.0.1:9987
(3)
metaOmics
Settings
Preprocessing
Saved Data
Toolsets
Working Directory
/Users/caleb/Desktop/
Active Study
No active study
(2)
List of saved data
Show 10 entries
Search:
data type
numeric nature
study type
features
sample size
Balgobind_internal.csv microarray continuous single 5135 74
Kohlmann_internal.csv microarray continuous single 5135 105
Verhaak_internal.csv microarray continuous single 5135 89
Showing 1 to 3 of 3 entries
Previous
1
Next
Selected Datasets
Balgobind_internal.csv Kohlmann_internal.csv
Verhaak_internal.csv
(1)
Merging and Filtering Datasets
mean:
0.3
variance:
0.3
Study Name:
Merge from Selected Datasets
(4)
Danger Zone
Delete Selected Data

# MetaQC


metaOmics
Settings
Preprocessing
Saved Data
Toolsets
Working Directory
/Users/matianzhou/Doc
Active Study
merged_1234567
Download Csv File
(1)
Options
Perform gene filtering:
Yes
No
(2)
Use adjusted p-value for selecting DE genes
Yes
No
p-value cutoff for selecting DE genes
0.05
Use adjusted p-value for selecting pathways
Yes
No
p-value cutoff for selecting pathways
0.05
(3)
Advanced Options
(4)
Run MetaQC Analysis

Working Directory /Users/matianzhou/Doc  Active Study merged_1234567

(1)

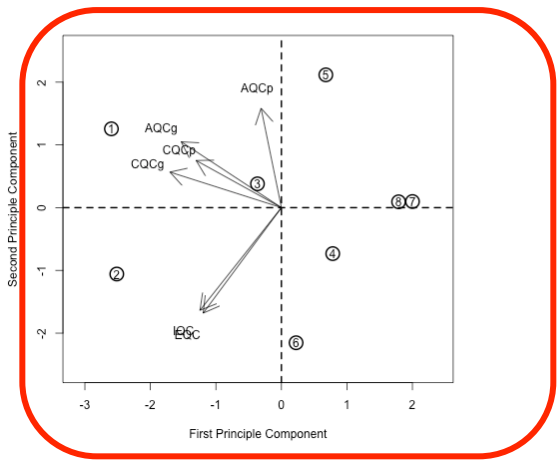
Show 10 entries  Search:

| | IQC | EQC | AQCg | AQCp | CQCg | CQCp | SMR |
|---|---|---|---|---|---|---|---|
| study1.csv | 4.62972117515165 | 4.42080140017298 | 28.7506408159351 | 19.6553215724074 | 168.178161321905 | 29.1728506116653 | 2 |
| study2.csv | 9.49476305430643 | 9.54232695746311 | 22.8328911582152 | 18.5608278598915 | 161.156270084427 | 5.90587620132403 | 2 |
| study3.csv | 3.54459359448249 | 3.53185328209592 | 23.7550333901066 | 12.5641055466726 | 90.629894007444 | 0 | 4.08333333333333 |
| study4.csv | 4.24828698811111 | 4.64040800688361 | 4.1114791659993 | 8.25400998207925 | 18.7230783709056 | 0 | 4.58333333333333 |
| study5.csv | 0.894687963415149 | 0.960893673815512 | 15.2051724608639 | 64.5423701027504 | 45.0875412933291 | 0 | 4.75 |
| study6.csv | 8.16660524920825 | 8.34978165196621 | 0.00323872133424415 | 5.62346862034754 | 0.0000724622147555651 | 0 | 5.08333333333333 |
| study7.csv | 0.813497306130717 | 0.48153373919226 | 0 | 0 | 0.389817980078202 | 0 | 7.41666666666667 |
| study8.csv | 0.936649618643111 | 1.27979174672063 | 0.739905960624053 | 4.14217226240963 | 8.02899021611631 | 0 | 6.08333333333333 |

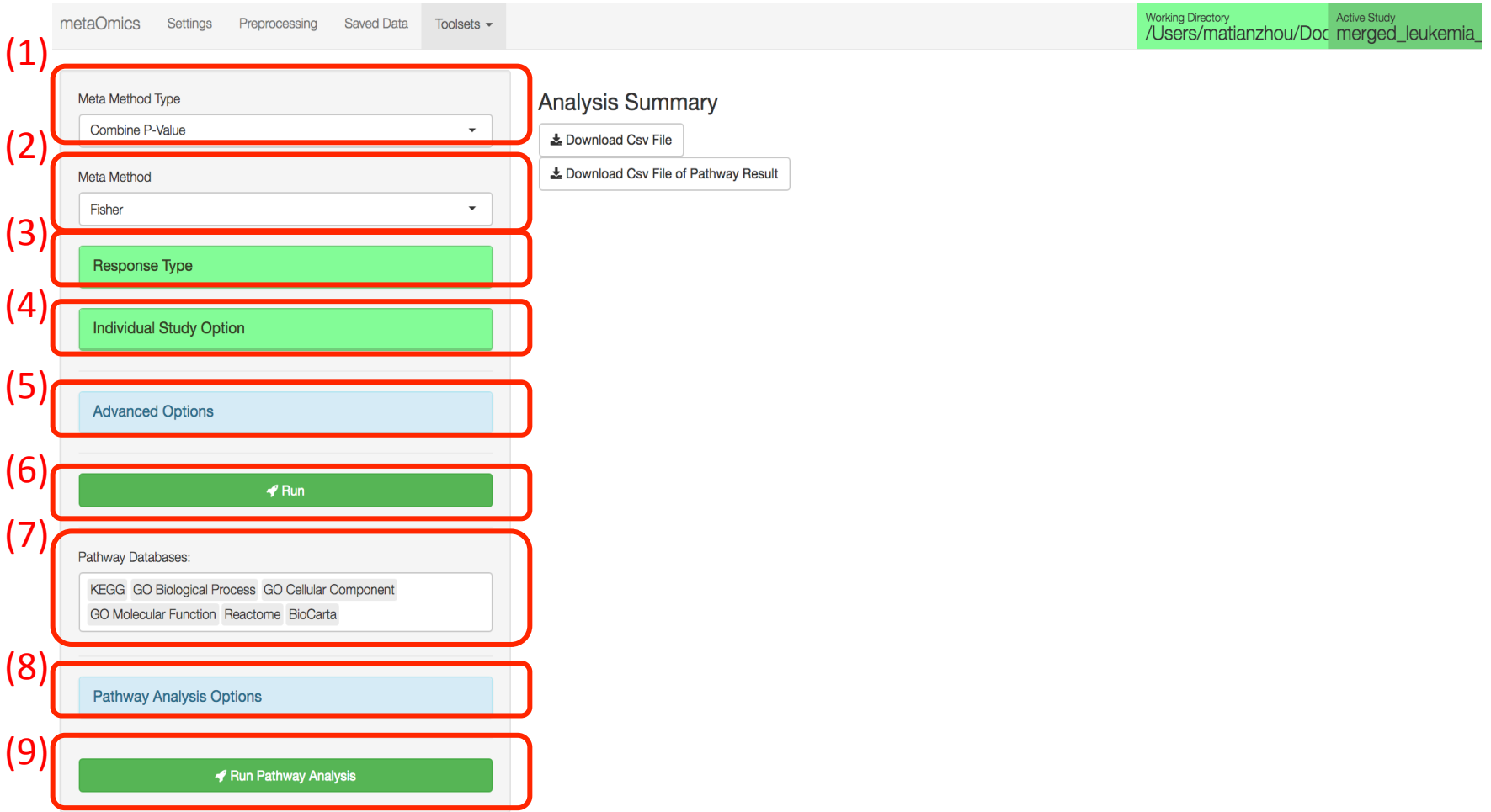
Showing 1 to 8 of 8 entries  Previous 1 Next

Download Csv File

(2)



# MetaDE


metaOmics
Settings
Preprocessing
Saved Data
Toolsets
Working Directory
/Users/matianzhou/Doc
Active Study
merged_leukemia_
(1)
Meta Method Type
Combine P-Value
(2)
Meta Method
Fisher
(3)
Response Type
(4)
Individual Study Option
(5)
Advanced Options
(6)
Run
(7)
Pathway Databases:
KEGG
GO Biological Process
GO Cellular Component
GO Molecular Function
Reactome
BioCarta
(8)
Pathway Analysis Options
(9)
Run Pathway Analysis
Analysis Summary
Download Csv File
Download Csv File of Pathway Result

FDR Cutoff

0.000000001

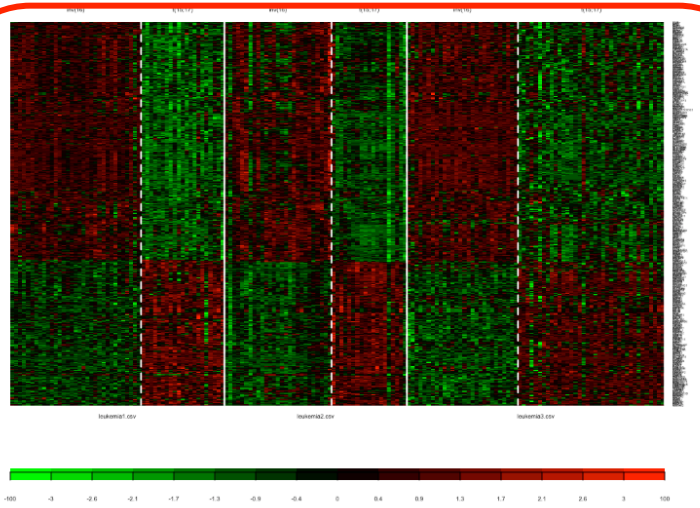
476 genes left after cut off

Image Size

0.5 1.2 1.9 2.6 3.3 4

Plot DE Genes Heatmap

(1)



Analysis Summary

Download Csv File

(2)

Show 10 entries

Search:

| | ind.stat.leukemia1.csv | ind.stat.leukemia2.csv | ind.stat.leukemia3.csv | ind.p.leukemia1.csv | ind.p.leukemia2.csv | ind.p.leukemia3.csv | stat |
|---|---|---|---|---|---|---|---|
| XIST | 1.75894517870996 | 1.57341698663743 | 0.0621319973857489 | 0.0465466256513682 | 0.0962121687544035 | 0.480139337084587 | 12.2843582663452 |
| RPS4Y1 | -1.43080240329004 | -1.37073434139571 | -0.0324220964001872 | 0.0749967751149047 | 0.0362759662985079 | 0.601813317409207 | 12.8294359860048 |
| VCAN | -5.36061923204762 | -3.92302844692982 | -0.452776646196597 | 2.31027467700219e-29 | 3.84677403324962e-14 | 7.34328056595729e-22 | 290.97928809875 |
| STAB1 | 2.65390600821645 | 4.10091167397856 | 0.230107822617278 | 6.64233621441893e-16 | 7.121387106178 84e-29 | 9.86047301212157e-20 | 287.045861276912 |
| AREG | -3.04807348087879 | -4.78541000735867 | -0.250165669520792 | 7.1482301506152e-10 | 1.03694874505757e-17 | 0.00000223014939911103 | 146.360184387848 |
| HLA-DRB4 | -2.33227273313853 | -0.735722949436647 | -0.392207119772102 | 0.000725219996012073 | 0.0546692216680428 | 2.50856662961504e-10 | 64.4832586265324 |
| S100A12 | -4.31591811888744 | -3.56116977637037 | -0.237606239566241 | 1.60546633800265e-21 | 1.75916492696931e-13 | 1.73394041388372e-9 | 194.845017987147 |
| CTSG | 4.0219313879697 | 2.8727325801306 | 0.266604868457814 | 6.54055486019511e-13 | 1.26271973633199e-13 | 1.17728497209957e-12 | 170.447465397976 |

(3)

Download Csv File of Pathway Result

Show 10 entries

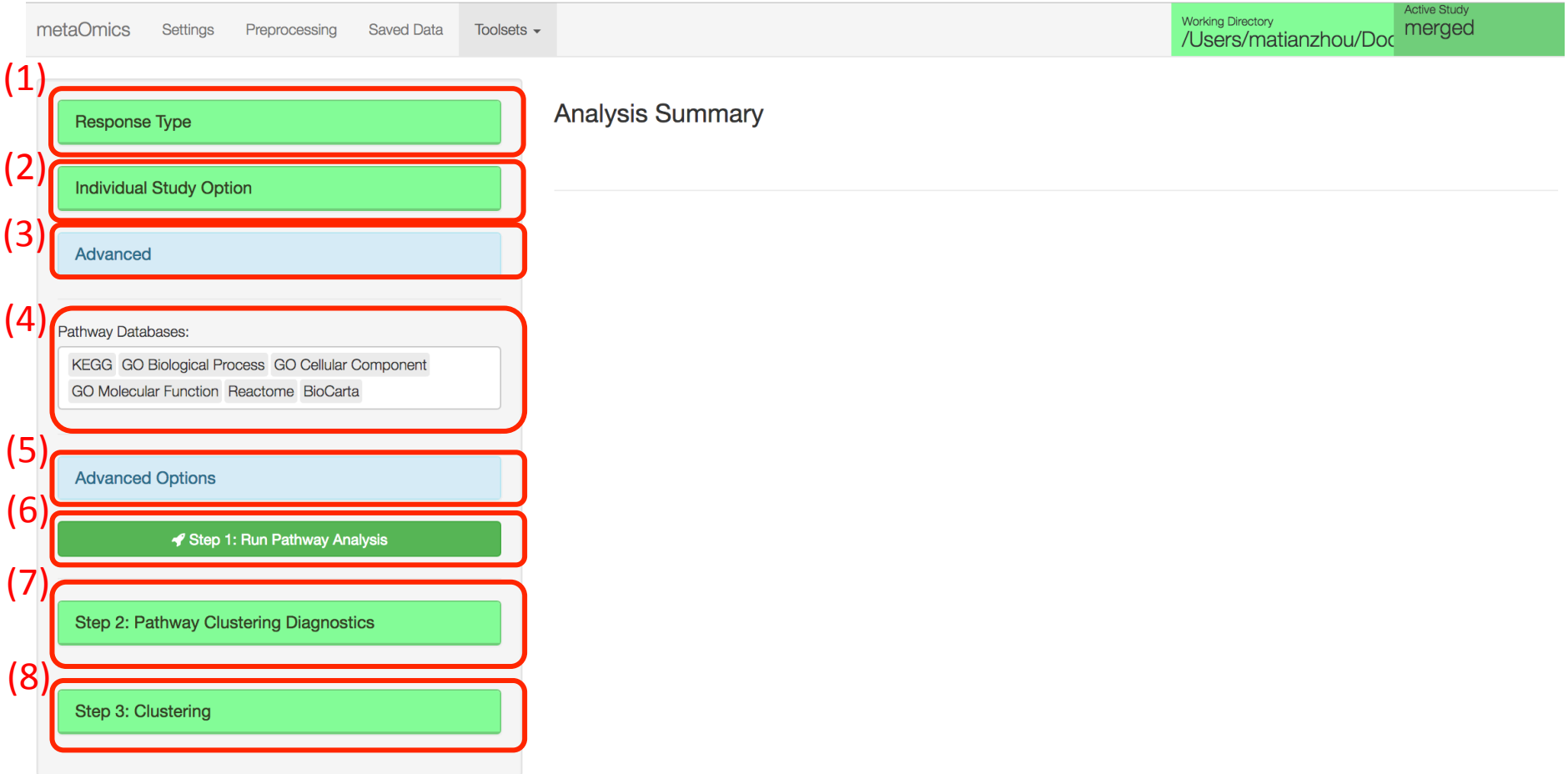
Search:

| | pvalue | qvalue |
|---|---|---|
| KEGG Glycolysis / Gluconeogenesis | 0.802757387123335 | 0.999995330023358 |
| KEGG Citrate cycle (TCA cycle) | 0.803334097527091 | 0.999995330023358 |
| KEGG Pentose phosphate pathway | 0.154769551640228 | 0.848505112559124 |
| KEGG Pentose and glucuronate interconversions | 0.416541246542213 | 0.999995330023358 |
| KEGG Fructose and mannose metabolism | 0.830677498437588 | 0.999995330023358 |
| KEGG Galactose metabolism | 0.0255936536718409 | 0.598893684244145 |
| KEGG Ascorbate and aldarate metabolism | 0.922240213199199 | 0.999995330023358 |
| KEGG Fatty acid metabolism | 0.80965895400645 | 0.999995330023358 |
| KEGG Steroid biosynthesis | 0.391621817077732 | 0.998221132687578 |
| KEGG Primary bile acid biosynthesis | 0.396360007151662 | 0.998221132687578 |

Showing 1 to 10 of 1,901 entries

Previous 1 2 3 4 5 … 191 Next

# MetaPath


metaOmics
Settings
Preprocessing
Saved Data
Toolsets
Working Directory
/Users/matianzhou/Doc
Active Study
merged
(1)
Response Type
(2)
Individual Study Option
(3)
Advanced
(4)
Pathway Databases:
KEGG
GO Biological Process
GO Cellular Component
GO Molecular Function
Reactome
BioCarta
(5)
Advanced Options
(6)
Step 1: Run Pathway Analysis
(7)
Step 2: Pathway Clustering Diagnostics
(8)
Step 3: Clustering
Analysis Summary

# Analysis Summary

Show 10 entries

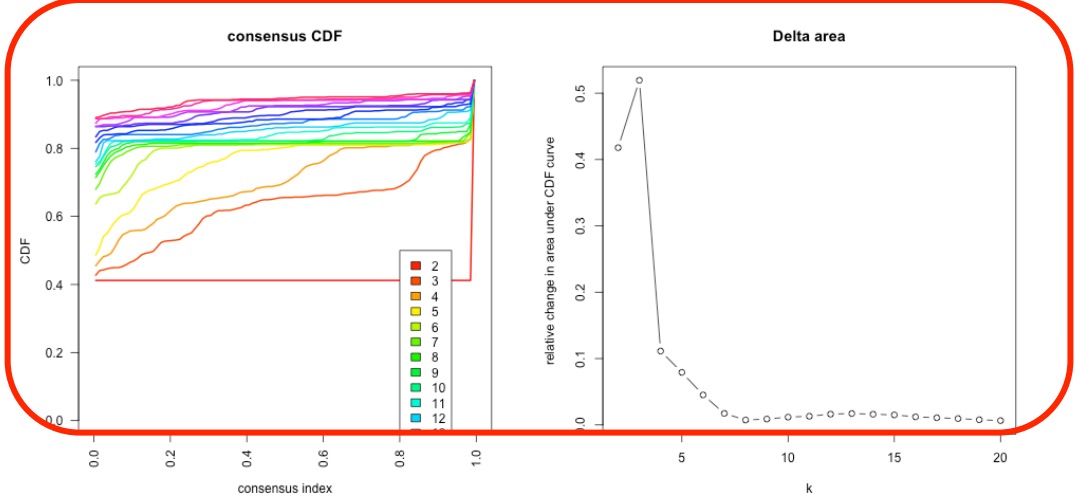
Search:

(1)

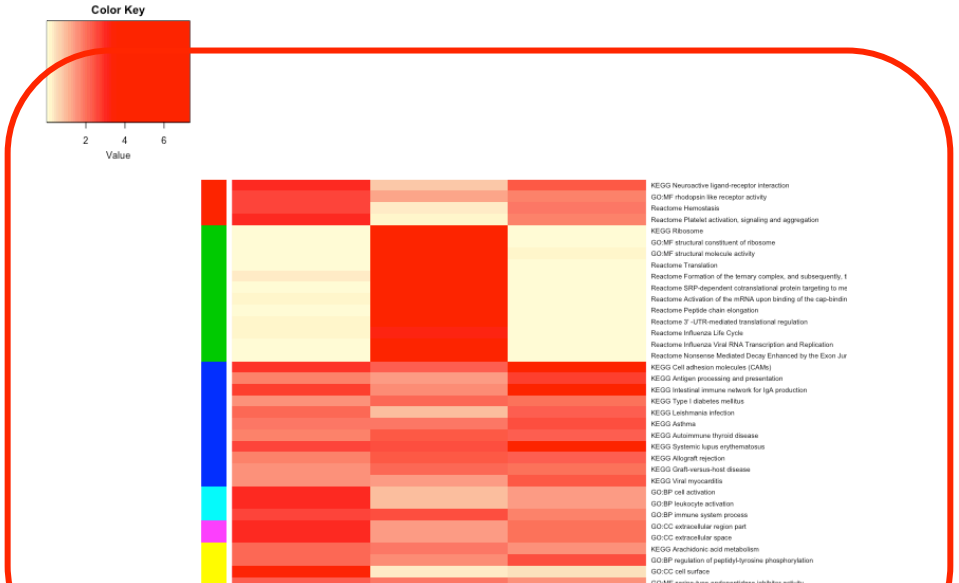
| | q_value_meta | p_value_meta | leukemia1.csv | leukemia2.csv | leukemia3.csv |
|---|---|---|---|---|---|
| KEGG Glycolysis / Gluconeogenesis | 0.999997344007533 | 0.742702273327691 | 0.365812198422891 | 0.630811182760298 | 0.83066172560152 |
| KEGG Citrate cycle (TCA cycle) | 0.999997344007533 | 0.287274297784932 | 0.102583720153995 | 0.968778328449648 | 0.84506657539453 |
| KEGG Pentose phosphate pathway | 0.999997344007533 | 0.255579356462519 | 0.112084202050741 | 0.848695951159788 | 0.158102461624005 |
| KEGG Pentose and glucuronate interconversions | 0.999997344007533 | 0.350457149547908 | 0.565391468440809 | 0.130584580056393 | 0.474391991314713 |
| KEGG Fructose and mannose metabolism | 0.999997344007533 | 0.816249181501483 | 0.969060893236398 | 0.433318456990639 | 0.497791781474735 |
| KEGG Galactose metabolism | 0.677819988918544 | 0.0479116594906807 | 0.033663660016924 | 0.552460821338628 | 0.0548424200492012 |
| KEGG Ascorbate and aldarate metabolism | 0.999997344007533 | 0.923957276303375 | 0.880497604349819 | 0.575390597923188 | 0.840021678292876 |
| KEGG Fatty acid metabolism | 0.999997344007533 | 0.800399377995137 | 0.528384935493589 | 0.809952362991652 | 0.417356029535636 |
| KEGG Steroid biosynthesis | 0.999997344007533 | 0.470352276256348 | 0.18949789554244 | 0.514711313510736 | 0.345766475371192 |
| KEGG Primary bile acid biosynthesis | 0.999997344007533 | 0.954579830451634 | 0.697154525601612 | 0.644375166133531 | 0.987501243892513 |

Showing 1 to 10 of 1,825 entries

(2)


consensus CDF
CDF
consensus index
2
3
4
5
6
7
8
9
10
11
12
Delta area
relative change in area under CDF curve
k

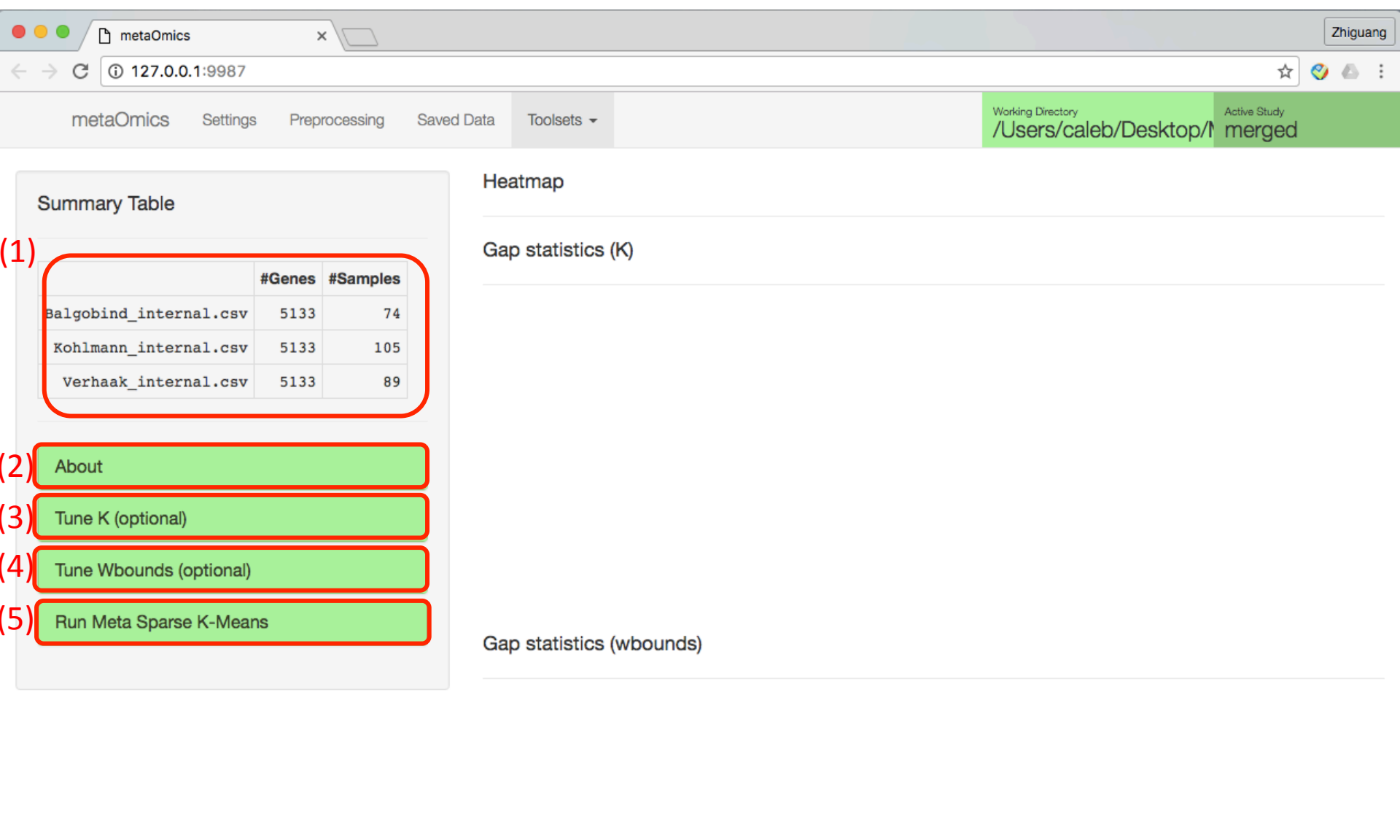
(3)


Color Key
Value
KEGG Neuroactive ligand-receptor interaction
GO:MF rhodopsin-like receptor activity
Reactome Hemostasis
Reactome Platelet activation, signaling and aggregation
KEGG Ribosome
GO:MF structural constituent of ribosome
GO:MF structural molecule activity
Reactome Translation
Reactome Formation of the ternary complex, and subsequently, t
Reactome SRP-dependent cotranslational protein targeting to me
Reactome Activation of the mRNA upon binding of the cap-bindin
Reactome Peptide chain elongation
Reactome 3'-UTR-mediated translational regulation
Reactome Influenza Life Cycle
Reactome Influenza Viral RNA Transcription and Replication
Reactome Nonsense Mediated Decay Enhanced by the Exon Jur
KEGG Cell adhesion molecules (CAMs)
KEGG Antigen processing and presentation
KEGG Intestinal immune network for IgA production
KEGG Type I diabetes mellitus
KEGG Leishmania infection
KEGG Asthma
KEGG Autoimmune thyroid disease
KEGG Systemic lupus erythematosus
KEGG Allograft rejection
KEGG Graft-versus-host disease
KEGG Viral myocarditis
GO:BP cell activation
GO:BP leukocyte activation
GO:BP immune system process
GO:CC extracellular region part
GO:CC extracellular space
KEGG Arachidonic acid metabolism
GO:BP regulation of peptidyl-tyrosine phosphorylation
GO:CC cell surface

(4)

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | ID | Term | NumGeneTotalInSet | Study_p-value | Study_p-value | Study_p-value | | | | | | | | | | |
| 2 | Cluster 1 | | | | | | | | | | | | | | | |
| 3 | Key words | activation | platelet activation | coupled recepto | g-protein | adenosine | adhesion | ADP | aggregation | agonist | cascade | cleavage | fibrinogen | platelet | thromboxan | vascular trauma |
| 4 | q_value | 0.0011988 | 0.001198801 | 0.001198801 | 0.001198801 | 0.001198801 | 0.0011988 | 0.0011988 | 0.0011988 | 0.0011988 | 0.0011988 | 0.0011988 | 0.0011988 | 0.0011988 | 0.0011988 | 0.0011988 |
| 5 | count | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 |
| 6 | KEGG Neuroactive ligand-receptor | | 272 | 0.000988699 | 0.165623281 | 0.004705548 | | | | | | | | | | |
| 7 | GO:MF rhodopsin like receptor act | | 135 | 0.002354604 | 0.057090475 | 0.016814203 | | | | | | | | | | |
| 8 | Reactome Hemostasis | | 466 | 0.002640089 | 0.455069786 | 0.013257929 | | | | | | | | | | |
| 9 | Reactome Platelet activation, signa | | 208 | 0.00099527 | 0.645386771 | 0.016801587 | | | | | | | | | | |
| 10 | | | | | | | | | | | | | | | | |
| 11 | Cluster 2 | | | | | | | | | | | | | | | |
| 12 | Key words | mRNA | RNA | initiation | polypeptide | subunit | template | structural int | translation ir | translation ir | nascent poly | peptide | elongation | ribosome | synthesis | occurs |
| 13 | q_value | 0.0011239 | 0.001123876 | 0.001123876 | 0.001123876 | 0.001123876 | 0.00112388 | 0.00112388 | 0.00112388 | 0.00112388 | 0.00112388 | 0.00112388 | 0.00112388 | 0.00112388 | 0.00112388 | 0.00112388 |
| 14 | count | 5 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 |
| 15 | KEGG Ribosome | | 88 | 0.921335968 | 1.22E-06 | 0.91118369 | | | | | | | | | | |
| 16 | GO:MF structural constituent of rib | | 80 | 0.912643351 | 4.79E-08 | 0.816680675 | | | | | | | | | | |
| 17 | GO:MF structural molecule activity | | 244 | 0.784928345 | 2.74E-05 | 0.623950541 | | | | | | | | | | |
| 18 | Reactome Translation | | 222 | 0.879174023 | 2.48E-05 | 0.808403848 | | | | | | | | | | |
| 19 | Reactome Formation of the ternar | | 74 | 0.486640239 | 2.32E-05 | 0.96709482 | | | | | | | | | | |
| 20 | Reactome SRP-dependent cotransl | | 179 | 0.852923945 | 1.57E-06 | 0.817211067 | | | | | | | | | | |
| 21 | Reactome Activation of the mRNA | | 84 | 0.634771363 | 0.000118894 | 0.955314989 | | | | | | | | | | |
| 22 | Reactome Peptide chain elongatio | | 153 | 0.867879263 | 7.76E-08 | 0.922028213 | | | | | | | | | | |
| 23 | Reactome 3' -UTR-mediated transl | | 176 | 0.713811611 | 1.86E-07 | 0.958396231 | | | | | | | | | | |
| 24 | Reactome Influenza Life Cycle | | 203 | 0.725052637 | 0.000509546 | 0.97961918 | | | | | | | | | | |
| 25 | Reactome Influenza Viral RNA Tran | | 169 | 0.831490623 | 8.03E-07 | 0.877061392 | | | | | | | | | | |
| 26 | Reactome Nonsense Mediated Dec | | 176 | 0.849690552 | 5.83E-08 | 0.900043304 | | | | | | | | | | |
| 27 | | | | | | | | | | | | | | | | |

# MetaClust


metaOmics
Zhiguang
127.0.0.1:9987
metaOmics
Settings
Preprocessing
Saved Data
Toolsets
Working Directory
/Users/caleb/Desktop/M
Active Study
merged
Summary Table
(1)
#Genes
#Samples
Balgobind_internal.csv
5133
74
Kohlmann_internal.csv
5133
105
Verhaak_internal.csv
5133
89
(2)
About
(3)
Tune K (optional)
(4)
Tune Wbounds (optional)
(5)
Run Meta Sparse K-Means
Heatmap
Gap statistics (K)
Gap statistics (wbounds)

| | #Genes | #Samples |
|---|---|---|
| Balgobind_internal.csv | 5133 | 74 |
| Kohlmann_internal.csv | 5133 | 105 |
| Verhaak_internal.csv | 5133 | 89 |

About

Tune K (optional)

This panel is for tuning number of clusters K

(1) Maximum of K: 5

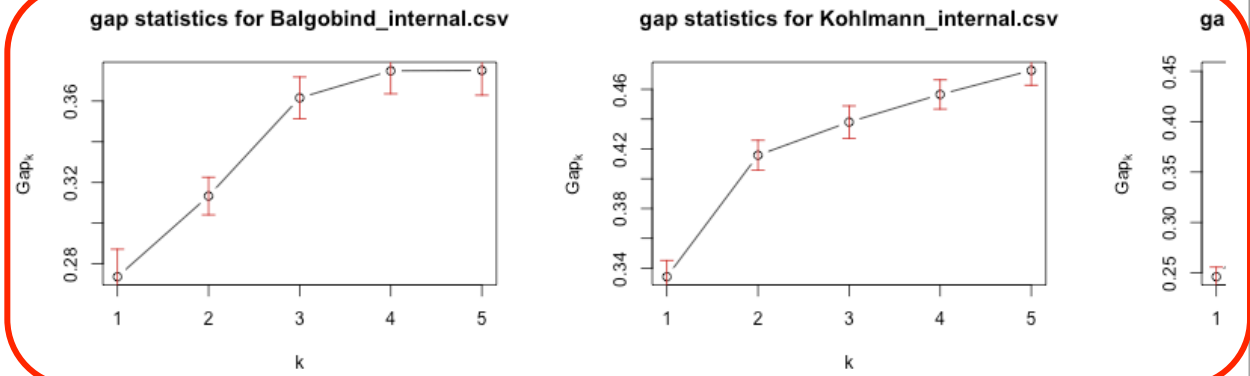
(2) Top percentage by larger variance: 0.1

(3) Number of permutations: 10

(4) Select studies to be tuned: Balgobind_internal.csv, Kohlmann_internal.csv, Verhaak_internal.csv

## Gap statistics (K)

(5)




## Gap statistics (wbounds)

## Tune Wbounds (optional)

This panel is for tuning Wbounds

(1) Number of clusters for tuning wbounds: 3

(2) Iterations: 2

(3) Minimum of wbounds: 2 | Maximum of wbounds: 16 | Step of wbounds: 2

(4) Tune wbounds

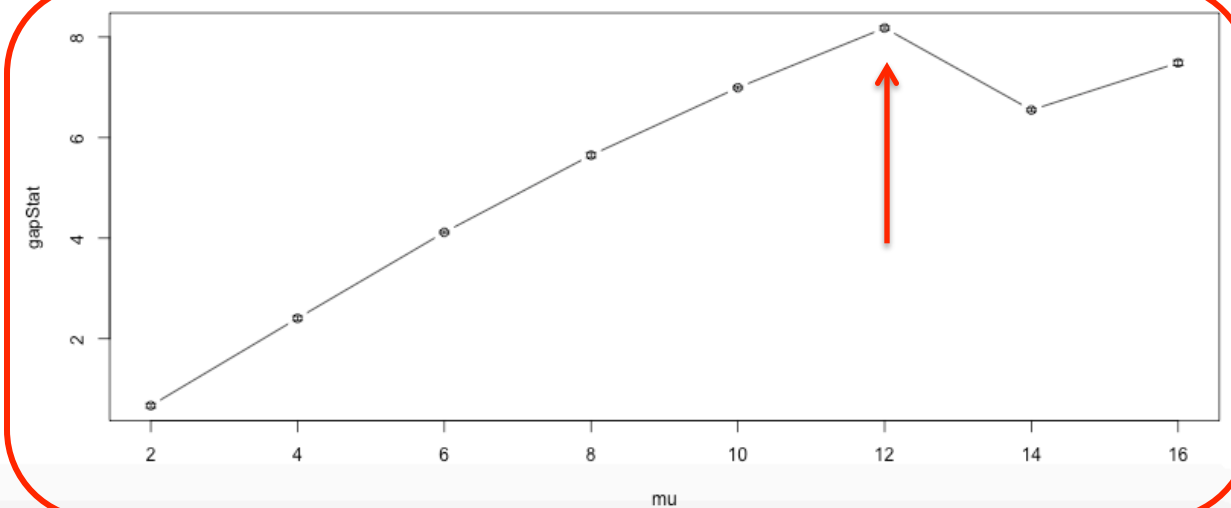
## Run Meta Sparse K-Means

1 2 3 4 5 1 2 3 4 5 1

k k

## Gap statistics (wbounds)

(5)



| | | |
|---|---|---|
| Balgobind_internal.csv | 5133 | 74 |
| Kohlmann_internal.csv | 5133 | 105 |
| Verhaak_internal.csv | 5133 | 89 |

About

Tune K (optional)

Tune Wbounds (optional)

Run Meta Sparse K-Means

This panel is for running meta sparse K means. Not optional (obviously)

(1) Number of clusters: 3

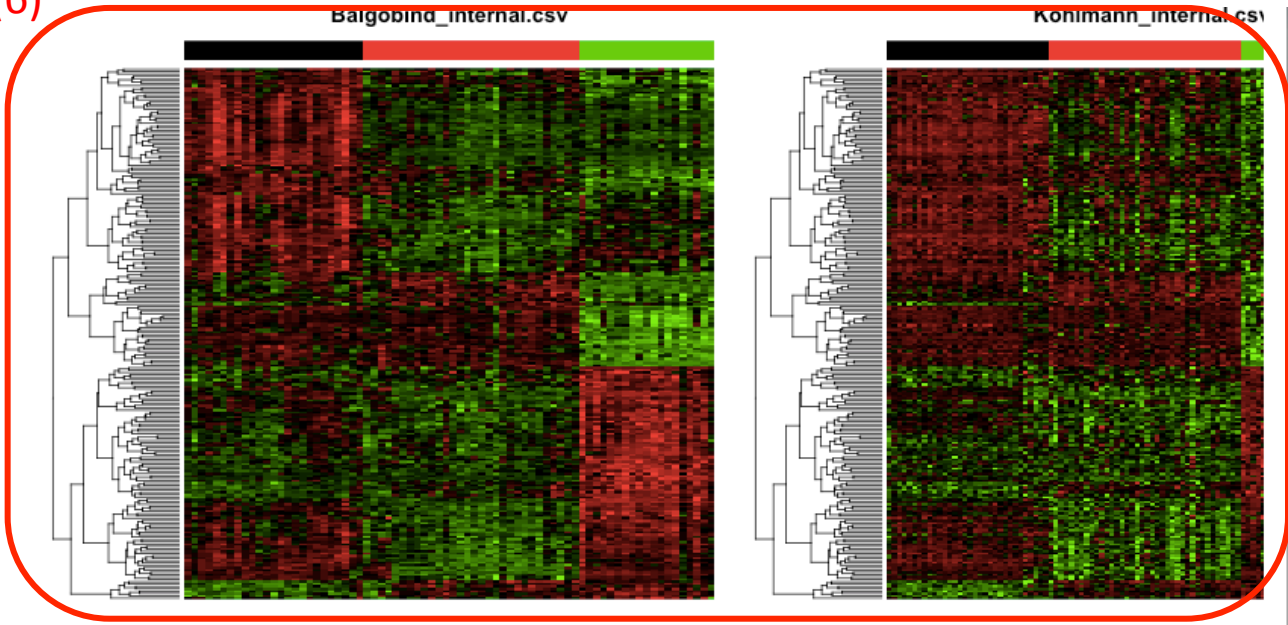
(2) Wbounds: 12

(3) Methods for meta sparse K means: Exhaustive

(4) Adjust sample size

(5) Run meta sparse K means

(6)




Gap statistics (K)