

1. Consider the Haldane map function,  $r = (1 - e^{-2d})/2$ , and the Kosambi map function,  $r = \tanh(2d)/2 = (e^{4d} - 1)/[2(e^{4d} + 1)]$ . (a) Find the inverse of these two functions (i.e., express  $d$  in terms of  $r$ ). (b) Calculate the genetic distance (in cM) corresponding to  $r = 0.01, 0.05, 0.10$  and  $0.20$ .
2. Use Mather's formula to derive the map function for the C-L model when the distribution of the number of chiasmata on the four-strand bundle is  $\mathbf{p} = (p_0, p_1, p_2, \dots)$ . (Let  $L = \sum_i ip_i/2$  denote the genetic length of the chromosome.) Use your result to show that in the case  $p_n = \exp(-2L)(2L)^n/n!$ , one obtains the Haldane map function.
3. Show that if the locations of chiasmata on the four-strand bundle follow a stationary Poisson process, then under no chromatid interference, the locations of crossovers on a random meiotic product also follow a stationary Poisson process.
4. Propose penetrance (emission) probabilities  $e_i(v) = \Pr(\text{observe } O_i | v_i = v)$  for an intercross, to account for possible genotyping errors. Take  $v \in \{AA, AB, BA, BB\}$  (phase-known genotypes) and  $O \in \{A, H, B, C \text{ (not AA)}, D \text{ (not BB)}, - \text{ (missing)}\}$ .
5. Consider a nested sequence of models with  $i = 0, 1, \dots, k$  markers giving  $RSS_0 > RSS_1 > \dots > RSS_k$ . Let  $B_i(\delta) = \ln(RSS_i) + i\delta \log n/n$  (the BIC- $\delta$  criterion) and  $LOD(i) = (n/2) \log_{10}(RSS_{i-1}/RSS_i)$  (a conditional LOD score). Show that picking the model for which  $B_i(\delta)$  is minimized is essentially equivalent to placing a threshold on the conditional LOD score.