

# Instruction of using MidtermScript.r

---

*Dan Jin. Oct. 15, 2012*

**To run this script, please copy MidtermScript.r to the same fold where containing two input data files, then type the following lines in R.**

```
source("MidtermScript.r")
result.ls=list()
result.ls=control.function()
```

## **Result of this script:**

1. return one list, **result.ls**, that includes all results required.
2. create **5 plots** in png format. (See below for more details)

## **Summary of the content in result.ls:**

1. \$beta.MLE: beta.MLE (note: includes all beta.MLE for each test);
2. \$pval: p value (note: includes all p value for each test);
3. \$hits.ls: all genotype marker (marker number and their p value) significant than Bonferroni correction;
4. \$hit.set.ls: distinct sets;
5. \$sig.hit.ls: the most significant marker in each set (marker number and the associated p value);
6. \$sig.hit.ls: MAF for the most significant genotype markers in each set;
7. \$sig.hit.GWAS: the most significant genotype marker in GWAS overall (marker number and its p value);
8. \$corr.ls: correlation of Xa between this marker and one of the markers to its left and right colomn. correlation of Xa between this marker and marker 409

## **Structure of result.ls:**

```
result.ls
|-$beta.MLE
|-$pval
|-$hits.ls
|  |-$position
|  |-$pval
|
|-$hit.set.ls
|-$sig.hit.ls
|  |-$position
|  |-$pval
|  |-$MAF
|
|-$sig.hit.GWAS
|  |-$position
|  |-$pval
```

```
|
|-$corr.ls
|  |
|  |-position.left
|  |-corr.left
|  |-position.right
|  |-corr.right
|  |-corr.409
```

### List of .png image files.

1. Q2-Histogram of the phenotypes.png
2. Q3-beta.a\_hat.png
3. Q3-beta.d\_hat.png
4. Q5-Manhattan Plot.png
5. Q6-Manhattan Plot with Bonferroni correction.png

### The following is a quick view of the data in result.ls:

```
> source("MidtermScript.r")
> result.ls=list()
> result.ls=control.function()
> result.ls
```

```
$beta.MLE
      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
[1,]  0.1906589 -1.6173730 -0.83658533 -1.5872665 -2.1088089 -0.8319530
[2,] -1.8521048  1.0918100 -0.37447354  0.4522081  1.0114511 -0.2210134
[3,] -0.3843263  0.7963517  0.04401317  0.1032542  0.1349533  0.2534198
...
```

```
$pval
 [1] 4.944906e-02 6.673668e-03 8.579912e-01 8.044802e-01 3.694046e-01
...
```

```
$s1
[1] "#####"
```

```
$hits.ls
$hits.ls$positon
 [1] 186 193 202 204 206 213 274 277 281 282 283 284 287 290
[15] 291 292 294 296 298 300 301 302 808 811 813 816 818 819
[29] 820 822 1166 1167 1173 1174 1182 1185 1188 1191
```

```
$hits.ls$pval
 [1] 4.457882 13.070888 4.798361 4.823398 9.372000 5.431085 4.388118
 [8] 5.712318 5.178458 6.710362 6.134569 6.665158 6.701824 4.833773
[15] 6.401800 6.704053 6.704053 6.423896 6.742694 6.727083 6.521027
[22] 6.484797 8.734447 14.781594 4.694469 13.914018 14.524456 14.476910
[29] 14.205841 5.413049 4.995273 5.081697 5.635441 5.560703 15.262291
[36] 5.394543 5.619389 5.536150
```

```
$s2
[1] "#####"
```

```

$hit.set.ls
$hit.set.ls[[1]]
[1] 186 193 202 204 206 213

$hit.set.ls[[2]]
[1] 274 277 281 282 283 284 287 290 291 292 294 296 298 300 301 302

$hit.set.ls[[3]]
[1] 808 811 813 816 818 819 820 822

$hit.set.ls[[4]]
[1] 1166 1167 1173 1174 1182 1185 1188 1191

$s3
[1] "#####"

$sig.hit.ls
$sig.hit.ls$position
[1] 193 298 811 1182

$sig.hit.ls$pval
[1] 8.493990e-14 1.808449e-07 1.653509e-15 5.466501e-16

$sig.hit.ls$MAF
[1] 0.222 0.288 0.430 0.259

$s4
[1] "#####"

$sig.hit.GWAS
$sig.hit.GWAS$position
[1] 1182

$sig.hit.GWAS$pval
[1] 5.466501e-16

$s5
[1] "#####"

$corr.ls
$corr.ls$position.left
[1] 1112

$corr.ls$corr.left
[1] -0.02848561

$corr.ls$position.right
[1] 1185

$corr.ls$corr.right
[1] 0.568552

$corr.ls$corr.409
[1] -0.0005280443

```