User Manual for Genome-wide Composite Interval Mapping (GCIM)

1. Introduction

GCIM, an R package, aims to provide a user-friendly interface to conduct linkage analysis via Genome-wide Composite Interval Mapping (GCIM) and to visualize its results. This GCIM software is within the software of **mrMLM** (multi-locus random-SNP-effect Mixed Linear Model). It works on the platforms of Windows, Linux and MacOS. The GUI is based on available add-on package RGtk2, via the aid of another package WidgetsRGtk2. The visualization of the results is based on package ggplot2, the plot of LOD score against genome position (cM).

2. Installation

2.1 Install GTK+

You may need to install GTK+ before installing RGtk2, because RGtk2 depends on GTK+.

For **Windows** user, you do as below:
Download GTK+ here
(http://sourceforge.net/projects/gladewin32/files/gtk%2B-win32 runtime/2.10.11/gtk-2.10.11-win32-1.exe).
Run the resulting file (gtk-2.10.11-win32-1.exe), which is an automated installer that will help you complete the installation of Gtk2 libraries.

For **Mac OS** users, you do as below:
Download GTK+ here (http://sourceforge.net/projects/gtk-osx/files/latest/download).
Extract and run the resulting file (gtk-osx-docbook-1.2.tar.gz).

For **Linux** users, you do as below:
You may or may not upgrade the GTK libraries depending on your distribution.
There are more details on RGtk2 at RGtk2's home page (http://www.ggobi.org/rgtk2/).

2.2 Install R

Download R from CRAN (https://cran.r-project.org/) and install it by running the downloaded file.

2.3 Install the R packages

The following R packages are necessary: RGtk2, cairoDevice, gWidgets, RGtk2Extras, openxlsx, ggplot2, gWidgetsRGtk2 and stringr, which can be downloaded from CRAN (https://cran.r-project.org/).

Install them in the order, as some depend on others. Within R environment, these packages can be installed directly using the below command:
install.packages(pkgs=c("RGtk2", "gWidgets", "gWidgetsRGtk2", "RGtk2Extras", "ggplot2(1.0.1)", "openxlsx", "stringr"))

2.4 Install mrMLM

The software GCIM within the mrMLM package is freely available at the CRAN (https://cran.r-project.org/web/packages/mrMLM/index.html or soyzhang@mail.hzau.edu.cn or soyzhang@hotmail.com), you can download or request this R software. Within R environment, the GCIM software can be installed directly using the below command: *install.packages(pkgs="mrMLM")*

3. Running

The **RUN** steps are described as below. Within R environment, launch the GCIM by command: *library(mrMLM)*, then the following dialog will appear after users press the GCIM button.

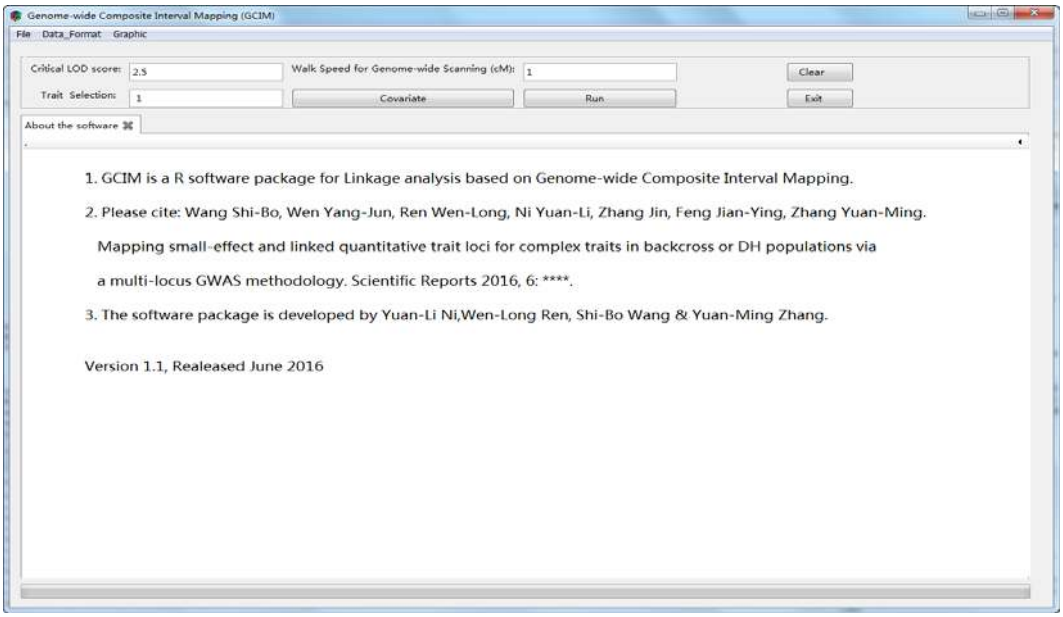


Figure 1. The GUI for **GCIM** in the software **mrMLM**

To restart the GUI, the command *mrMLM()* can be issued.

3.1 Data File Format for GCIM

3.1.1 GCIM Format

To click GCIM will appear GCIM dialog box. In the dialog box, there are four steps. Firstly, the **Genotype**, **Phenotype** and **Linkage Map** buttons are used to input genotype, phenotype and linkage map datasets, respectively. Once one file is successfully uploaded, one tabbed page is added to the software notebook. Secondly, the user selects the required the population type, including **BC_1 (F_1 × P_1)**, **BC_2 (F_1 × P_2)**, **DH**, **RIL** and **Chromosome Segment Substitution Lines (CSSL)**. Thirdly, users should give the symbols in the marker translation table that users indicate genotypes. Users can enter any alpha numeric character(s) as these symbols. In this software, these symbols will translate into numeric variables in our method. Fourthly, the user selects the required **QTL-effect model type**: **Random** and **Fixed** models. Finally, some things will be implemented in this step: 1) to upload the above three files; 2) to select population type; 3) to conduct marker-genotype translation; and 4) to select QTL-effect model. Once users press the **DO** button, these things may be executed, until GCIM Format dialog box disappear and **info** window is appeared. When click **Continue** button, the next work is to select covariate and to run the program. If click **Cancel** button, the next work is not to execute these above things and GCIM Format dialog box is also disappeared.

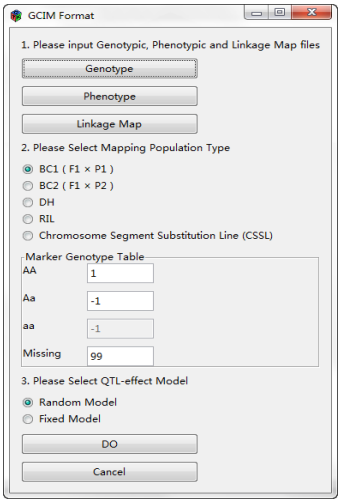


Figure 2. The **GCIM Format** dialog

3.1.2 QTLIciMaping Format

To click QTLIciMaping Format will appear QTLIciMaping dialog box. In the dialog box, there are three steps. Firstly, **QTLIciMaping_Format** button is used to input QTLIciMaping format datasets. Once the file is successfully uploaded, one tabbed page is added to the software notebook. Secondly, the user selects the required population type (see §3.1.1). Thirdly, the users select the required QTL-

effect model type (see §3.1.1). Finally, two things will be implemented in this step: 1) to upload QTLIciMaping-formatted files; and 2) to select population and model types. Once users press the **DO** button, the two things may be executed. Three tabbed pages (Genotype, Phenotype and Linkage map) will be added to the software notebook, and QTLIciMaping Format dialog box will be disappeared. To click **Cancel** button is not to execute the above things and QTLIciMaping Format dialog box is also disappeared.

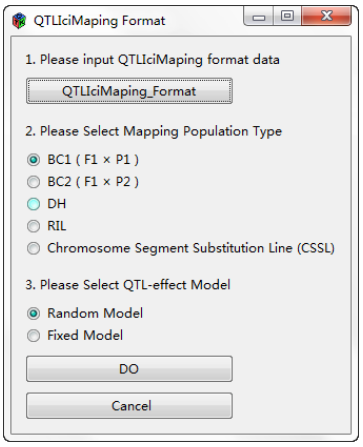


Figure 3. The **QTLIciMapping Format** dialog

3.3 WinQTLCart Format

To click WinQTLCart will appear WinQTLCart dialog box. In the dialog box, there are three steps. Firstly, **WinQTLCart_Format** button is used to input WinQTLCart format datasets. Once the related files are successfully uploaded, the tabbed pages are added to the software notebook. Secondly, the users select the required population type (see §3.1.1), and the users select the required model type (see §3.1.1). Finally, two things will be implemented in this step: 1) to upload WinQTLCart format files; and 2) to select population and model types. Once users press the **DO** button, the two things may be executed, three tabbed pages (Genotype, Phenotype and Linkage map) will be added to the software notebook, and WinQTLCart Format dialog box will be disappeared. If to click **Cancel** button, the next work is not to execute the above two things and WinQTLCart Format dialog box is also disappeared.

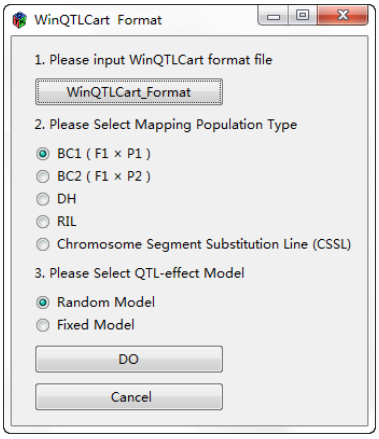


Figure 4. The **WinQTLCart** Format dialog

3.1.4. Covariate

To click **Covariate** button will appear **Covariate** dialog box. In the dialog box, covariate(s) may be not included in the genetic model if there is no covariate. If not, the covariates should be included in the genetic model. Once the covariate file is successfully uploaded, the tabbed page will add to the software notebook.

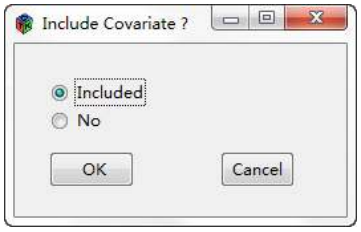


Figure 5. The **Covariate** dialog

Note: About the **input file formats** in details, please see **Direction 1** at the end of the manual.

3.2 Run Program

Before run the program, please set up **the Critical LOD score**, which is defaulted by the 2.5 (LOD) value. If a LOD score for a putative QTL is larger than the Critical LOD score, the putative QTL is viewed as true. If not, the putative QTL is viewed as false. Of course, the critical LOD score may be determined by permutation tests. If doing so, the software **WinQTLCart** is available. **Walk Speed for Genome-wide Scanning (cM)** is defaulted by the 1.0 (cM) value, which may be modified by users. **Trait Selection** is defaulted by the first trait. If user wants to analyze the third trait, the value in Trait Select column is set up by "3". In the GCIM, to click Run button will execute the software. If the program runs, a progress bar with the "**Please be patient...**" words will appear in the bottom of the interface. If the program finished, a bar with the "**All done.**" will appear.

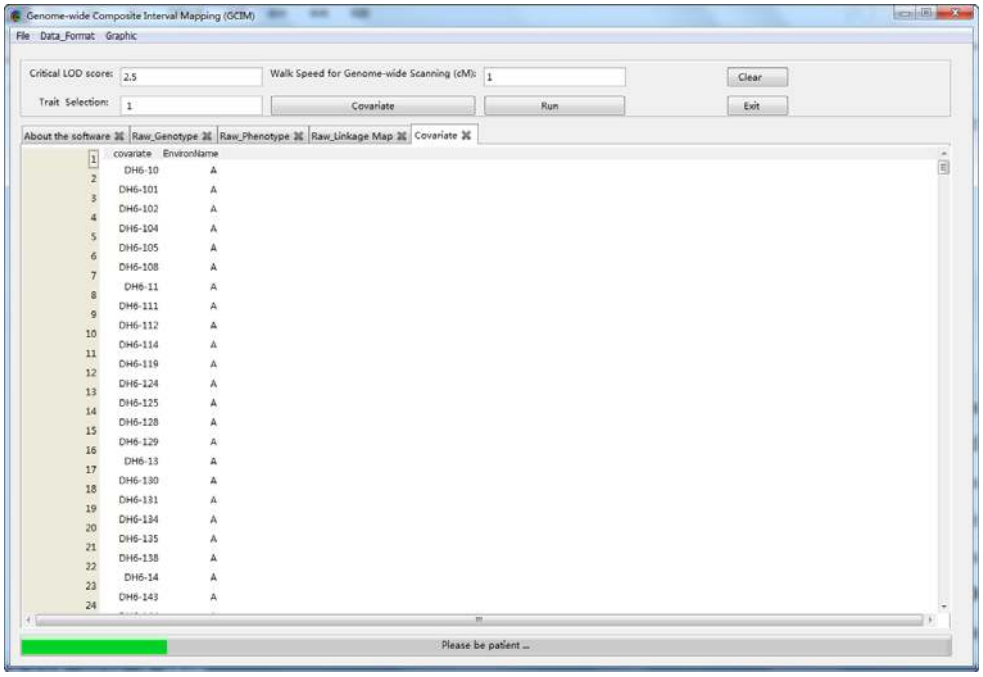


Figure 6. A running program interface

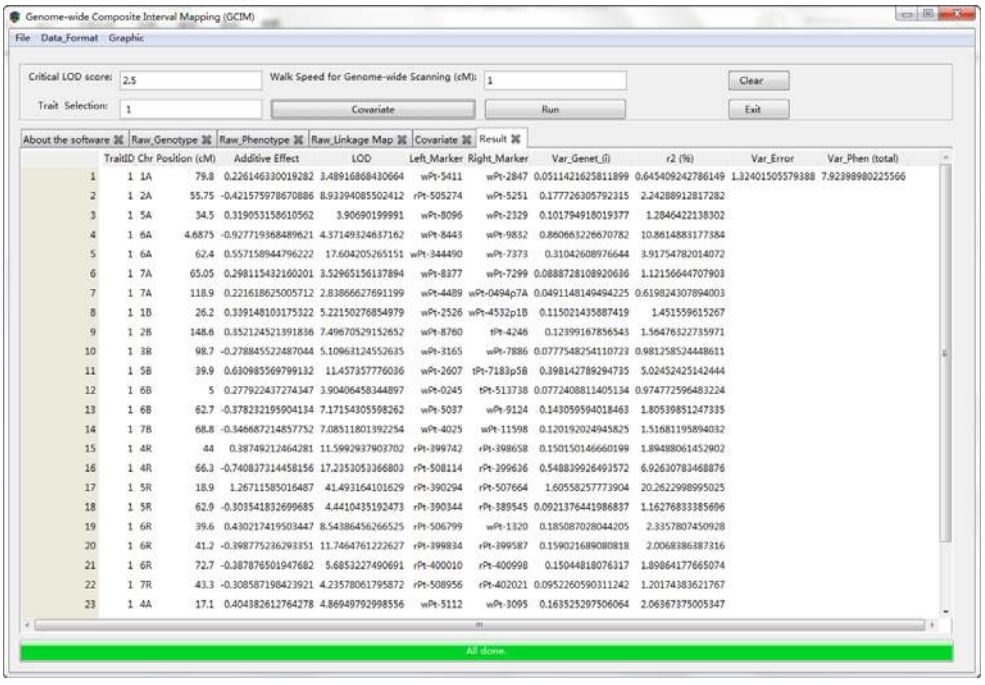


Figure 7. A finished program interface (the GCIM Results: Trait 1)

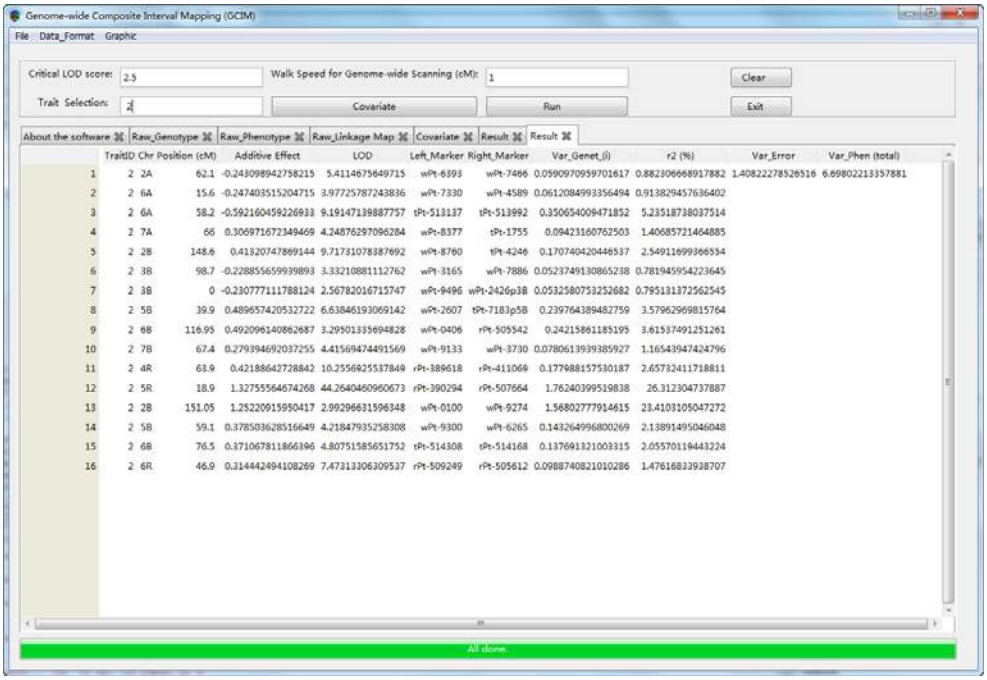


Figure 8. A finished program interface (the GCIM Results: Trait 2)

3.3 Save results

To click **save** button in the **File** menu is used to save the result as *.csv file. When a trait is analyzed, the results may be saved, a dialog is used to select the pathway and the file name for the saved file.

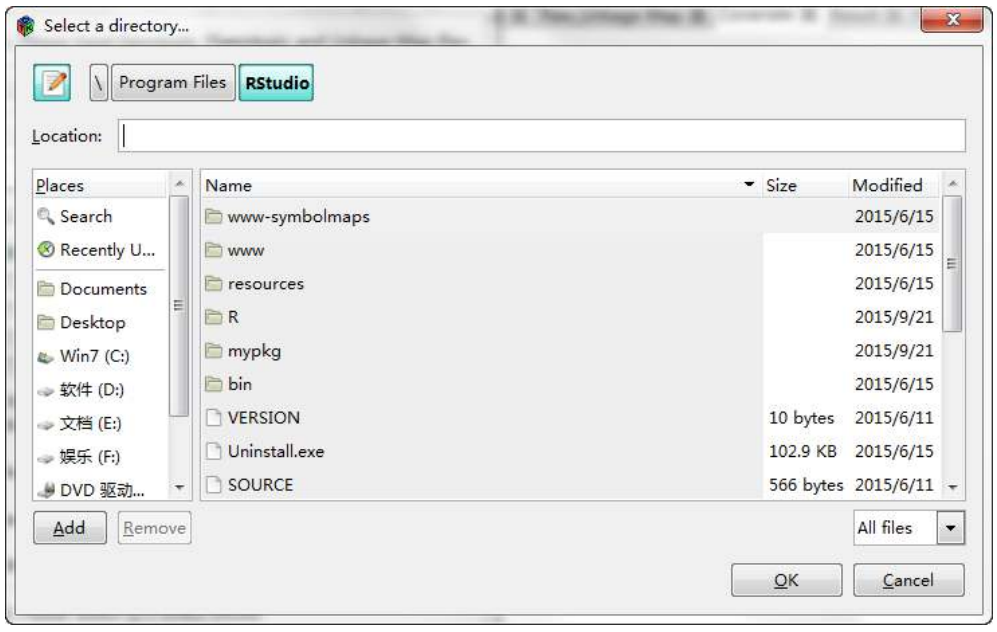


Figure 9. The **Save** dialog

Warning: It is better not to include other languages except English in the pathway and file name. Otherwise, there may be something wrong.

4. Visualization of Results

If the running is ended, user may visualize the result by selecting **plot** button in the Graphic menu. Before clicking **Save** button in the **Plot of LOD Score against Genome Position** window, you can set up the **width** (mm), **height** (mm) and **precision** (dpi).

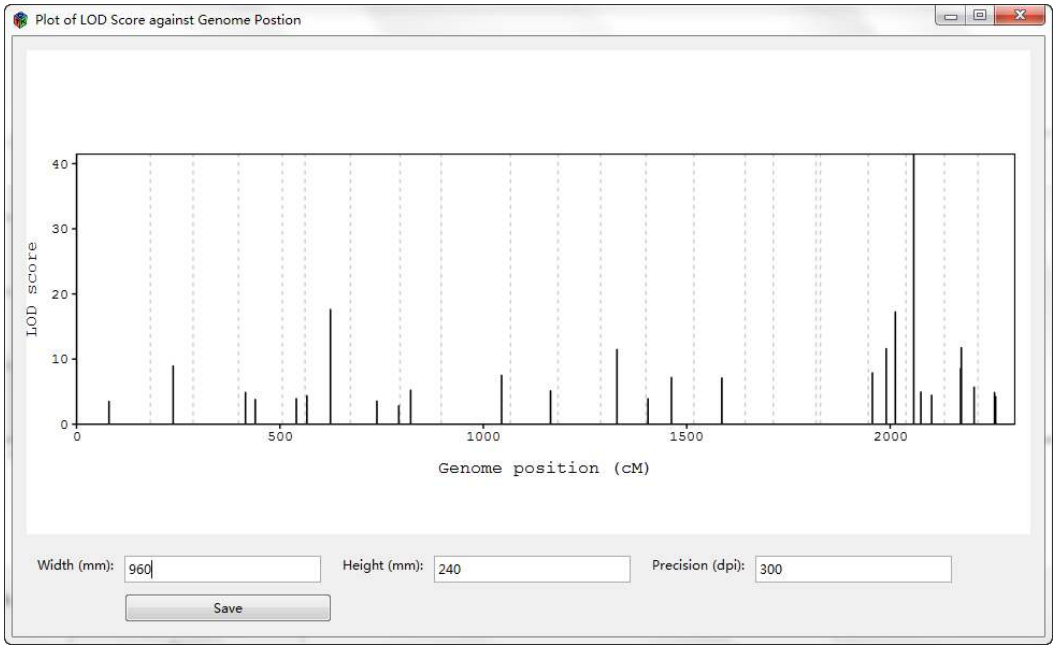


Figure 10. The **Plot of LOD Score against Genome Position (cM)**

Directions

Direction 1: Explanation of input files in details

D1.1 GCIM format

D1.1.1 The Genotypic file

The **Genotypic** file should be a ***.csv** format file. In the first column, "**genotype**" is showed in the first row and marker names are appeared from row 2 to row *m*+1 (*m* is the number of markers). In the column 2, **individual ID or individual names** is appeared in the first row and marker genotypes for all the markers are listed in the other rows. For the other rows, it is similar to the column 2.

Population Type. At present, GCIM can analyze five population types derived from two parental lines. $F_1 = P_1 \times P_2$.

1. BC_1: $F_1 \times P_1$. 1 stands for AA, -1 stands for Aa, and 99 stands for missing genotypes.

2. BC_2: $F_1 \times P_2$. 1 stands for Aa, -1 stands for aa, and 99 stands for missing genotypes.

3. DH: doubled haploid lines derived from F_1. 1 stands for AA, -1 stands for aa, and 99 stands for missing genotypic value.

4. RIL: recombinant inbred lines derived from repeatedly selfing since F_1. 1 stands for AA, -1 stands for aa, and 99 stands for missing genotypes.

5. Chromosome Segment Substitution Line (CSSL): 1 stands for AA, -1 stands for aa, 99 stands for missing genotypes.

	A	B	C	D	E	F	G	H	I	J	K	L
1	genotype	DH6-10	DH6-101	DH6-102	DH6-104	DH6-105	DH6-108	DH6-11	DH6-111	DH6-112	DH6-114	DH6-119
2	wPt-9752	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
3	wPt-8770	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
4	wPt-1167	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
5	wPt-5876	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
6	wPt-3870	1	1	1	1	1	1	1	1	1	1	1
7	wPt-6280	1	1	1	1	1	1	1	1	1	1	1
8	wPt-3867	1	1	1	1	1	1	1	1	1	1	1
9	wPt-5411	1	1	1	1	1	1	1	1	1	1	1
10	wPt-7339	-1	-1	-1	1	-1	-1	1	1	1	-1	-1
11	wPt-2847	1	1	1	1	1	1	1	1	1	1	1
12	wPt-8016	1	1	1	-1	1	1	-1	-1	-1	1	1
13	wPt-4658	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
14	tPt-51378	-1	-1	-1	-1	-1	-1	1	1	-1	-1	1
15	wPt-7430	-1	-1	-1	-1	-1	-1	1	1	-1	-1	1
16	wPt-9757	-1	1	-1	-1	-1	-1	1	1	-1	-1	1
17	wPt-7030	-1	1	-1	1	-1	-1	1	1	-1	-1	1
18	wPt-4765	-1	1	-1	1	-1	-1	1	1	-1	-1	1
19	wPt-7184	1	-1	1	1	1	1	-1	1	1	1	-1
20	wPt-9429	-1	1	-1	1	-1	-1	1	1	-1	-1	1
21	tPt-51377	-1	1	-1	1	-1	-1	1	1	-1	-1	1
22	wPt-5941	-1	1	-1	1	-1	-1	1	1	-1	-1	1

Figure D1.1.1 The **genotypic** file with **GCIM** format

D1.1.2 The Phenotypic file

The **Phenotypic** file should be a ***.csv** format file. In the first column, “phenotype” is appeared in the first row and **individual ID or individual names** are listed in the other rows, such as DH6-10, DH6-101 and DH6-101. In the second column, the phenotypic values for the first trait are listed. The trait name is appeared in the first row, such as DS1–BLUEs, and observations are listed in the other rows. In the other columns, it is similar to the column 2. Missing phenotypic values is indicated by **NA**.

	A	B	C	D
1	phenotyp	DS1 BLUEs	DS2 BLUEs	DS3 BLUEs
2	DH6-10	46.4832	68.34811	82.22822
3	DH6-101	45.38132	67.97619	81.51473
4	DH6-102	45.70267	68.53223	82.31631
5	DH6-104	43.89463	67.94785	81.42319
6	DH6-105	43.40711	66.44586	80.5653
7	DH6-108	48.77381	68.71128	82.75909
8	DH6-11	46.7418	68.83311	82.12227
9	DH6-111	43.48794	67.78476	81.60943
10	DH6-112	44.66737	68.73259	82.8079
11	DH6-114	41.28731	62.52602	81.75011
12	DH6-119	48.44181	69.23856	82.49072
13	DH6-124	42.89888	68.03529	81.5066
14	DH6-125	45.83477	68.47224	82.69455
15	DH6-128	42.55648	65.3753	81.21193
16	DH6-129	46.34065	68.75757	80.89524
17	DH6-13	44.57828	68.37544	81.3758
18	DH6-130	46.14527	68.61368	81.3821
19	DH6-131	45.31128	68.45102	82.70197
20	DH6-134	46.16461	68.66404	81.19782
21	DH6-135	47.26563	69.00265	82.5961
22	DH6-138	42.18055	66.37762	81.28508

Figure D1.1.2 The **Phenotypic** file with **GCIM** format

D1.1.3 The Linkage Map file

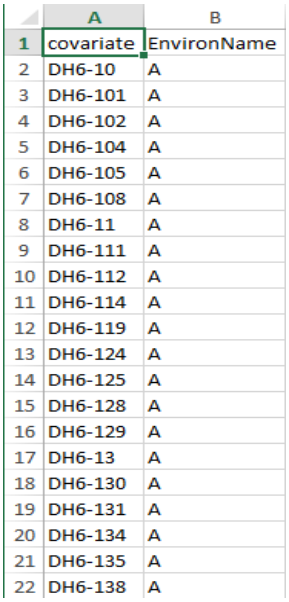
The **Linkage Map** file should be a ***.csv** format file. In the first column, “marker” is appeared in the first row, and marker names are listed in the other rows. In the second column, “chr” is chromosome and appeared in the first row, and chromosome information for all the markers are listed in the other rows. In the third column, “pos” is marker position information, marker position (cM) are listed in the other rows. Note that the marker position is not interval length.

	A	B	C
1	marker	chr	pos
2	wPt-9752	1A	0
3	wPt-8770	1A	1.6
4	wPt-1167	1A	2.3
5	wPt-5876	1A	3
6	wPt-3870	1A	5
7	wPt-6280	1A	6.6
8	wPt-3867	1A	40.8
9	wPt-5411	1A	62.4
10	wPt-7339	1A	79.8
11	wPt-2847	1A	80.1
12	wPt-8016	1A	80.7
13	wPt-4658	1A	81.3
14	tPt-513785	1A	107.7
15	wPt-7430	1A	111
16	wPt-9757	1A	116.1
17	wPt-7030	1A	117.9
18	wPt-4765	1A	118.8
19	wPt-7184	1A	119.5
20	wPt-9429	1A	120.1
21	tPt-513770	1A	121.4
22	wPt-5941	1A	121.6

Figure D1.1.3 The **linkage map** file with **GCIM** format

D1.1.4 The Covariate file

The **Covariate** file should be a ***.csv** format file. In the first column, "covariate" is appeared in the first row and **individual names** or **individual ID,** such as DH6-10, DH6-101 and DH6-101, are listed in the other rows. In the second column, the name for the first covariate is appeared in the first row and covariate information is listed in the other row. The other columns are similar to the second column if there are several covariates.



	A	B
1	covariate	EnvironName
2	DH6-10	A
3	DH6-101	A
4	DH6-102	A
5	DH6-104	A
6	DH6-105	A
7	DH6-108	A
8	DH6-11	A
9	DH6-111	A
10	DH6-112	A
11	DH6-114	A
12	DH6-119	A
13	DH6-124	A
14	DH6-125	A
15	DH6-128	A
16	DH6-129	A
17	DH6-13	A
18	DH6-130	A
19	DH6-131	A
20	DH6-134	A
21	DH6-135	A
22	DH6-138	A

Figure D1.1.4 The **Covariate** file with **GCIM** format

D1.2 QTLIciMaping format

Please see the QTLIciMaping software in details. Here we introduce simply. QTLIciMaping have five sheets, including GeneralInfo, Chromosome, LinkageMap, Genotype and Phenotype. Note that only LinkageMap, Genotype and Phenotype sheets will be showed in the software.

D1.2.1 Genotypic format

The first column stands for marker ID. And each of the remaining columns stands for one individual. In QTL IciMapping, 2 was used to represent the marker genotype of the first parent (P_1), 0 for the second parent (P_2), 1 for the F_1, and -1 for missing genotypes.

	A	B	C	D	E	F	G	H	I	J	K	L
1	RCA3(1)	0	-1	0	2	0	0	2	2	2	-1	0
2	wPt-6358	0	-1	-1	-1	-1	0	2	2	2	-1	0
3	Hplc2	2	2	0	2	0	0	2	2	2	0	0
4	wPt-9752	2	-1	-1	-1	-1	-1	2	2	2	-1	0
5	abc156a	2	2	0	2	0	0	0	0	2	0	-1
6	RCA36b(2)	2	-1	0	2	-1	0	0	0	2	-1	0
7	bcd98	0	2	0	2	0	0	0	0	2	0	2
8	wmc24	0	2	0	2	0	0	0	0	2	0	2
9	ksuG9c	0	2	0	2	0	0	0	0	2	0	2
10	wPt-2436	0	-1	-1	-1	-1	0	0	0	0	-1	2
11	wPt-4886	0	-1	-1	-1	-1	0	0	0	0	-1	2
12	wmc120	0	2	0	2	0	0	0	0	0	2	2
13	cdo105	0	2	0	2	0	0	0	0	0	2	2
14	wPt-6074	0	-1	-1	-1	-1	0	0	0	0	-1	2
15	GluA1	0	2	0	2	0	2	0	0	0	2	2
16	bcd808b	0	2	2	0	0	2	0	2	0	0	2
17	wis-2	0	2	2	0	0	2	0	2	0	-1	2
18	wPt-5316	0	-1	-1	-1	-1	2	0	2	0	-1	2
19	ksuH9b	0	2	2	0	0	2	0	2	0	0	2
20	RCA24(1)	0	-1	2	0	-1	2	0	2	0	-1	2
21	wPt-5274	0	-1	-1	-1	-1	2	0	2	0	-1	2
22	wPt-6005	0	-1	-1	-1	-1	2	0	2	0	-1	2

Figure D1.2.1 The **genotypic** file in the **QTLIciMaping** software

D1.2.2 Phenotypic format

The first column stands for trait ID. And each of the remaining columns stands for the phenotypic value of every individual. Note that -100 stands for missing phenotypes.

	A	B	C	D	E	F	G	H	I	J	K	L
1	T15	103	111.7	106.7	92.67	122	93.67	108	118.3	102.3	-100	130
2	T19	75.33	105	96.33	81	101.7	89	82.67	133.3	105	-100	104.7

Figure D1.2.2 The **phenotypic** format in the **QTLIciMaping** software

D1.2.3 Linkage map format

The linkage map file has three columns. The first column stands for marker ID, the second column stands for chromosome, and the third column is marker position (cM) in the chromosome.

	A	B	C
1	RGA3(1)	1	0
2	wPt-6358	1	3.034
3	Hplc2	1	8.8291
4	wPt-9752	1	10.1452
5	abc156a	1	41.3408
6	RGA36b(2)	1	43.8429
7	bcd98	1	51.9122
8	wmc24	1	54.5814
9	ksuG9c	1	55.3333
10	wPt-2436	1	59.1871
11	wPt-4886	1	61.7209
12	wmc120	1	62.4012
13	cdo105	1	63.0679
14	wPt-6074	1	69.7745
15	GluA1	1	81.5246
16	bcd808b	1	105.233
17	wis-2	1	114.697
18	wPt-5316	1	122.159
19	ksuH9b	1	122.796
20	RGA24(1)	1	134.641
21	wPt-5274	1	137.31
22	wPt-6005	1	138.515

Figure D1.2.3 The **Linkage map** format in the **QTLIciMaping** software

D1.3 WinQTLCart format

Please see the WinQTLCart software in details. Here we introduce simply. Between the first "–start" and "–stop" information, marker information is listed, including **chromosome name**, **marker name** and **position (interval length)**. Between the second "–start" and "–stop", genotypic information is showed. Between the third "–start" and "–stop", phenotypic information is appeared. If variable information is included, it will be **otrait** information between the fourth "–start" and "–stop".

```
#FileID 1438801284
#bychromosome
 -type position
 -function 1
 -Units cM
 -chromosomes 3
 -maximum 13
 -named yes
 -start
 -Chromosome C1
  AXR-1          0.0000
  HH.335C-COL    9.3000
  EC.480C       17.2000
  EC.650C       29.9000
  GC.845L       38.7000
  G23554        52.8000
  CH.160L-COL   57.8000
  DF.701L       72.4000
  AD.333C       76.6000
  GBB.80L       93.2000
  GD.97L        97.0000
  FD.8411L     115.5000
  MXF-F-001    116.5000
```

Figure D1.3 The **mcd** file in the **WinQTLCart** software

D2.1 Explanation of Result file

The **Results** are listed in ten columns for the GCIM (Genome-wide Composite Interval Mapping) method. The corresponding column names are as follows:

TraitID: Trait ID represented by an integer number.

Chr: Raw name of chromosome or chromosome ID represented by an integer number.

Position (cM): The scanning position (cM) on the chromosome.

Additive Effect: Estimated additive effect of the putative QTL.

LOD: LOD score for the putative QTL.

Left_Marker: Left flanking marker name of current scanning position (or putative QTL).

Right_Marker: Right flanking marker name of current scanning position (or putative QTL).

Var_Genet_(i): Genetic variance for all the detected QTL

r2 (%): proportion of phenotypic variance explained by single QTL.

Var_Error: residual variance for the full model.

Var_Phen (total): Phenotypic variance

	A	B	C	D	E	F	G	H	I	J	K
1	TraitID	Chr	Position (cM)	Additive Effect	LOD	Left_Marker	Right_Marker	Var_Genet_(i)	r2 (%)	Var_Error	Var_Phen (total)
2	1	1A	79.8	0.22614633	3.489168684	wPt-5411	wPt-2847	0.051142163	0.645409	1.324015	7.923989802
3	1	2A	55.75	-0.421575979	8.933940855	rPt-505274	wPt-5251	0.177726306	2.242889		
4	1	5A	34.5	0.319053159	3.906902	wPt-8096	wPt-2329	0.101794918	1.284642		
5	1	6A	4.6875	-0.927719368	4.371493246	wPt-8443	wPt-9832	0.860663227	10.86149		
6	1	6A	62.4	0.557158945	17.60420527	wPt-344490	wPt-7373	0.31042609	3.917548		
7	1	7A	65.05	0.298115432	3.529651561	wPt-8377	wPt-7299	0.088872811	1.121566		
8	1	7A	118.9	0.221618625	2.838666277	wPt-4489	wPt-0494p7A	0.049114815	0.619824		
9	1	1B	26.2	0.339148103	5.221502769	wPt-2526	wPt-4532p1B	0.115021436	1.45156		
10	1	2B	148.6	0.352124521	7.496705292	wPt-8760	tPt-4246	0.123991679	1.564763		
11	1	3B	98.7	-0.278845522	5.109631246	wPt-3165	wPt-7886	0.077754825	0.981259		
12	1	5B	39.9	0.63098557	11.45735778	wPt-2607	tPt-7183p5B	0.398142789	5.024524		
13	1	6B	5	0.277922437	3.904064583	wPt-0245	tPt-513738	0.077240881	0.974773		
14	1	6B	62.7	-0.378232196	7.171543056	wPt-5037	wPt-9124	0.143059594	1.805399		
15	1	7B	68.8	-0.346687215	7.085118014	wPt-4025	wPt-11598	0.120192025	1.516812		
16	1	4R	44	0.387492125	11.59929379	rPt-399742	rPt-398658	0.150150147	1.894881		
17	1	4R	66.3	-0.740837314	17.23530534	rPt-508114	rPt-399636	0.548839926	6.926308		
18	1	5R	18.9	1.26711585	41.4931641	rPt-390294	rPt-507664	1.605582578	20.2623		
19	1	5R	62.9	-0.303541833	4.441043519	rPt-390344	rPt-389545	0.092137644	1.162768		
20	1	6R	39.6	0.43021742	8.543864563	rPt-506799	wPt-1320	0.185087028	2.335781		
21	1	6R	41.2	-0.398775236	11.74647612	rPt-399834	rPt-399587	0.159021689	2.006839		
22	1	6R	72.7	-0.387876502	5.685322749	rPt-400010	rPt-400998	0.150448181	1.898642		
23	1	7R	43.3	-0.308587198	4.235780618	rPt-508956	rPt-402021	0.095226059	1.201744		
24	1	4A	17.1	0.404382613	4.86949793	wPt-5112	wPt-3095	0.163525298	2.063674		
25	1	4A	41.1	-0.263567278	3.790975912	wPt-5428	wPt-5951	0.06946771	0.876676		
26	1	4R	9.9	0.649501366	7.885505762	wPt-8336	wPt-7840	0.421852024	5.323733		
27	1	5R	36.5	0.404239323	4.928059606	rPt-509673	rPt-398691	0.16340943	2.062212		
28	1	7R	40.7	0.316359724	4.862103473	rPt-505765	rPt-401366	0.100083475	1.263044		

Figure D2.1.1. Results in the **GCIM** (Result: **Trait 1**)

	A	B	C	D	E	F	G	H	I	J	K	L
1	TraitID	Chr	Position (cM)	Additive Effect	LOD	Left_Marker	Right_Marker	Var_Genet_(i)	r2 (%)	Var_Error	Var_Phen (total)	
2	2	2A	62.1	-0.243098943	5.411468	wPt-6393	wPt-7466	0.059097096	0.882307	1.408223	6.698022	
3	2	6A	15.6	-0.247403515	3.977258	wPt-7330	wPt-4589	0.061208499	0.913829			
4	2	6A	58.2	-0.592160459	9.191471	tPt-513137	tPt-513992	0.350654009	5.235187			
5	2	7A	66	0.306971672	4.248763	wPt-8377	tPt-1755	0.094231608	1.406857			
6	2	2B	148.6	0.413207479	9.717311	wPt-8760	tPt-4246	0.17074042	2.549117			
7	2	3B	98.7	-0.22885566	3.332109	wPt-3165	wPt-7886	0.052374913	0.781946			
8	2	3B	0	-0.230777112	2.56782	wPt-9496	wPt-2426p3B	0.053258075	0.795131			
9	2	5B	39.9	0.489657421	6.638462	wPt-2607	tPt-7183p5B	0.239764389	3.57963			
10	2	6B	116.95	0.492096141	3.295013	wPt-0406	rPt-505542	0.242158612	3.615375			
11	2	7B	67.4	0.279394692	4.415695	wPt-9133	wPt-3730	0.078061394	1.165439			
12	2	4R	63.9	0.421886427	10.25569	rPt-389618	rPt-411069	0.177988158	2.657324			
13	2	5R	18.9	1.327555647	44.26405	rPt-390294	rPt-507664	1.762403995	26.3123			
14	2	2B	151.05	1.25220916	2.992966	wPt-0100	wPt-9274	1.568027779	23.41031			
15	2	5B	59.1	0.378503629	4.218479	wPt-9300	wPt-6265	0.143264997	2.138915			
16	2	6B	76.5	0.371067812	4.807516	tPt-514308	tPt-514168	0.137691321	2.055701			
17	2	6R	46.9	0.314442494	7.473133	rPt-509249	rPt-505612	0.098874082	1.476168			

Figure D2.1.2 Results in the **GCIM** (Result: **Trait 2**)