



FIGURE 27.7. A simple hidden Markov model for a sequence alignment. (*Left*) An alignment is shown for five related peptides, each with three amino acids. These three columns are used to create a model of the sequence patterns of this peptide group. (*Right*) Hidden Markov model for these five peptides. The columns are modeled by the match states (boxes labeled m1, m2, and m3), each of which has 20 possible residues with the probability for each determined from the alignment column. One can also model the probability of insertions and deletions relative to the model (deletion possibilities are shown in the circles d1, d2, and d3). (*b and e circles*) Beginning and ending probabilities. The *arrows* represent transition probabilities between states. (Modified from Eddy S.R. *Bioinfo. Rev.* **14**: 755–763, Fig. 2, © 1998 Oxford University Press.)