

preprocessing

metaOmics tutorial figures

metaOmics

127.0.0.1:9987

metaOmics Settings Preprocessing Saved Data Toolsets

Working Directory /Users/caleb/Desktop/

Active Study No active study

Session Information

protocol: http:
hostname: 127.0.0.1
port: 9987
server type: local

Directory for Saving Output Files: ?

Select a directory

Toolsets

Package	Status
Meta DE	<input checked="" type="checkbox"/> installed
Meta Clust	<input checked="" type="checkbox"/> installed
Meta Path	Meta PATH is not installed: install
Meta PCA	We are sorry, this package is currently not supported
Meta KTSP	We are sorry, this package is currently not supported

(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

Preprocessing

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	3.788
ND2	3.56125898755002	3.82034719791393	3.62373629251127	3.73730911305576	3.81997541825845	3.798

metaOmics

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metaOmicsSettingsPreprocessingSaved DataToolsets

Working Directory
/Users/caleb/Desktop/

Active Study
No active study

Selected Datasets ?
Balgobind_internal.csv Kohlmann_internal.csv
Verhaak_internal.csv

(1) Merging and Filtering Datasets ?
mean:

variance:

Study Name:

(4) Danger Zone

(2) List of saved data

Show 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

PreviousNext

MetaQC

[Download Csv File](#)

Options

Perform gene filtering:

☐ Yes ☒ No

Use adjusted p-value for selecting DE genes

☒ Yes ☐ No

p-value cutoff for selecting DE genes

Use adjusted p-value for selecting pathways

☒ Yes ☐ No

p-value cutoff for selecting pathways

Advanced Options

[Run MetaQC Analysis](#)

Show 10 entries

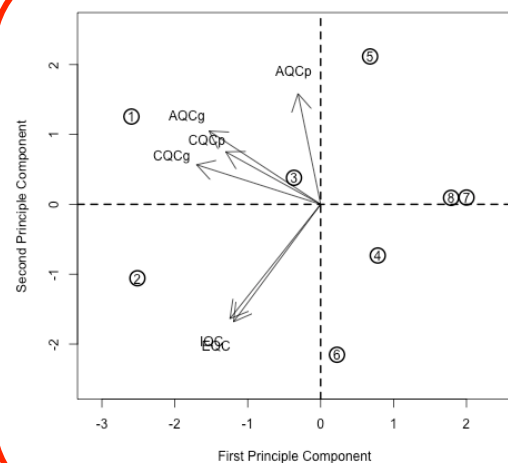
Search:

	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



(1)

(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

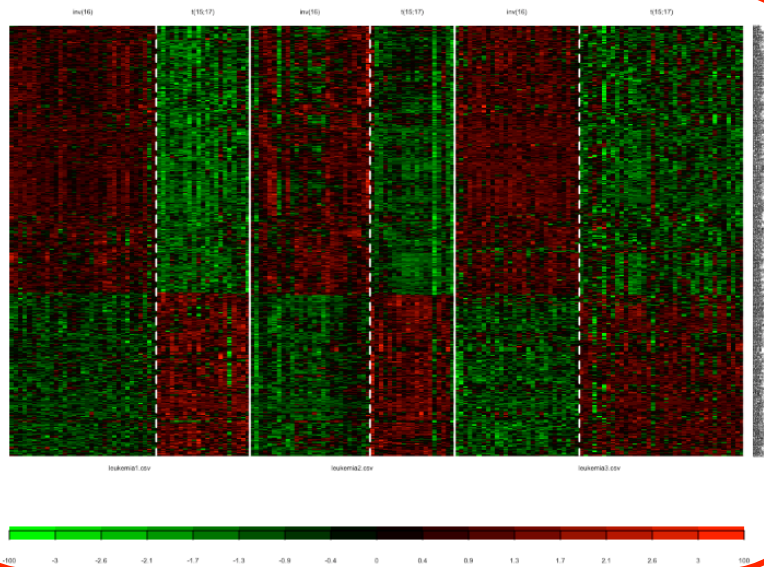
476 genes left after cut off

Image Size

0.5 1.2 1.9 2.6 3.3 4

Plot DE Genes Heatmap

(1)



Analysis Summary

Download Csv File

Show entriesSearch:

(2)



	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	7.12138710617884e-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-12	1.17728497209957e-12	170.447465397976

 Download Csv File of Pathway Result

Show entries

Search:

(3)

	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 2 3 4 5 ... 191 Next

MetaPath

Analysis Summary

(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

Show 10 entries

Search:

	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

Previous

1

2

3

4

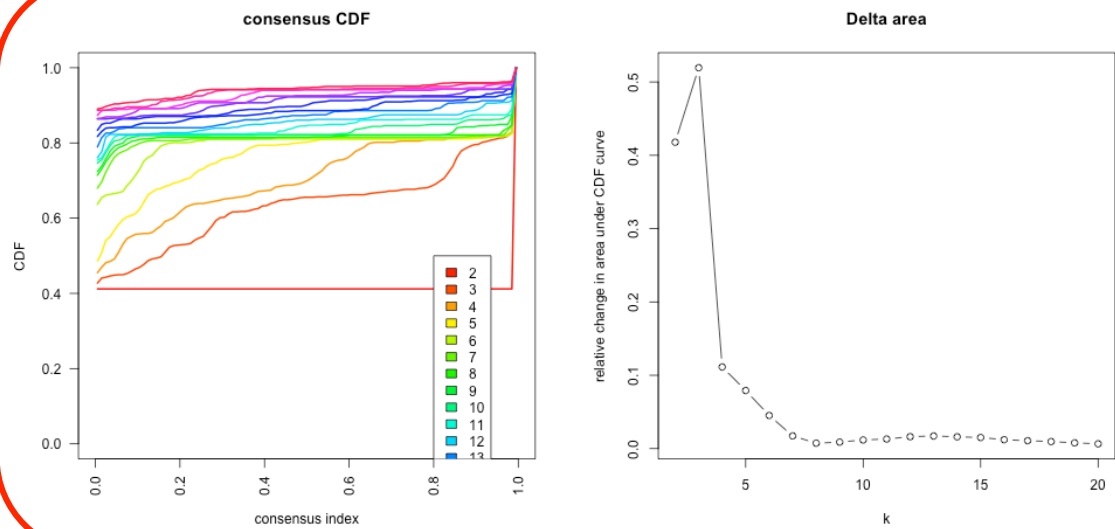
5

...

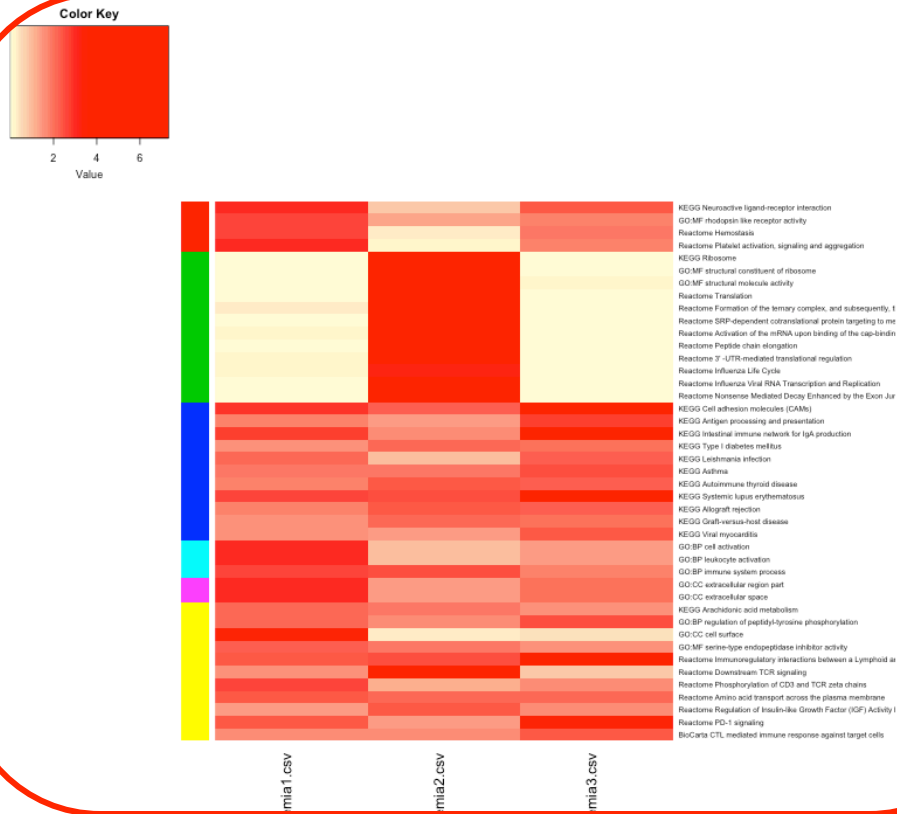
183

Next

(2)



(3)



(4)

[illegible]

MetaClust

Summary Table

	#Genes	#Samples
balgobind_internal.csv	5133	74
Kohlmann_internal.csv	5133	105
Verhaak_internal.csv	5133	89

Heatmap

Gap statistics (K)

Gap statistics (wbounds)

About

Tune K (optional)

Tune Wbounds (optional)

Run Meta Sparse K-Means

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	#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

Tune K

Gap statistics (K)

(5)

gap statistics for Balgobind_internal.csv

gap statistics for Kohlmann_internal.csv

ga

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

Maximum of K:

5

Top percentage by larger variance:

0.1

Number of permutations

10

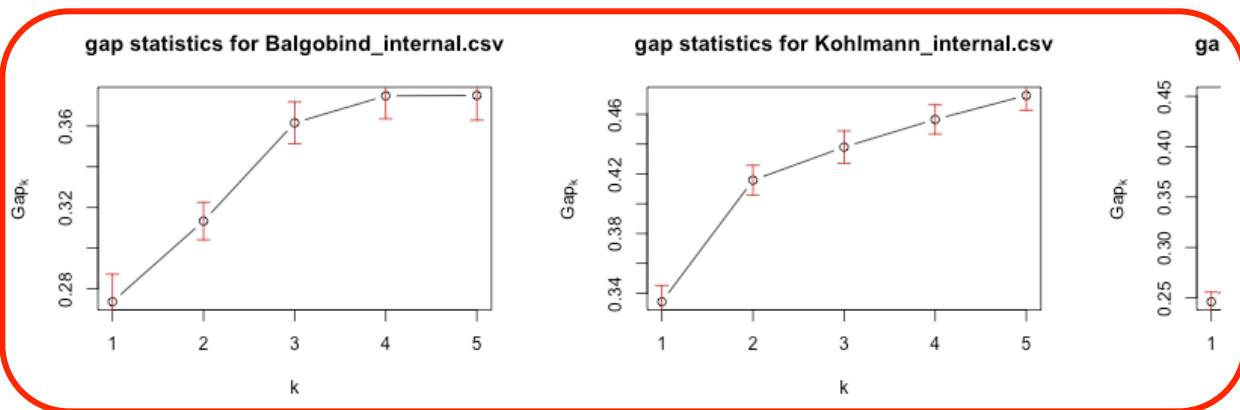
Select studies to be tuned

Balgobind_internal.csv Kohlmann_internal.csv
Verhaak_internal.csv

Tune K

Gap statistics (K)

(5)



Gap statistics (wbounds)

Tune Wbounds (optional)

This panel is for tuning Wbounds

Number of clusters for tuning wbounds

3

Iterations:

2

Minimum of
wbounds:


2

Maximum of
wbounds:

16

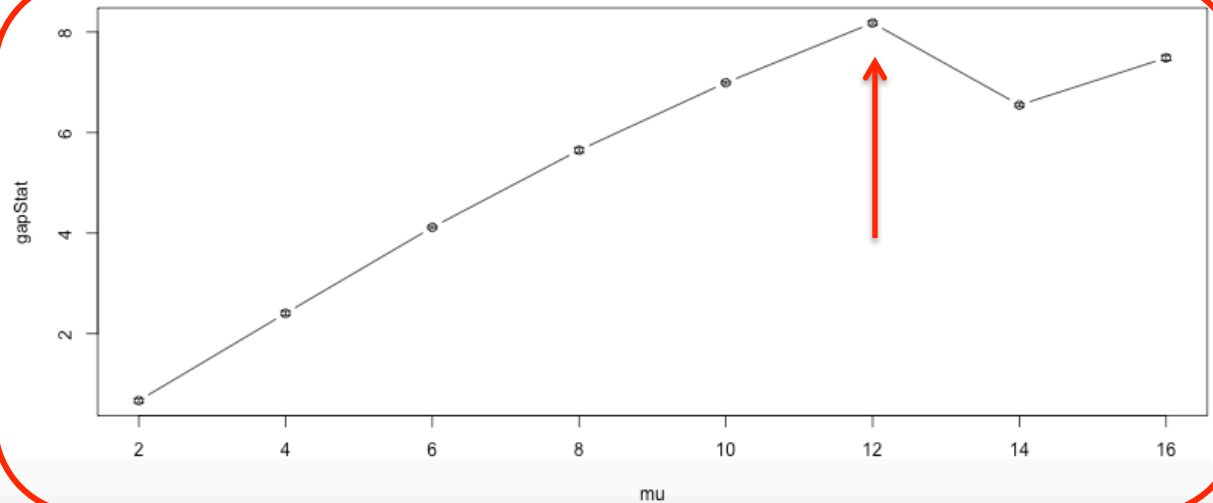
Step of
wbounds:

2

 Tune wbounds

Run Meta Sparse K-Means

Gap statistics (wbounds)



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)

Number of clusters:

3

Wbounds:

12

Methods for meta sparse K means

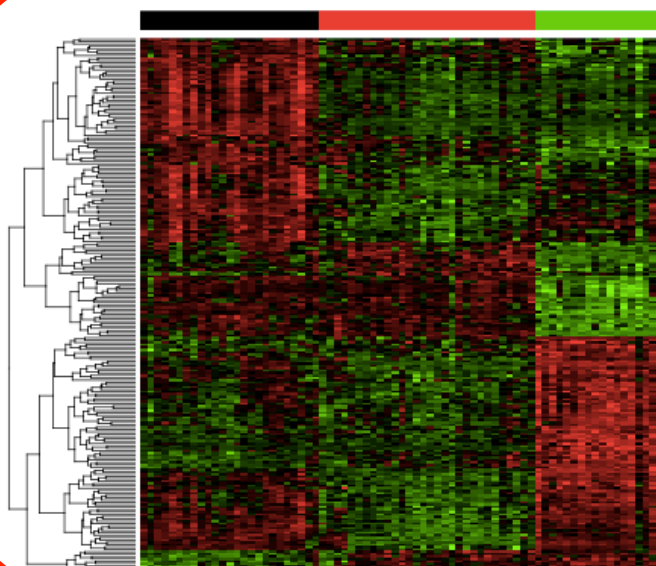
Exhaustive

☐ Adjust sample size

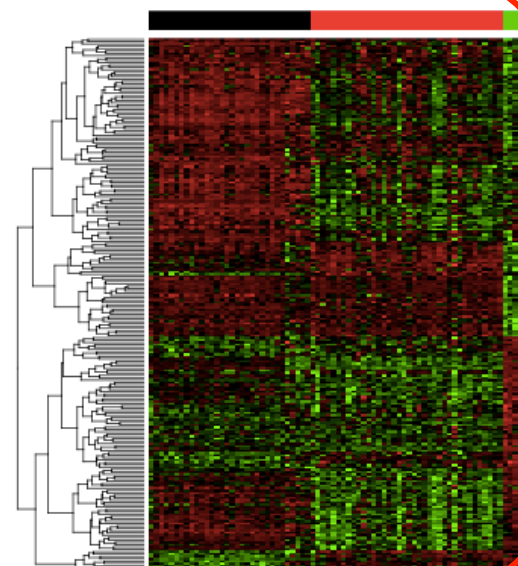
 Run meta sparse K means

(6)

Balgobind_internal.csv

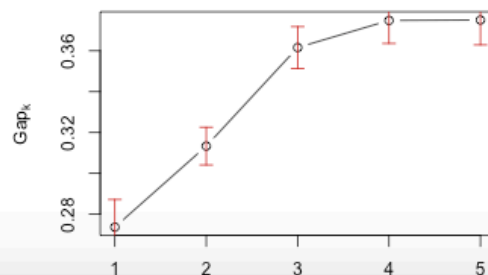


Kohlmann_internal.csv

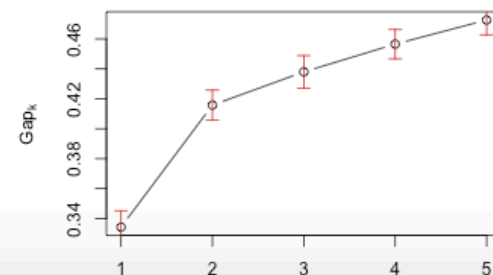


Gap statistics (K)

gap statistics for Balgobind_internal.csv



gap statistics for Kohlmann_internal.csv



ga

