



FIGURE 25.22. Model to estimate admixture in populations. **P** is the founder population. **H** is a hybrid population formed by members of the **P₁** and **P₂** parental populations. The impact of genetic drift on allele frequencies in all populations depends on the time elapsed and the effective population sizes (N_1 , N_h , N_2). Models such as these can be used to estimate the time since a hybrid population was formed (scaled by population size) and/or the proportion of input from each parental population.

25.22, adapted from Barbujani G. et al., *Annu. Rev. Genomics Hum. Genet.* **5**: 119–150, © 2004 Annual Reviews, www.annualreviews.org