**Mapping vQTL(& QTL)**

To map vQTL(& QTL) you need to have the following files in the folder “Vqtl-interactions”:

* 1. getphenogeno.R
  2. mapping.R
  3. getpeaks.R
  4. BF\_test.R

System Requirements:

1. For best results “R” version 3.1 or above
2. The following R packages must be installed
   1. rqtl
   2. parallel
   3. doparallel
   4. foreach

You may need to run the command

***install.packages(package\_name)***

in R to install each one of them.

Once the above requirements are met, follow the below steps to perform mapping vQTL(&QTL):

**Step 1**: Place your desired phenogeno input file in the folder “Vqtl-interactions” and rename the input file to “phenogeno.csv” (A sample file is supplemented for illustration purposes.)

**Step 2**: Open “mapping. R” in a text editor and set the 2 variables ***no\_of\_env***and ***nperm***according to requirements*.*

**Step 3***:* Open “get\_peaks.R” in a text editor and set the desired LODBF cutoff defined by the variable and enter the chromosome starting and ending locations.

**Step 4:** Open R and change the working directory of R to Vqtl-interactions.

**Step 5:** Execute the following two commands in R:

***source(“mapping.R”)***

***source(“get\_peaks.R”)***

**Check your output in the file “DataFile1.csv”.**

Note: After executing the command ***source(“mapping.R”)***, the folder Vqtl-interactions/vQTL will contain a csv file named according to the environments. The BFLOD values for all the markers are present in them. The BFLOD plots will be generated in the Vqtl-interactions/vQTL/Plots folder.

The above codes also map QTL simultaneously. For QTL output you may want to check the folder “Vqtl-interactions/QTL”.

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**Deming Deviations**

To calculate the Deming deviations, you need to have the following files in the folder Vqtl-interactions/bins:

1. DemingDeviations.R
2. Bins.csv
3. First\_markers\_of\_bins.csv
4. QTL\_and\_vQTL.csv

The R package “mcr” must be installed.

Once the requirements are met, perform the following steps:

Step 1: Change the working directory of R to “Vqtl-interactions\Bins”

Step 2: Run the following script:

**source(“DemingDeviations.R”)**

**Your output will be available in the file “DataFile2.csv” in the Maps\_QTL\Bins folder.**

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**Interactions**

To get the 2QTL and 2vQTL interactions, you need to have the following files in the folder Vqtl-interactions/interactions:

1. interaction.R
2. vQTL\_vQTL.py

Once the requirements are met, perform the following steps:

Step 1: After performing peak extraction from getpeaks.R, place the 2 folders “QTL” and “vQTL” in the folder Vqtl-interactions/interactions

Step 1: Change the working directory of R to “Vqtl-interactions\Bins”

Step 2: Execute the Python script ***vQTL\_vQTL.py***

vQTL\_vQTL interactions will be generated in the folder 2vQTL.

(Two folders 2QTL and 2vQTL are given for illustrative purposes.)

Step 3: To collate the data, set the environments in ***interaction.R*** and run the R script

***source(“interaction.R”)***

**Your output will be available in the file “DataFile3.csv” in the Vqtl-interactions\interactions folder.**

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