

Software / IQI v1.0 (Java)

Introduction

IQI v1.0 (Java) has the following main functions.

- 1、 Calculate the degree (IQI) of regulation between SNP and the quantitative phenotype for each single sample.
- 2、 Perform the standard hypothesis testing method - DQ test, to accurately detect the QTL regulation changes in disease state.

Note: The two functions are implemented by one command line.

Pre-installation

IQI v1.0 (Java) is implemented by Java. Before using it, please install [Java programing environment](#) (Java 8 or update) first.

Download

[IQI v1.0 \(Java, Command-line running\)](#)

Usage

command-line example:

```
java -jar IQI.jar -DQ.test -input.pheno_1 phenotype\_1.txt -input.pheno_0 phenotype\_0.txt -input.geno_0 genotype\_0.txt -input.geno_1 genotype\_1.txt -output.IQI_0 IQI\_0.txt -output.IQI_1 IQI\_1.txt -output.eQe_test DQ\_test\_result.txt
```

parameters:

- DQ.test: Perform the DQ test;
- input.pheno_1: Input the phenotype information of the case group;
- input.pheno_0: Input the phenotype information of the control group;
- input.geno_0: Input the SNP genotype data of the case group;
- input.geno_1: Input the SNP genotype data of the control group;
- output.IQI_0: Specify the file name of the IQI values of the SNP-phenotype pairs of all samples in the control group;
- output.IQI_1: Specify the file name of the IQI values of the SNP-phenotype pairs of all samples in the case group;
- output.eQe_test: Specify the file name of the results of DQ test.

Input phenotype file

please see [phenotype_1.txt](#) and [phenotype_0.txt](#) for more information

```
Gene→sample1→sample2→sample3→sample4→sample5→sample6→sample7→sample8→sample9→sample10→
Gene1→7.277892592→7.131781215→4.739206133→3.293924424→5.519652169→7.263166
Gene2→-0.749986321→-0.486092578→0.440564831→-0.967294794→-0.022983214
Gene3→1.607443978→1.89183677→2.371212104→1.705601189→2.30635606→1.876922
Gene4→1.554325189→1.882135295→2.905419185→2.14552173→2.78595273→1.996336
Gene5→2.455953556→0.325004256→-1.646837322→-1.313823954→-0.90075176→
Gene6→0.854339273→7.590108599→2.640719759→0.692701539→3.941547344→4.541120
Gene7→6.290496647→5.798508771→6.111434888→7.280799496→2.830754116→6.086360
Gene8→-1.932175133→-4.349342775→-0.759426544→-1.550274264→0.61
Gene9→2.079321501→4.661192454→4.72414281→3.634468298→2.392000371→2.543756
Gene10→-0.333984057→0.974384607→0.724378605→1.175572621→2.219008096→-1.0
```

column 1: (e.g. Gene1) is the ID or name of a phenotype.

column 2 to the last: (e.g. 7.277892592) is the phenotype information of each sample.

Input genotype file

please see [genotype_1.txt](#) and [genotype_0.txt](#) for more information

```

SNP>ALLELE→MINOR.ALLELE→sample1>sample2>sample3>sample4>sample5>sample6>
rs10001>G/A>G→AA→AA→AA→AA→AA→AG→AA→AG→AA→AA→AA→AA→GG→AA→AA→
rs10002>T/C>T→CT→CC→CC→CC→TT→CC→CT→CC→CC→CC→CC→CT→CC→CC→CC→
rs10003>T/C>C→TT→TC→TT→TT→TT→TT→TC→TC→CC→TC→CC→TT→TT→TC→TC→
rs10004>T/C>T→CC→CC→TT→CT→CT→CC→CC→CC→CT→CT→CC→TT→CC→CT→CC→
rs10005>T/C>T→CC→CT→CT→CC→CT→CT→CC→CC→CC→CT→CC→TT→CT→CC→CC→
rs10006>A/G>G→AA→AA→AA→AG→AA→AA→GG→AG→AG→GG→AG→AA→AA→AA→AG→
rs10007>A/G>A→GG→GA→AA→GG→GG→GA→GA→GA→GG→AA→GA→GG→GG→AA→AA→
rs10008>A/G>G→AA→AA→AA→AA→AG→GG→AG→AA→AA→AA→GG→GG→AA→AA→AA→
rs10009>G/A>A→GG→GG→GA→GG→GA→GG→GA→GA→GG→GA→GA→GG→GG→GG→GA→
rs10010>G/A>A→GG→GA→GG→AA→GA→GG→GG→GA→AA→GG→GG→GG→GA→GA→GG→

```

column 1: (e.g. rs10001) is the name of an SNP.

column 2: (e.g. G/A) is the two alleles.

column 3: (e.g. G) is the minor allele.

column 4 to the last: (e.g. AA) is the genotype of each sample.

Output IQI file

please see [IQI_1.txt](#) and [IQI_0.txt](#) for more information

```

SNP_Gene→sample1>sample2>sample3>sample4>sample5>sample6>sample7>sample8>
rs10010_Gene1→-0.677544→-1.131207→-0.659939→0.930822→1.086707→0.16143
rs10008_Gene1→-0.707659→1.056176→-0.689271→-0.300311→1.099180→0.14019
rs10009_Gene1→-0.746355→1.113930→0.721169→-0.316732→1.061582→0.15184
rs10004_Gene1→-0.690956→1.031248→1.997642→0.288569→0.974955→0.13111
rs10005_Gene1→-0.703929→-1.129078→0.736847→-0.298728→1.084661→0.17528
rs10006_Gene1→-0.707205→1.055499→-0.688829→0.302529→-1.013977→0.18904
rs10007_Gene1→-0.695570→-1.142820→2.169127→-0.295181→-0.997295→0.16187
rs10001_Gene1→-0.718828→1.072846→-0.700149→-0.305051→-1.030641→0.16522
rs10002_Gene1→1.507467→1.010818→-0.659670→-0.287414→5.293809→0.13388
rs10003_Gene1→-0.683192→-1.044428→-0.665439→-0.289928→-0.979547→0.15671
rs10010_Gene2→2.374625→1.285338→-1.690329→-0.352866→0.491422→0.17364
rs10008_Gene2→2.480169→-1.200084→-1.765458→0.113845→0.497062→0.18904
rs10009_Gene2→2.615788→-1.265706→1.847159→0.120070→0.480060→0.13111
rs10004_Gene2→2.421631→-1.171759→5.116644→-0.109394→0.440886→0.16187
rs10005_Gene2→2.467096→1.282919→1.887317→0.113245→0.490496→0.17528
rs10006_Gene2→2.478579→-1.199315→-1.764326→-0.114686→-0.458532→0.18904
rs10007_Gene2→2.437801→1.298533→5.555876→0.111900→-0.450989→0.16187
rs10001_Gene2→2.519313→-1.219025→-1.793322→0.115642→-0.466068→0.13388
rs10002_Gene2→-5.283299→-1.148546→-1.689639→0.108956→2.393922→0.15671
rs10003_Gene2→2.394418→1.186736→-1.704418→0.109909→-0.442963→0.17364

```

column 1: (e.g. rs10010_Gene1) is the name of the SNP-phenotype pair.

column 2 to the last: (e.g. -0.677544) is IQI of each sample.

DQ test results

please see [DQ_test_result.txt](#) for more information

```

SNP_Gene→change_type>beta_1→SE_1→p_1>beta_0→SE_0→p_0>dx1_x0→Sx1_x0→df→eQe_mean_1→eQe_mean_0→sample_num
rs10001_Gene1→GOE,-/O→-2.037791→0.073848→2.1228E-102→0.029417→0.077993→0.706205→-2.067208→0.16143
rs10001_Gene2→LOE,O/+→-0.076519→0.116169→0.510398→0.232988→0.080879→0.004139→-0.309507→0.14019
rs10002_Gene2→GOE,+/O→1.969310→0.074698→1.5567E-96→0.049207→0.085511→0.565248→1.920103→0.15184
rs10003_Gene3→LOE,O/-→0.027906→0.065411→0.669837→-1.519056→0.063573→1.2232E-84→1.546962→0.13111
rs10004_Gene4→LOE,O/+→0.023216→0.067263→0.730122→0.901411→0.066669→1.054E-35→-0.878195→0.10844
rs10005_Gene5→ROE,+/-→1.825745→0.065499→9.9926E-104→-1.736576→0.072568→8.2097E-85→3.562321→0.17528
rs10004_Gene6→LOE,O/+→-0.075922→0.111471→0.496129→0.243735→0.108733→0.025428→-0.319656→0.15770
rs10006_Gene6→ROE,-/+→-1.965373→0.070023→1.2194E-104→2.000344→0.065844→1.8389E-115→-3.965717→0.18904
rs10007_Gene7→SOE,--/-→-1.947513→0.068132→4.4395E-107→-0.945750→0.066752→1.5783E-38→-1.001762→0.16187
rs10008_Gene8→SOE,++/+→1.971503→0.067759→1.764E-109→1.081841→0.068378→5.6507E-46→0.889661→0.16522
rs10005_Gene8→GOE,+/O→0.288813→0.103515→0.005472→-0.092004→0.083323→0.270047→0.380818→0.13388
rs10009_Gene9→WOE,-/--→-0.910509→0.064703→4.1685E-38→-1.953974→0.065978→6.5642E-112→1.043465→0.15671
rs10010_Gene10→WOE,+/-→0.981220→0.070475→1.8835E-37→2.020827→0.068436→1.6678E-111→-1.039607→0.17364

```

It contains 18 columns:

SNP_Gene -> the name of SNP-phenotype pair;
change_type -> change type of QTL regulation;
beta_1 -> the traditional regression based QTL analysis results of the case group;
SE_1 -> the standard error in the case group;
p_1 -> the p value in the case group;
beta_0 -> the traditional regression based QTL analysis results of the control group;
SE_0 -> the standard error in the control group;
p_0 -> the p value in the control group;
dx1_x0 -> the mean difference between case and control groups;
Sx1_x0 -> the standard error between case and control groups;
df -> the degree of freedom;
eQe_mean_1 -> the average IQI in the case group;
eQe_mean_0 -> the average IQI in the control group;
sample_num_1 -> the sample size of the case group;
sample_num_0 -> the sample size of the control group;
fold_change -> the fold change value;
t -> the DQ statistics;
tp -> the p value.

The simulated data and results were offered to test: [Download](#)