

Answers to Part 1 Questions

Q.1.2

phenotypic variance = 15.10257

genotype counts are

0	1	2
474	1021	505

genotype frequencies are

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> 474/2000
[1] 0.237 (aa)
> 1021/2000
[1] 0.5105 (Aa, aA)
> 505/2000
[1] 0.2525 (AA)
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Q.1.4a & b

Yes

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.1464	0.1511	27.438	< 2e-16 ***
QTLA1T1	0.9180	0.1226	7.491	1.02e-13 ***

Multiple R-squared: 0.02732

Given $\alpha=0.005$, we reject the null hypothesis $b_1=0$, as $p < \alpha$. We conclude that there is association. The proportion of explained variance equal .02732, so the additive coded QTL explain 2.732% of the phenotypic variance (variance component = $.02732 \times 15.10257 = 0.412$).

Q 1.5

The total explained proportion is .02732, so that unexplained proportion is $1 - 0.02732 = 0.97268$

The unexplained variance is $(1 - .03658) \times 15.102 = 14.68941$

Q. 1.6

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-4.98016	0.32547	-15.301	<2e-16 ***
QTLA1T1	0.86835	0.10136	8.567	<2e-16 ***
QTLA2T1	0.96957	0.10139	9.563	<2e-16 ***
QTLA3T1	0.93857	0.09918	9.464	<2e-16 ***
QTLA4T1	0.96458	0.09929	9.715	<2e-16 ***
QTLA5T1	0.84703	0.10211	8.296	<2e-16 ***
QTLA6T1	1.15908	0.10013	11.576	<2e-16 ***
QTLA7T1	0.91373	0.10076	9.068	<2e-16 ***
QTLA8T1	1.16146	0.09896	11.737	<2e-16 ***
QTLA9T1	1.21302	0.10060	12.058	<2e-16 ***
QTLA10T1	0.97548	0.10247	9.519	<2e-16 ***

Multiple R-squared: 0.3395

The proportion is .3395, i.e., 33.95% of the variance. The explained variance equals $.3395 \times 15.102 = 5.127$.