FIGURE 16.13. Wright's F_{ST} is related to the mean coalescence time between pairs of genes within demes, compared with the mean coalescence time between randomly chosen pairs: $F_{ST} = (\overline{T} - T_w)/\overline{T}$. These coalescence times, and hence F_{ST}, can be estimated from the number of mutations that separate each pair of genes (assuming the infinite sites model; see p. 424). In this example, seven genes are sampled from three demes; mutations are indicated by *red circles*. On average, there are 8.1 differences between pairs of genes sampled at random compared with 2.0 differences between genes within the same deme. Hence, F_{ST} is estimated to be $(8.1 - 2.0)/8.1 = 0.753$.

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