

MetCleaning v0.99.0

Xiaotao Shen(shenxt@sioc.ac.cn) and Zhengjiang Zhu

2016-12-29

Introduction

MetCleaning provides an integrated and automatic pipeline for data cleaning and statistical analysis of large scale mass spectrometry (MS) based-metabolomic data. It includes missing value (MV) filtering and imputation, zero value filtering, data normalization, data integration, data quality assessment, univariate statistical analysis, multivariate statistical analysis such as PCA and PLS-DA, potential marker selection and show. This document describes how to use the integrated functions, *MetClean* and *MetStat* in *MetCleaning* utilizing demo data.

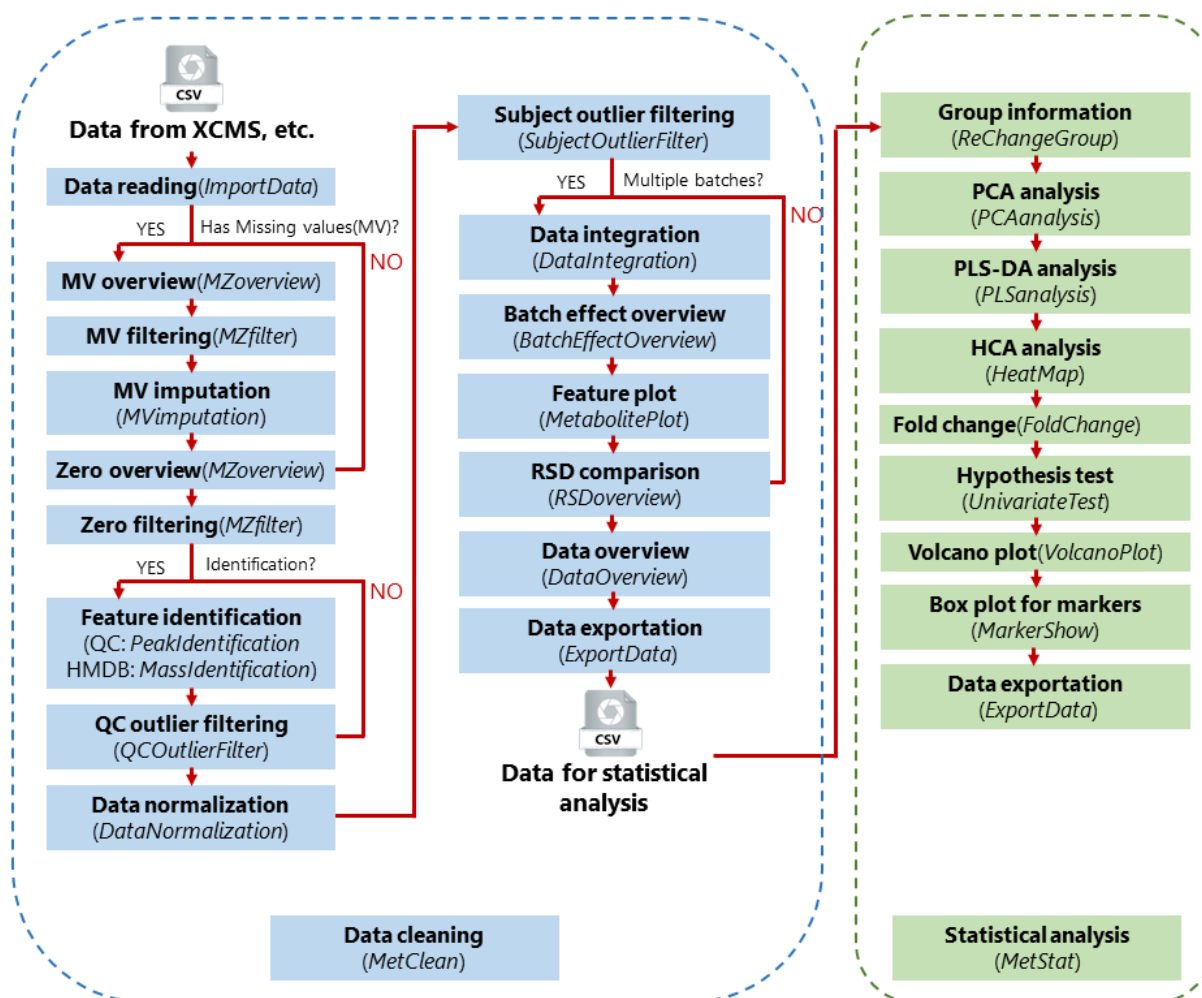


Figure 1: Figure1 Workflow of *MetCleaning*

Installation and help

MetCleaning is published in github (link). So you can install it via to github.

code 1: Installation of *MetCleaning*

```
##pcaMethods and impute should be installed form bioconductor
##pcaMethods
source("http://bioconductor.org/biocLite.R")
  biocLite("pcaMethods")
##impute
source("http://bioconductor.org/biocLite.R")
  biocLite("impute")
if(!require(devtools)) {
  install.packages("devtools")
}
library(devtools)
install_github("jaspershen/MetCleaning")
library(MetCleaning)
help(package = "MetCleaning")
```

Data cleaning

Data cleaning is integrated as a function named as *MetClean* in *MetCleaning*. We use the demo data as the example. Copy the code below and paste in you R console.

code 2: Demo data of *MetClean*

```
##demo data
data(data, package = "MetCleaning")
data(sample.information, package = "MetCleaning")
##demo work directory
dir.create("Demo for MetCleaning")
setwd("Demo for MetCleaning")
##write files
write.csv(data, "data.csv", row.names = FALSE)
write.csv(sample.information , "sample.information.csv", row.names = FALSE)
```

The demo data have been added in your work directory and organized in your work directory as Figure 2 shows. It contains two files, “data.csv” and “sample.information.csv”.

1. “data.csv” is the metabolomic dataset you want to process. Rows are features and columns are feature abundance of samples and information of features. The information of features must contain “name” (feature name), “mz” (mass to charge ratio) and “rt” (retention time). Other information of features are optional, for example “isotopes” and “adducts”. The name of sample can contain “-”, but cannot contain “-” and space. And the start of sample name cannot be number. For example, “A210.a” and “A210a” are valid, and “210a” or “210-a” are invalid.

2. “sample.information.csv” is sample information for metabolomic dataset. Column 1 is “sample.name” which is the names of subject and QC samples. Please confirm that the sample names in “sample.information.csv” and “data.csv” are completely same. Column 2 is “injection.order” which is the injection order of QC and subject samples. Column 3 is “class”, which is used to distinguish “QC” and “Subject” samples. Column 4 is “batch” to provide acquisition batch information for samples. Column 5 is “group”, which is used to label the group of subject sample, for example, “control” and “case”. The “group” of QC samples is labeled as “QC”.

Then you can run *MetClean* function to do data cleaning of data. All the arguments of *MetClean* can be found in the other functions in *MetCleaning*. You can use *help(package = “MetCleaning”)* to see the help page of *MetCleaning*.

code 3: Running of *MetClean*

```
##demo data
MetClean(polarity = "positive")
```

Running results of *MetClean*

1.Missing or zero values filtering. In the missing or zero value filtering step, if there are samples which beyond the threshold you set, you should decide to filter them or not. We recommend to remove all of them as Figure 3 shows.

2.Sample filtering. In the QC or subject sample filtering step (based on PCA), if there are samples which beyond the threshold you set, you should decide to filter them or not. We don’t recommend to remove them as Figure 4 shows, because they should be considered combined other information.


3.Output files. Output files of *MetClean* are listed as Figure 5 shows.


(1) “1MV overview”, “2MV filter”, “3Zero overview” and “4Zero filter” are missing and zero values filtering information.

(2) “5QC outlier filter” and “6Subject outlier filter” are sample filtering based on PCA information.

(3) “7Normalization result” is the data normalization information for each batch.

Feature name		m/z	rt	Other information of features		QC and subject sample abundance			
	A	B	C	D	E	F	G	H	
1	name	mz	rt	isotopes	QC22	QC23	QC12	QC24	
2	M72T49	72.080982	49.212	[1][M]+	1812140	1544984	1794878	1659980	
3	M76T31	76.075904	30.995	[2][M]+	516119.9	516731.3	545147.1	378761.9	
4	M84T38	84.081043	37.514	[3][M]+	2062165	1926203	1821621	1691399	
5	M86T74	86.096638	73.766	[4][M]+	3450548	3086142	3430762	3144320	
6	M86T90	86.096646	89.873	[5][M]+	2390322	2160545	2448855	1921855	
7	M100T149	100.07584	149.427	[6][M]+	4369935	3627019	4198031	3978860	
8	M103T150	103.05438	149.991	[7][M]+	191304.8	154571.8	176281.5	171652.6	
9	M104T30	104.10736	29.5285	[8][M]+	10220169	9599432	10928312	8911149	
10	M110T652	110.02015	652.103	[9][M]2+	642884.8	564758.9	799711.5	528291.8	
11	M114T32	114.06639	32.413	[10][M]+	1369850	1362086	1795623	1643309	
12	M118T36	118.08637	36.0715	[11][M]+	12726533	13111893	12571014	12803860	
13	M119T379	119.08572	378.5005	[12][M]+	94376	78369.41	114665.7	86013.00	
14	M120T150	120.08085	149.995	[13][M]+	4001522	3321928	3837926	3555599	
15	M122T160	122.09645	159.657	[14][M]+	232127.1	204514.5	238401.2	2144170	
16	M126T165	126.0915	164.642	[15][M]+	296192.1	226613.8	281846.4	256782.6	
17	M130T64	130.05002	63.6625	[16][M]+	513595.2	378566.3	398876.5	503552.9	
18	M130T157	130.06516	157.058	[17][M]+	239890.3	186114.1	252431.1	213720.7	
19	M130T38	130.08644	38.384	[18][M]+	336137	506422.3	367187.6	368729.7	

 data.csv

 sample.information.csv

Sample name		Injection order	Sample class	Sample batch	Sample group
	A	B	C	D	E
1	sample.name	injection.order	class	batch	group
2	QC11		1 QC		1 QC
3	A5551		2 Subject		1
4	A4880		3 Subject		1
5	C1282		4 Subject		0
6	C1492		5 Subject		9
7	A5730		6 Subject		1
8	X1421		7 Subject		0
9	X2		8 Subject		0
10	C1059		9 Subject		1
11	QC12		10 QC		1 QC
12	C1397		11 Subject		0
13	A5819		12 Subject		1
14	C1137		13 Subject		0
15	A3867		14 Subject		1
16	C1223		15 Subject		0
17	C1295		16 Subject		0
18	C1510		17 Subject		0
19	C1121		18 Subject		0

Figure 2: Figure2 Data organisation of MetCleaning

Missing values filter...
 No QC should be removed.
 x257 A5546 x231 sholud be removed!!!
 Subject shoulde be removed are:
 65 160 177
 which subject you want to remove(please type the index of subject sample,65,160,177|
 and separate them using comma,
 if you don't want to remove any subject, please type n):

Figure 3: Figure3 Missing or zero value filtering

```

Subject outlier filtering...
x2 x217 c1126 c1283 c1242 x1 x214 are outliers!!!
c1238 c1248 x5121 x209 x208 x211 x218 are outliers!!!
Batch 1
-----
Subject should be removed are:7 40 54 63 90 130 198
which subject you want to remove(please type the index of subject sample,n|
and separate them using comma,
if you don't want to remove any subject, please type n):

```

Figure 4: Figure4 Sample filtering

- (4) “8Batch effect” is the batch effect both in before and after data cleaning.
- (5) “9metabolite plot” is the scatter plot for each feature.
- (6) “10Data overview” is the overview of data.
- (7) “11RSD overview” is the RSD distribution for each batch both before and after data cleaning.
- (8) “data_after_pre.csv”, “qc.info.csv” and “subject.info” are the data and sample information after data cleaning.
- (9) “intermediate” is the intermediate data during processing.

Statistical analysis

Data statistical analysis is integrated as a function named as *MetStat* in *MetCleaning*. We use the demo data as the example. Please note that now *MetStat* can only process two class data. Copy the code below and paste in you R console.

code 4: Demo data of *MetStat*

```

data("met.data.after.pre", package = "MetCleaning")
data(new.group, package = "MetCleaning")
##create a folder for MetStat demo
dir.create("Demo for MetStat")
setwd("Demo for MetStat")
## export the demo data as csv
write.csv(new.group, "new.group.csv", row.names = FALSE)

```

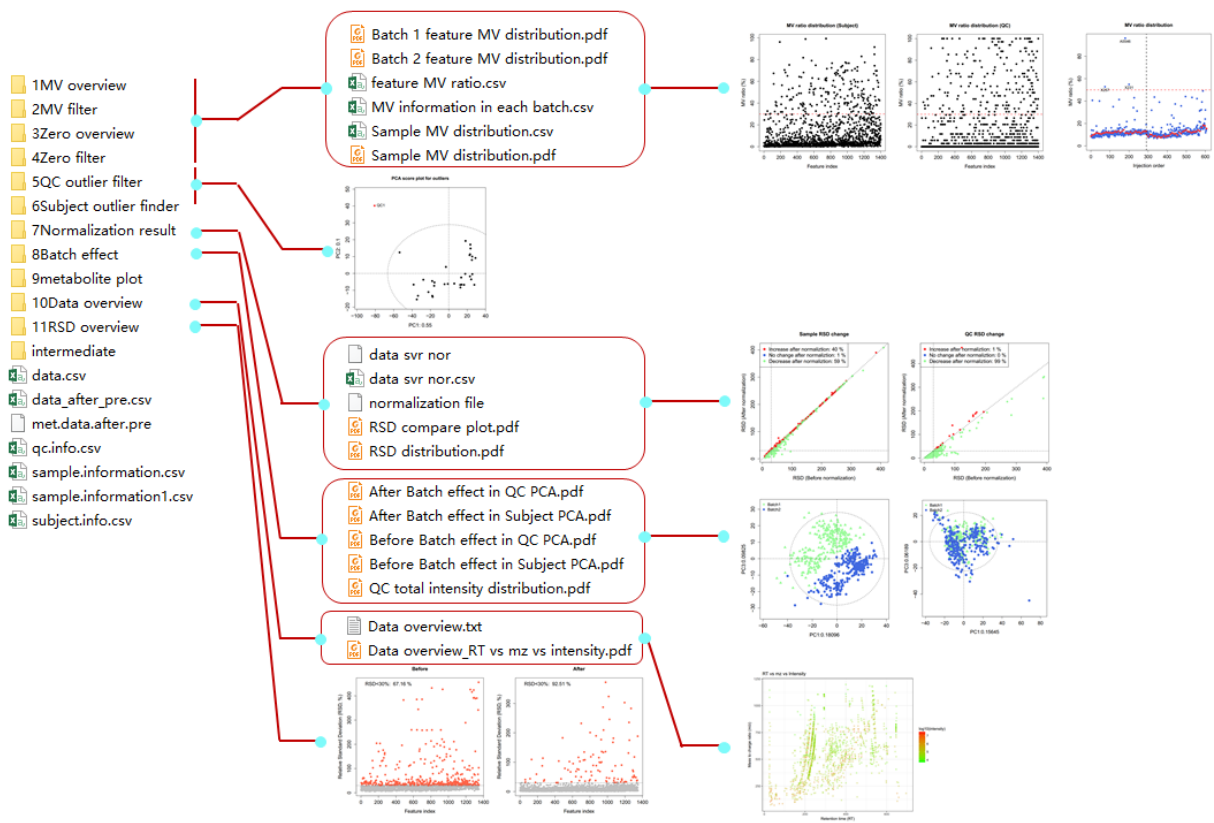


Figure 5: Figure5 Output files of *MetClean*

The demo data have been added in your work directory. “new.group.csv” is a sample.information which has been changed the group information you want to use for statistical analysis. For the sample which you don’t want to use them for statistical analysis, you can set they group information as NA like Figure 6 shows.

Sample.information.csv					New.group.csv				
sample.name	injection.order	class	batch	group	sample.name	injection.order	class	batch	group
QC11		1 QC		1 QC	QC11		1 QC		1 QC
A5551		2 Subject		1	A5551		2 Subject		1 NA
A4880		3 Subject		1	A4880		3 Subject		1 case
C1282		4 Subject		1	C1282		4 Subject		1 control
C1492		5 Subject		1	C1492		5 Subject		1 NA
A5730		6 Subject		1	A5730		6 Subject		1 case
X1421		7 Subject		1	X1421		7 Subject		1 control
X2		8 Subject		1	X2		8 Subject		1 control
C1059		9 Subject		1	C1059		9 Subject		1 case
QC12		10 QC		1 QC	QC12		10 QC		1 QC
C1397		11 Subject		1	C1397		11 Subject		1 control
A5819		12 Subject		1	A5819		12 Subject		1 case
C1137		13 Subject		1	C1137		13 Subject		1 control
A3867		14 Subject		1	A3867		14 Subject		1 case
C1223		15 Subject		1	C1223		15 Subject		1 control
C1295		16 Subject		1	C1295		16 Subject		1 control
C1510		17 Subject		1	C1510		17 Subject		1 control
C1121		18 Subject		1	C1121		18 Subject		1 control
QC13		19 QC		1 QC	QC13		19 QC		1 QC

Figure 6: Figure6 new group information

code 5: Running of *MetStat*

```
MetStat(MetFlowData = met.data.after.pre, new.group = TRUE)
```

Running results of *MetStat*

1.Sample removing. Firstly, you need to confirm the samples which you want to remove form dataset as Figure 7 shows.

Change group information

The samples you want to remove from dataset are:

A5551 C1492 FA13 A5134 A3820 M135 M134 M133 C1262 C1442 X1 A5520 C1458
7 C1485 M139 A5636 C1430 M132 A3657 M140 A4994 C1371

Right(y) or wrong(n)?y|

Figure 7: Figure7 sample removing confirmation

2.Number of component selection in PLS-DA analysis. In PLS-DA analysis, you should manually select the best choice of the number of component. When the Console show “How many comps do you want to see?”, you can type 10 and enter “Enter” key. Then a MSE plot is showing, and the best number of component is the one has the smallest CV values. So type the number (in this example is 4) and enter “Enter” key.

3.Output files. Output files of *MetStat* are listed as Figure 9 shows.

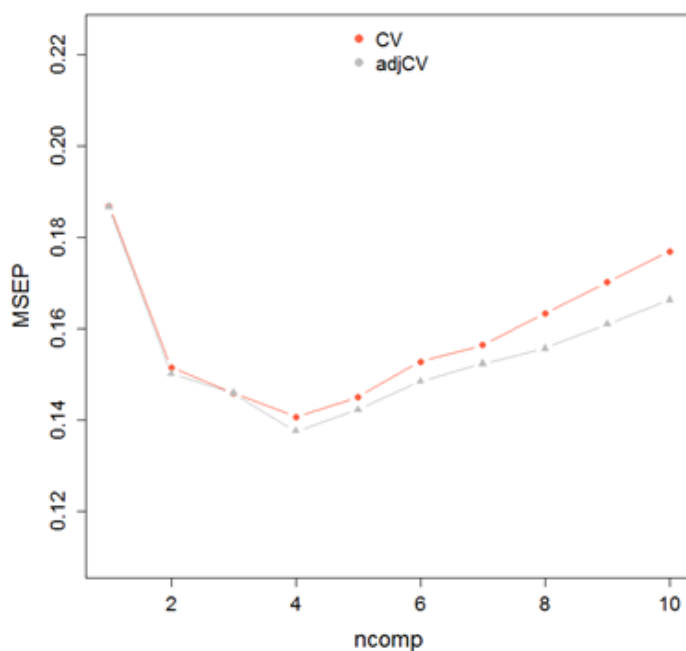
Step 1

PLS analysis

How many comps do you want to see?10|



Step 2



Step 3

PLS analysis

How many comps do you want to see?10

Do you want to see the next plot? (y/n)n

Please type number and press Enter to continue:4

Figure 8: Figure8 Number of component selection in PLS-DA analysis

- (1) “12PCA analysis” is the PCA score plot.
- (2) “13PLS analysis” contains the PLS-DA results.
- (3) “14heatmap” is the heatmap.
- (4) “15marker selection” contains the information of markers, volcano plot and boxplots of markers.
- (5) “data__after__stat.csv”, “qc.info.csv” and “subject.info” are the data and sample information after statistical analysis.
- (6) “intermediate” is the intermediate data during processing.

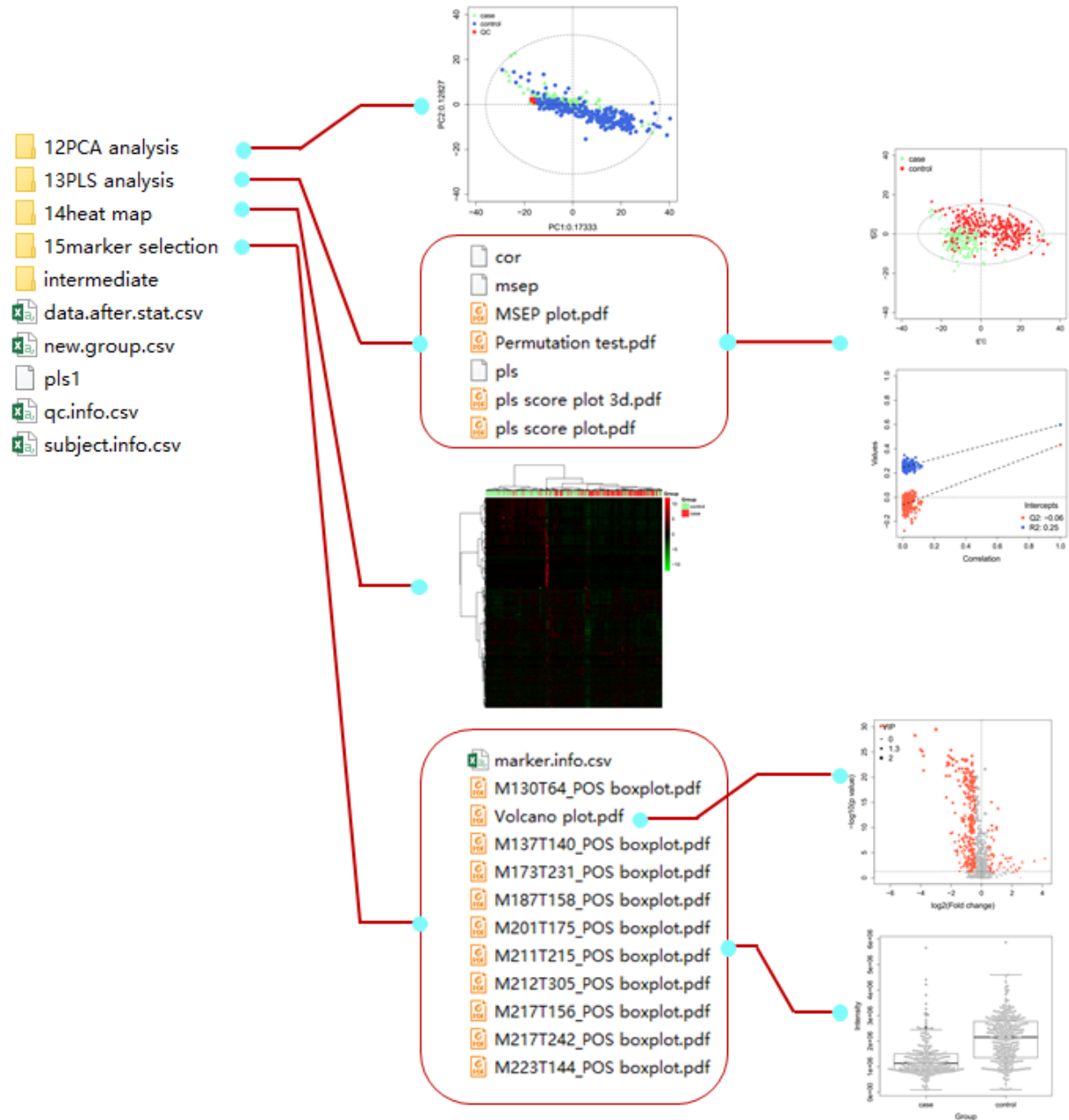


Figure 9: Figure9 Output files of *MetStat*