

## Appendix A

Given the described pseudo-doubled backcross, our preferential pairing mechanism assumes that each informative chromosome ( $MQ, M, Q$ ) is paired with a noninformative chromosome ( $\emptyset$ ). Because of this, there are only three pairing configurations to consider. The matrix  $\mathbf{C}$  for the three pairs is:

$$\mathbf{C} = \begin{array}{c} \text{Possible Pairing Configurations} \\ \hline \begin{array}{ccc} MQ \times \emptyset & M \times \emptyset & Q \times \emptyset \\ \hline \left[ \begin{array}{cc} \frac{1}{2}(1-r) & \frac{1}{2}r \\ \frac{1}{2}r & \frac{1}{2}(1-r) \end{array} \right] & \left[ \begin{array}{c} \frac{1}{2} 0 \\ \frac{1}{2} 0 \end{array} \right] & \left[ \begin{array}{c} \frac{1}{2} \frac{1}{2} \\ 0 0 \end{array} \right] \end{array} \end{array}$$

Notice that only the  $MQ \times \emptyset$  pair provides any information concerning  $r$ . Because we consider, for a given  $d_M$  and  $d_Q$ , only the configuration which maximizes the number of  $MQ$  chromosomes, our situations use only the configurations which provide the most information concerning  $r$ . This not only reduces the number of models we consider (one model for each  $d_M, d_Q$  combination), but because we are looking at the most opportunistic setting, it also provides us with a upper limit on power for the selected progeny sizes.

**Example of Computing Configuration Probabilities.** The following is an example demonstrating the matrix multiplication procedure to obtain the probabilities for each contribution to the gamete under both preferential pairing and random pairing. Consider the configuration of the informative parent being  $M_2Q$  where  $k = 6$ . This would mean there is 1  $MQ$  chromosome, 1  $M$  chromosome and 4  $\emptyset$  chromosomes.

**Preferential Pairing.** Under the preferential pairing mechanism, each informative chromosome pairs with an  $\emptyset$  chromosome. Thus, we need to consider only two  $\mathbf{C}$  matrices, and these matrices represent the  $MQ \times \emptyset$  and  $M \times \emptyset$  pairs. The Kronecker product of these two matrices is

$$\begin{bmatrix} \frac{1}{2}(1-r) & \frac{1}{2}r \\ \frac{1}{2}r & \frac{1}{2}(1-r) \end{bmatrix} \otimes \begin{bmatrix} \frac{1}{2} & 0 \\ \frac{1}{2} & 0 \end{bmatrix} = \begin{bmatrix} \frac{1}{4}(1-r) & 0 & \frac{1}{4}r & 0 \\ \frac{1}{4}(1-r) & 0 & \frac{1}{4}r & 0 \\ \frac{1}{4}r & 0 & \frac{1}{4}(1-r) & 0 \\ \frac{1}{4}r & 0 & \frac{1}{4}(1-r) & 0 \end{bmatrix}$$

For the purpose of collapsing the previous matrix to a  $3 \times 3$  matrix, we multiply by  $\mathbf{A}_2$ , and its transpose, where

$$\mathbf{A}_2 = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

The resulting matrix is

$$\begin{bmatrix} \frac{1}{4}(1-r) & \frac{1}{4}r & 0 \\ \frac{1}{4} & \frac{1}{4} & 0 \\ \frac{1}{4}r & \frac{1}{4}(1-r) & 0 \end{bmatrix}$$

**Random Pairing.** In this case, there are two situations for possible  $\mathbf{C}$  matrices. The one described in the preferential pairing section, and one in which the two informative chromosomes pair ( $MQ \times M$ ). The latter pairing occurs with probability  $\frac{1}{5}$ , whereas the previous pairing will occur with probability  $\frac{4}{5}$ . As a result, the overall configuration probabilities are

$$\frac{4}{5} \begin{bmatrix} \frac{1}{4}(1-r) & \frac{1}{4}r & 0 \\ \frac{1}{4} & \frac{1}{4} & 0 \\ \frac{1}{4}r & \frac{1}{4}(1-r) & 0 \end{bmatrix} + \frac{1}{5} \begin{bmatrix} 0 & 0 & 0 \\ \frac{1}{2} & \frac{1}{2} & 0 \\ 0 & 0 & 0 \end{bmatrix} = \begin{bmatrix} \frac{1}{5}(1-r) & \frac{1}{5}r & 0 \\ \frac{3}{10} & \frac{3}{10} & 0 \\ \frac{1}{5}r & \frac{1}{5}(1-r) & 0 \end{bmatrix}$$

where the second matrix on the left is computed in a similar fashion as the first.

**Summary of Contribution Probabilities.** Table 6 summarizes the contribution probabilities associated with the 16 models considered for octaploid ( $k = 8$ ) simulations. Whether dosage of the marker is observed or not, we only need to know the probabilities associated with each dosage of the QTL and the presence/absence of the marker. Using the fact that

$$p(Q_d) + p(MQ_d) = \binom{d_Q}{d} \left(\frac{1}{2}\right)^d,$$

Table 6 displays only  $p(Q_d)$ .

**Table 6. Contribution probabilities of specific parental configurations**

Dosage		Probability of gamete				
$M$	$Q$	$\emptyset$	$Q$	$Q_2$	$Q_3$	$Q_4$
1	1	.5(1-r)	.5r			
1	2	.25(1-r)	.25	.25r		
1	3	.125(1-r)	.125(2-r)	.125(1+r)	.125r	
1	4	.0625(1-r)	.0625(3-2r)	.1875	.0625(1+2r)	.0625r
2	1	.25(1-r)	.25r			
2	2	.25(1-r) <sup>2</sup>	.5r(1-r)	.25r <sup>2</sup>		
2	3	.125(1-r) <sup>2</sup>	.125(1-r <sup>2</sup> )	.125r(2-r)	.125r <sup>2</sup>	
2	4	.0625(1-r) <sup>2</sup>	.125(1-r)	.0625(1+2r-2r <sup>2</sup> )	.125r	.0625r <sup>2</sup>
3	1	.125(1-r)	.125r			
3	2	.125(1-r) <sup>2</sup>	.25r(1-r)	.125r <sup>2</sup>		
3	3	.125(1-r) <sup>3</sup>	.375r(1-r) <sup>2</sup>	.375r <sup>2</sup> (1-r)	.125r <sup>3</sup>	
3	4	.0625(1-r) <sup>3</sup>	.0625(1-r) <sup>2</sup> (1+2r)	.1875r(1-r)	.0625r <sup>2</sup> (3-2r)	.0625r <sup>3</sup>
4	1	.0625(1-r)	.0625r			
4	2	.0625(1-r) <sup>2</sup>	.125r(1-r)	.0625r <sup>2</sup>		
4	3	.0625(1-r) <sup>3</sup>	.1875r(1-r) <sup>2</sup>	.1875r <sup>2</sup> (1-r)	.0625r <sup>3</sup>	
4	4	.0625(1-r) <sup>4</sup>	.25r(1-r) <sup>3</sup>	.375r <sup>2</sup> (1-r) <sup>2</sup>	.25r <sup>3</sup> (1-r)	.0625r <sup>4</sup>