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Correction: Detection of linkage between quantitative trait loci and restriction fragment length polymorphism using inbred lines

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It has been drawn to my attention that Table 2 and Table 3 in Simpson (1989) are in error. This arose as a consequence of poor convergence during maximum likelihood estimation for small gene effects, d, and for recombination rates, r, close to 0.5, which led to incorrect interpretation of the results. Table 1 presented here gives the mean maximum likelihood ratio test statistic for 200 observations based on 100 replicates using the NAG algorithm E04JAF (Numerical Algorithms Group 1990), which converges well, even for small values of d and r close to 0.5, and the expected *t*-statistic from comparing marker genotype means. Table 2 and Table 3 should replace those published. Table 2 shows that the numbers of inbred lines required to detect linkage are similar for the *t*-test and the maximum likelihood ratio test. For small values of d and r close to 0.5 there appear to be large differences between the numbers of lines needed for the two tests, however the standard error of the estimate of the mean of the likelihood ratio test statistic is large compared with the mean, and the estimates of the numbers of lines needed in these cases will have a wide confidence interval. Table 3 shows that the powers of the two tests are similar.

To validate these results, data sets were generated using sample sizes given in Table 2 for a range of values of d and r and replicated 100 times, and the resulting powers of 5% significance tests were close the the expected value of 0.5.

Table 1. Mean likelihood ratio test statistics and expected *t*-statistics

Standardised difference between means $d = (m_1 - m_2)$		Recombination rate – r^c							
		Selfing				Brother-sister mating			
		0.05	0.10	0.20	0.30	0.05	0.10	0.20	0.30
d = 0.25	χ^{2a}	2.58	2.45	1.28	1.23	2.50	1.84	1.25	1.48
	t^b	1.44	1.17	0.75	0.44	1.22	0.88	0.48	0.25
d = 0.50	χ^2	8.27	6.57	3.22	1.56	5.92	3.65	1.69	1.31
	t	2.86	2.32	1.48	0.86	2.41	1.73	0.94	0.49
d = 0.75	χ^2	18.39	10.75	5.49	2.60	12.12	7.51	2.94	1.59
	t	4.24	3.41	2.15	1.25	3.54	2.52	1.36	0.71
d = 1.00	χ^2	29.57	18.27	7.95	3.63	22.14	10.75	4.14	1.54
	t	5.56	4.42	2.76	1.59	4.60	3.24	1.74	0.91
d = 2.00	χ^2	83.35	54.07	20.71	8.83	56.41	29.28	9.85	3.14
	t	10.03	7.56	4.50	2.54	7.94	5.35	2.78	1.44
d = 3.00	χ^2	123.44	79.77	31.12	11.74	86.52	42.24	12.46	4.37
	t	13.14	9.43	5.40	3.01	9.97	6.47	3.30	1.69

[a] χ^2 denotes likelihood ratio test statistic

[b] t denotes comparison of marker genotype means

[c] Proportion recombinant is $R = 2r/(1+2r)$ for selfing and $R = 4r/(1+6r)$ for brother-sister mating

Table 2. Total number of inbred lines needed to detect linkage at 5% significance level

Standardised difference between means $d=(m_1-m_2)$		Recombination rate – r[c]							
		Selfing				Brother-sister mating			
		0.05	0.10	0.20	0.30	0.05	0.10	0.20	0.30
d=0.25	χ^2[a]	485	531	2,704	3,278	512	915	3,126	1,602
	t[b]	369	558	1,355	3,990	517	995	3,352	12,227
d=0.50	χ^2	106	138	346	1,362	156	290	1,118	2,513
	t	94	143	352	1,041	132	257	874	3,195
d=0.75	χ^2	44	79	171	479	69	118	395	1,304
	t	43	66	166	495	61	121	415	1,522
d=1.00	χ^2	27	44	110	292	36	79	244	1,421
	t	25	39	101	303	36	73	254	937
d=2.00	χ^2	9	14	39	98	14	27	87	359
	t	8	13	38	119	12	27	99	372
d=3.00	χ^2	6	10	25	72	9	19	67	228
	t	4	9	26	85	8	18	71	268

[a] χ^2 denotes likelihood ratio test statistic

[b] t denotes comparison of marker genotype means

[c] Proportion recombinant is $R=2r/(1+2r)$ for selfing and $R=4r/(1+6r)$ for brother-sister mating

Table 3. Power of a 5% test using a total of 200 inbred lines

Standardised difference between means $d=(m_1-m_2)$		Recombination rate – r[c]							
		Selfing				Brother-sister mating			
		0.05	0.10	0.20	0.30	0.05	0.10	0.20	0.30
d=0.25	χ^2[a]	0.24	0.20	0.09	0.07	0.25	0.20	0.07	0.12
	t[b]	0.30	0.21	0.11	0.06	0.23	0.14	0.07	0.04
d=0.50	χ^2	0.81	0.66	0.32	0.10	0.62	0.37	0.12	0.09
	t	0.82	0.64	0.31	0.13	0.67	0.41	0.15	0.07
d=0.75	χ^2	0.98	0.92	0.53	0.25	0.97	0.72	0.29	0.13
	t	0.99	0.92	0.58	0.24	0.94	0.71	0.28	0.11
d=1.00	χ^2	0.98	0.96	0.79	0.35	1.00	0.85	0.41	0.13
	t	1.00	0.99	0.79	0.36	1.00	0.90	0.41	0.15
d=200	χ^2	1.00	1.00	1.00	0.87	1.00	1.00	0.84	0.32
	t	1.00	1.00	0.99	0.72	1.00	1.00	0.79	0.30
d=3.00	χ^2	1.00	1.00	1.00	0.87	1.00	1.00	0.98	0.45
	τ	1.00	1.00	1.00	0.85	1.00	1.00	0.91	0.40

[a] χ^2 denotes likelihood ratio test statistic

[b] t denotes comparison of marker genotype means

[c] Proportion recombinant is $R=2r/(1+2r)$ for selfing and $R=4r/(1+6r)$ for brother-sister mating

In the light of these results, the conclusion on the relative power of the two tests must be revised, and it is now concluded that comparison of marker genotype means and the likelihood ratio test have similar power. Although the test statistic for comparison of marker genotype means is easier to calculate than the maximum likelihood ratio test statistic, maximum likelihood estimation is a useful tool for estimation of the recombination rate and the size of the effect of the quantitative trait locus.

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References

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