Pea Lodging Final Report

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1 Introduction

Jamin is a Ph.D. student in the Department of Plant Sciences and Plant Pathology at MSU. The primary focus is his research is to associate variation in genetic expression with variation in the expression of several phenotypic traits. Genotypic and pheynotypic data were collected on 257 varieties of pea, from two locations (Bozeman and Moccasin), over 4 years. Phenotypic data includes percent lodging, tendril length, tendril node length, nodes at 1st flow, maximum number of nodes, germination, number of branches, plant height, plant length, average total yield, main stem diameter, tiller diameter, "comp" tiller diameter, and maturation time, totaling 14 traits. Data from 609 genetic markers were collected. The end result of Jamin's research will include a quantitative trait loci (QTL) analysis. Prior to the QTL analysis, understanding of the data and methods are necessary. The report includes:

- Evaluation of correlations in pheynotypic data
- Analysis of combining data from the different sites and years
- Exploration of the rate of missing data
- Explanation of significance thresholds for QTL
- Suggestions for future work

2 Correlation Plots

Correlation describes the strength and direction of a linear association. Specifically, this analysis examines Pearson Correlations because the variables are measured on a quantitative scale. Correlation is measured on a scale between -1 (a perfect negative linear association) and 1 (a perfect positive linear association). Correlation does not imply causal relationships. In examining, for instance, the relationship between lodging and stem width, the Pearson Correlation would only give information about the linear association between the two variables. A strong association between the two variables cannot be interpreted that changes in stem width cause changes in lodging; rather, we would simply say that the two variables are associated with each other. Other confounding variables, such as climate, may be driving both. Since the phenotypes in each year at each site are considered separate response values, we consider examining plots of correlation matrices for each site/year combination as well as for the entire dataset. This allows for direct examination of linear relationships between covariates; however, non-linear relationships may not be accurately measured by Pearson correlation. Further investigation of outlying values in the data may be necessary as Pearson correlations are sensitive to the presence of outliers in the data.

2.1 Sites and Years Combined

The correlation between pairwise explanatory variables of the phenotypic data were assessed using the a pairwise correlation matrix. We assessed the pairwise correlations across sites for pairs of explanatory variables which were measured within these sites at least two different years.

In Moccasin, only four variables were observed to have been measured both in 2015 and 2016. Of these variables, the length and main stem diameter of the plants are moderately correlated (r=0.55). Also, the main stem diameter and root diameter of the plants are moderately correlated (r=0.45).

2.2 Bozeman in All Years

The pairwise correlation matrix below shows that germination which was measured in Bozeman for all 3 years has weak correlation against all the variables measured. Also results from Bozeman shows that tendril length node of the plant was moderately to strongly correlated with the average length and tendril length of the plant with correlation coefficients of 0.61 and 0.48 respectively. The branch number and tiller diameter of the plant were also moderately correlated (r = 0.47). The maturity time of the plant was strongly and moderately correlated with the maximum nodes (r=0.65) and nodes of 1st flow (r=0.48). In addition, a correlation coefficient of 0.81 was observed for nodes 1st flow and maximum nodes of the plants.

```
'data.frame': 787 obs. of 14 variables:
                   : num 17.3 NA 52.4 22.7 29.4 ...
$ prcnt_lodging
$ branch_numb
                     : num
                            3.07 3.12 3 3 2 ...
$ plant_height
                     : num
                            42.4 NA 30 34 31.2 ...
$ plant_length
                     : num
                            51.4 NA 63 44 44.2 ...
$ mat_time
                     : num NA NA NA NA NA NA NA NA NA ...
                     : Factor w/ 60 levels "","#DIV/0!","10",..: 55 1 25 4 28 50 21 50 23 21 ...
$ germ
$ tendril_length
                     : num 19.9 14.2 21.5 15 17 ...
                     : num 2.74 NA 2.33 NA 3.04 ...
$ main_stm_diam
$ tendril_length_node: num 18.2 14.2 20.3 15 14.8 ...
$ nodes_1st_flow
                   : num 16.5 20 14 19 15 ...
$ max_nodes
                     : num 21 25.5 23 23 19 18 24 19 22 19 ...
$ avg_total_yield
                     : num 14.9 NA 10.8 10.9 12.9 ...
$ tiller_diam
                     : num 3.27 NA 3.3 NA 3.39 ...
$ comp_tiller_diam : num 0.791 NA 1.218 NA 0.858 ...
```

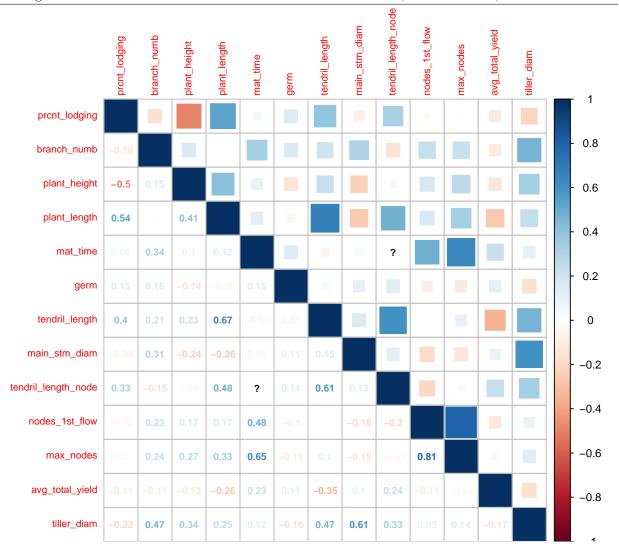


Figure 1: Correlation Plot for Bozeman (In All Years)

2.3 Bozeman by Year

We assessed the pairwise correlation of the different sites each year. In 2014, twelve pairs of explanatory variables had correlation coefficients between 0.42 and 0.91. The pairwise correlations are shown in the matrix below. Germination and total yield was strongly correlated (r=0.66) while the length and internode length of the plants recorded a very high correlation coefficient (r=0.91). In 2015 and 2016, of the pairwise combinations assessed, 28 combinations yielded correlation coefficients between 0.40 and 0.85. The results are presented in the pairwise correlation matrices below.

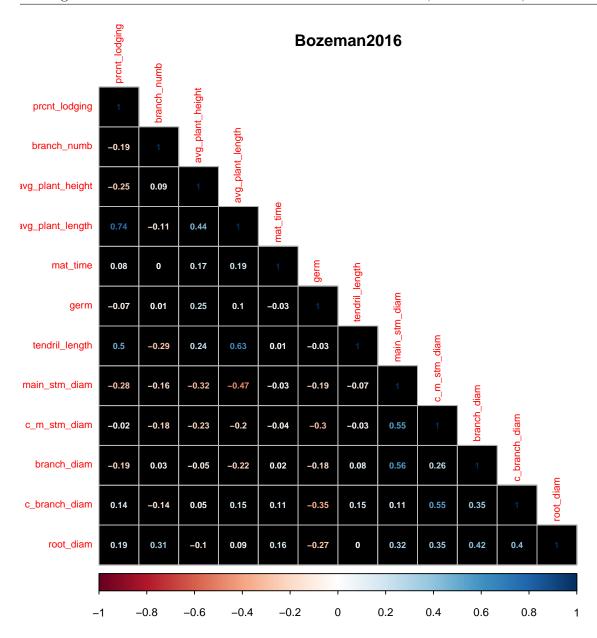


Figure 2: Correlation Plot for Bozeman in 2016

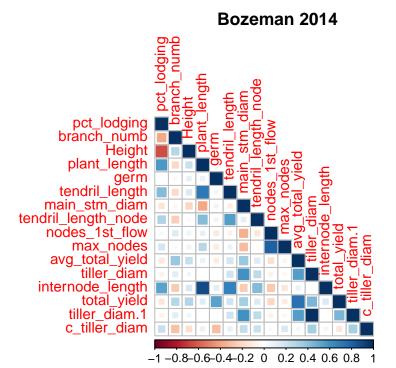


Figure 3: Correlation Matrix for Bozeman in 2014

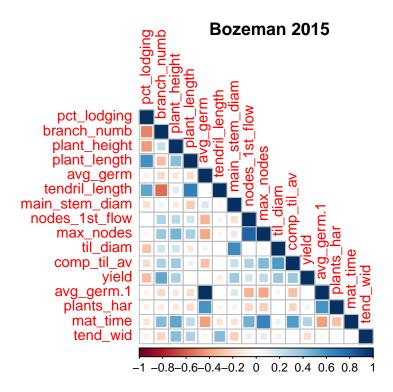


Figure 4: Correlation Matrix for Bozeman in 2015

2.4 Moccasin by Year

Examining the phenotypes at Moccasin in each year, we can see that several of the variables were relatively highly correlated in 2016. The strongest correlations were between tendril length and plant length, which makes sense, as well as between percent lodging and plant length. While none of the correlations would be interpreted as very strong, there are moderate postive and negative relationships in both years.

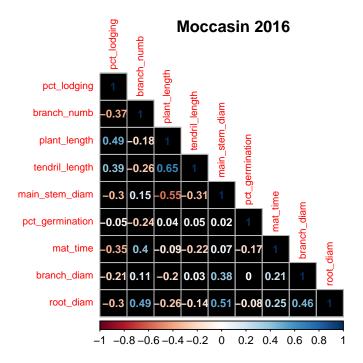


Figure 5: Correlation Matrix for Moccasin in 2016

In Moccasin in 2015, several notable correlations were found. Stress minus equation was strongly negatively correlated with tiller diameter, tiller compressed, tiller compressed flex, and flex after crushing. Lodging was found to be correlated with plant height as expected.

Moccasin 2015

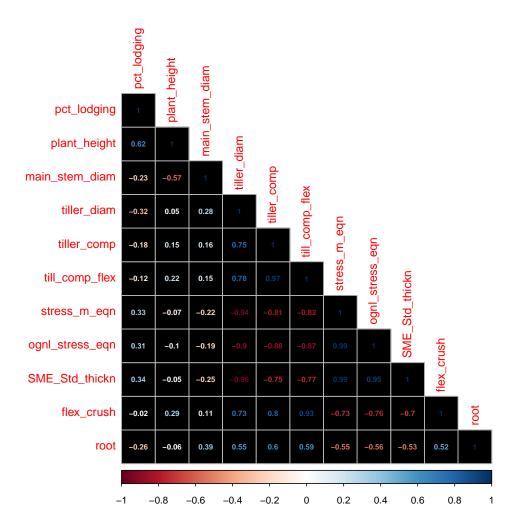


Figure 6: Correlation Matrix for Moccasin in 2015

Figure 7: Correlation Matrix for Moccasin (In All Years)

0

0.2

0.4

0.6

8.0

-0.2

-0.8

-0.6

-0.4

3 Site Year Combinations for Lodging

3.1 Exploratory Analysis

The data were collected over a period of 4 field seasons at sites in Bozeman and 2 field seasons in Moccasin. Phenotypic data were analyzed in order to determine whether conditions were similar enough at each year/site combination to consider as a single dataset, or if they differ by enough that the sites and years need to be considered as different groups.

Though QTL analyses of all phenotypic traits is of interest, lodging is considered the primary response. Therefore, we examine the Percent Lodging measured at each site/year combination. Note that Percent Lodging is not measured in the 2013 Bozeman data; we did not include it in this analysis.

Visually, we can create beanplots (Kampstra 2008) to assess the differences mean percent lodging at each year/site combination. These show both the variability of the distribution, like a traditional boxplot would, as well as information about the skew and modes. Over all years in Bozeman it appears that the distribution of lodging was slightly more variable than for sites in Moccasin; however, for some reason in 2016 the Bozeman site exhibited positive skew. This indicates that in 2016, the majority of pea plants were lodged to a lesser degree than in 2015 or 2014. The thin horizontal black bars indicate the original data values; the bold black lines indicate group means.

BZ14 BZ15 BZ16 Moc15 Moc16

Lodging at each site/year combination

Figure 8: Comparative Beanplot of Site/Year Combinations

3.2 Interaction Plot

If the sites are reasonably similar, we would expect to see parallel lines that are either overlapping or very near each other. The dashed red line for Bozeman indicates that average percent lodging was higher in Bozeman than in Moccasin in both 2015 and 2016. The bars indicate the variability of lodging for each year in Bozeman - it appears that for most years, Bozeman was slightly more variable than Moccasin. While the blue line and red line are both decreasing from 2015 to 2016, the difference in slopes indicates that there may be some interaction between year/site combinations. This visualization indicates some evidence of a difference in lodging in each location and year. However, since there are no observations from Moccasin in 2014, we cannot formally test for a site by year interaction.

Interaction plot of lodging based on year and site

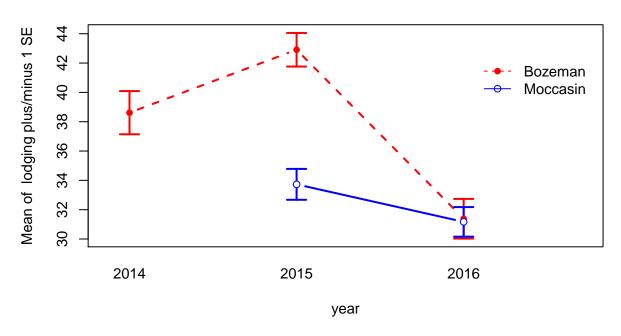


Figure 9: Interaction Plot for Sites and Years

3.3 Regression Model and Pairwise Comparisons

A model was fit to include all site and year combinations in order to test for differences between the combinations. Bozeman 2014 was treated as the baseline group. An overall F test using 4 and 1205 degrees of freedom to assess evidence against all site-year combinations yields a p-value less than 0.000001. There is strong evidence that the site/year combinations do not have all the same mean percent lodging.

We include 95 percent confidence intervals for the true mean percent lodging at each site-year combination. In order to get a better sense for which groups differ, we performed Tukey-Kramer pairwise comparisons to adjust for multiple testing. The results of that analysis are included below. The plot below shows differing pairwise combinations were between Bozeman 2015 and Bozeman 2014, as well as between Moccasin 2015 and Bozeman 2016, and between Moccasin 2016 with Bozeman in 2015 and 2016. Given that Bozeman 2015 had such a large mean relative to the other site/year combinations, this is not a surprising result.

F Test Results and	Confidence Interv	als for Lodging a	t Each Site										
Coefficients	Mean	Lower Bound	Upper Bound										
Bozeman 2014 38.62% 36.08% 41.14%													
Bozeman 2015	42.91%	40.55%	45.26%										
Bozeman 2016	31.38%	29.07%	33.69%										
Moccasin 2015	33.73%	31.36%	36.09%										
Moccasin 2016	31.17%	28.86%	33.47%										
F Test Results	$F_{4,1205} = 17.99$	P-valu	e: <0.00001										

95% family-wise confidence level

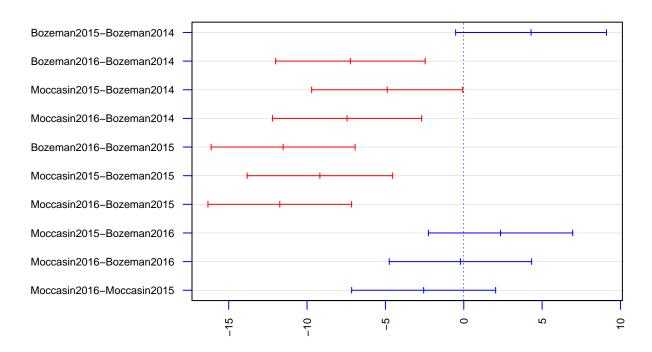


Figure 10: Multiple Comparisons of Lodging at Sites and Years

3.4 Discussion

This analysis indicates that the measurements taken at each site in each year should be treated separately; they should not be considered homogeneous enough to be taken as a single group. The inclusion of 2013 into the data is unlikely to change the results of this study because the differences between the combinations already considered are enough to justify splitting the dataset into separate groups. However, it may facilitate future calculations to consider converting lodging measurements in Bozeman in 2013 from likert-scale format (on a 1-4 scale) to the same "percent-lodging" variable that is used in subsequent years.

4 Missing Genetic Data

Quality of the genetic data can be explored through the percentage of varieties missing information at each genetic marker. Reviewing QTL literature may provide insight to acceptable missing rates. Plots are provided below to visualize the amount of missing data at each genetic marker and across each variety genotyped. Tables of missing rates are provided in the appendix. As the number of genetic markers and varieties are large, the tables will be more informative on the exact varieties with certain missing rates. Rates of missing-ness at each genetic marker are first shown across all makers, and then are broken into plots subsetted by genetic markers with less than 25% missing, less than between 35% and 30% missing, less than between 30% and 35% missing, and less than between 35% and 40%. All genetic markers had at least 60% of the data across all varieties.

4.1 All Markers

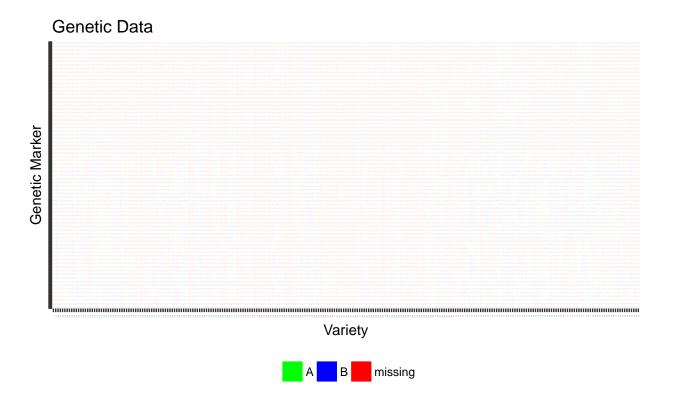


Figure 11: Missing Genetic Data Plot

4.2 Less than 25% Missing by Genetic Marker

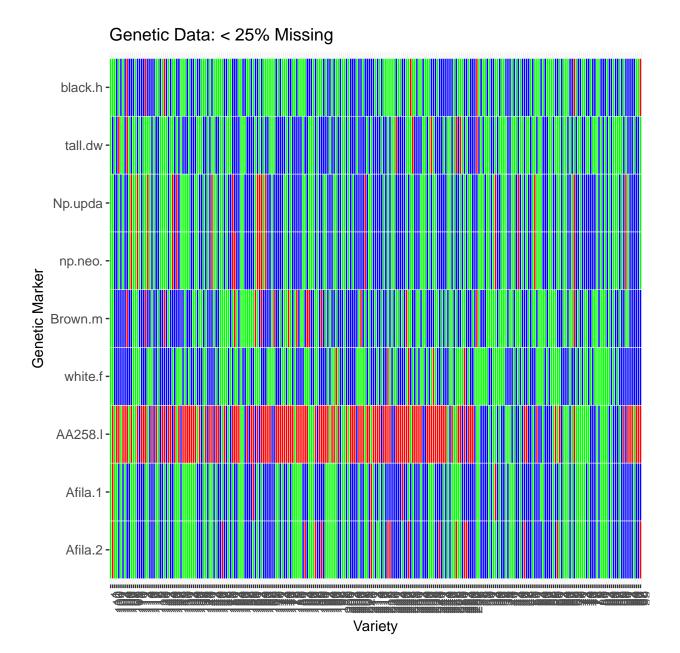


Figure 12: Less Than 25 Percent Missing

missing

4.3 25% - 30% Missing by Genetic Marker

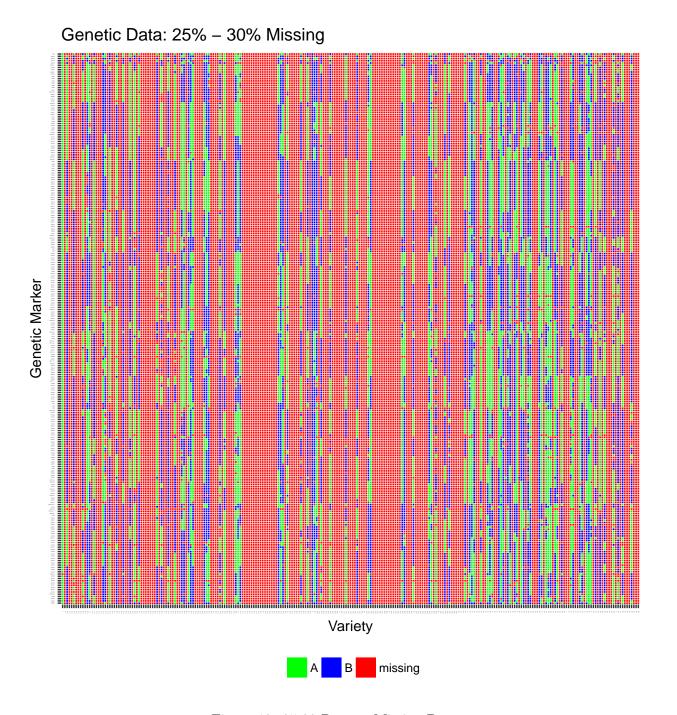
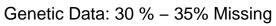


Figure 13: 25-30 Percent Missing Data

4.4 30% - 35% Missing by Genetic Marker



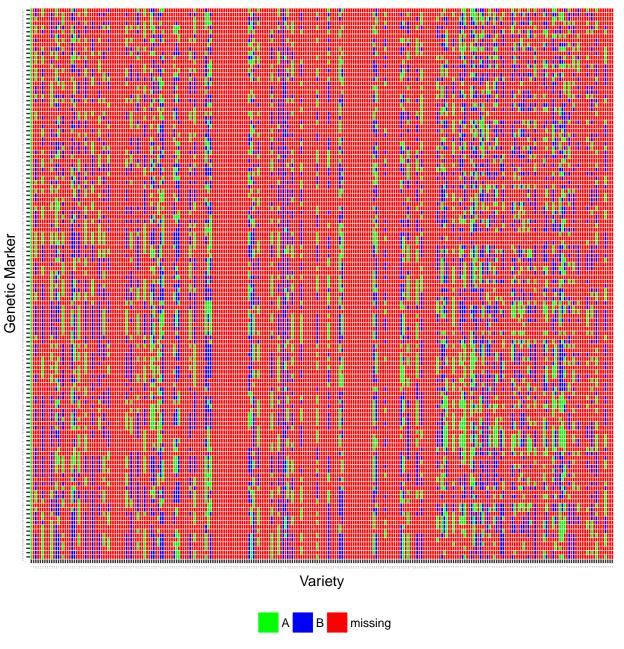


Figure 14: 30-35 Percent Missing Data

4.5 35% - 40% Missing by Genetic Marker

Genetic Data < 35 % - 40% Missing

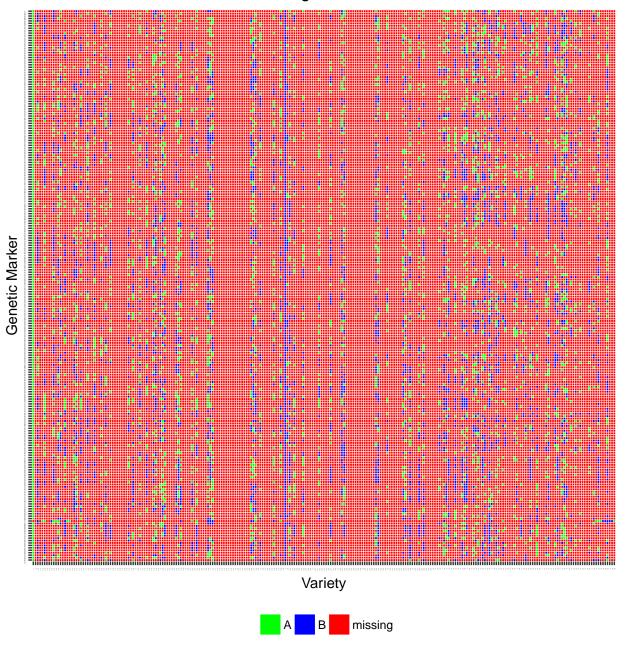


Figure 15: 35-40 Percent Missing Data

5 Setting Significance Thresholds

The pea genetic data include over 600 genetic markers. When a QTL analysis is done, a significance test is done at each genetic marker to test for an association between the average quantiative trait and the genotype. Multiple testing problems are quite common in genetic analyses. Jamin mentioned he would like to use LOD for setting a significance threshold. LOD is an abbreviation for the log-odds. LOD is the log_{10} likelihood ratio comparing the null that there is not a QTL to the alternative, that there is.

Null Model, $H_o: y_i \sim N(\mu, \sigma^2)$ i.e., there is no genetic dependency between the phenotype and the genotype. We define the Residual Sum of Squares (RSS_0) to be the squared difference between the expected mean lodging for each marker and the overall mean lodging under the null model.

- Where the maximum likelihood estimates (MLEs) for parameter estimates $\mu = \bar{y}; \sigma^2 = RSS_o/n$ are used.

Alternative Model, $H_a: y_i|g_i \sim N(\mu_{g_i}, \sigma^2)$

- Where g_i = genotype of individual i at the marker (loci); each genotype group has a different mean; σ^2 = pooled RSS = RSS_1 ; again the MLEs.

$$LOD = \frac{n}{2} \times log_{10}(\frac{RSS_o}{RSS_1})$$

LOD is related to the F statistic. LOD = $\frac{n}{2} \times [F(\frac{df}{n-df-1}+1)]$ and similar to the F statistic, large LOD values are associated with strong evidence against the null hypothesis, suggesting that there is a relationship between the genetic loci and the phenotype. Since F statistics help find p-values, and LOD is related to F statistics, by setting genome wide adjusted LOD thresholds, we can easily convert these back to genome wide adjusted p-values. Broman and Sen (2009) provide a simulation based method for generating genome wide adjusted LOD thresholds, and the corresponding genome-wide adjusted p-value thresholds in Section 4.3 using the QTL package in R (Broman et al. 2003).

6 Future Work

Future work with Jamin should be more focused with the QTL analysis and developing p-value based thresholds for drawing statistical conclusions. Jamin currently is using the MapDisto macro in Excel and QTL Cartographer to do preliminary QTL analyses. Both programs provide extensive documentation on their functions. R is a common program for statisticians to use, and discussion around whether packages such as QTL in R or outside programs should be used in the final analysis would be beneficial. While identifying specific genetic markers associated with the most variation in phenotypic traits is the end goal of the project, a QTL analysis has many steps that should be taken before using outputted results. Broman and Sen (2009) is a good reference for a basic QTL

analysis. Because Jamin is interested in genetic variation associated with all phenotypic traits, the correlations between the traits should be accounted for in the final analysis. Adding in the recommendation to not combine across sites and years, we suggest the direction of the final QTL analysis done to be in a multi-trait, multi-environment setting. A resource for an introduction to the multi-trait, multi-environment setting in QTL analyses is referenced by Margarido et al. (2015).

References

Margarido et al. 2015. Multi-trait multi-environment quantitative trait loci mapping for a sugarcane commercial cross provides insights on the inheritance of important traits. Mol Breeding 35:175.

Broman and Sen. 2009. A guide to QTL mapping with R/QTL. New York: Spring Science+Business Media. Retrieved from

http://link.springer.com/book/10.1007%2F978-0-387-92125-9.

Appendix

Tables of Missing Rates by Genetic Marker

	A2594	A1617	A1621	A1619	A1618	A1624	A1615	A1622	A7578	C20B	AD51.ba	a A673	4 A6720	6 A6730	A6732	A6733	3 A6731	A6737	A6724	A6729
Count		194.00	199.00	202.00	195.00 0.32	199.00 0.33	185.00 0.30	163.00 0.27	163.00 0.27	170.00 0.28	166.00	0 209.0	0 162.00	161.00	161.00	210.00	166.00	190.00	163.00 0.27	182.00 0.30
	A6738									A1325					A1409	A1408	A2407	A1405	A1404	A1402
Percent										161.00 0.26	161.00 0.26			161.00 0.26	161.00 0.26	161.00 0.26	161.00 0.26	187.00 0.31	169.00 0.28	193.00 0.32
		A1024 :	ad147.l 163.00	A7384 162.00		A7302 A	A7302.1 211.00	A2197 226.00	A6889 164.00	A6891 163.00	A2259 187.00	A2257 170.00	A2256 201.00			A2340 162.00	A26 161.00	A26.dpn 165.00	A26.dpr	
Percent	0.29	0.27	0.27	0.27	0.27	0.27	0.35	0.37	0.27	0.27	0.31	0.28	0.33	0.26	0.27	0.27	0.26	0.27	0.	.27 0.30
	A.C.1. O	A C1 - 1	A C1 - 1	A A OFO 1	ADEL I	- 1 ACO	F9 AF1	00 107	E7 A07	FF A.C.C	40 4 4	(79 I A	6760 A	erro A	1990 1	A 409.4	A 4020	A A F A F: 1	1 1 270	T Lite 6
Count Percent		Afila.l 163.00 0.27	Afila.1 5.00 0.01	AA258.1 129.00 0.21		5.00 218.	00 192.	00 171.		00 161.0	00 16		62.00 16	6758 Az 62.00 0.27		A4834 161.00 0.26	A4832 163.00 0.27	AA5.Mid 171.00 0.28	166.	00 5.00
				-																
	A608						A4500	A337	A4495	A4496	A7738		A4497	A298	A7055	A4292	A6470	A5495	A5502	A220
Coun							163.00 0.27	172.00 0.28	173.00 0.28	195.00 0.32	208.00 0.34	215.00 0.35	205.00 0.34	162.00 0.27	169.00 0.28	161.00 0.26	162.00 0.27	199.00 0.33	166.00 0.27	171.00 0.28
Count	A5501 184.00	A5494 166.00	A5499 190.00	A5491 169.00	A5498 198.00	A299 202.00	A1561 181.00	A7736 180.00			A4502 162.00	A4501 161.00	A7729 166.00	165.00	161.00	219.00	163.00	164.00 1	167.00	AD51.Ba 171.00
Percent	0.30	0.27	0.31	0.28	0.33	0.33	0.30	0.30	0.27	0.27	0.27	0.26	0.27	0.27	0.26	0.36	0.27	0.27	0.27	0.28
	A5204	A5213	A5165	A5193	A5191	Brown.m	A60	A56	A61	A55	A57	A59	A5226	A58	A5229	LKA.F	5. A718	34 A718;	3 A7181	1 A7185
Count Percent	223.00 0.37	224.00 0.37	206.00 0.34	217.00 0.36	227.00 0.37	16.00 0.03		182.00 0.30	190.00 0.31	168.00 0.28	165.00 0.27	193.00 0.32	220.00 0.36	208.00 0.34	189.00 0.31	186.0 0.3				
Count	A7182 163.00	A2446 162.00	A7188 161.00	A7186 169.00	A7187 200.00	A7356 207.00	A7357 178.00	A7298 166.00	A4307 196.00	AA107 164.00	A6492 163.00	A7814 161.00	A7814.							A7369 217.00
Percent	0.27	0.27	0.26	0.28	0.33	0.34	0.29	0.27	0.32	0.27	0.27	0.26	0.3	1 0.35	0.32	2 0.3	5 0.3	6 0.35	0.35	0.36
	A7348	A2431	A6253	A6252	A6254	A6622 A	4829 A	D73.f.	AB111.L	A6075	A6995	A4460	AA5I	о А446	1 A699	4 A224	6 A102	5 AD17	4.L. CD	C.27. A836
								164.00 0.27	162.00 0.27	163.00 0.27	181.00 0.30	162.00	162.0	0 165.0	0 199.0	0 169.0	0 162.0	0 164		70.00 161.00 0.28 0.26
	A836.1 213.00	NCPA.F 219.0						A422 163.00		A432 184.00	A421 189.00	A423 207.00	A425 186.00	np.neo. 18.00	Np.up		270.L ta			1066 A1064 63.00 162.00
Percent	0.35	0.3						0.27	0.33	0.30	0.31	0.34	0.31	0.03			0.28			0.27 0.27
	179.00	AA285.I	0 162.0	00 162.0	0 166.0	0 162.00	182.0		00 200.0	0 206.0	0 220.0		00 187.0	0 208.00	162.0	0 202.0	00 183.0	00 190.00	0 163.00	164.00
Percent	0.29	0.2	7 0.2	27 0.2	7 0.2	7 0.27	0.3	30 0.2	28 0.3	3 0.3	4 0.3	36 0.3	37 0.3	1 0.3	1 0.2	27 0.3	33 0.5	30 0.3	1 0.27	7 0.27
	A1224	A2012	A2008	A1223	A2007	A2341	A2001	A7189	A7192	A7193	A7197	A7196	A296	AGAT.H	i A2181	1 A4598	8 A774	9 A4852	A6542	A1785
Count Percent	166.00 0.27	176.00 0.29	162.00 0.27	163.00 0.27	163.00 0.27	162.00 0.27	161.00 0.26	161.00 0.26			164.00 0.27	168.00 0.28	162.00 0.27	185.00 0.30	185.00		162.00	228.00		161.00 0.26
Count	A1788 161.00	A1783 161.00	A1787 161.00	A1782 169.00	A1786 167.00	A30 164.00							A5398 194.00	AA315.L 163.00	A5517 183.00	A4825 227.00		A4824 205.00	AB23.lg 161.00	
Percent	0.26	0.26	0.26	0.28	0.27	0.27	0.26	0.30	0.27	0.27	0.28	0.27	0.32	0.27	0.30	0.37	0.37	0.34	0.26	

Missing Data and LOD

Nnamdi Ezike, Paul Harmon, and Andrea Mack

V1100111			na D								110111		zike,		1 110				larca	11100
Count		A4804 162.00									A2144 I 195.00	205.0						A7613 164.00		
Percent	0.26	0.27	0.29	0.27	0.27	0.27	0.27	0.27	0.27	0.28	0.32	0.3	4 0.3					0.27		0.28
Count	A7604 164.00	A7608 162.00	A7607 162.00	A7602 162.00	A7601 162.00	A7615 163.00	A7614 163.00	A7603 163.00	A7619 162.00	A446 161.00	A2518 164.00	A448 163.00	A451 163.00	A452 163.00	A449 161.00	A447 163.00	A445 194.00 2		A4546 . 192.00	AA374.1 163.00
Percent	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.26	0.27	0.27	0.27	0.27	0.26	0.27	0.32	0.33	0.32	0.27
Count	AA224.l 161.00	A7224 165.00	A7223 163.00	A1580 161.00	A5439 161.00	A5420 161.00	A7133 162.00	A7134 162.00	A7132 161.00	A7131 161.00	AA335.1 161.0							A1003 173.00		
Percent	0.26	0.27	0.27	0.26	0.26	0.26	0.27	0.27	0.26	0.26	0.2	6 0.3	1 0.3	1 0.29	0.27	7 0.3	0.28	0.28	0.27	0.26
Count	A998 161.00	A997 161.00				A6634 162.00	black.h 7.00	A4409 162.00	AC76b.l 163.00	A1555 226.00	A6561 167.00	A1915 165.00	A1916 201.00	A6560 163.00	A6563 162.00	A1912 203.00	RPL15S.	A64		
Percent	0.26	0.26	0.27	0.27	0.26	0.27	0.01	0.27	0.27	0.37	0.27	0.27	0.33	0.27	0.27	0.33	0.28	0.26	6 0.27	7 0.26
Count	A645 171.00	A640 162.00	A638 161.00	A647 161.00	A7763 163.00	A4828 206.00	aa456 161.00	A1978 161.00	A1980 166.00	aa416 164.00	A258 215.00	A260 222.00	A246 224.00	A66 219.00	A253 214.00	A259 224.00	A236 221.00	A250 221.00	A5553 224.00	A5574 222.00
Percent	0.28	0.27	0.26	0.26	0.27	0.34	0.26		0.27	0.27		0.36	0.37	0.36	0.35	0.37	0.36	0.36	0.37	0.36
Count	A5562 223.00				A5552 224.00		A5545 218.00		A5547 217.00	A1434 206.00	A1551 209.00	A6408 184.00	A470 230.00	A474 226.00	A6451 219.00	A6449 221.00	A6454 219.00	A846 222.00	A6751 215.00	A850 213.00
Percent				0.36	0.37				0.36	0.34	0.34	0.30	0.38	0.37	0.36	0.36	0.36	0.36	0.35	0.35
Count	A2680 222.00	A3067 220.00	A3050 217.00	A635 205.00	A3598 199.00	A5728 211.00	A5477 208.00	A5478 209.00	A5479 206.00	A6575 171.00					A4690 206.00	A791 .	A6751.1 215.00	A846.1 222.00	A850.1 213.00	A5311 192.00
Percent	0.36	0.36	0.36	0.34	0.33	0.35	0.34	0.34	0.34	0.28	0.35	0.36	0.36	0.33	0.34	0.36	0.35	0.36	0.35	0.32
Count	A5895 223.00			A1058 191.00	A5537 226.00	A244 216.00	A257 220.00	A232 223.00	A243 219.00	A237 213.00	A240 215.00	A6955 219.00	A6934 217.00	A4750 217.00	A4734 216.00	A4757 225.00	A2714 180.00	A6947 214.00	A938 203.00	A4792 220.00
Percent				0.31	0.37				0.36	0.35	0.35	0.36	0.36	0.36	0.35	0.37	0.30	0.35	0.33	0.36
Count	A4786 223.00	A4783 224.00	A4779 222.00	A2316 220.00	A2303 222.00	A2319 225.00	A2317 214.00	A2672 165.00	A2672.1 224.00			A7378 215.00	A7075 189.00	A6222 224.00	A7013 230.00	A7008 231.00	A1185 189.00	A4855 205.00	A5951 215.00	A6557 226.00
Percent	0.37	0.37	0.36	0.36	0.36	0.37	0.35	0.27	0.37			0.35	0.31	0.37	0.38	0.38	0.31	0.34	0.35	0.37
Count	A6574 224.00	A6554 225.00		A4511 222.00	A4512 220.00		A5063 228.00		A948 208.00	A6573 221.00	A6550 223.00	A6532 214.00	A5654 216.00	A5623 231.00	A3512 224.00	A1461 205.00		A3634 219.00	A790 219.00	A785 218.00
Percent				0.36	0.36			0.33	0.34	0.36	0.37	0.35	0.35	0.38	0.37	0.34	0.31	0.36	0.36	0.36
Count	A786 215.00										A7245 223.00	A653 222.00	A660 223.00	A661 227.00	A657 217.00	A652 219.00		A5988 197.00	A6817 210.00	A6820 213.00
Percent										0.37	0.37	0.36	0.37	0.37	0.36	0.36	0.36	0.32	0.34	0.35
Count	A6819 212.00								A6512 226.00	A6506 220.00	A6496 219.00	A6127 226.00	A6123 224.00	A6120 229.00	A6122 221.00	A6125 223.00		A6121 217.00	A4028 195.00	A4641 207.00
Percent				0.37	0.38				0.37	0.36	0.36	0.37	0.37	0.38	0.36	0.37	0.36	0.36	0.32	0.34
Count	A340 193.00								A5828 224.00	A4766 222.00	A5826 219.00	A5815 223.00	A5814 226.00	A5830 221.00	A5816 216.00	A5810 219.00		A5817 221.00	A780 227.00	A693 218.00
Percent					0.37				0.37	0.36	0.36	0.37	0.37	0.36	0.35	0.36	0.35	0.36	0.37	0.36
-	A771											A1096	A5750	A1452	A6363	A1758		A2041	A5972	A391
Count Percent										219.00 0.36	220.00 0.36	227.00 0.37	217.00 0.36	224.00 0.37	192.00 0.32	217.00 0.36	220.00 0.36	211.00 0.35	226.00 0.37	222.00 0.36

Missing Data and LOD

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	A393	A392	A6422	A6415	A6411	A6403	A6418	A3936	A3934	A3935	A2556	A5188	A4079	A4101	A7222	A7221	A7220	A1868	A1867	A1665
Count	218.00	210.00	227.00	223.00	223.00	221.00	215.00	217.00	216.00	226.00	213.00	217.00	230.00	225.00	226.00	221.00	229.00	218.00	203.00	214.00
Percent	0.36	0.34	0.37	0.37	0.37	0.36	0.35	0.36	0.35	0.37	0.35	0.36	0.38	0.37	0.37	0.36	0.38	0.36	0.33	0.35
	A811	A5703	A1060	A1046	A7643	A7633	A7300	A2443	A7301	A7276	A6789	A7274	A7148	A7147	A7139	A6218	A6217	A6219	A5752	A5733
Count	221.00	196.00	225.00	217.00	227.00	224.00	225.00	214.00	219.00	229.00	198.00	222.00	227.00	228.00	218.00	223.00	223.00	223.00	223.00	225.00
Percent	0.36	0.32	0.37	0.36	0.37	0.37	0.37	0.35	0.36	0.38	0.33	0.36	0.37	0.37	0.36	0.37	0.37	0.37	0.37	0.37
	A5775	A4430	A4428	A4427	A4425	A4365	A1038	A3654	A5779	A1348	A1349	A1350	A1343	A5228	A5259	A1123	A1109	A20	A927	A928
Count	225.00	219.00	223.00	224.00	229.00	225.00	224.00	209.00	215.00	227.00	216.00	222.00	215.00	190.00	224.00	222.00	226.00	176.00	221.00	227.00
Percent	0.37	0.36	0.37	0.37	0.38	0.37	0.37	0.34	0.35	0.37	0.35	0.36	0.35	0.31	0.37	0.36	0.37	0.29	0.36	0.37

	A926	A930	A925	A6359	A6360	A6357	A6060	A6058	A6056
Count	214.00	222.00	223.00	227.00	218.00	225.00	224.00	217.00	210.00
Percent	0.35	0.36	0.37	0.37	0.36	0.37	0.37	0.36	0.34

Tables of Missing Rates by Variety

	X1	X2	Х3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18	X19	X20
Count			600.00				605.00			603.00			230.00		223.00				221.00	294.00
Percent	0.01	0.01	2.33	0.67	1.04	0.88	2.35	0.79	2.33	2.35	0.94	2.33	0.89	2.33	0.87	2.33	0.70	2.33	0.86	1.14
	X21	X22	X23	X24	X25	X26	X27	X28	X29	X30	X31	X32	X33			X36	X37	X38		
Count Percent	602.00 2.34	603.00 2.35	601.00 2.34	261.00 1.02		600.00 2.33	603.00 2.35	600.00 2.33	246.00 0.96	190.00 0.74	238.00 0.93	212.00 0.82	600.00 2.33			600.00 2.33	600.00 2.33	195.00 0.76		
	X41	X42	X43	X44	X45	X46	X47	X48	X49	X50	X51	X52	X53	X54	X55	X56	X57	X58	X59) X60
Count	600.00	184.00	210.00	195.00	601.00	213.00	177.00	602.00	165.00	599.00	194.00	238.00	601.00	292.00	233.00	600.00	600.00	600.00	224.00	600.00
Percent	2.33	0.72	0.82	0.76	2.34	0.83	0.69	2.34	0.64	2.33	0.75	0.93	2.34	1.14	0.91	2.33	2.33	2.33	0.87	2.33
Count	X61 269.00	X62 308.00	X63 252.00	X64 600.00	X65 209.00	X66 291.00	X67 600.00	X68 189.00	X69 600.00	X70 600.00	X71 242.00	X72 216.00	X73 600.00			X76 235.00	X77 600.00	X78 165.00		
Percent	1.05	1.20	0.98	2.33	0.81	1.13	2.33	0.74	2.33	2.33	0.94	0.84	2.33			0.91	2.33	0.64		
	X81	X82	X83	X84	X85	X86	X87	X88	X89	X90	X91	X92	X93	X94	X95	X96	X97	X98	X99	X100
Count Percent	244.00 0.95	600.00 2.33	248.00 0.96	600.00 2.33	280.00 1.09	600.00 2.33	600.00 2.33	600.00 2.33	282.00 1.10	267.00 1.04	600.00 2.33	190.00 0.74	600.00 2.33			173.00 0.67	600.00 2.33	600.00 2.33		
Count	X101 601.00	X102 601.00	X103 170.00	X104 601.00	X105 601.00	X106 603.00	X107 164.00	X108 602.00	X109 200.00	X110 603.00	X111 187.00	X112 600.00	X113 600.00			X116 205.00	X117 601.00	X118 194.00		
Percent	2.34	2.34	0.66	2.34	2.34	2.35	0.64	2.34	0.78	2.35	0.73	2.33	2.33			0.80	2.34	0.75		
	X121	X122	X123	X124	X125	X126	X127	X128	X129	X130	X131	X132	X133			X136	X137	X138		
Count Percent	601.00 2.34	603.00 2.35	174.00 0.68	601.00 2.34	601.00 2.34	226.00 0.88	601.00 2.34	227.00 0.88	601.00 2.34	601.00 2.34	601.00 2.34	601.00 2.34	601.00 2.34			601.00 2.34	209.00 0.81	601.00 2.34		
	X141	X142	X143	X144	X145	X146	X147	X148	X149	X150	X151	X152	X153			X156	X157	X158		
Count Percent	207.00 0.81	601.00 2.34	603.00 2.35	182.00 0.71	601.00 2.34	601.00 2.34	209.00 0.81	178.00 0.69	601.00 2.34	185.00 0.72	178.00 0.69	603.00 2.35	603.00 2.35			209.00 0.81	198.00 0.77	209.00 0.81		
	X161	X162	X163	X164	X165	X166	X167	X168	X169	X170	X171	X172	X173			X176	X177	X178		
Count Percent	602.00 2.34	195.00 0.76	603.00 2.35	171.00 0.67	604.00 2.35	601.00 2.34	603.00 2.35	601.00 2.34	156.00 0.61	178.00 0.69	601.00 2.34	601.00 2.34	601.00 2.34			601.00 2.34	602.00 2.34	601.00 2.34		
Count	X181 601.00	X182 601.00	X183 601.00	X184 602.00	X185 602.00	X186 186.00	X187 167.00	X188 194.00	X189 602.00	X190 601.00	X191 603.00	X192 601.00	X193 601.00			X196 601.00	X197 601.00	X198 183.00		
Percent	2.34	2.34	2.34	2.34	2.34	0.72	0.65	0.75	2.34	2.34	2.35	2.34	2.34			2.34	2.34	0.71		

Missing Data and LOD

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	X201	X202	X203	X204	X205	X206	X207	X208	X209	X210	X211	X212	X213	X214	X215	X216	X217	X218	X219	X220
Count	601.00	209.00	601.00	601.00	601.00	200.00	601.00	602.00	601.00	601.00	601.00	192.00	601.00	601.00	601.00	601.00	178.00	601.00	601.00	602.00
Percent	2.34	0.81	2.34	2.34	2.34	0.78	2.34	2.34	2.34	2.34	2.34	0.75	2.34	2.34	2.34	2.34	0.69	2.34	2.34	2.34

	X221	X222	X223	X224	X225	X226	X227	X228	X229	X230	X231	X232	X233	X234	X235	X236	X237	X238	X239	X240
Count	172.00	186.00	602.00	601.00	601.00	602.00	601.00	602.00	603.00	602.00	601.00	601.00	601.00	601.00	173.00	169.00	601.00	601.00	602.00	601.00
Percent	0.67	0.72	2.34	2.34	2.34	2.34	2.34	2.34	2.35	2.34	2.34	2.34	2.34	2.34	0.67	0.66	2.34	2.34	2.34	2.34

	X241	X242	X243	X244	X245	X246	X247	X248	X249	X250	X251	X252	X253	X254	X255	X256	X257
Count	601.00	602.00	601.00	601.00	601.00	179.00	219.00	601.00	249.00	601.00	602.00	189.00	602.00	186.00	601.00	601.00	601.00
Percent	2.34	2.34	2.34	2.34	2.34	0.70	0.85	2.34	0.97	2.34	2.34	0.74	2.34	0.72	2.34	2.34	2.34