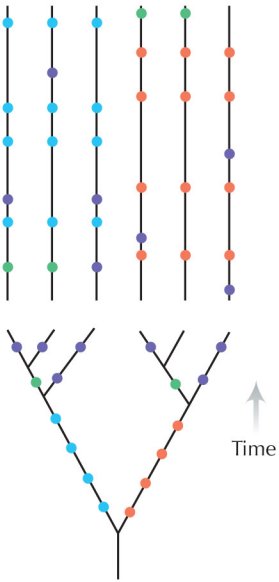

FIGURE 26.5. Any short region of genome will share the same ancestral genealogy (*bottom*). Six sampled sequences are shown on the *top*. These carry any mutations that occurred on the lineages leading down to them (*colored dots*). Every mutation is assumed to occur at a unique place in the genome (i.e., the **infinite-sites model**). The sequences fall into two distinct haplotypes corresponding to the two main branches of the genealogy. The haplotype could be determined by scoring any one of the *red* or *light blue* mutations, which could therefore act as tagging single-nucleotide polymorphisms (tSNPs).