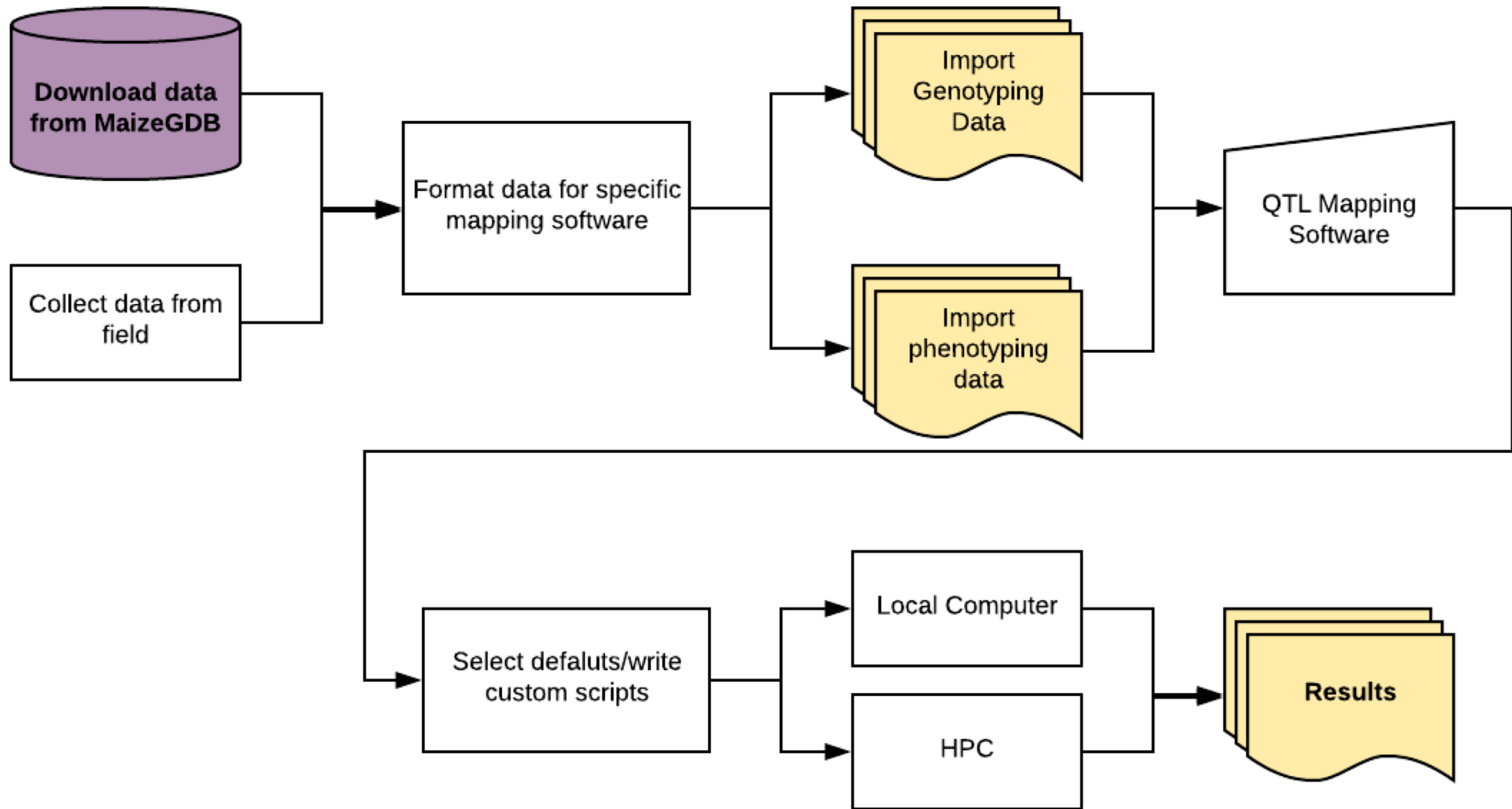


QTL Mapping in Maize

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Buckler Lab Presentation

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Existing QTL Mapping Software

Name	OS	Last Update
ICI Mapping	Windows	2013
PLABMQTL	Windows	2010
MapQTL	Windows	2013
QTL Cartographer	Windows	2012
QTL/QTL2	R	Feb 2018

QTL Cartographer

markers per
chromosome

1	C1	175
2	C2	127
3	C3	130
4	C4	111
5	C5	139
6	C6	78
7	C7	78
8	C8	106
9	C9	85
10	C10	77

Reduced marker names for
each chromosome

1	m0001	m0002	m0003
2	m0176	m0177	m0178
3	m0303	m0304	m0305
4	m0433	m0434	m0435
5	m0544	m0545	m0546
6	m0683	m0684	m0685
7	m0761	m0762	m0763
8	m0839	m0840	m0841
9	m0945	m0946	m0947
10	m1030	m1031	m1032

Distances
between markers

1	0
2	0.9
3	3.7
4	5.1
5	9.7
6	11.5
7	13.4
8	15.6
9	15.6
10	16.2
11	17.4
12	17.9
13	17.9

RIL IDs, genotypes,
phenotypes

1	RIL Marker						
2	Z014E0001	0	0	0	0	0	0
3	Z014E0002	2	2	2	2	2	2
4	Z014E0004	0	0	0	0	2	2
5	Z014E0005	0	0	0	0	0	0
6	Z014E0007	2	2	2	2	2	2
7	Z014E0008	2	2	2	2	0	0
8	Z014E0009	0	0	0	0	0	0
9	Z014E0011	2	2	2	2	2	2
10	Z014E0012	2	2	2	2	2	2
11	Z014E0013	0	0	0	0	0	0

QTL Cartographer

WinQTLCart - C:\WCSU\WinQTLCart2.5\Examples\Maize ----- Source Data.mcd

1. Title Bar

2. Menus

3. Toolbar

4. Tree Pane

- Messages
- Source Files
 - wqcart-samp3.mcd
 - Maize.mcd
- Result Files
 - nLtest-C.qrt
 - Maize-C.qrt
- Text Files
 - nLtest-C-all-pm.txt

5. Form Pane

Summary information

File name: Maize.mcd

File ID number: 901540162

Chromosome numbers: 1

Cross type: SF2

Sample size: 171

Trait numbers: 1

Other trait numbers: 0

Source data view and modify

Marker values

Chromosome 1 --- C1

Markers...

Trait values

Trait View... OTrait View...

Analysis

Single Marker Analysis

GO

Source data manipulations

Basic Info... Individual... Chromosome... Trait... OTrait...

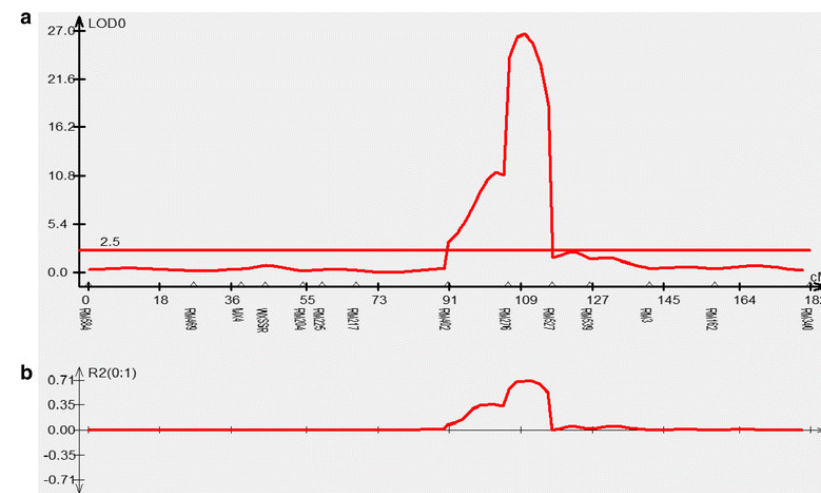
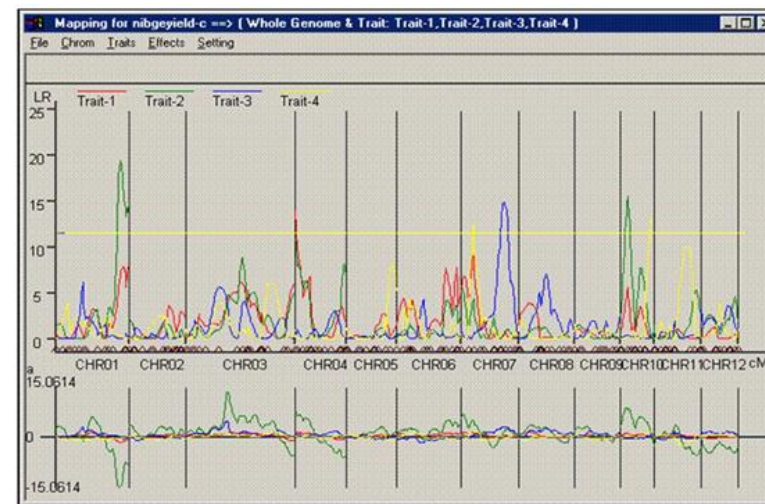
6. Data Pane

```
#FileID 901540162
#bychromosome
/* One way to make comment
on data source file */
-type position //default is interval
-function 1 //default is 1
-Units cM //default is cM
-chromosomes 1
-maximum 12
-named yes
-start
-Chromosome C1
// Another way to comment
Mk01_01 0.0000
Mk01_02 37.8000
Mk01_03 49.1000
Mk01_04 59.8000
Mk01_05 62.8000
Mk01_06 86.7000
Mk01_07 92.7000
Mk01_08 108.2000
Mk01_09 112.5000
Mk01_10 134.6000
Mk01_11 140.0000
Mk01_12 149.8000
-stop
```

7. Status Bar

For Help, press F1

Thu, Feb 10, 2005 9:33 AM



R/qtl + qtl2

Example input for R/qtl

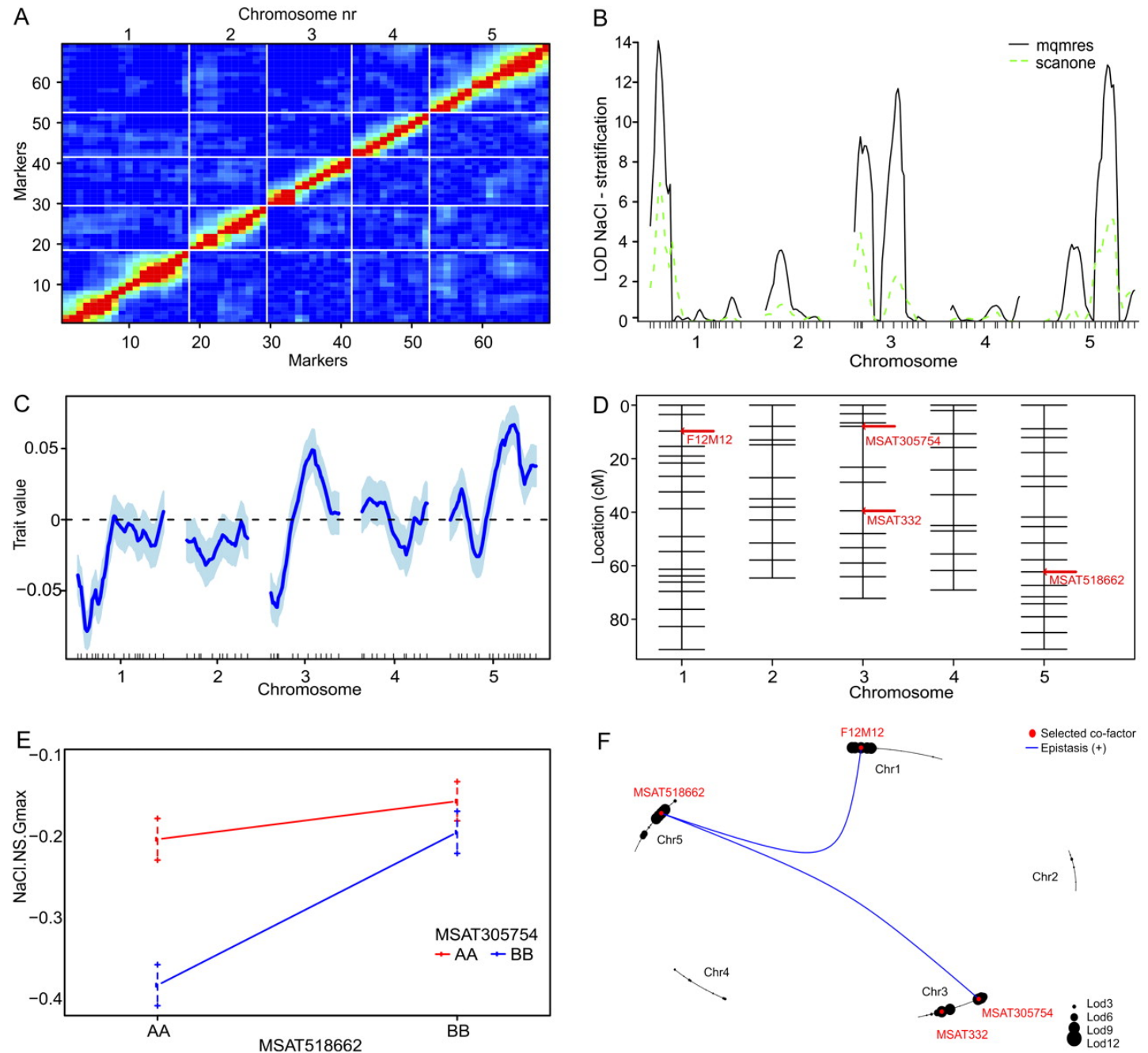
1	Bins	p-umc135	p-phi056	p-tub1	p-dmt103	p-umc117	p-umc156
2		1	1	1	1	1	1
3		0	-2.3	2.5	10.5	10.5	16.5
4	0 B	B	B	B	B	A	A
5	0.6 B	B	B	B	B	B	B
6	0.4 A	-	-	A	A	A	A
7	0.2 B	B	B	B	B	B	B
8	B	B	B	B	B	B	B
9	0.6 B	B	B	B	B	B	B
10	0 A	A	A	A	A	A	A
11	1.25 A	A	A	A	A	A	A
12	0 A	A	A	A	A	A	A
13	0 -	A	A	A	A	A	A
14	3.4 B	-	-	A	A	A	B

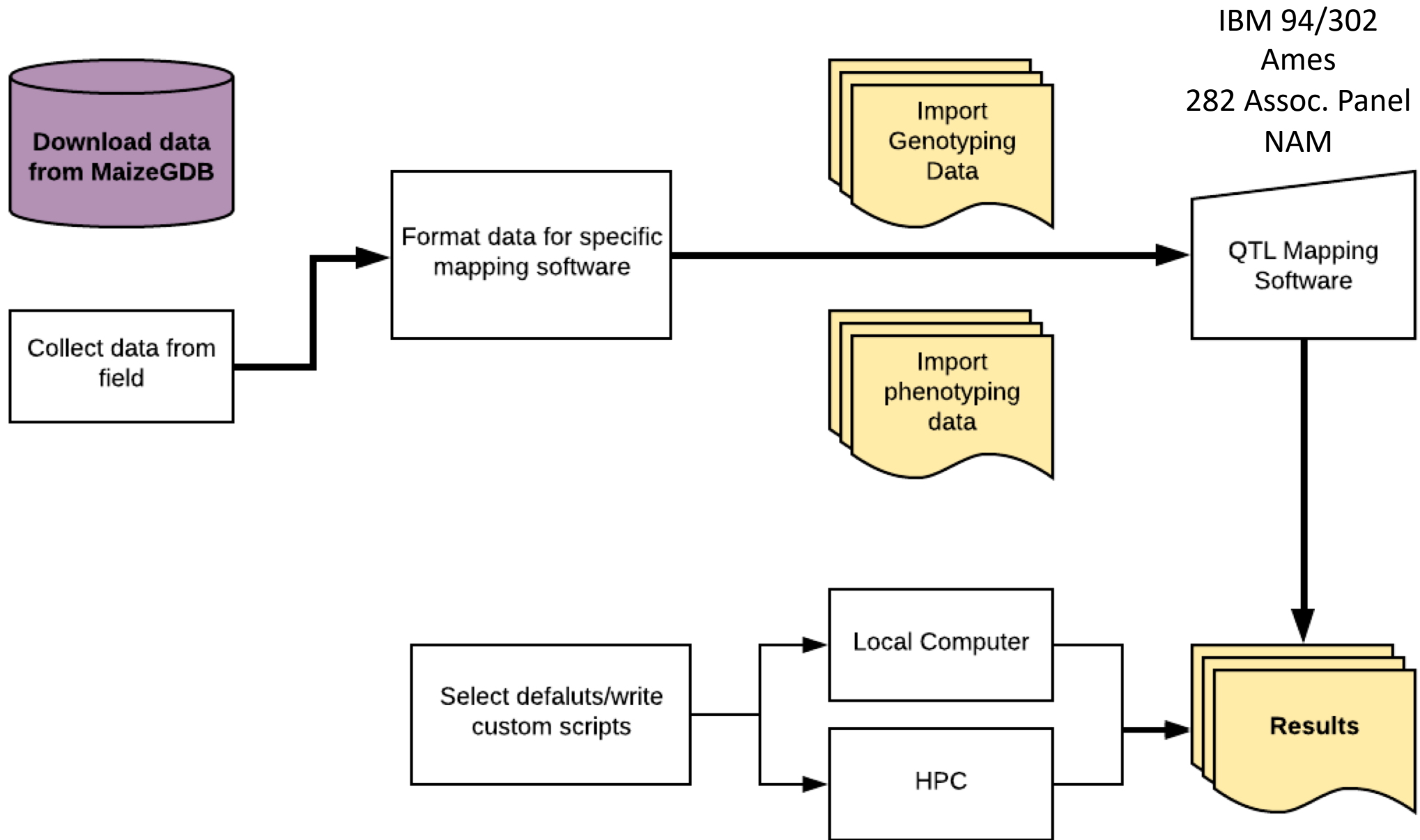
R/qtl + qtl2

Example output for R/qtl

Cons:

- Require extensive data formatting (error prone)
- Long runtimes
- Knowledge of running jobs on HPCs for permutation tests
- Intermediate file sizes large





gQTL for collaborative cross mouse RILs

gQTL v1.0

Need Help?

CURRENT ANALYSIS

New

Name

Field Separator Options

Upload Phenotype File

Save Analysis

Close & Create New Analysis

Header

File delimiter

Tab

Semicolon

Comma

Quote

None

Double Quote

Single Quote

Select Data Transformation

log

sqrt

rankZ

auto

auto: Shapiro-Wilk's test chooses best transform between log and sqrt.
rankZ: Recommended if you have hundreds or thousands of phenotypes.

Genotyping Array

MegaMUGA (77K Markers)

GigaMUGA (141K Markers)

Genome Build (Founder Probabilities) *

Build 37 (mm9)

Build 38 (mm10)

* Read CC Status before making a decision to choose genome build.

Prune Probability Matrix

Prune Low Genotype Probabilities

Checking this option will set all the CC founder genotype probability values below 0.005 to a very low value, 1e-20.

Permutations

10

Run options

Rerun QTL analysis on selected phenotypes

Perform QTL Analysis and Render Plots

Warning: it will take a while!

Run QTL on single phenotype

Generate Report

Generate PDF Report

esayGWAS, 4 species, data preloaded

easyGWAS

Home

GWAS Center

Public Data

Private Data

FAQ

mbb262

GWAS Center

Manhattan Plots

QQ-Plots

SNP Annotations

Summary/Downloads

Create Experiments

Overview

New GWAS

New Meta-Analysis

New Intersection Analysis

Experiment overview

My temporary history

My experiments

Public experiments

Project overview

My projects

Public projects

Brief Summary

Experiment Type: Genome-wide Association Study

Species: Arabidopsis thaliana

Dataset: APolyDB (call method 75, Horton et al.)

Phenotype: FLC (ID: AT_P_43)

Algorithm: EMMAX

Parameters: MAF: 0.0, SNP Encoding: Additive, Transformation: None

Detailed SNP View (Chr5: 10172992)

Allele Information

Phenotypic Values for FLC (ID: AT_P_43) [None transformed]

Linkage Disequilibrium (LD) Plot

SNPs

SNP (Focal SNP)

Allele Information

Phenotypic Values for FLC (ID: AT_P_43) [None transformed]

Linkage Disequilibrium (LD) Plot

SNPs

SNP (Focal SNP)