



**FIGURE 5.12.** Evolutionary character state reconstruction. The trees show the evolutionary relationships between five species for which data about a single homologous trait are available. This trait comes in two states, A or G (e.g., nucleotides in a conserved position in a gene). Species 1, 2, and 3 have the G state and species 4 and 5 have the A state. Character state reconstruction methods allow one to infer which character state is ancestral and which is derived. (A,D) Two different trees relating the five species. (B,E) The character states are overlaid onto the trees. (C,F) Character state reconstruction methods are used to infer the likely states present in ancestral nodes. In C the ancestral state is A and in F it is G. Thus, the two different species trees lead to different inferences regarding which state is ancestral.