Chapter 6

Likelihoods on Pedigrees

6.1 The Baum algorithm and "Peeling"

We review here the algorithm given by Baum (1972) for the computation of the likelihood in a hidden Markov model. The procedure is general to any stochastic system with discrete-valued latent variables $S_{\bullet,j}$ with a first-order Markov structure, and outputs $Y_{\bullet,j}$ depending only on $S_{\bullet,j}$. However, for convenience, we retain the notation of section 4.7 with meiosis indicators $S_{\bullet,j}$ and phenotypic data $Y_{\bullet,j}$ for locus j, with loci ordered $j = 1, \ldots, L$ along a chromosome. The dependence structure is shown in Figure 6.1. The Baum algorithm can proceed in either direction, and both formulations will be given. For closer analogy with pedigree peeling (section 6.3), we consider first the backwards computation, which is less natural for time series. On a pedigree, data are usually on the final generations. In time series or signal processing, on the other hand, data are observed forwards in time and prediction is often the question of interest.

For data observations $\mathbf{Y} = (Y_{\bullet,j}, j = 1, \ldots, L)$, we want to compute $\Pr(\mathbf{Y})$. Due to the first-order Markov dependence of the $S_{\bullet,j}$, equation (4.10) can be written

$$\begin{aligned} \Pr(\mathbf{Y}) &= \sum_{\mathbf{S}} \Pr(\mathbf{S}, \mathbf{Y}) = \sum_{\mathbf{S}} \Pr(\mathbf{Y} \mid \mathbf{S}) \Pr(\mathbf{S}) \\ &= \sum_{\mathbf{S}} \left(\Pr(S_{\bullet,1}) \prod_{j=2}^{L} \Pr(S_{\bullet,j} \mid S_{\bullet,j-1}) \prod_{j=1}^{L} \Pr(Y_{\bullet,j} \mid S_{\bullet,j}) \right). \qquad (6.1) \end{aligned}$$

Now define

$$R_j(s) = \Pr(Y_{\bullet,k}, k = (j+1), \ldots, L \mid S_{\bullet,j} = s)$$

with $R_L(s) = 1$ for all s. The conditional independence structure (Figure 6.1), provides that $\{Y_{\bullet,k}, k = (j+1), \ldots, L\}$, $Y_{\bullet,j}$, and $S_{\bullet,j-1}$ are mutually independent given $S_{\bullet,j}$.