A Population Genetic Report

using PopGenReport Ver. 1.6.6

Adamack & Gruber (2013)

December 13, 2013

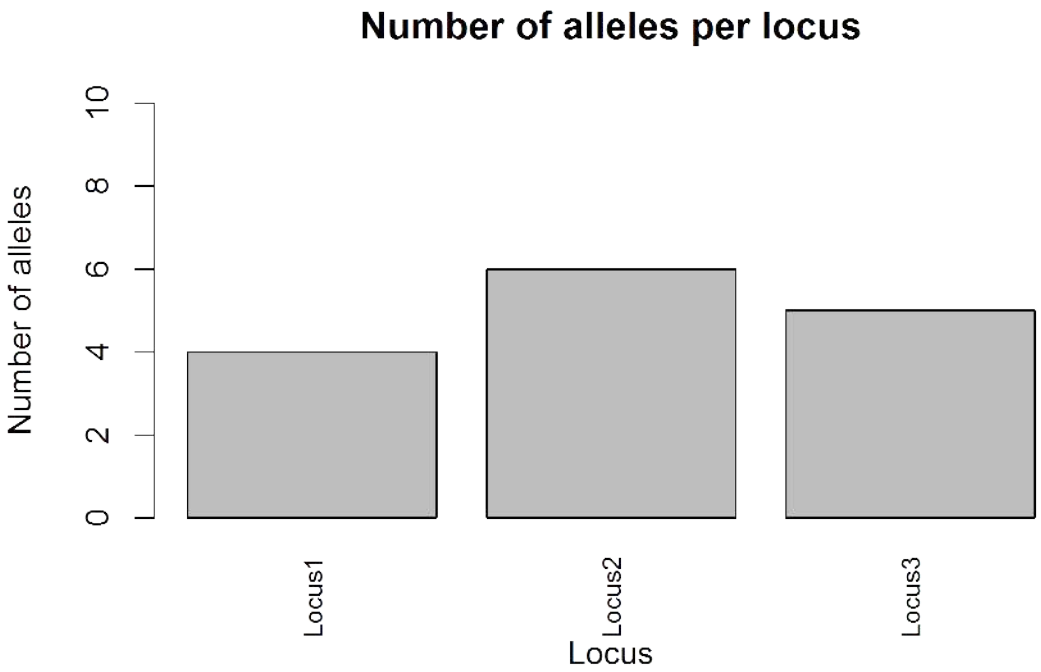
Contents

1 Counts

This analysis looks at 71 individuals.

The mean number of alleles per locus (across all locations): 5

The percentage of missing data was 0%.



The individuals were sampled from the following locations in the following numbers:

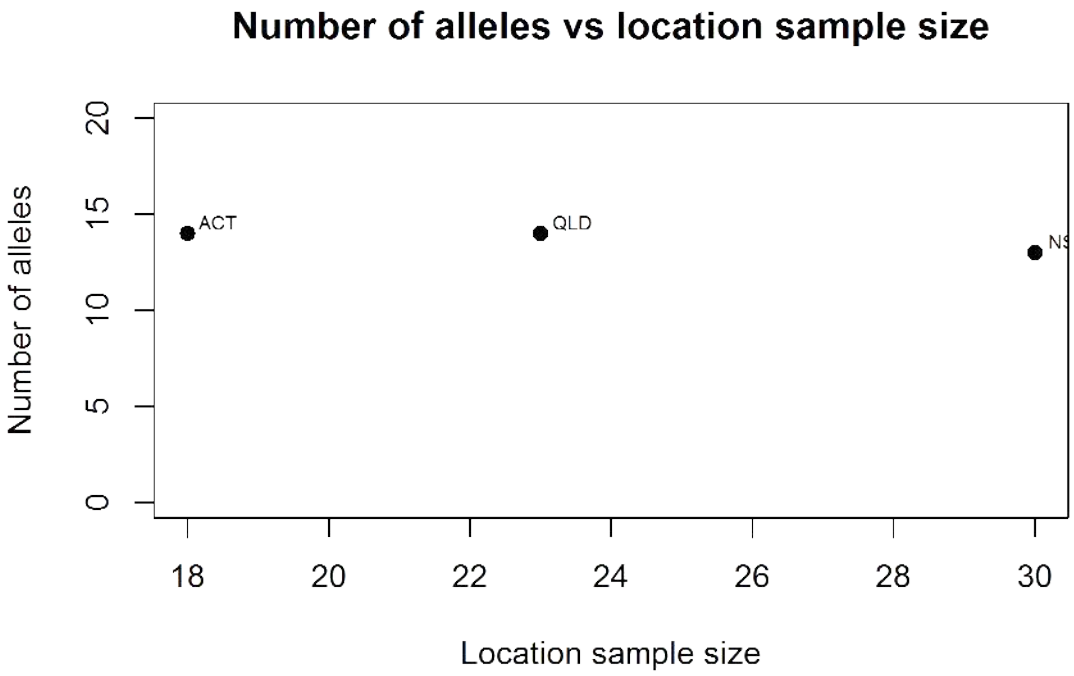
population	ACT	NSW	QLD
# ind	18	30	23

Table 1: Number of individuals per population

The total number of alleles sampled across all locations was 15
The total number of alleles seen in each sampling location was:

population	ACT	NSW	QLD
# alleles	14	13	14

Table 2: Number of alleles per population



The number of alleles per locus (across all subpopulations):

locus	Locus1	Locus2	Locus3
# alleles	4	6	5

Table 3: Number of alleles per locus across all subpopulations

2 Sampling locations

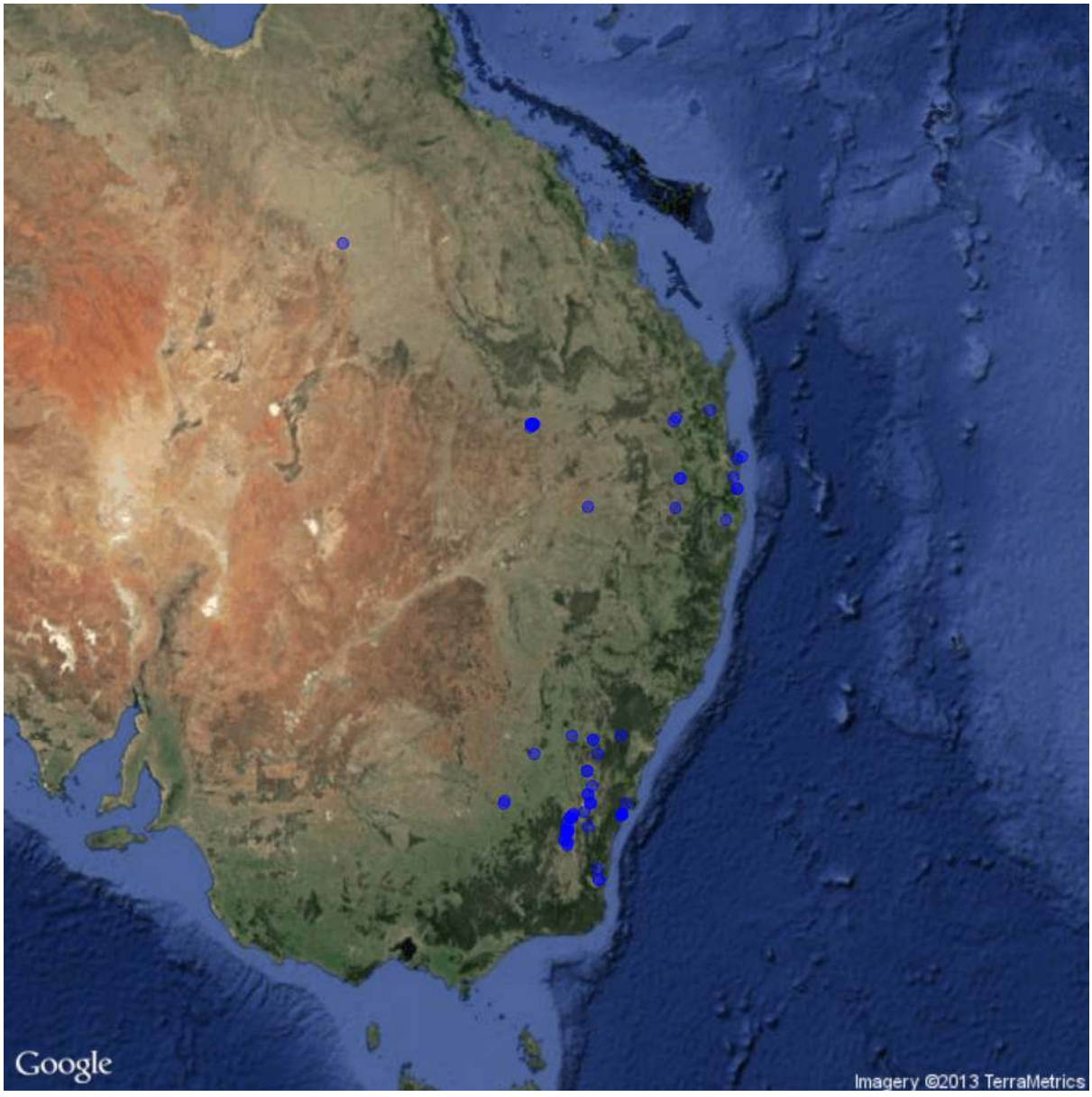


Figure 1: Sample locations

3 Population-wide test for heterozygosity

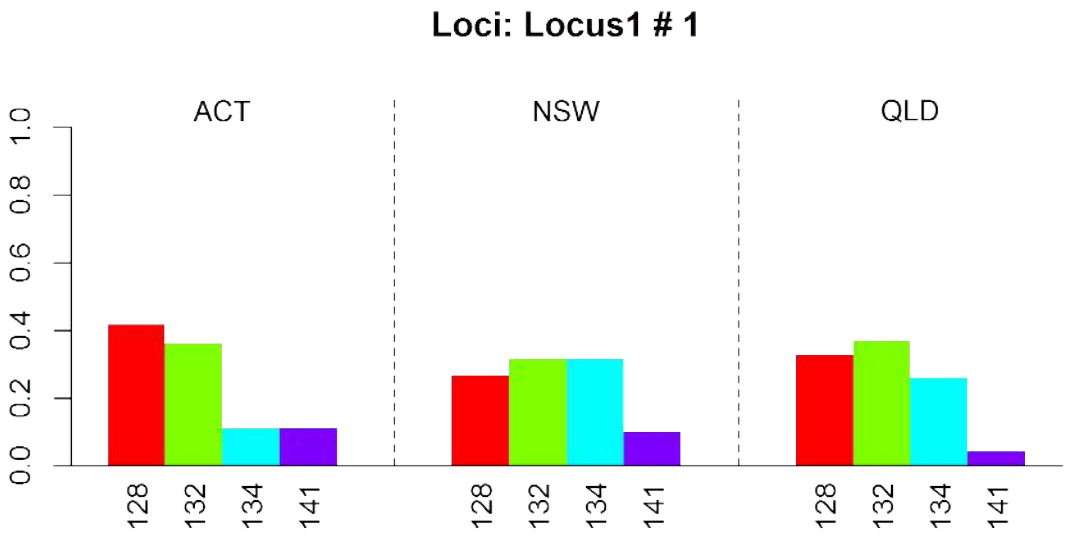
Locus	Expected	Observed	% difference
Locus1	0.708	0.718	-1.443
Locus2	0.691	0.746	-8.055
Locus3	0.710	0.718	-1.202

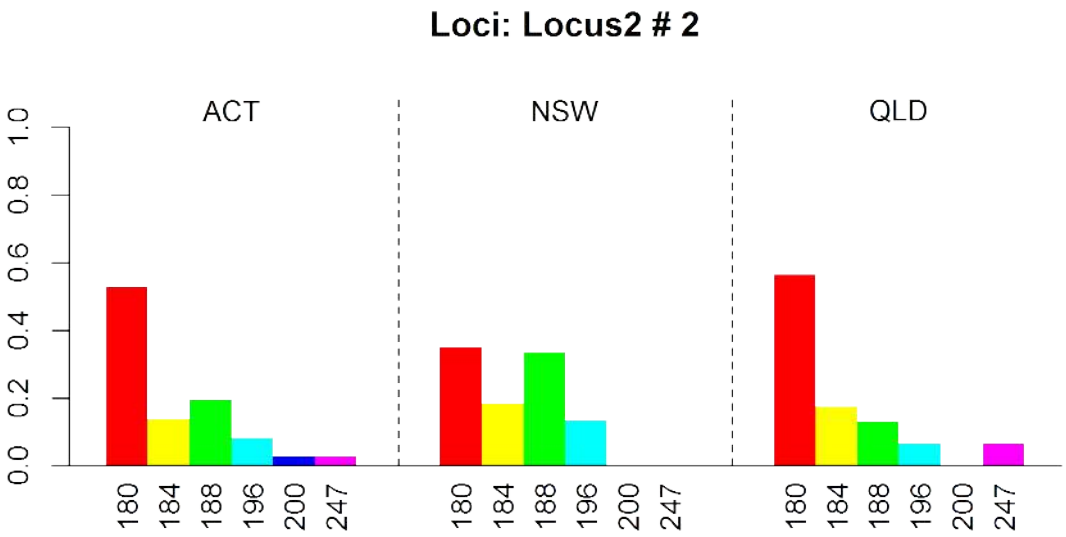
Table 4: The population-wide expected and observed heterozygosity and percent difference ((E-O)/E*100) at each locus

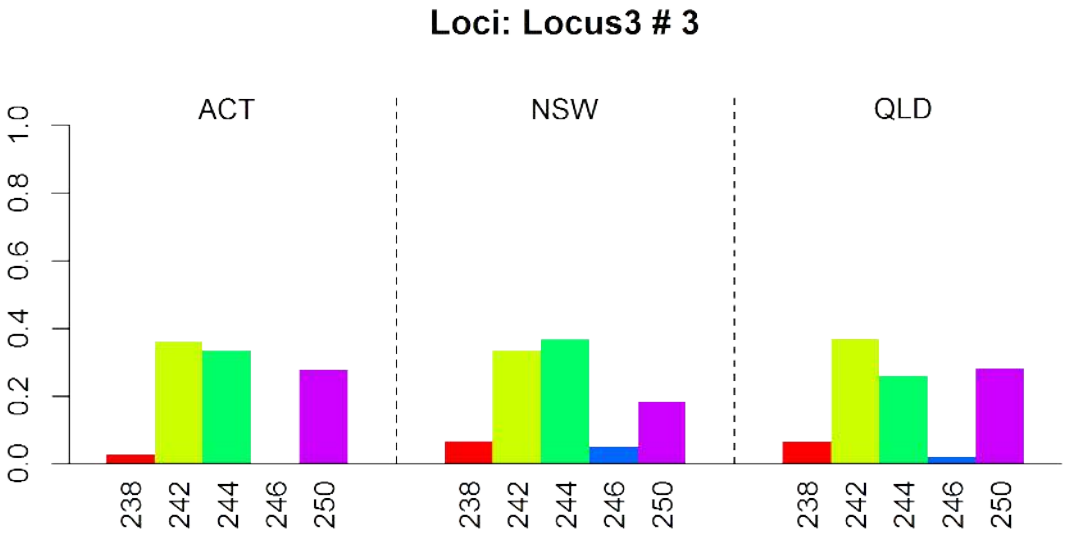
Bartlett test of homogeneity of variance. This test compares observed vs. expected heterozygosity. A significant result indicates that the population departs from HWE.
Bartlett's K-squared: 0.299, df = 1, p-value = 0.5846

4 Distribution of alleles by subpopulation and loci

4.1 Allele frequency plots for all subpopulations and loci







4.2 Heatmaps of allele frequencies for all subpopulation and loci

Cell colors indicate the proportion of the the total number of alleles in a subpopulation (e.g. 2N) that are of a particular allele type. The numbers within a cell are the counts of the number of alleles in a particular population.

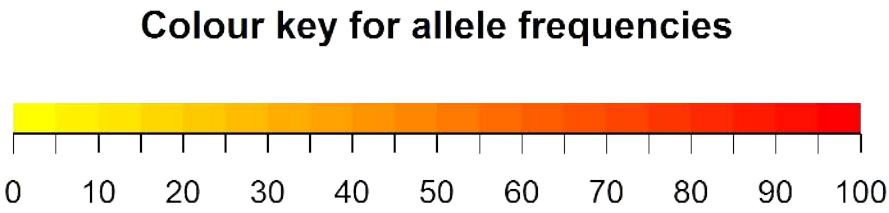
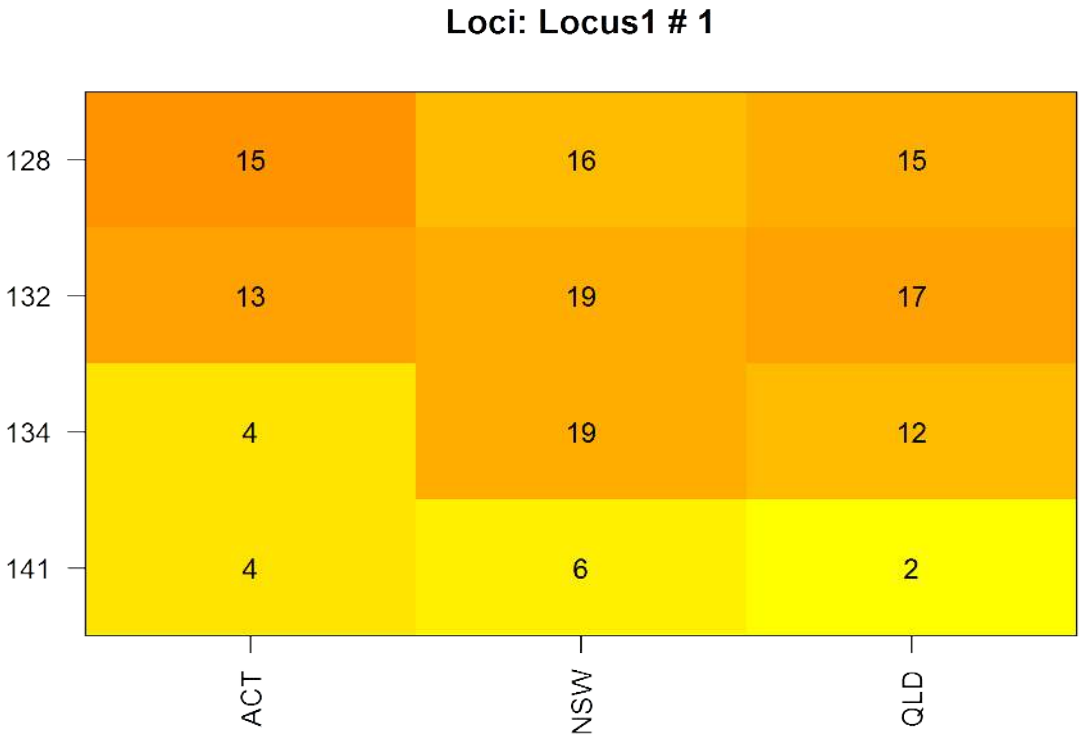
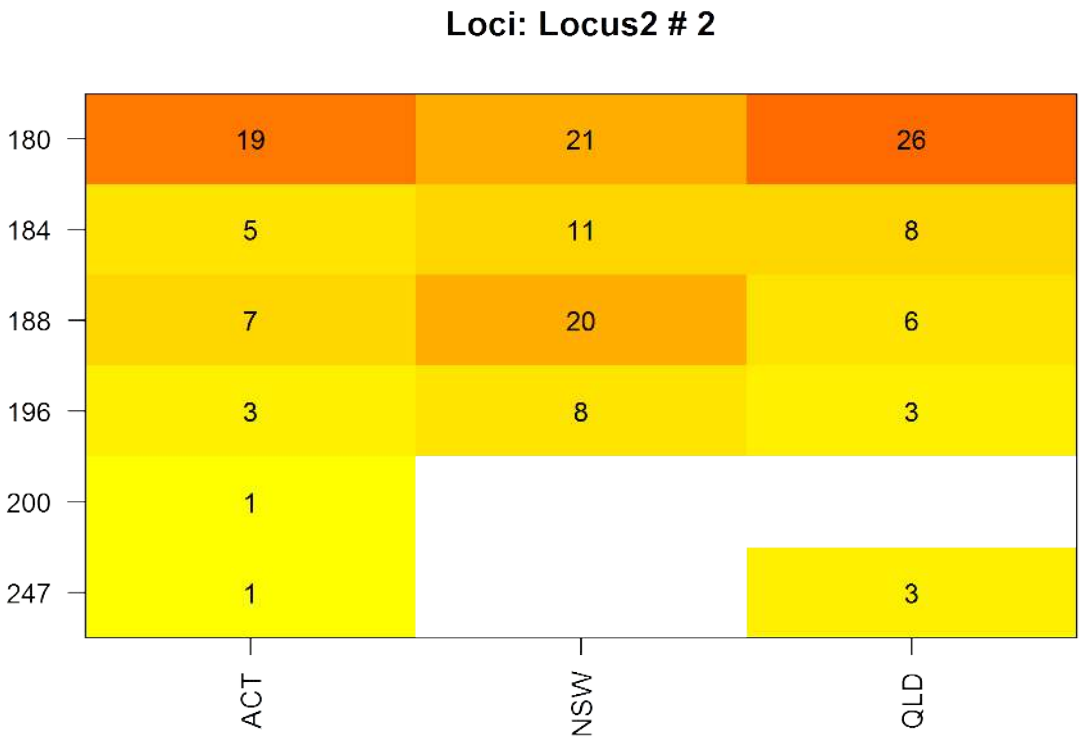
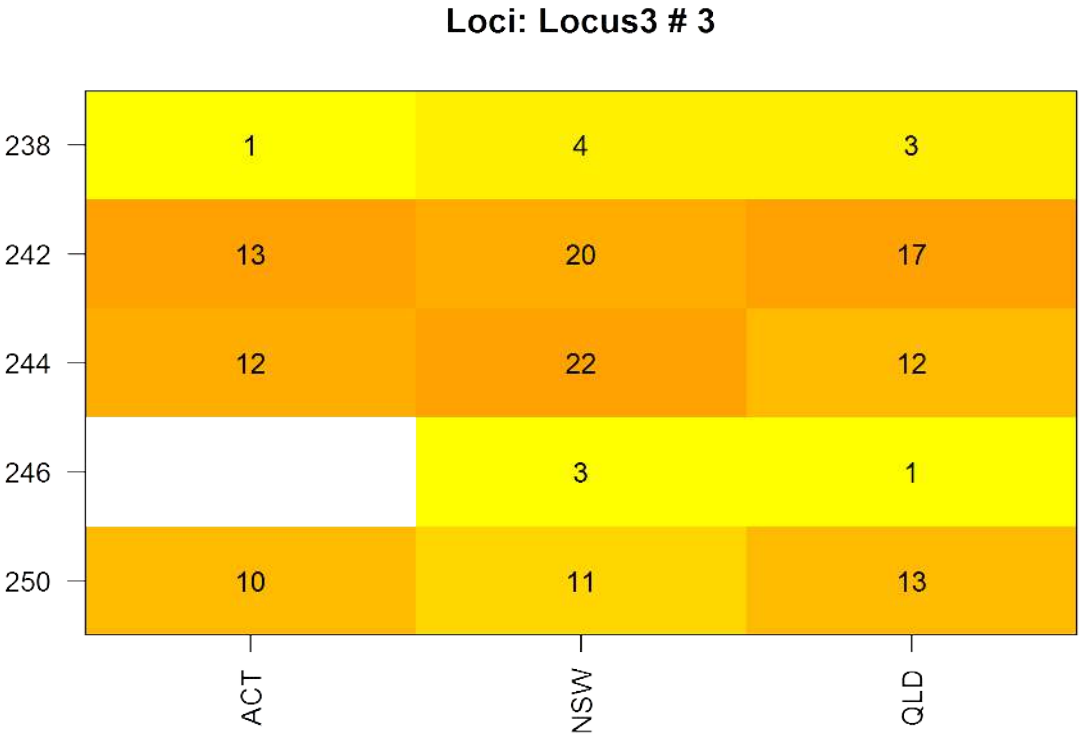


Figure 2: Color indicates the proportion of the total number of alleles in a subpopulation




Loci: Locus2 # 2
180
184
188
196
200
247
19
21
26
5
11
8
7
20
6
3
8
3
1
1
3
ACT
NSW
QLD


Loci: Locus3 # 3
238
242
244
246
250
1
4
3
13
20
17
12
22
12
3
1
10
11
13
ACT
NSW
QLD

4.3 Private Alleles

4.3.1 All private alleles

	Population	Allele
Locus2	ACT	200

Table 5: List of private alleles by locus and population

4.3.2 Number of private alleles by population

	ACT
Number of private alleles	1

Table 6: Number of private alleles by population

5 Calculation of F statistics for each locus across all sampling locations

	Fit	Fst	Fis
Locus3	-0.0084	-0.0103	0.0019
Locus1	-0.0060	0.0040	-0.0100
Locus2	-0.0645	0.0247	-0.0915

Table 7: Population wide Fit, Fst, and Fst values for each locus. The table is sorted in ascending order based on Fst.

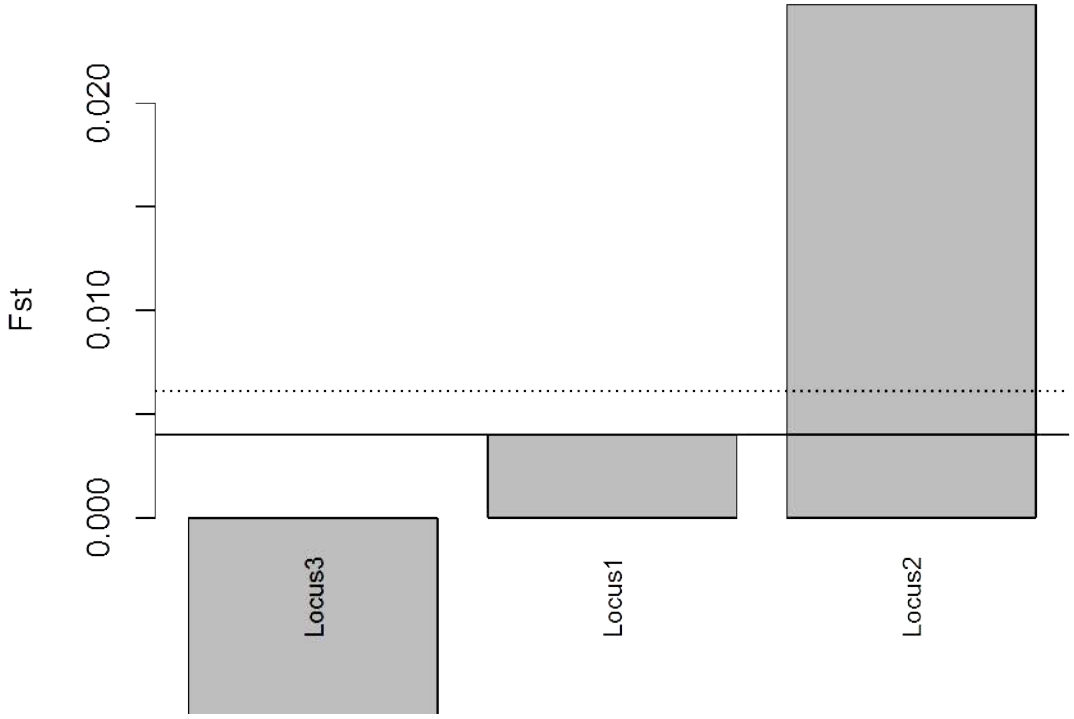


Figure 3: Fst across entire population at each locus. Solid line shows median Fst, dotted line shows mean Fst, dashed lines indicate 2.5th and 97.5th percentiles of Fst

6 Computation of Nei's pairwise Fst between all pairs of populations

	ACT	NSW	QLD
ACT	0.000		
NSW	0.015	0.000	
QLD	0.006	0.015	0.000

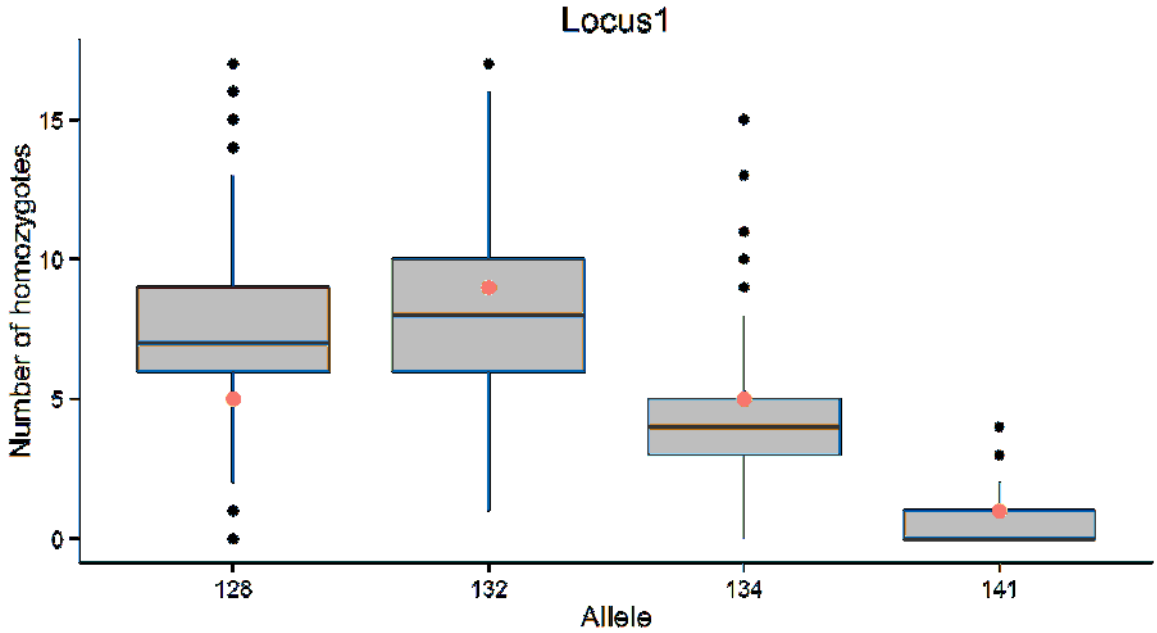
Table 8: Nei's pairwise Fst between all pairs of populations

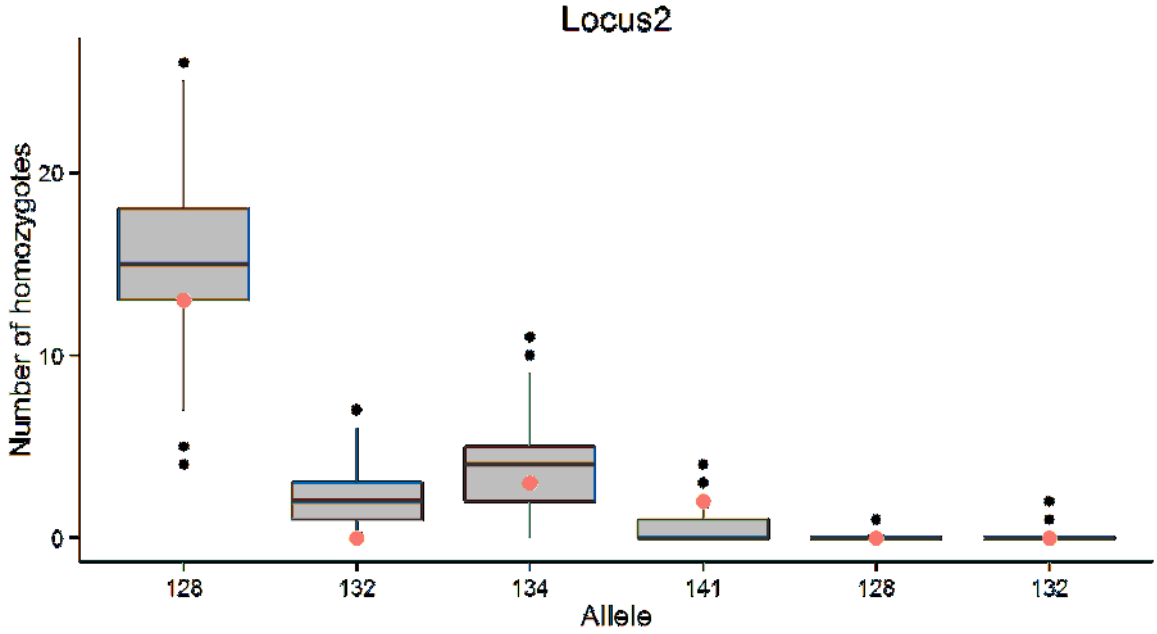
7 Testing for null alleles

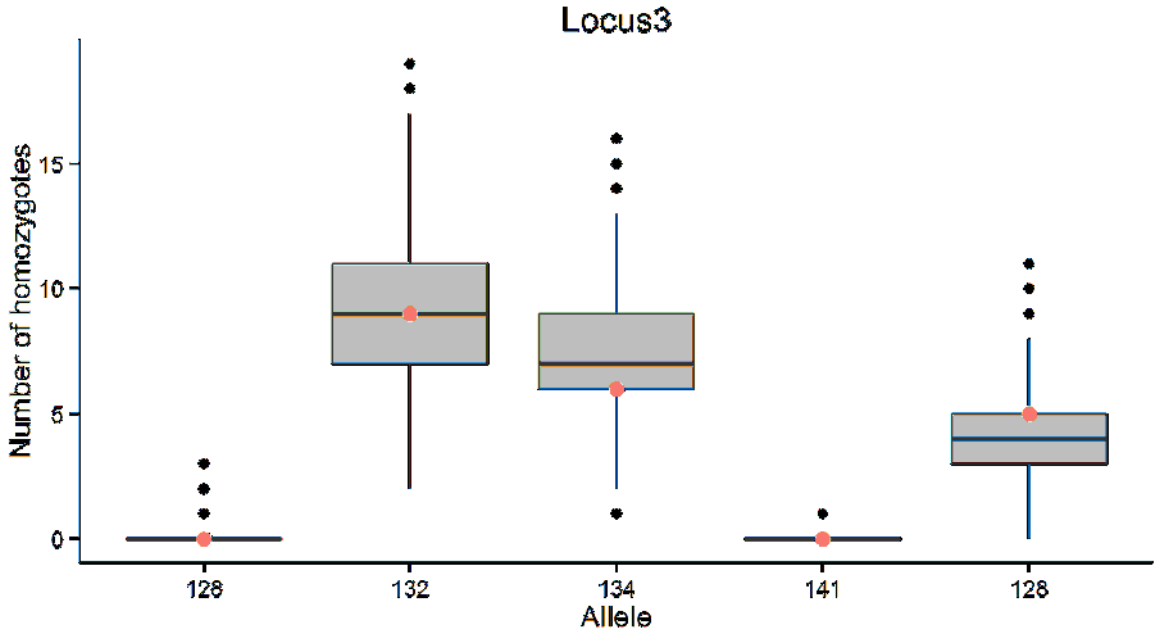
7.1 Comparison of the observed number of homozygotes vs. expected

Boxplots show the bootstrap distribution of the expected number of homozygotes for each allele with the boxes showing the 25th (lower edge), 50th (solid line), and 75th (upper edge) percentiles of the distribution and the whiskers showing 1.5 * the inter-quartile range. Solid black dots indicate outliers while red dots indicate the observed number of homozygotes for the allele. If the red dot is above the end of the whisker it suggests that there is an excess of homozygotes for that allele.

The probability of the observed number of homozygotes for each allele is available in the results object using null.all$homozygotes$probability.obs


Locus1
Number of homozygotes
15
10
5
0
128
132
134
141
Allele


Locus2
Number of homozygotes
20
10
0
128
132
134
141
128
132
Allele

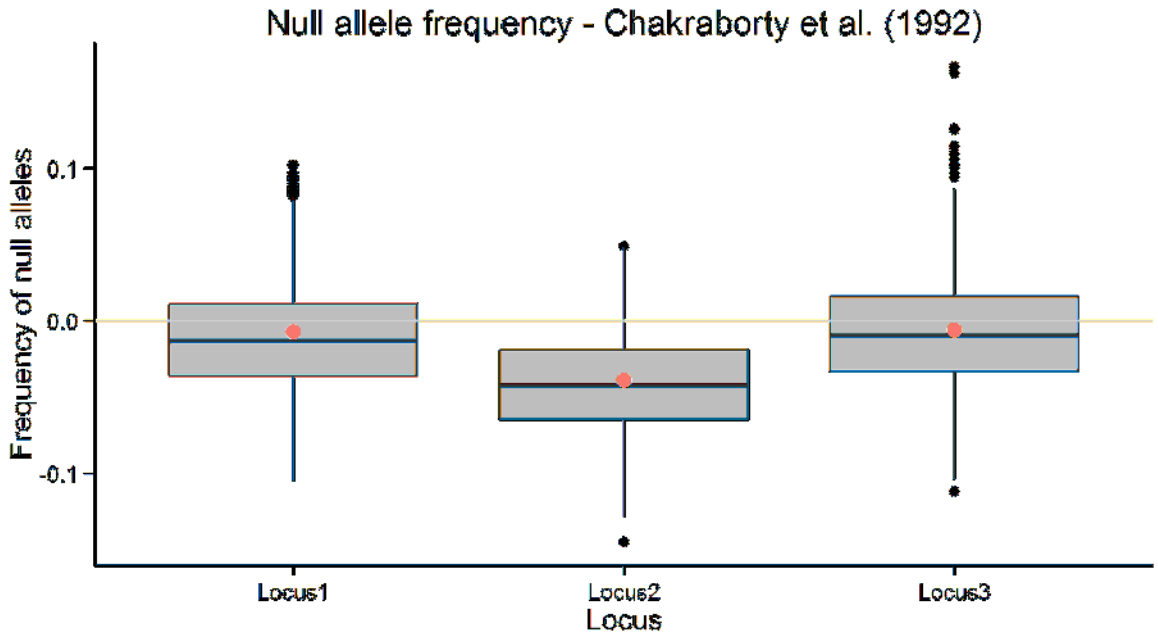


	Allele-1	Allele-2	Allele-3	Allele-4	Allele-5	Allele-6
Locus1	0.771	0.321	0.242	0.089		
Locus2	0.703	0.877	0.560	0.044	0.003	0.052
Locus3	0.183	0.374	0.604	0.059	0.210	

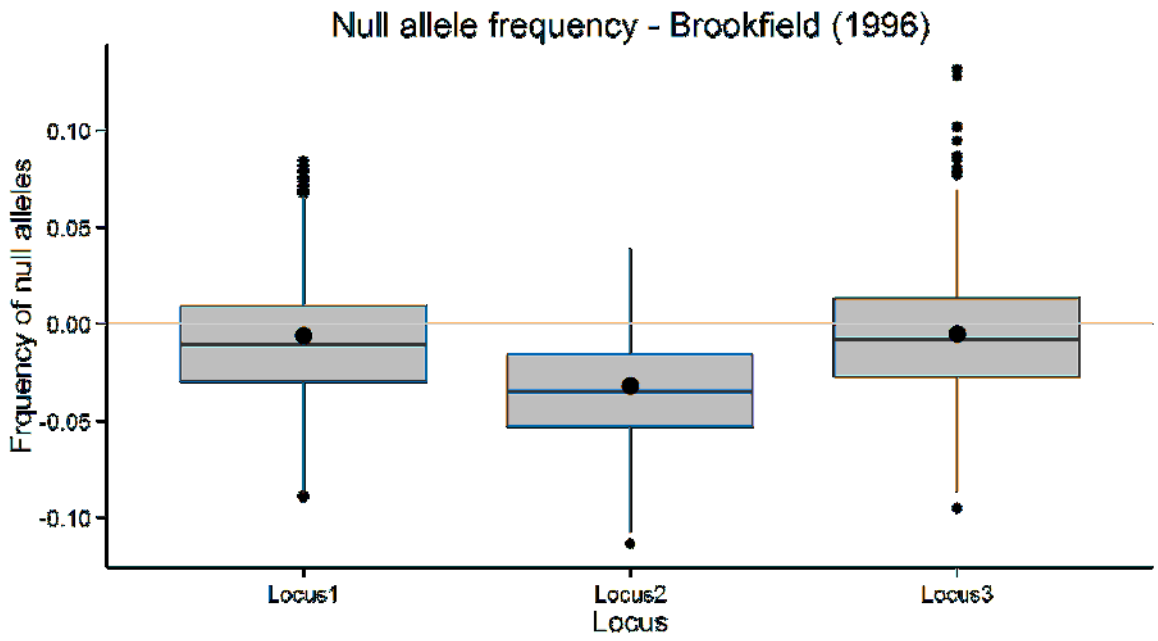
Table 9: Probability of the observed number of homozygotes

7.2 Frequency of null alleles

7.2.1 Determined using Chakraborty et al. (1992)



7.2.2 Determined using Brookfield (1996)



	Locus1	Locus2	Locus3
Observed frequency	-0.006	-0.032	-0.005
Median frequency	-0.011	-0.035	-0.008
2.5th percentile	-0.064	-0.082	-0.059
97.5th percentile	0.057	0.019	0.055

Table 10: Summary of null allele frequencies by locus for Brookfield (1996)

8 Allelic richness

Allelic richness for each locus and subpopulation was based on a subsample of 36 alleles.

	ACT	NSW	QLD
Locus1	4.000	3.997	3.957
Locus2	6.000	4.000	4.984
Locus3	4.000	4.919	4.775

Table 11: Allelic richness by locus and population

	ACT	NSW	QLD
Mean richness	4.667	4.305	4.572
Total richness	14.000	12.916	13.715

Table 12: Allelic richness summary statistics

9 Hs and Ht based population differentiation statistics

	Hs	Ht	Gst	Gprime_st	D
Locus1	0.708	0.710	0.003	0.017	0.012
Locus2	0.680	0.688	0.012	0.055	0.038
Locus3	0.718	0.712	-0.008	-0.041	-0.029

Table 13: Hs and Ht based estimates of differentiation: Gst, Gst and Dest for each locus

	Ht	Gst_est	Gprime_st	D_het	D_mean
0.702	0.704	0.002	0.012	0.008	

Table 14: Hs and Ht based global estimates of differentiation: Gst, Gst and Dest for each locus

	ACT	NSW	QLD
ACT			
NSW	0.025		
QLD	-0.027	0.029	

Table 15: mmod Jost's D pairwise

	ACT	NSW	QLD
ACT			
NSW	0.035		
QLD	-0.040	0.040	

Table 16: Pairwise Gst - Hedrick

	ACT	NSW	QLD
ACT			
NSW	0.005		
QLD	-0.006	0.006	

Table 17: Pairwise Gst - Nei

10 Testing for HWE for each combination of location and locus

10.1 Testing HWE for each combination of location and locus

The table below shows the p-value for the test of HWE for each combination of location and locus. The p-values shown here differ from those produced by GENALEX as the Chi-square test performed here includes the Yates continuity correction which GENALEX does not. As a large number of Chi-square tests are performed, $\alpha = 0.05$ cannot be used as Type I errors are likely to occur. Instead a Bonferroni adjustment is used $\alpha = (0.05/\ 9) = 0.0056$.

	ACT	NSW	QLD
Locus1	0.517	0.285	0.286
Locus2	0.167	0.029	0.800
Locus3	0.818	0.624	0.566

Table 18: Chi-square test of HWE p-values for each combination of location and locus

10.2 Combinations of location and locus that depart from HWE

There were no departures from HWE for any combination of sub-population and locus

11 Kosman and Leonard

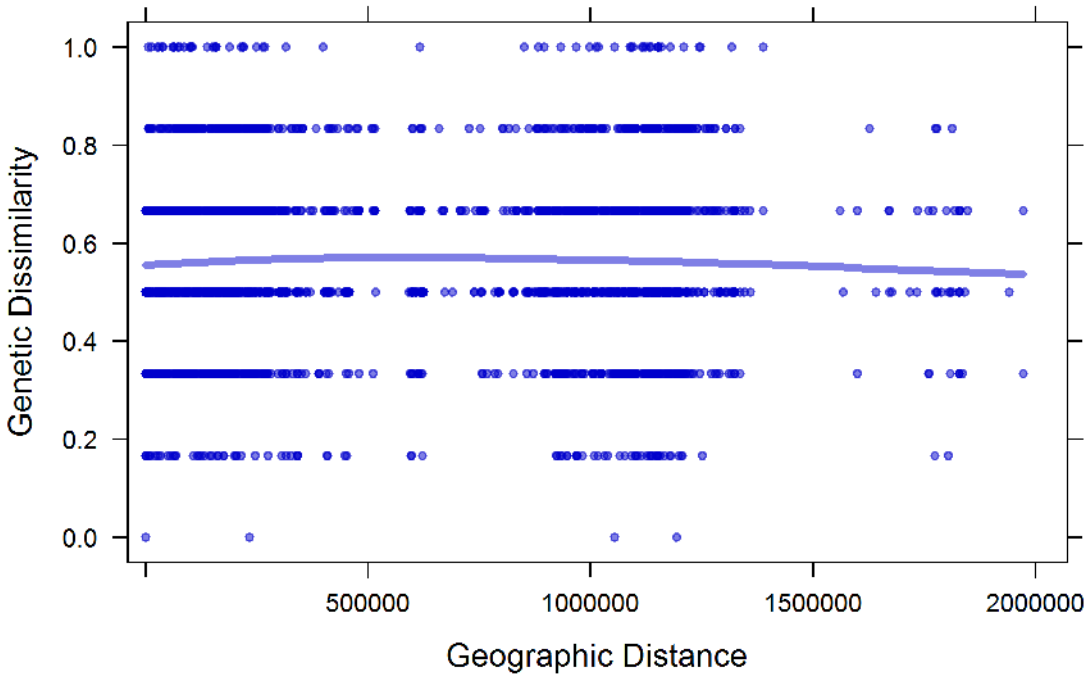


Figure 4: Genetic Dissimilarity (Kosman and Leonard 2005) vs Geographic Distance. The line represents the running average.

12 Genetic distance between individuals using Smouse and Peakall

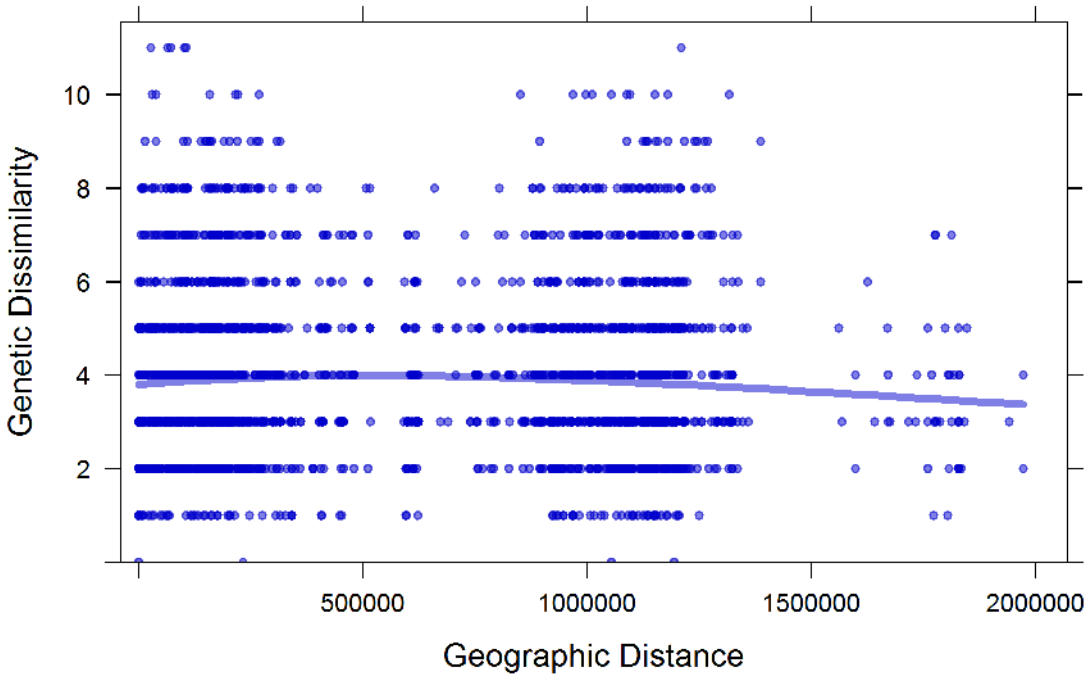


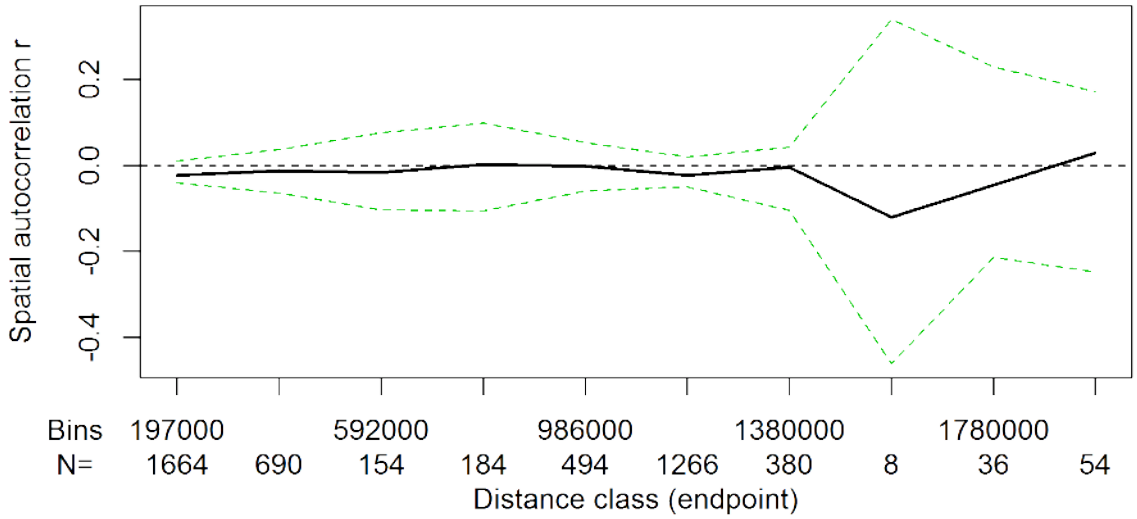
Figure 5: Genetic Dissimilarity (Smouse and Peakall 1999) vs Geographic Distance. The line represents the running average.

13 Spatial autocorrelation following Smouse and Pekall 1999

Global spatial autocorrelation is a multivariate approach combining all loci into a single analysis. The autocorrelation coefficient r is calculated for each pairwise genetic distance pairs for all specified distance classes. For more information see Smouse and Peakall 1999, Peakall et a. 2003 and Smouse et al. 2008. For full references refer to the help files by typing "?spautocor".

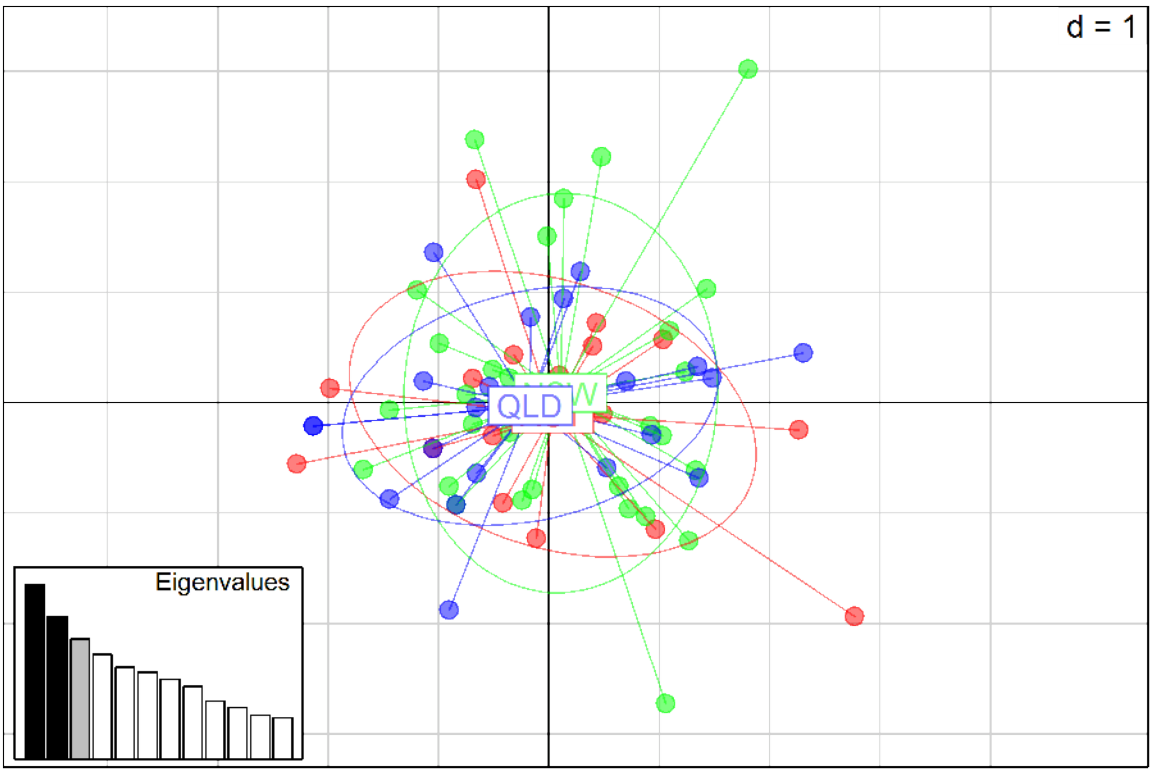
	bin	N	r	r.l	r.u
1	197300.000	1664	-0.023	-0.041	0.010
2	394600.000	690	-0.012	-0.065	0.036
3	591900.000	154	-0.017	-0.104	0.075
4	789200.000	184	0.002	-0.106	0.099
5	986500.000	494	-0.002	-0.060	0.053
6	1183800.000	1266	-0.023	-0.050	0.019
7	1381100.000	380	-0.004	-0.105	0.041
8	1578400.000	8	-0.120	-0.462	0.339
9	1775700.000	36	-0.045	-0.214	0.229
10	1973000.000	54	0.028	-0.248	0.172

Table 19: Spatial autocorrelation and bootstrap results using the approach of Smouse and Pekall 1999.



14 Principal Coordinate Analysis

Principal coordinate analysis. This plot, using the first two axes, visualises genetic diversity among sampled individuals. Missing data are replaced by the mean of the allele frequencies. Colors indicate subpopulation if specified in the genetic data set.


d = 1
QLD
Eigenvalues