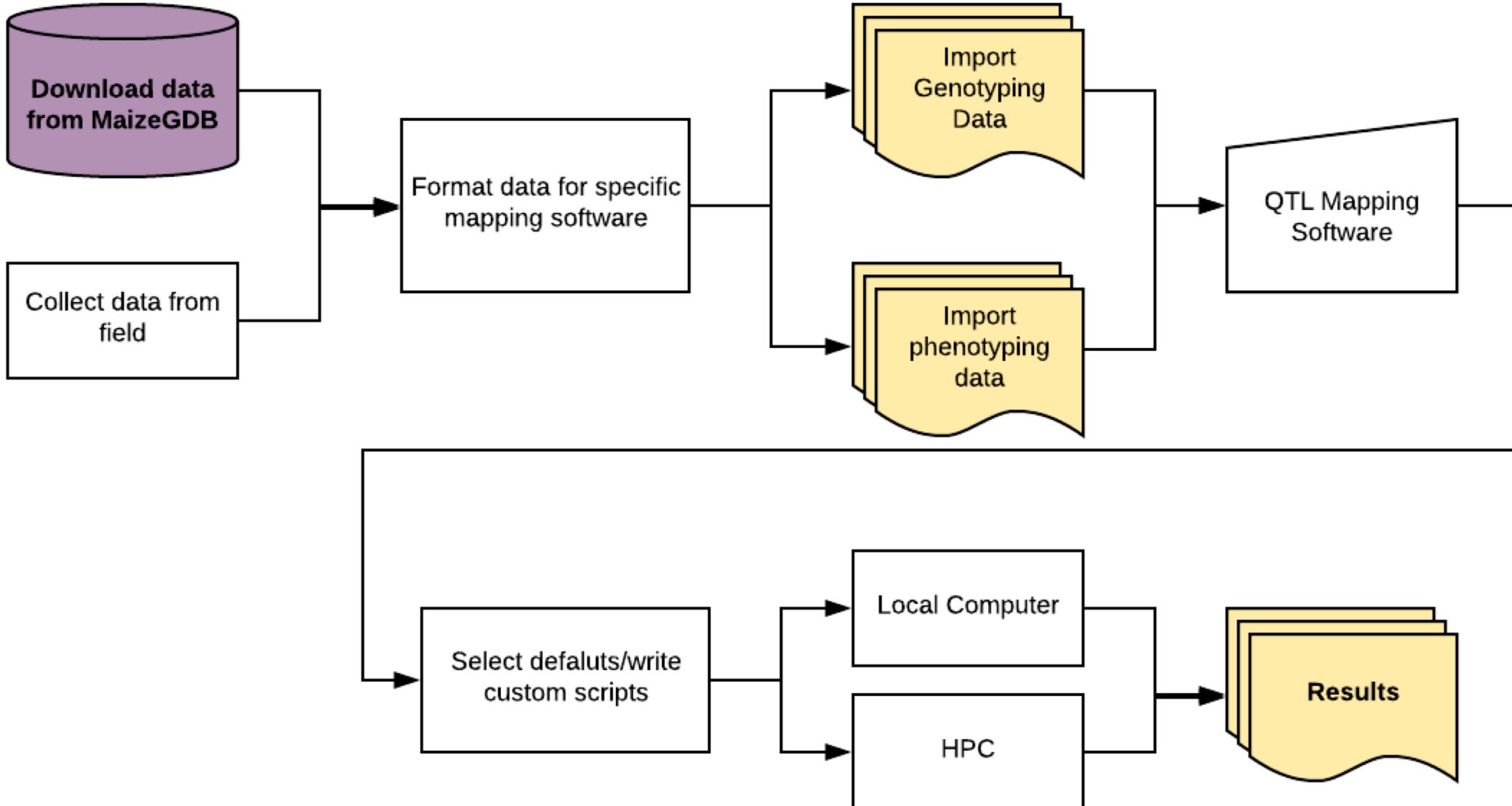


# QTL Mapping in Maize

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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

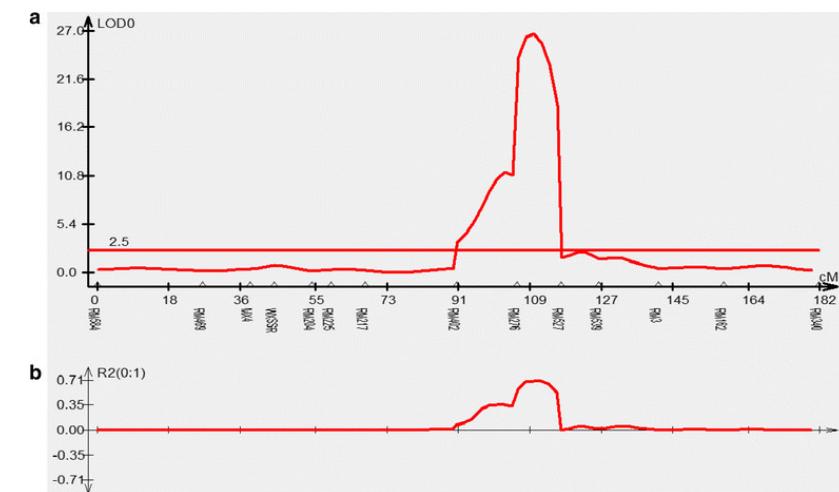
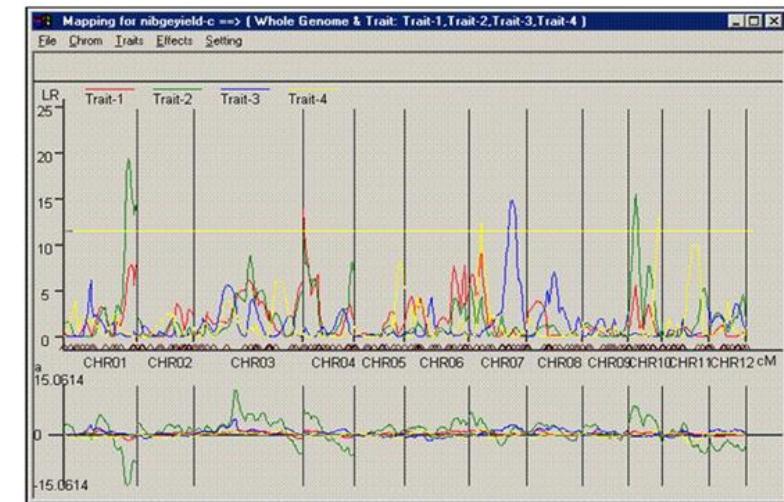
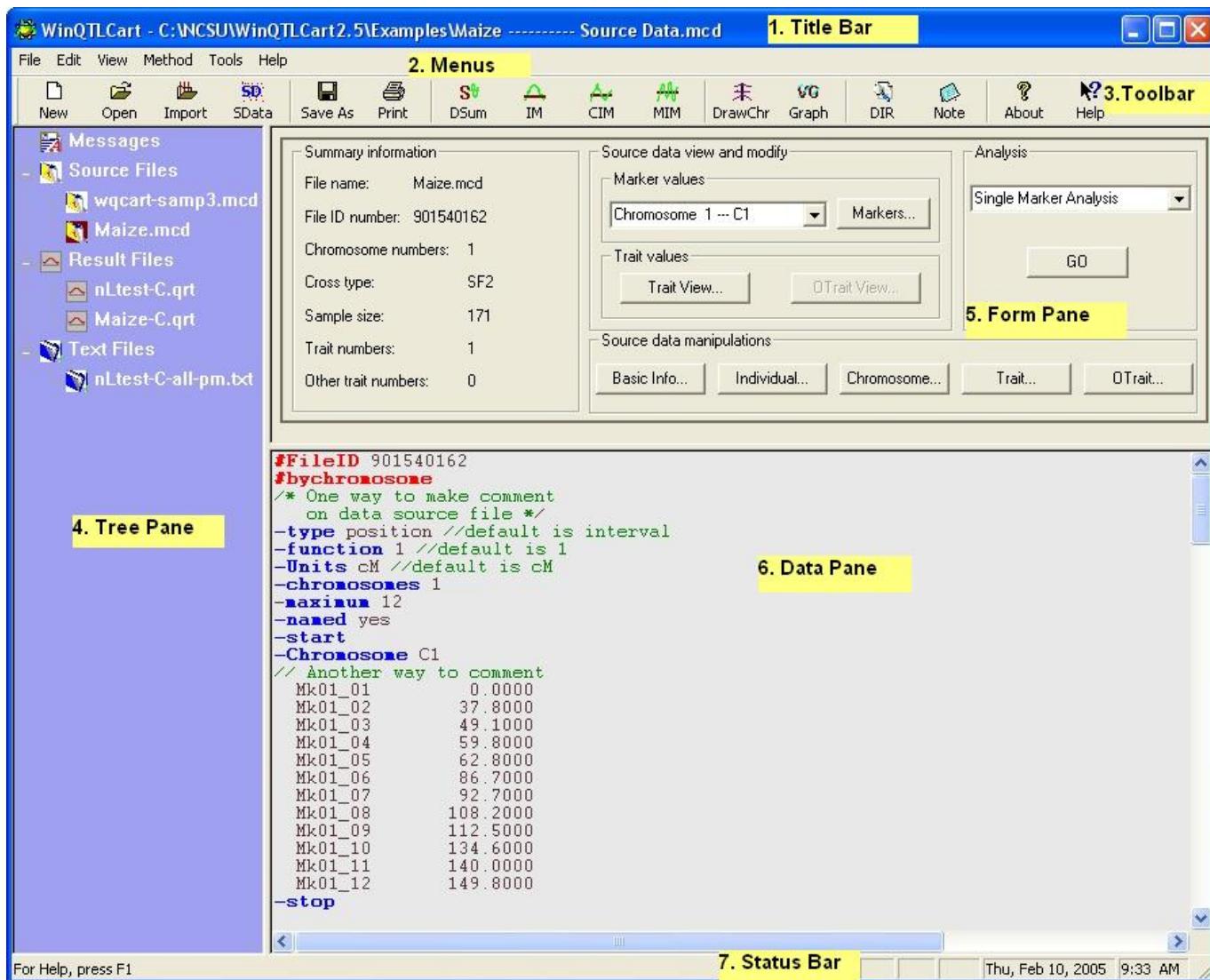
Distances between markers

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

# QTL Cartographer



# R/qtl + qtl2

Example input for R/qtl

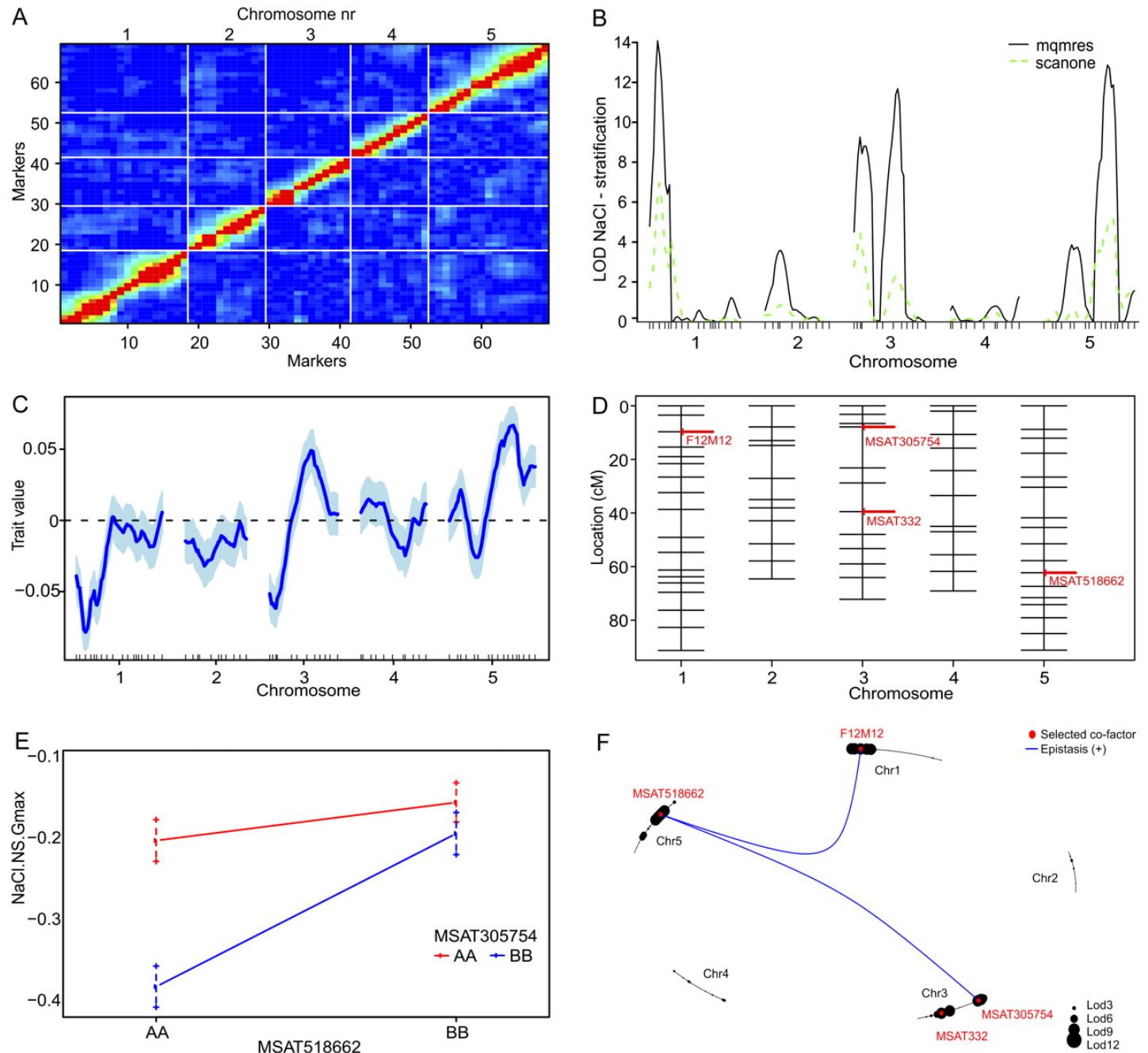
1	Bins	p-umc135	p-phi056	p-tub1	p-dmt103	p-umc117	p-umc156
2		1	1	1	1	1	1
3		0	-2.3	2.5	10.5	10.5	16.5
4	0 B	B	B	B	A	A	
5	0.6 B	B	B	B	B	B	
6	0.4 A	-	-	A	A	A	
7	0.2 B	B	B	B	B	B	
8	B	B	B	B	B	B	
9	0.6 B	B	B	B	B	B	
10	0 A	A	A	A	A	A	
11	1.25 A	A	A	A	A	A	
12	0 A	A	A	A	A	A	
13	0 -	A	A	A	A	A	
14	3.4 B	-	-	A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

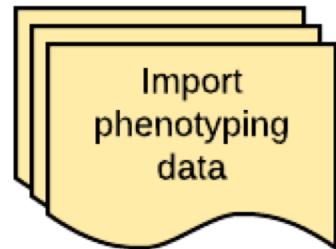
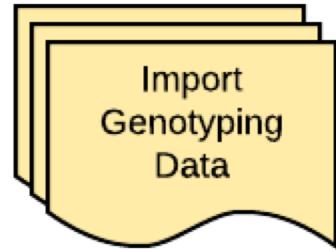
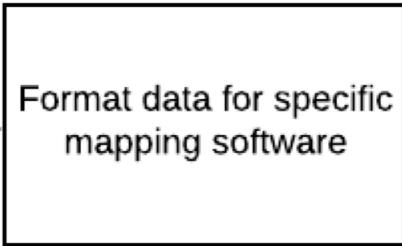
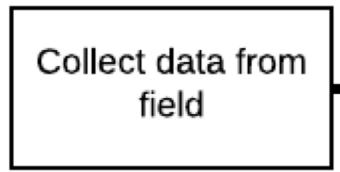
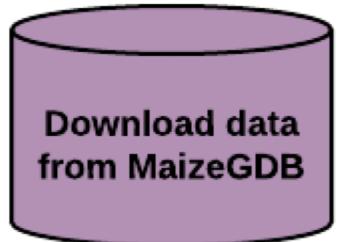
# R/qtl + qtl2

## Example output for R/qtl

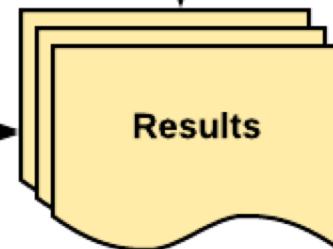
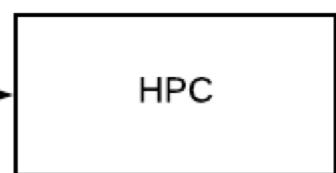
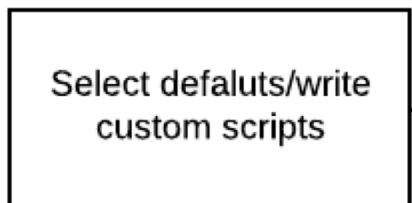
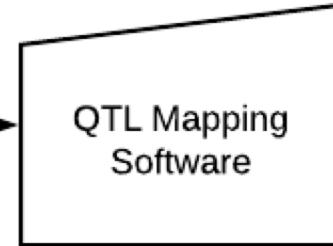
Cons:

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





IBM 94/302  
Ames  
282 Assoc. Panel  
NAM



# gQTL for collaborative cross mouse RILs

