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GenralPlot 作图包使用说明

版本

目前版本为 v1.0

说明

设计做8类的常见图形：柱形图，韦恩图，折线图，散点图，饼图，热图，频率直方图，箱线图

更新说明

暂无

流程说明

主程序：/Bio/User/liuyubin/pipeline/GeneralPlot/bin/general_plot.pl

模块路径：/Bio/User/liuyubin/pipeline/GeneralPlot/lib

示例路径：/state/partition1/WORK/Bio/Project/GBD0442/general_plot/example

使用方法

1. 通过general_plot.pl 画图

目前可以使用的方法：

```
$> perl general_plot.pl
```

Usage:

```
perl general_plot.pl <TYPE> [options]
```

the valid types are:

venn

scatter

pca

volcano

manhattan

line

bar

errorbar

histgram

density

pie

twopie

box

violin

splitviolin

correlation

correlation_old

cluster

单个图形可用的参数，图形后加-h或者-help:

```
$> perl general_plot.pl venn -h
```

```
GeneralPlot::Image::Venn->plot(%opts)
```

```
-method          => 'venn'
```

```
necessary:
```

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

```
optional:
```

```
-width           => 600
```

```
-height          => 600
```

```
-margin          => 30
```

```
-inwidth         => 1
```

```
-save            => T
```

```
-run             => T
```

```
-clean           => T
```

2. 通过GeneralPlot::Image 包编写脚本画图

```
use lib "/Bio/User/liuyubin/pipeline/GeneralPlot/lib";
```

```
use GeneralPlot::Image;
```

```
my $file = shift;
```

```
my $outp = shift;
```

```
my $pic = GeneralPlot::Image->new();
```

```
$pic->plot(-graph => 'correlation', -file => "$file", -outprefix => "$out  
p", -postype => "upper", -label => "T", -save => "T", -run => 'T');
```

plot() 函数可用参数与通过 general_plot.pl 作图时的参数相同。

使用示例

venn

参数:

```
GeneralPlot::Image::Venn->plot(%opts)
```

```
-method          => 'venn'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

optional:

```
-width           => 600
```

```
-height          => 600
```

```
-margin          => 30
```

```
-inwidth         => 1
```

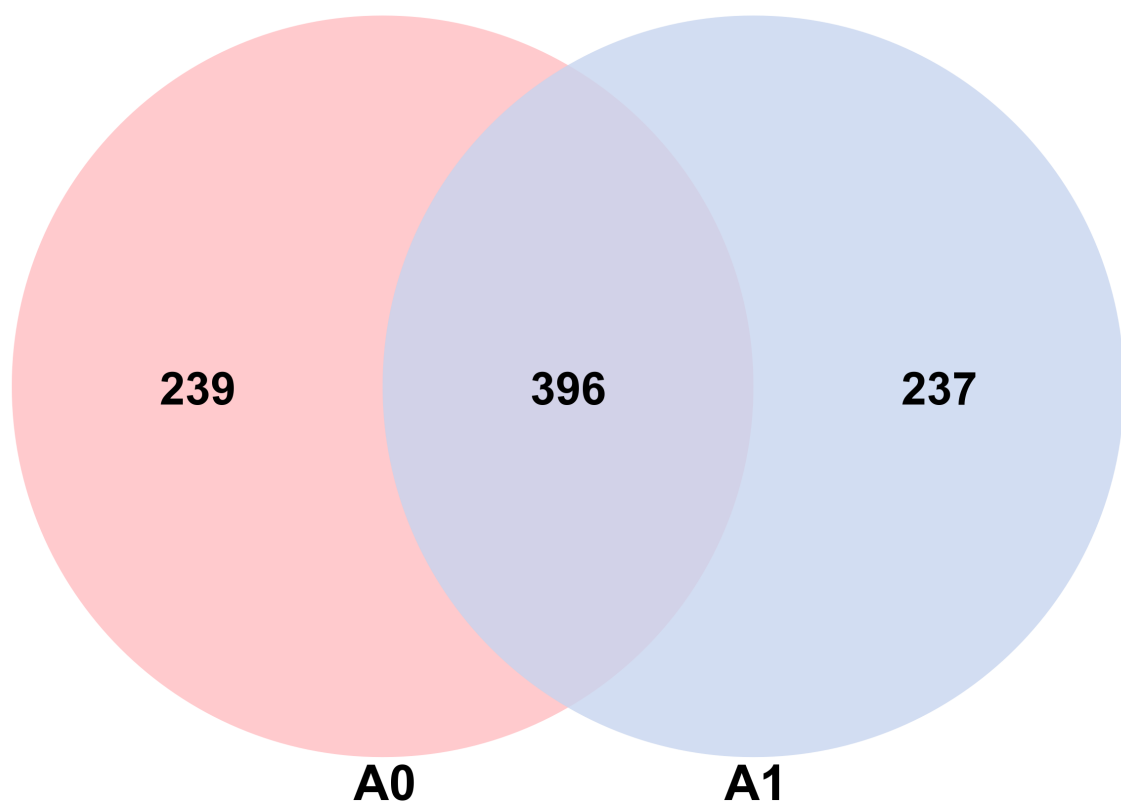
```
-save            => T
```

```
-run             => T
```

```
-clean           => T
```

示例:

```
perl general_plot.pl venn -file venn2.dat.txt -outprefix venn2
```



说明：对SBV包venn函数的封装，需要改venn图的同事可设置 -clean F 后手动编辑venn的配置文件。

scatter

参数：

```
GeneralPlot::Image::Dot->plot(%opts)
```

```
-method          => 'dot'
```

```
necessary:
```

```
-file
```

```
-outprefix
```

```
-outdir
```

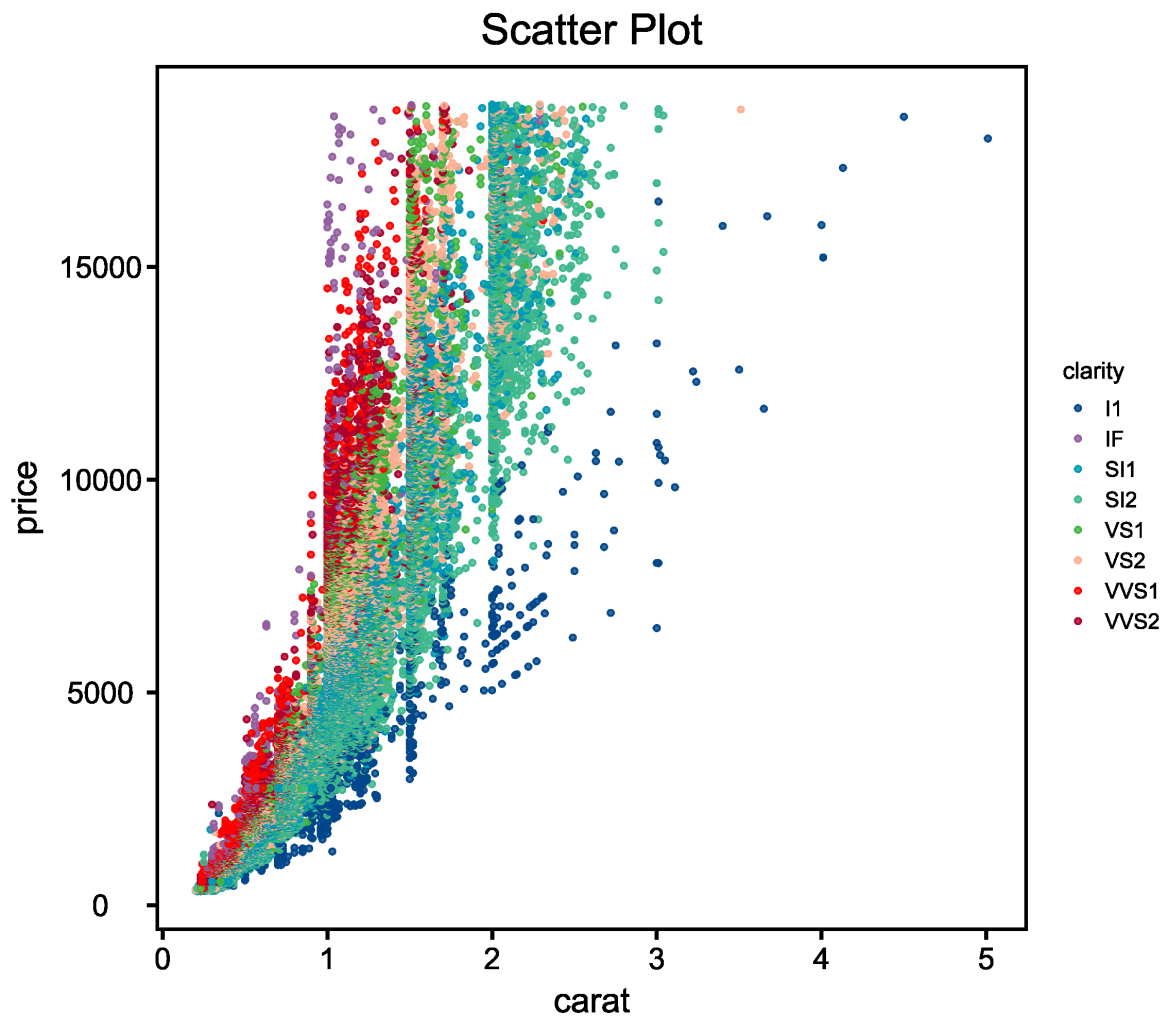
```
-outname
```

```
optional:
```

-colnpg	=> F
-collanc	=> F
-collist	=> 'none'
-x	=> 1
-y	=> 2
-group	=> 'none'
-header	=> T
-title	=> "Scatter Plot"
-xlab	=> ''
-ylab	=> ''
-legend	=> T
-width	=> 8
-height	=> 7
-save	=> T
-run	=> T
-clean	=> T

示例:

```
perl general_plot.pl scatter -file test.diamonds.txt -outprefix test -x 1  
-y 7 -group 4 -xlab carat -ylab price
```



pca

参数:

```
GeneralPlot::Image::Dot->plot(%opts)
```

```
-method          => 'pca'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

optional:

```
-group
```

```
-colnpg          => F
```

```
-collanc         => F
```

```
-collist         => 'none'
```

```

-ellipse      => F
-report       => T

-header       => T
-rowcol       => 'col'   [ col | row ]
-namefix      => 'none'  [ _fpkm ... ]

-title        => "PCA"
-label        => F
-legend       => T
-width        => 8
-height       => 8

-save         => T
-run          => T
-clean        => T

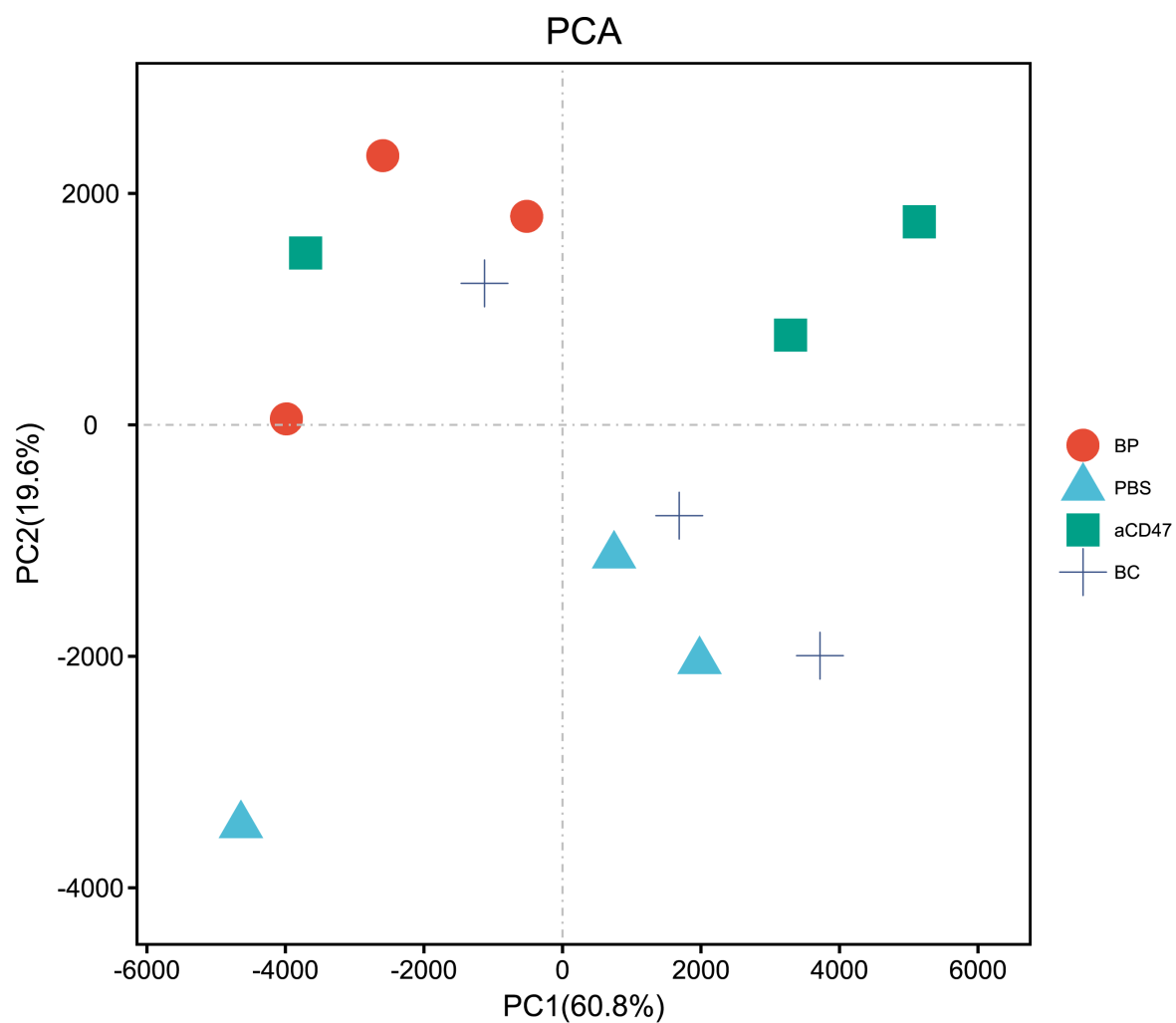
```

示例:

```

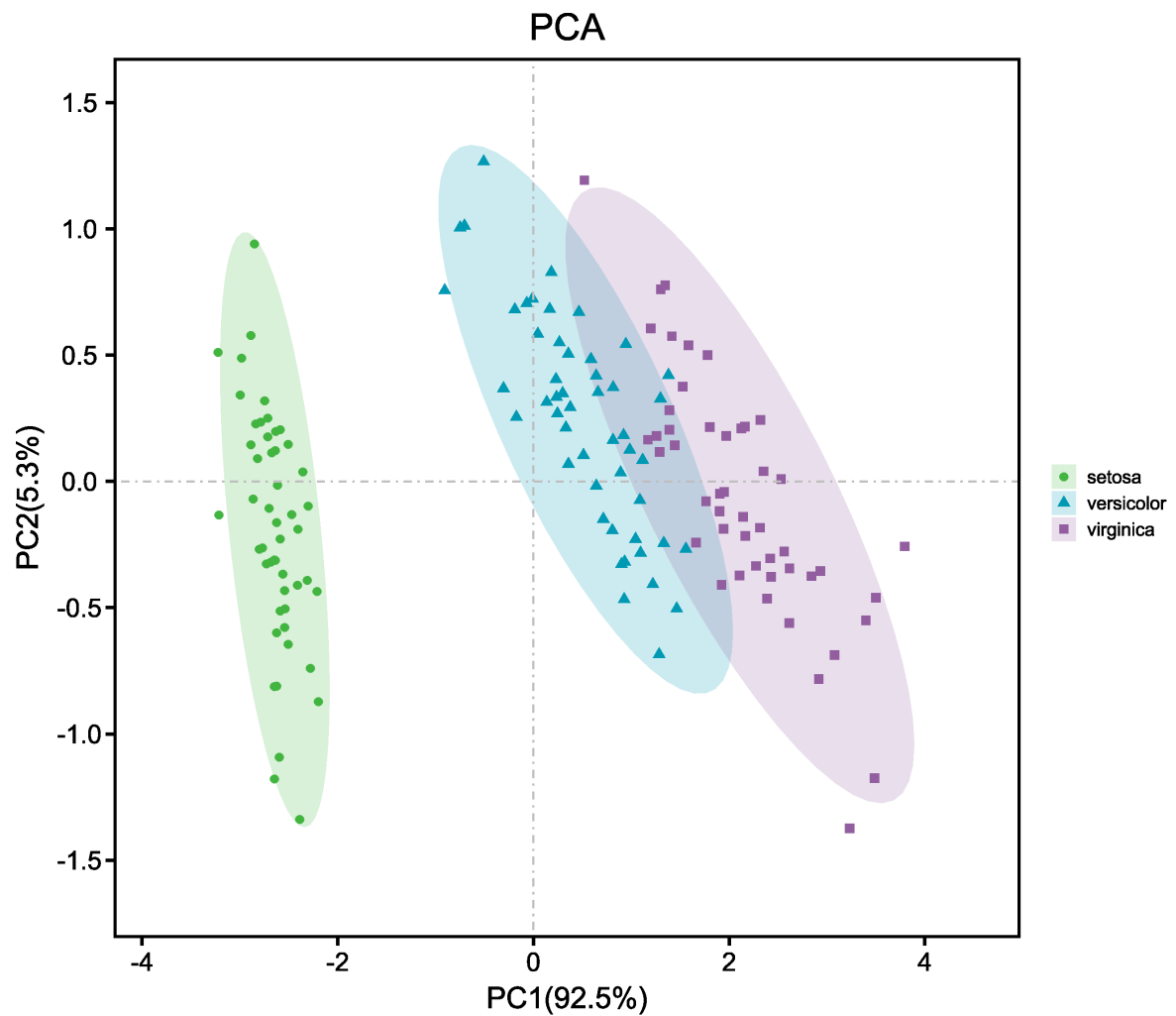
perl general_plot.pl pca -file all.samples.exp.xls -outprefix all.sample
-group group.list -colnpg T

```



添加置信椭圆，需要group信息，且对点的数目有要求。

```
perl general_plot.pl pca -file iris.txt -group iris.group.txt -outprefix  
iris -ellipse T
```



说明：PCA图暂时只能画PC1和PC2，后续添加可选择其他PC的选项。

volcano

参数：

```
GeneralPlot::Image::Dot->plot(%opts)
```

```
-method          => 'volcano'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

```

optional:
-header          => T
-rowcol          => 'col'      [ col | row ]
-namefix         => 'none'     [ _fpkm ... ]

-fccolname       => 'log2(fc)'
-pqcolname       => 'FDR'
-fccut           => 1
-pqcut           => 0.05
-fcformat        => 'none'     [ none | log2 ]
-pqformat        => '-log10'   [ none | -log10 ]

-collist         => 'none'

-title           => "Volcano Plot"
-xlab            => 'log2(fc)'
-ylab            => '-log10(FDR)'
-width           => 8
-height          => 7
-legend          => "T"

-save            => T
-run             => T
-clean           => T

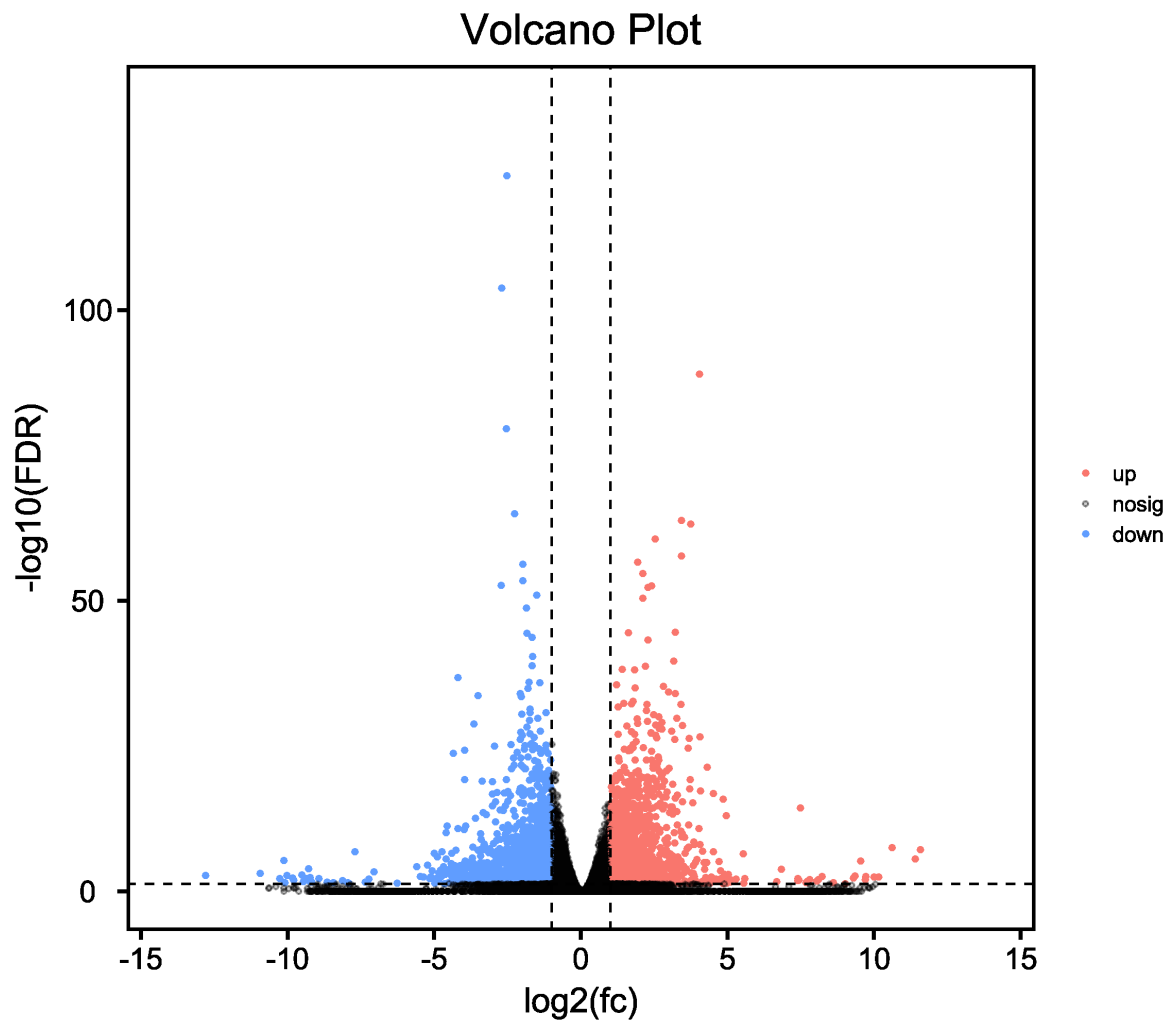
```

示例:

```

perl general_plot.pl volcano -file EL-vs-GL.all.xls -outdir . -outname volcano

```



manhattan

```
GeneralPlot::Image::Dot->plot(%opts)
```

```
-method          => 'manhattan'
```

```
necessary:
```

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

```
optional:
```

```
-chrlen
```

```
-header          => T
```

```
-datacol         => '1,2,3,4'
```

```
-thres           => '0.01,0.05',
```

```
-scale           => '-log10',
```

```
-space           => 'T',
```

```
-colnpg          => 'F',
```

```

-collanc      => 'F',
-collist      => 'none',

-title        => "Manhattan Plot"
-xlab         => 'Chromosomes'
-ylab         => '-log10(Pvalue)'
-legend       => "F"

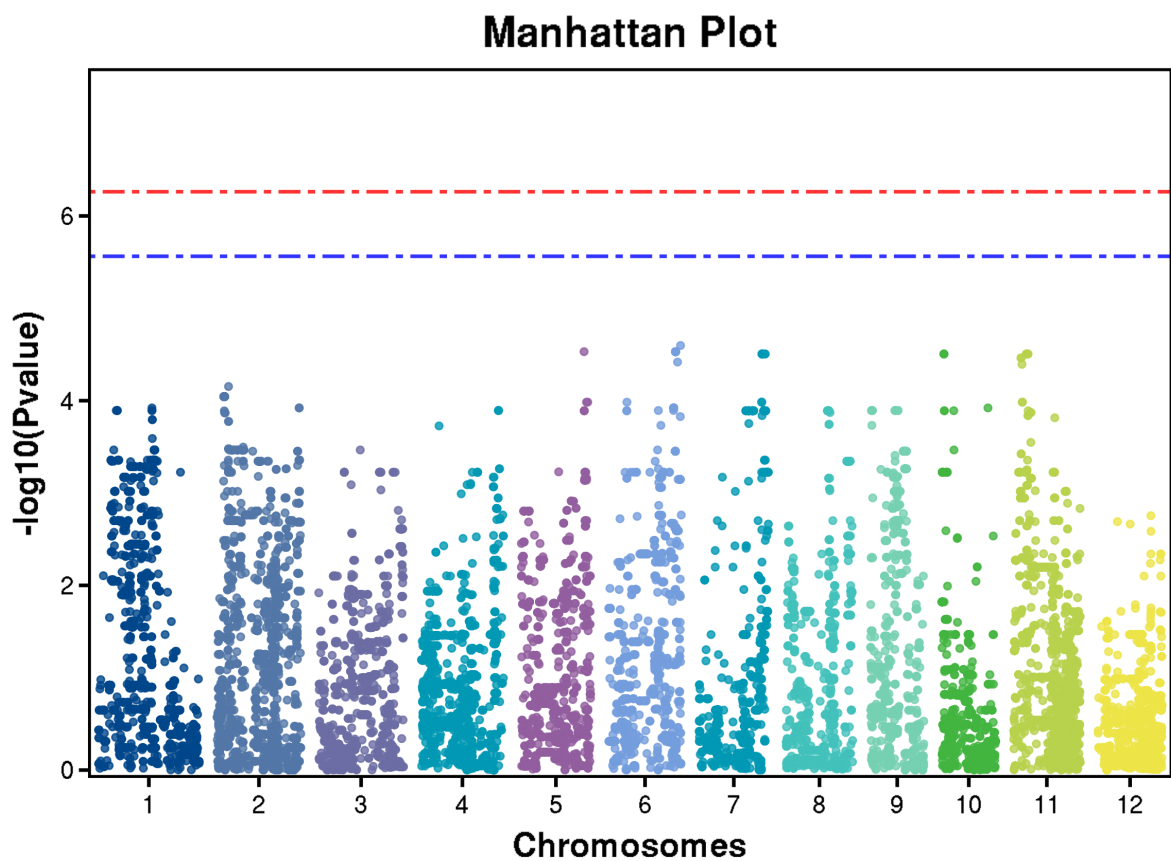
-width        => 8
-height       => 6

-save         => T
-run          => T
-clean        => T

```

示例：

```
perl general_plot.pl manhattan -file NAME.EPN.GLM.res.2 -outprefix rice
```



说明：-chrLen 可用两列的文本或直接用 samtools faidx 生成的索引文件，不加-chrLen的话，chr的长度为点在各个染色体的最大位置。

line

参数:

```
-method          => 'line'

necessary:
-file
-outprefix
-outdir
-outname

optional:
-header          => T

-colnpg          => 'F',
-collanc         => 'F',
-collist         => 'none',

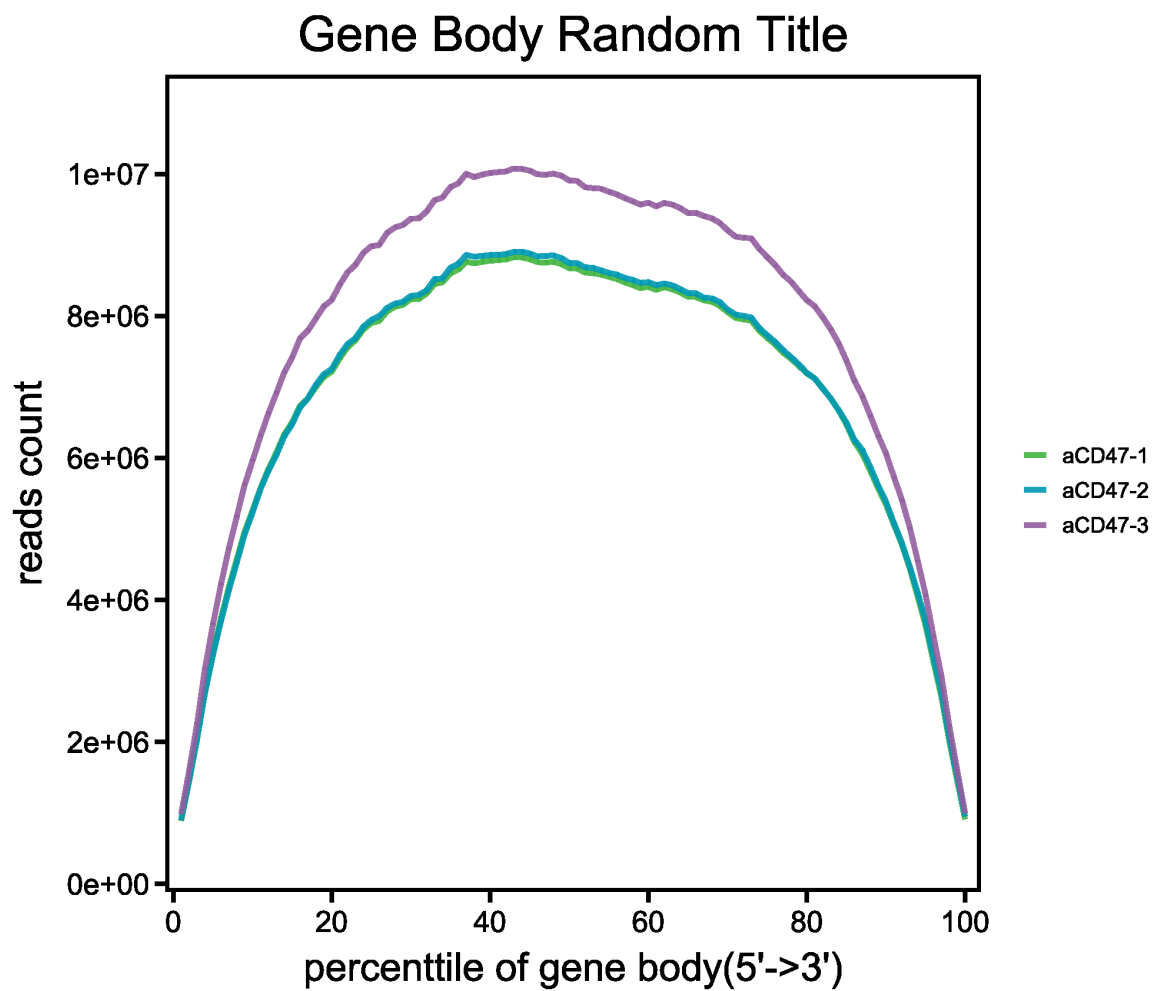
-title           => ""
-xlab            => ''
-ylab            => ''
-legend          => "T"

-width           => 7
-height          => 6

-save            => T
-run             => T
-clean           => T
```

示例:

```
perl general_plot.pl line -file line.3.random.xls -outprefix line.3 -title 'Gene Body Random Title' -xlab "percenttile of gene body(5'→3')" -ylab 'reads count'
```



说明：目前只提供基础函数。

bar

参数：

```
GeneralPlot::Image::Bar->plot(%opts)
```

```
-method          => 'bar'
```

```
necessary:
```

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

```
optional:
```

```
-header          => T
```

```
-barfill         => 'F'
```

```
-bardodge        => 'F'
```

```
-mulcolor        => 'F'
```

```
-colnpg         => 'F',
```

```

-collanc      => 'F',
-collist      => 'none',

-title       => ""
-xlab        => ''
-ylab        => ''
-label       => 'F'
-legend      => 'T'

-width       => 8
-height      => 6

-save        => T
-run         => T
-clean       => T

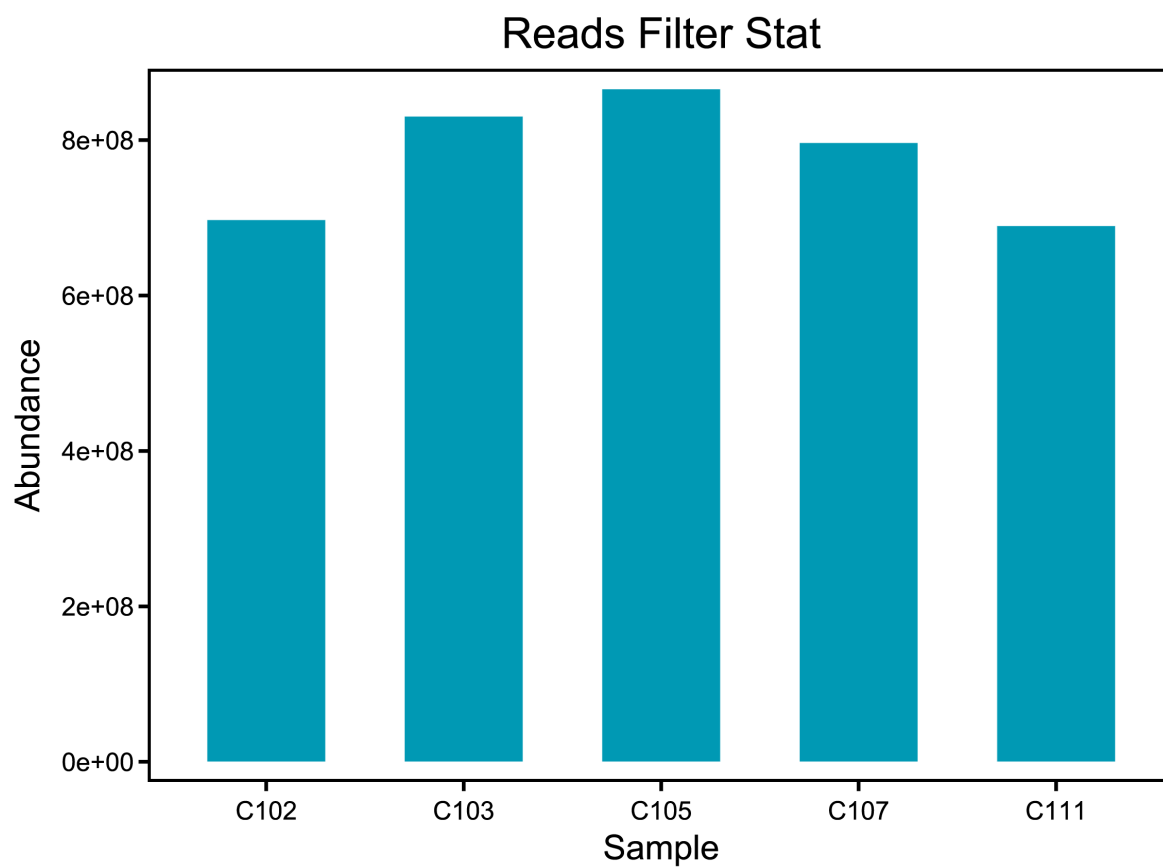
```

示例:

```

perl general_plot.pl bar -file bar.5.xls -outprefix bar.5 -title "Reads F
ilter Stat" -xlab "Sample" -ylab "Abundance"

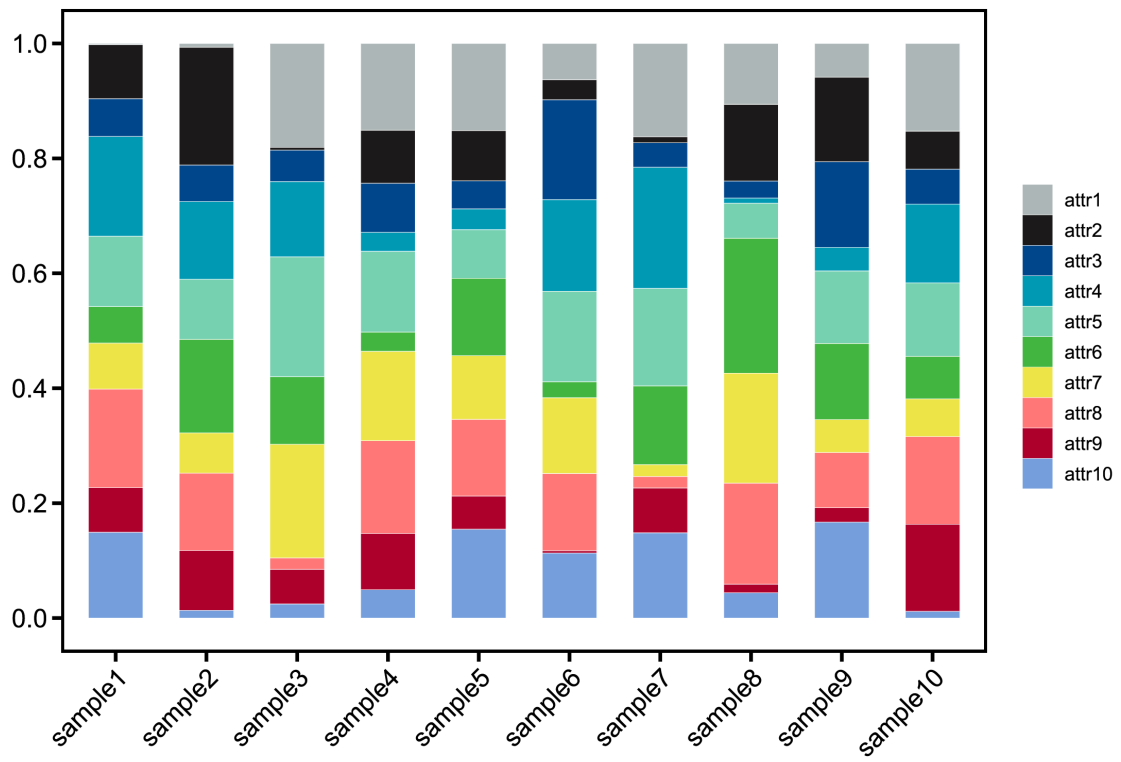
```



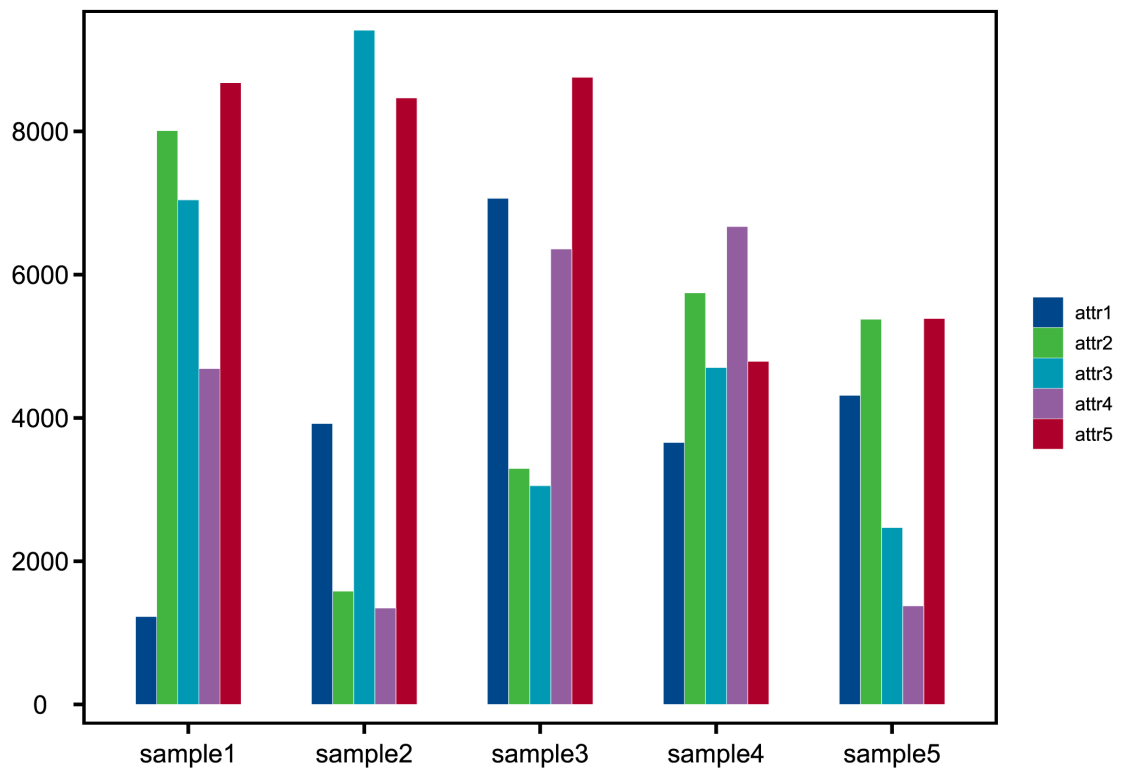
```

perl general_plot.pl bar -file dodgebar.10.10.xls -outprefix stack.10.10
-barfill T

```



```
perl general_plot.pl bar -file dodgebar.5.5.xls -outprefix dodgebar.5.5 -
bardodge T
```



errorbar

参数:

```
GeneralPlot::Image::Bar->plot(%opts)
```

```
-method          => 'errorbar'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

optional:

```
-header          => T
```

```
-mulcolor        => 'F'
```

```
-colnpg          => 'F',
```

```
-collanc         => 'F',
```

```
-collist         => 'none',
```

```
-title           => ""
```

```
-xlab            => ''
```

```
-ylab            => ''
```

```
-label           => 'F'
```

```
-legend          => 'T'
```

```
-width           => 8
```

```
-height          => 6
```

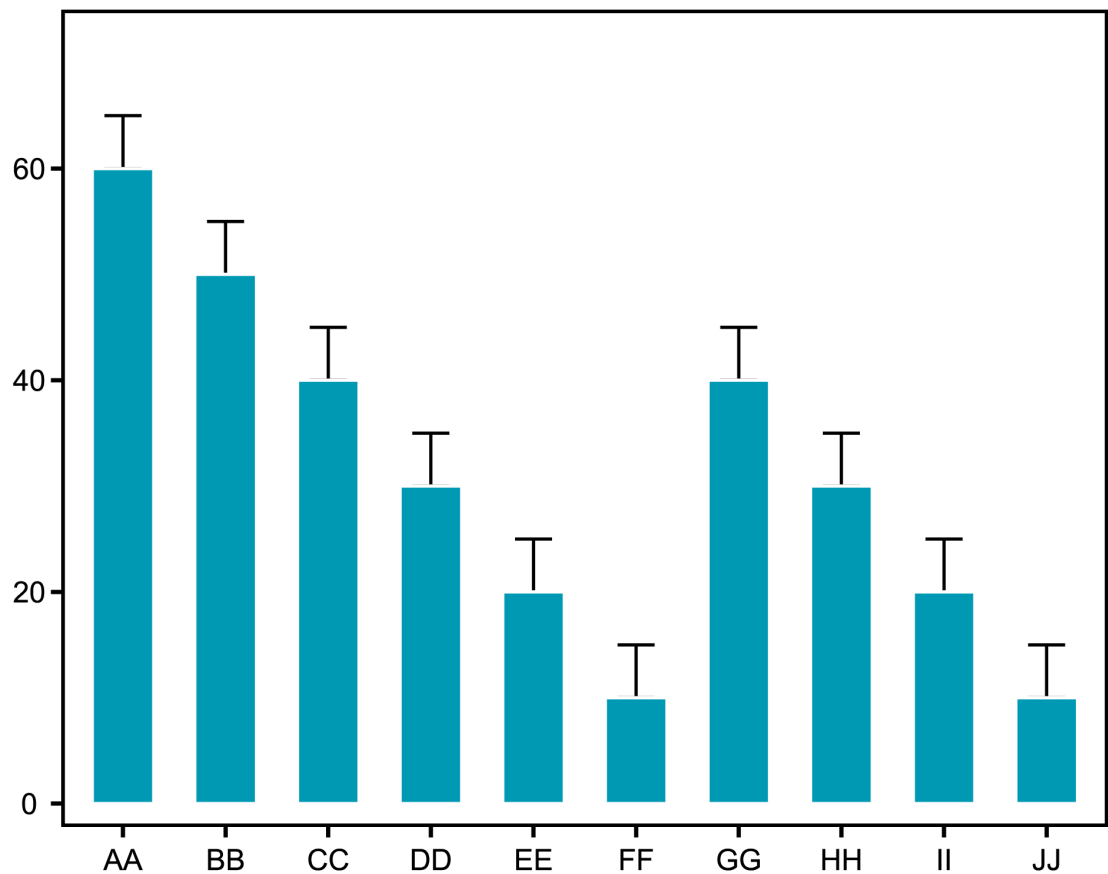
```
-save            => T
```

```
-run             => T
```

```
-clean           => T
```

示例:

```
perl general_plot.pl errorbar -file errorbar.10.table.xls -outprefix errorbar.10
```



histgram

参数:

```
GeneralPlot::Image::Hist->plot(%opts)
```

```
-method          => 'hist'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

optional:

```
-header          => T
```

```
-format          => 'table'      [ table | matrix ]
```

```
-colname         => 'NULL'
```

```
-facet           => 'F'
```

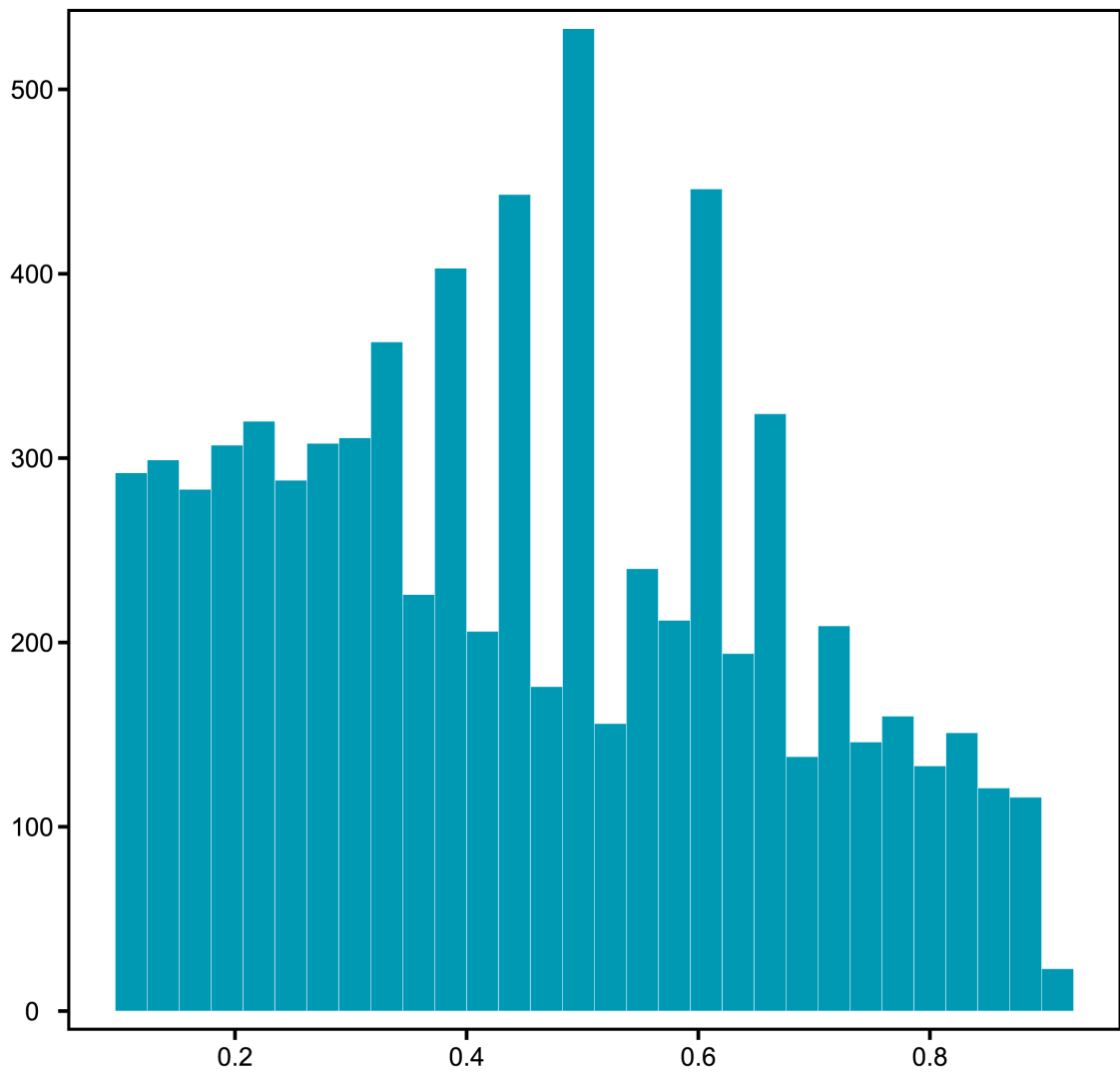
```
-identity        => 'F'
```

```
-density         => 'F'
```

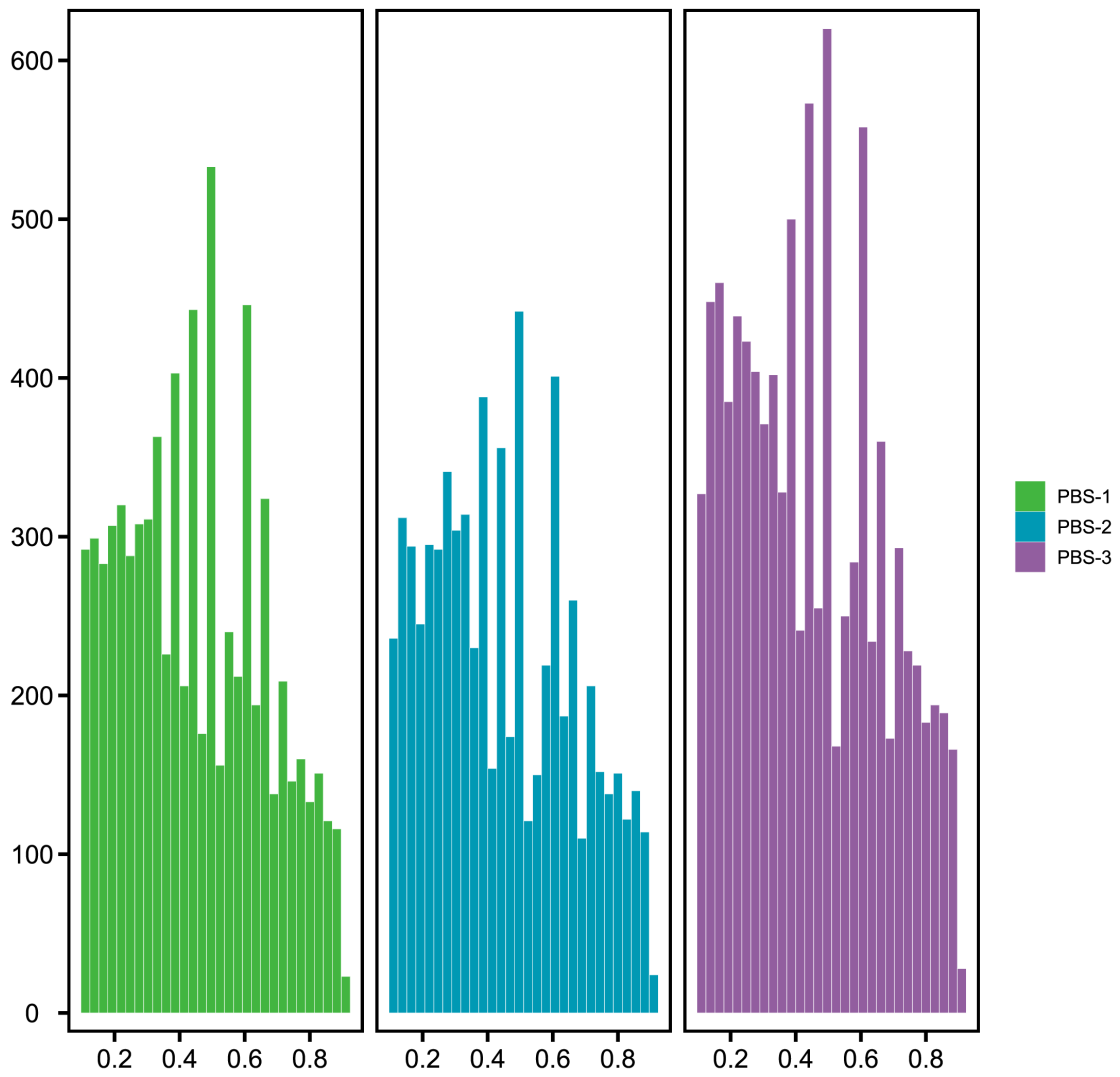
```
-colnpg      => 'F',  
-collanc     => 'F',  
-collist     => 'none',  
  
-title       => ""  
-xlab        => ''  
-ylab        => ''  
-legend      => 'T'  
  
-width       => 8  
-height      => 8  
-bins        => 30  
  
-save        => T  
-run         => T  
-clean       => T
```

示例:

```
perl general_plot.pl histogram -file hist.1.xls -outprefix hist.1
```



```
perl general_plot.pl histogram -file hist.3.xls -outprefix hist.3 -colname  
frequency -facet T
```



density

参数:

```
GeneralPlot::Image::Hist->plot(%opts)
```

```
-method          => 'density'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

optional:

```
-header          => T
```

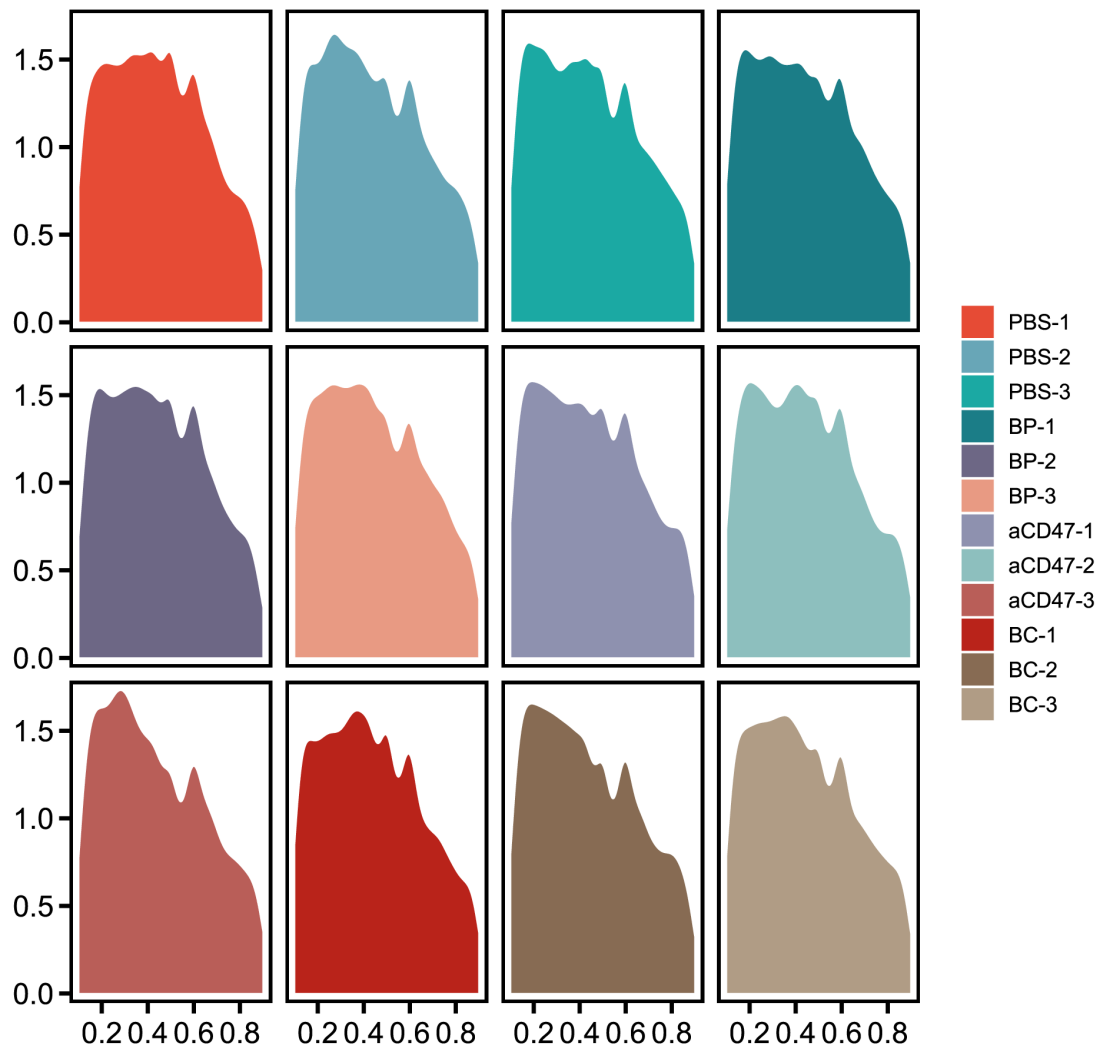
```
-format          => 'table'      [ table | matrix ]
```

```
-colname         => 'NULL'
```

-facet	=> 'F'
-inline	=> 'F'
-colnpg	=> 'F',
-collanc	=> 'F',
-collist	=> 'none',
-title	=> ""
-xlab	=> ''
-ylab	=> ''
-legend	=> 'T'
-width	=> 7
-height	=> 7
-save	=> T
-run	=> T
-clean	=> T

示例:

```
perl general_plot.pl density -file hist.12.xls -outprefix density.12 -for  
mat matrix -colnpg T -facet T -colname frequency
```



说明：对于matrix格式的数据（如表达量矩阵），histogram和density暂时没有-namefix，-scale之类的参数用于数据选择和转换。

pie

参数：

```
GeneralPlot::Image::Pie->plot(%opts)
```

```
-method          => 'pie'
```

necessary:

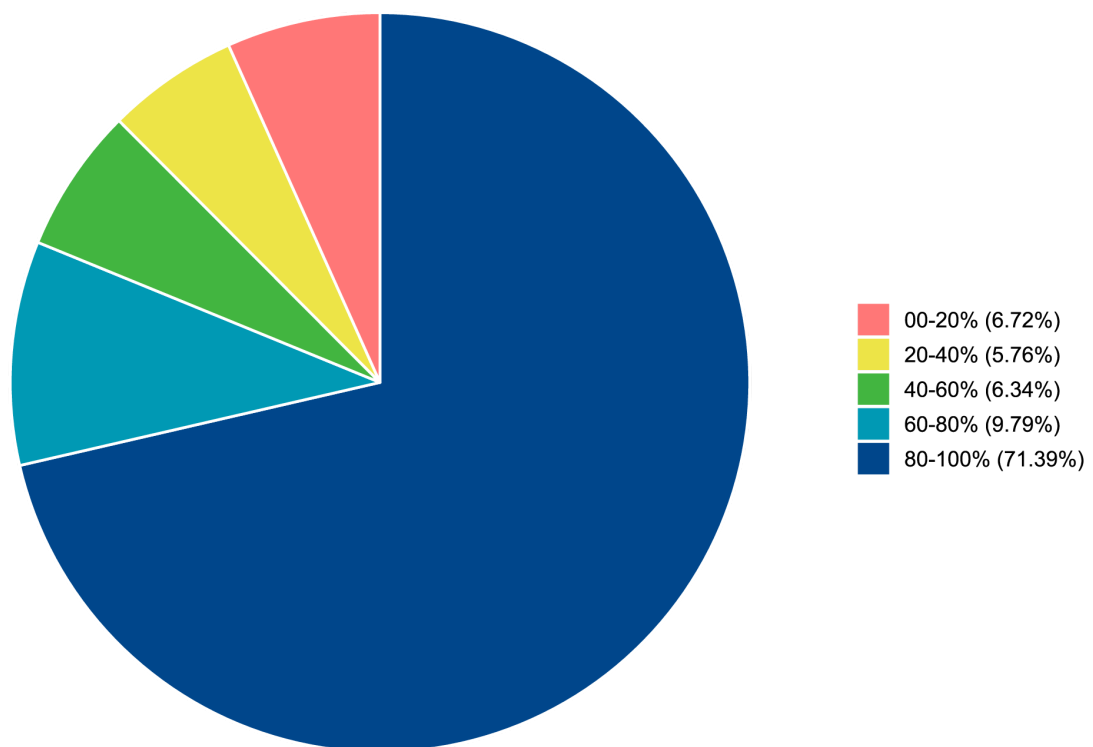
```
-file
-outprefix
-outdir
-outname
```

optional:

-header	=> T
-colnpg	=> 'F',
-collanc	=> 'F',
-collist	=> 'none',
-title	=> ""
-xlab	=> ''
-ylab	=> ''
-label	=> 'F'
-legend	=> 'T'
-width	=> 7
-height	=> 7
-save	=> T
-run	=> T
-clean	=> T

示例:

```
perl general_plot.pl pie -file pie.1.xls -outprefix pie.1
```

twopie

参数:

```
GeneralPlot::Image::Pie->plot(%opts)
```

```
-method          => 'twopie'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

optional:

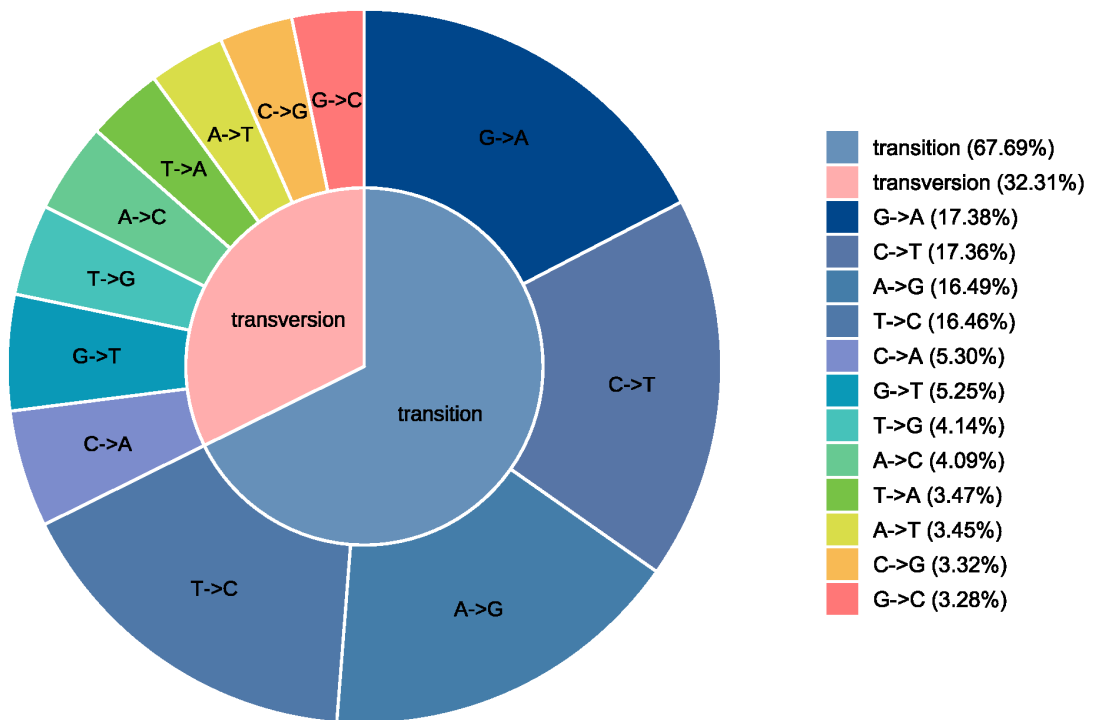
```
-header          => T
```

```
-colnpg          => 'F',
```

```
-collanc      => 'F',  
-collist      => 'none',  
  
-title        => ""  
-xlab         => ''  
-ylab         => ''  
-label        => 'F'  
-legend       => 'T'  
  
-width        => 7  
-height       => 7  
  
-save         => T  
-run          => T  
-clean        => T
```

示例:

```
perl general_plot.pl twopie -file twopie.1.xls -outprefix twopie.1 -label  
T
```



说明：twopie对数据做了排序，多个样本时可能出现样本间标签颜色不对应的情况。

box

参数：

```
GeneralPlot::Image::Box->plot(%opts)
```

```
-method          => 'box'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

optional:

```
-header          => T
```

```
-format          => 'matrix' [ matrix | table ]
```

```

-rowcol      => 'col'      [ col | row ]
-group       => 'none'

-namefix     => 'none'    [ _fpkm ... ]
-filter0     => 'F'
-scale       => 'none'    [ log2 | log10 ]

-colnpg      => 'F',
-collanc     => 'F',
-collist     => 'none',

-report      => 'T'

-title       => ""
-xlab        => ''
-ylab        => ''
-legend      => 'T'
-adddot      => 'F'

-width       => 8
-height      => 6

-save        => T
-run         => T
-clean       => T

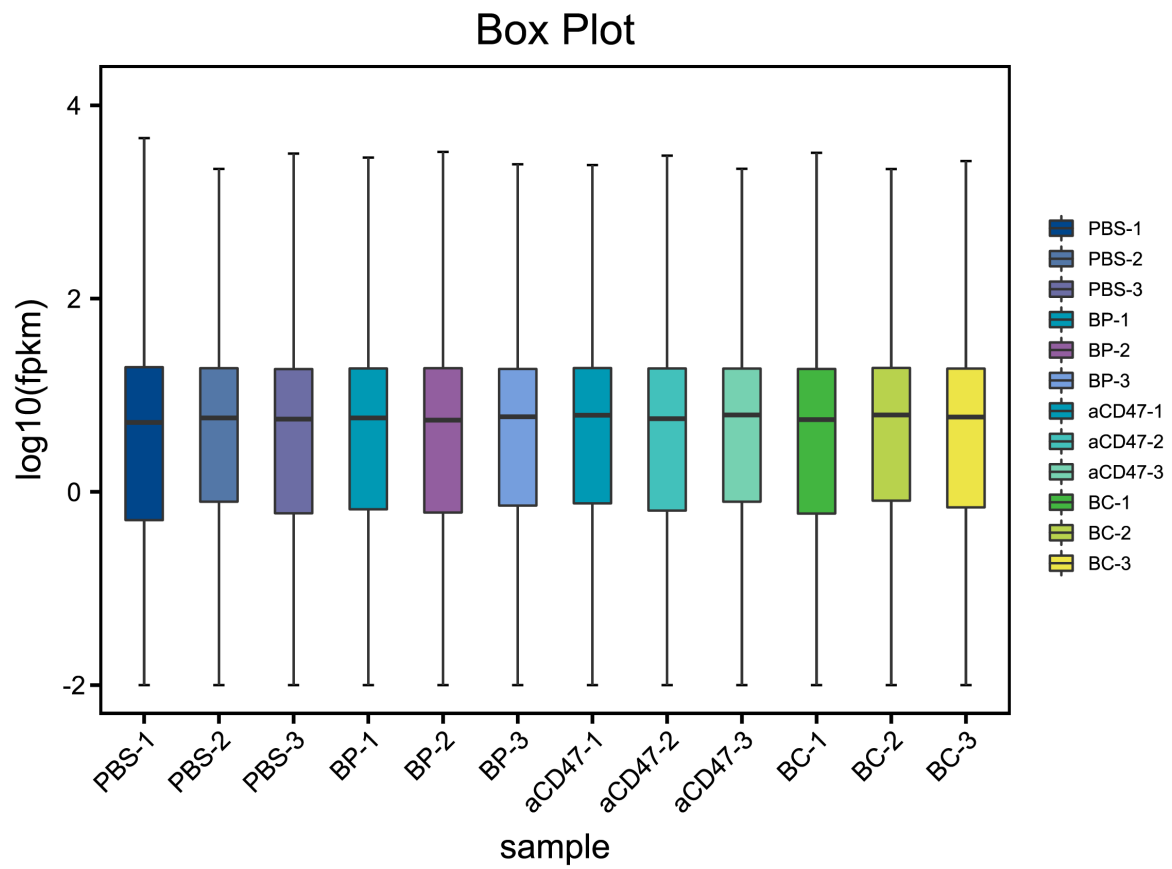
```

示例:

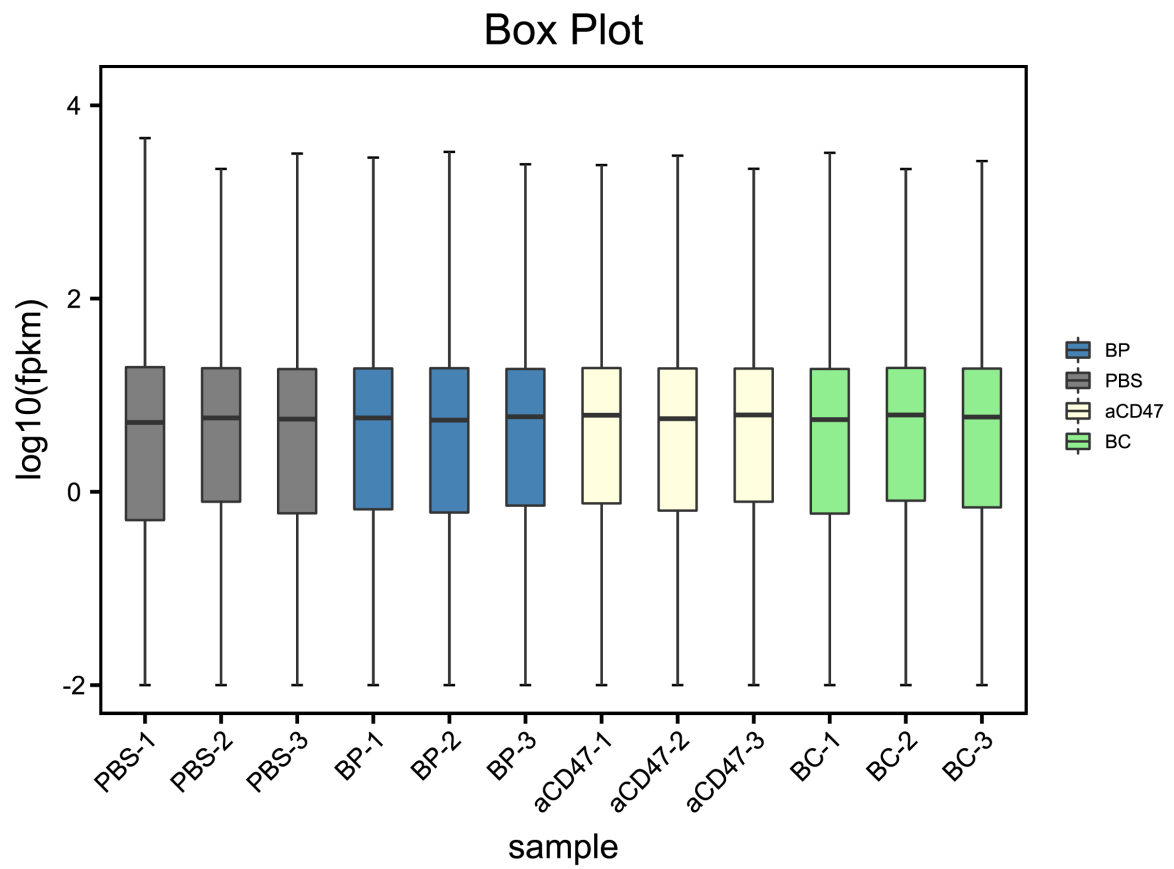
```

perl general_plot.pl box -file all.genes.expression.xls -outprefix all.genes
-filter0 T -namefix _fpkm -scale log10 -xlab sample -ylab "log10(fpkm)" -title "Box Plot"

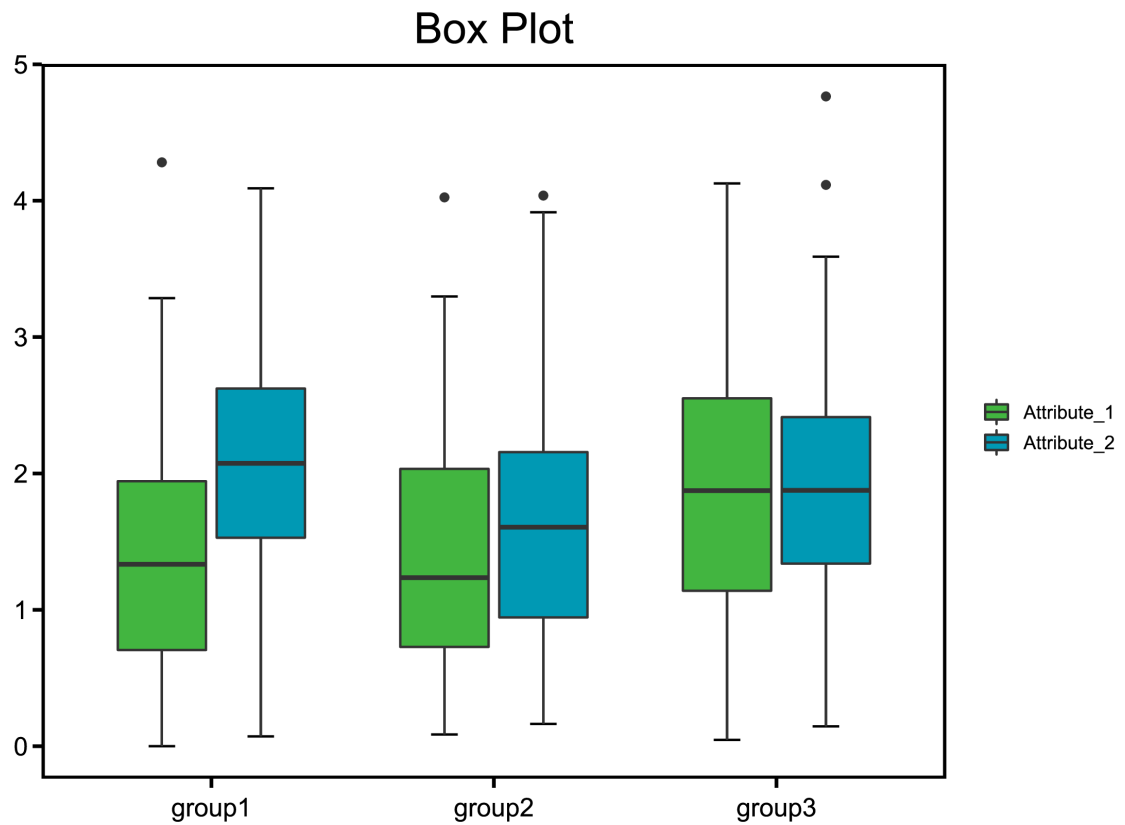
```



```
perl general_plot.pl box -file all.genes.expression.xls -outprefix all.genes.group -filter0 T -namefix _fpkm -scale log10 -xlab sample -ylab "log10(fpkm)" -title "Box Plot" -group group.list -collist 'steelblue, grey50, lightyellow, lightgreen'
```



```
perl general_plot.pl box -file text.txt -outprefix test.group -filter0 1
-namefix none -scale none -format table -adddot T
```



violin

violin函数的参数与box基本一致。

参数：

```
GeneralPlot::Image::Box->plot(%opts)

-method          => 'violin'

necessary:
-file
-outprefix
-outdir
-outname

optional:
-header          => T
-format          => 'matrix'      [ matrix | table ]
-rowcol          => 'col'         [ col | row ]
-group           => 'none'

-namefix         => 'none'        [ _fpkm ... ]
-filter0         => 'F'
-scale           => 'none'        [ log2 | log10 ]

-colnpg         => 'F',
-collanc         => 'F',
-collist         => 'none',

-report          => 'T'

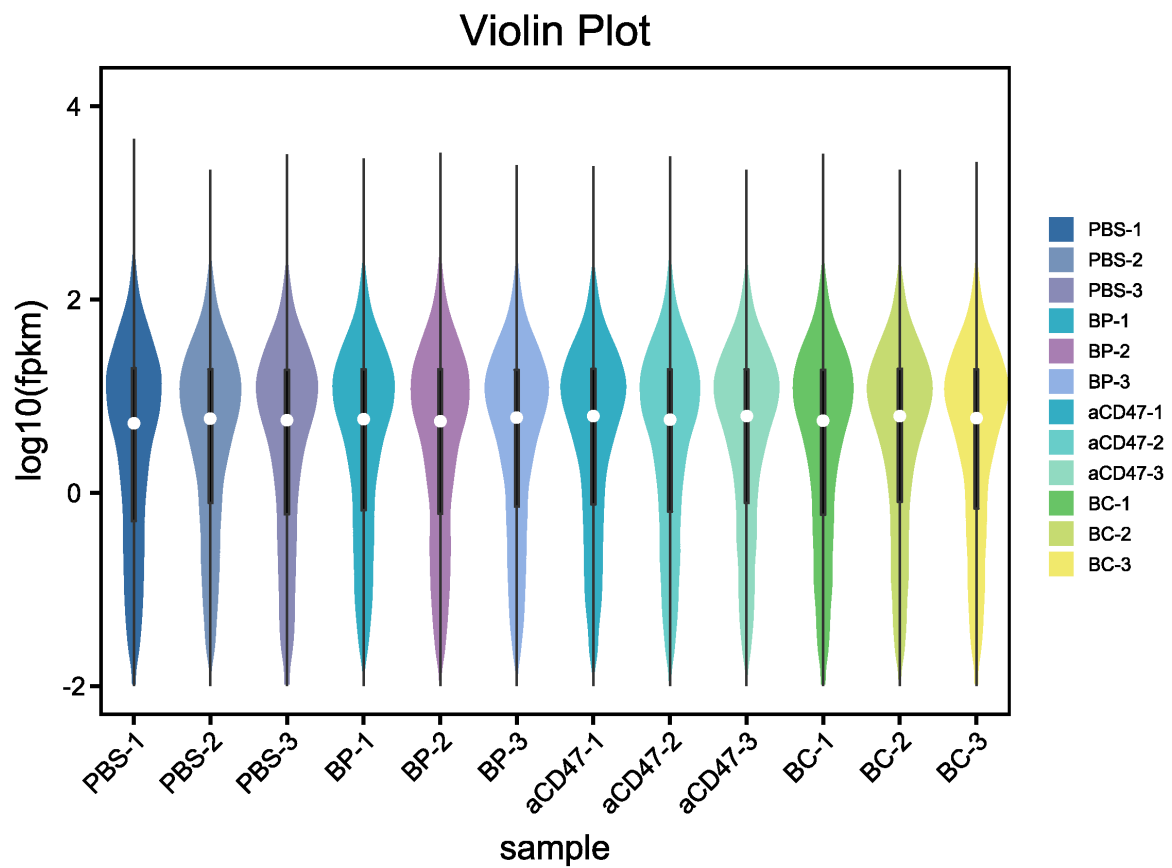
-title           => "Violin Plot"
-xlab            => ''
-ylab            => ''
-legend          => 'T'
-adddot          => 'F'

-width           => 8
-height          => 6

-save            => T
-run             => T
-clean           => T
```

示例：

```
perl general_plot.pl violin -file all.genes.expression.xls -outprefix
all.genes -filter0 T -namefix _fpkm -scale log10 -xlab sample -ylab "log1
0(fpkm)" -title "Violin Plot"
```



splitviolin

参数:

```
GeneralPlot::Image::Box->plot(%opts)
Notice: can only be used on 2 attrrs data
```

```
-method          => 'splitviolin'
```

necessary:

```
-file
-outprefix
-outdir
-outname
```

optional:

```
-header          => T
-rowcol          => 'col'          [ col | row ]

-filter0         => 'F'
-scale           => 'none'        [ log2 | log10 ]

-collist         => 'none',
```



```

-report      => 'T'

-title      => "Violin Plot"
-xlab       => ''
-ylab       => ''
-legend     => 'T'
-adddot     => 'F'

-width      => 8
-height     => 7

-save       => T
-run        => T
-clean      => T

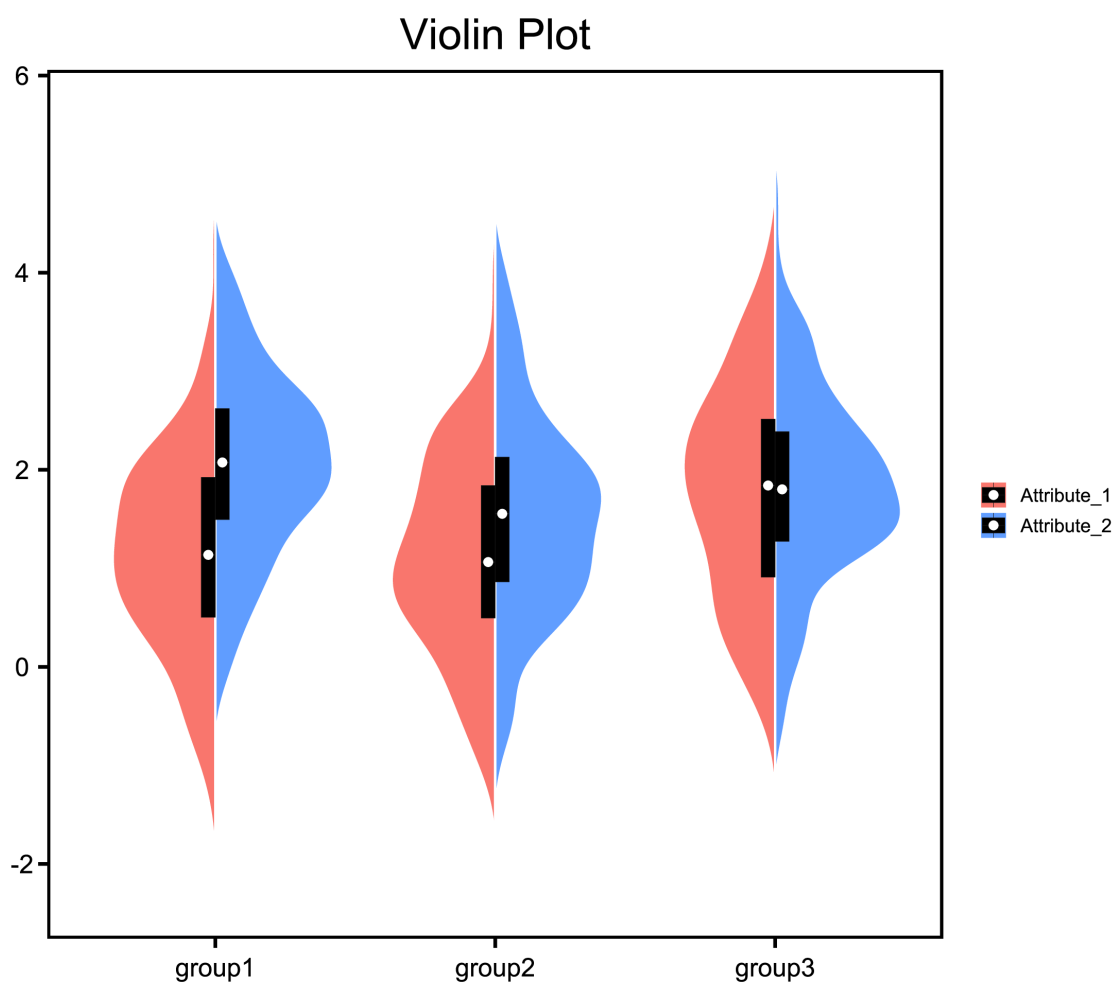
```

示例：

...

```
perl general_plot.pl splitviolin -file text.txt -outprefix test
```

...



说明：只接受table格式的数据，attribute是能有2个。

correlation

参数:

```
GeneralPlot::Image::Heatmap->plot(%opts)
```

```
-method          => 'ggcor'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

optional:

```
-header          => T
```

```
-rowcol          => 'col'          [ col | row ]
```

```
-namefix         => 'none'        [ _fpm ... ]
```

```
-cor             => 'pearson'     [ pearson | spearman | kendall ]
```

```
-cortest         => 'F'
```

```
-pvalue          => 0.05
```

```
-postype         => 'full'        [ upper | lower ]
```

```
-collist         => 'none',
```

```
-title           => "Sample Correlation"
```

```
-xlab            => ''
```

```
-ylab            => ''
```

```
-legend          => 'T'
```

```
-label           => 'F'
```

```
-width           => 7
```

```
-height          => 7
```

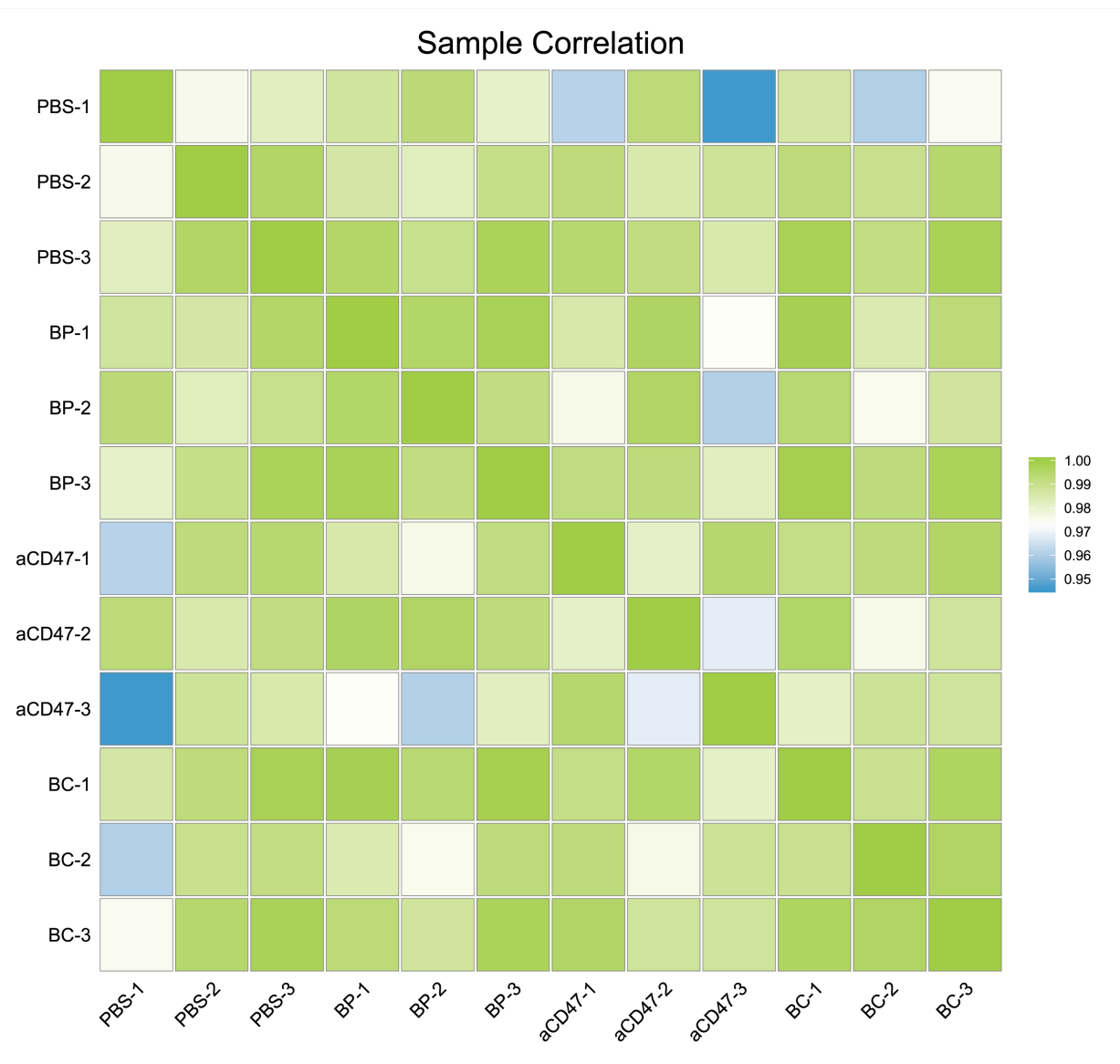
```
-save            => T
```

```
-run             => T
```

```
-clean           => T
```

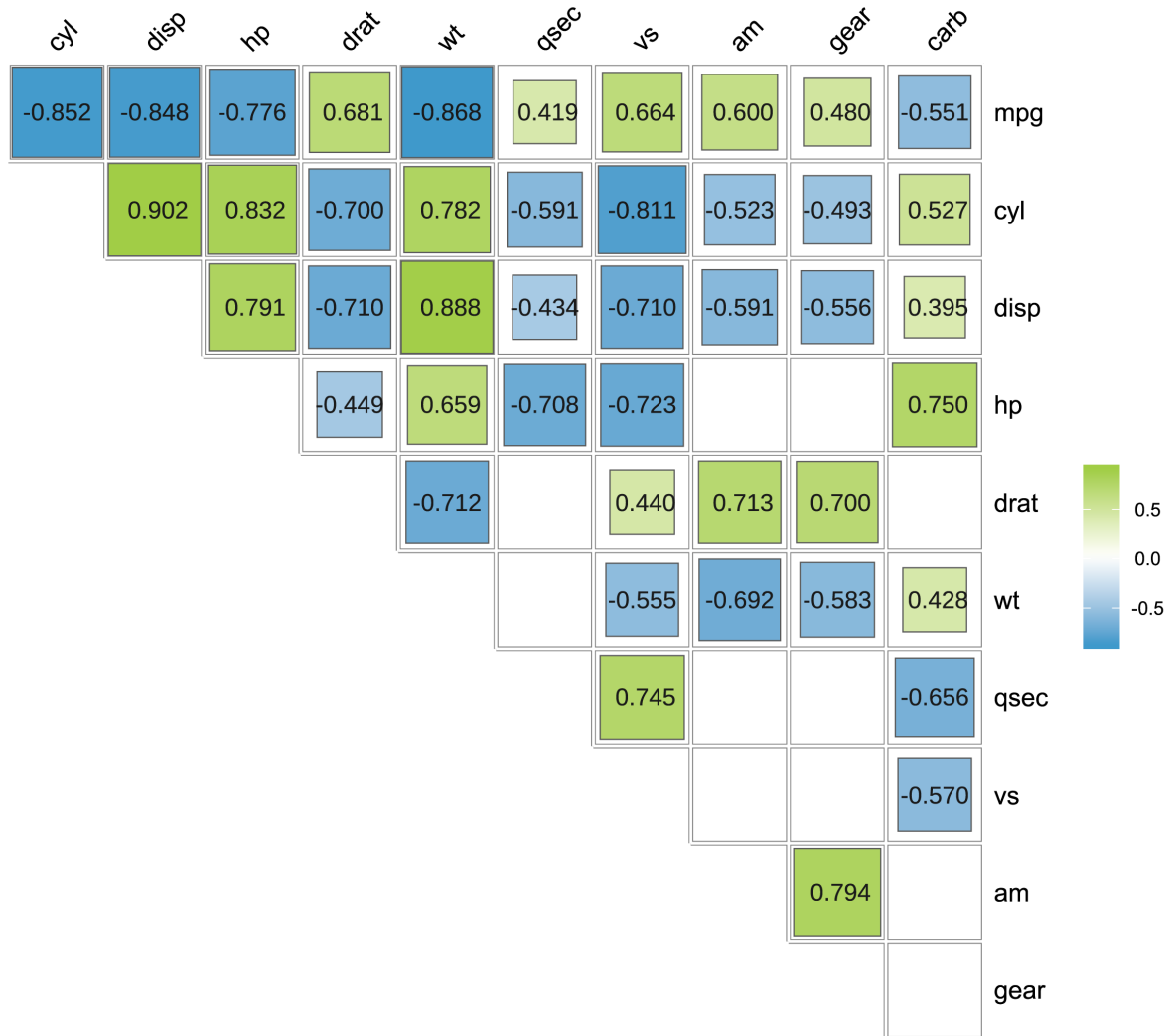
示例:

```
perl general_plot.pl correlation -file all.samples.exp.12.xls -outprefix  
all.samples.exp.12
```



```
perl general_plot.pl correlation -file mtcars.txt -outprefix test.mtcars  
-label T -cortest T -postype upper
```

Sample Correlation



cluster

参数:

```
GeneralPlot::Image::Heatmap->plot(%opts)
```

```
-method          => 'cluster'
```

necessary:

```
-file
```

```
-outprefix
```

```
-outdir
```

```
-outname
```

optional:

```
-header          => T
```

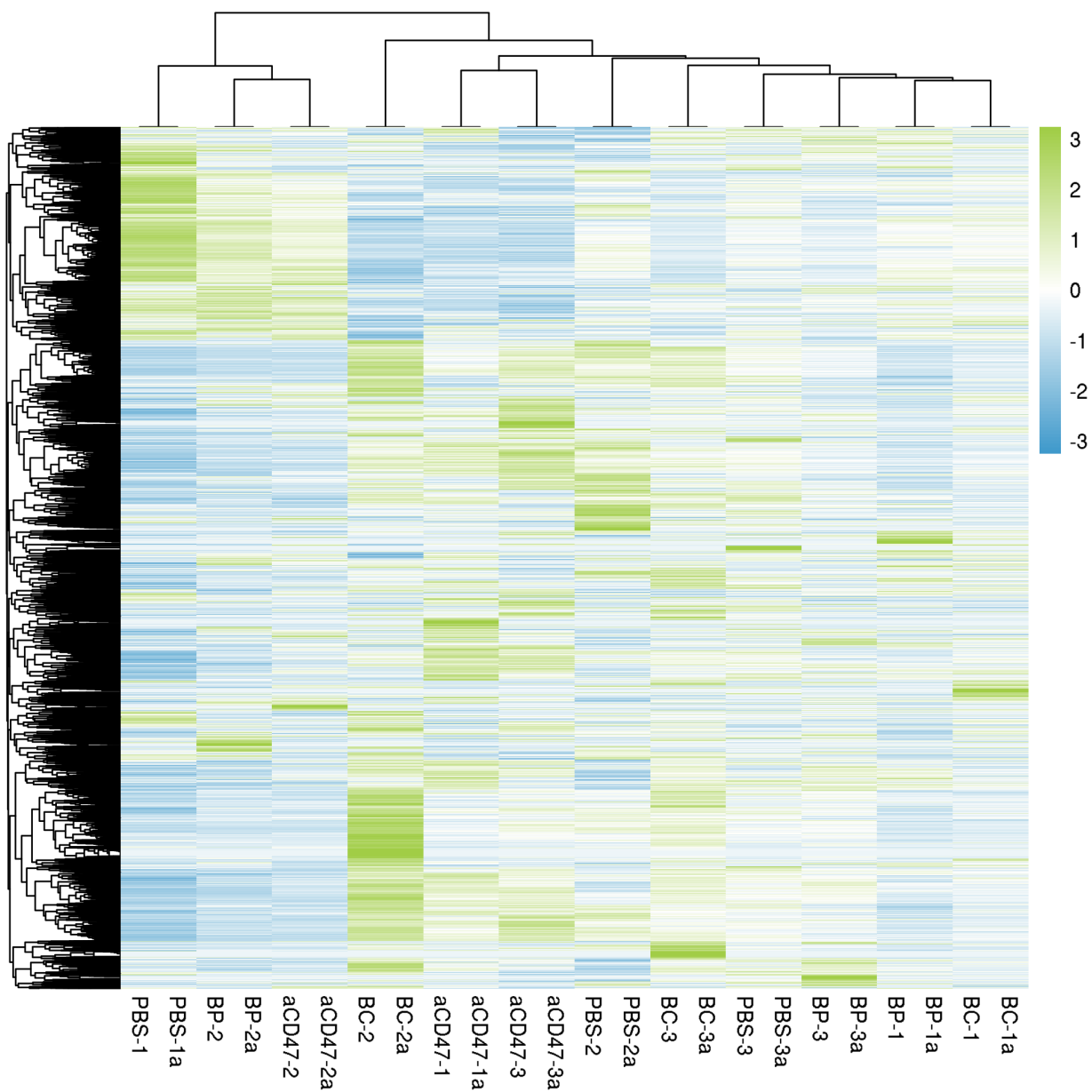
```
-rowcol          => 'col'          [ col | row ]
```

```
-namefix         => 'none'        [ _fpkm ... ]
```

```
-collist      => 'none',  
  
-title       => ""  
-xlab        => ''  
-ylab        => ''  
-legend      => 'T'  
-label       => 'F'  
  
-width       => 7  
-height      => 7  
  
-save        => T  
-run         => T  
-clean       => T
```

示例:

```
perl general_plot.pl cluster -file all.samples.exp.24.xls -outprefix all.  
samples.exp.24.cluster
```



补充说明

1、文件格式请参考示例目录，这里暂不列出。