



FIGURE 15.9. Genealogies relating genes from HIV reflect different population histories. (A) Relationship between sequences from the *gag* gene, sampled from 200 individuals from northern Britain in 1993. Coalescence tends to occur back in the past (toward the center of the diagram), a pattern characteristic of a rapidly growing population (cf. Fig. 15.8C). (B) Relationship between *env* genes sampled from within a single patient over 7 years. This example is unusual in that genes are sampled through time. The divergence of genes through time can be seen by following out from the original sequence (red) through to the most diverse population at year 7 (magenta). In this example, most coalescence occurs relatively recently, a pattern characteristic of a steady population (cf. Fig. 15.8A). (Both these genealogies are drawn **unrooted**, whereas Fig. 15.8 shows **rooted** genealogies.)

15.9, data courtesy of Leigh-Brown A.J., Centre for HIV Research, University of Edinburgh