

**Problem 1.1** The purple and red subunits are the easiest to 'parse'. In the purple subunit the E and F helices form a 'Vee', the E helix at the right, with the haem group between them. The D helix is just above the E helix. Therefore purple must be B. Red is equivalent, rotated by 180° around an axis perpendicular to the page.

**Problem 1.2** (a) Positioning of genes relative to control elements is determinative. (b) An example of this is the Corfu deletion. If homozygous, defective developmental switching results.

**Problem 1.3** From Figure 1.8, map the exons onto the amino acid sequence. Find the helix assignments from the PDB file, and map them onto the sequence also. Then, using the E and F helices as an anchor, map the exons onto the structure.

**Problem 1.4** Computing the number of genes/Mb is simple arithmetic. Assuming, for example, that the chloroplast was originally a fairly complete cyanobacterium, compare number of genes and gene density.

**Problem 1.5** (a) Assume 5 generations per century (b) Genetic markers were used to test the hypothesis that U.S. President Thomas Jefferson (1743-1826) was the father of Sally Hemmings.

**Problem 1.6** Calculate the overall allelic composition of the equilibrium population and distribute the alleles randomly among individuals.

**Problem 1.7** (a) 1 cM = 1% recombination frequency per generation. (b) probability of recombination + probability of non-recombination = 1. (c) Probability of no recombination in 2 generations = (probability of no recombination in one generation)<sup>2</sup>. Generalize this, and evaluate for part (d).

**Problem 1.8** Devise a pattern that recognizes complementarity of most base pairs in regions separated by an appropriate range of spacings. It would be convenient to adapt the 'dotplot' technique for searching for sequence similarities. (See p. 235 ff.)

**Problem 1.9** (a) Ask yourself: Would they be female? Could they be calico? In what ways, then, would they resemble Copycat? In what ways might they differ?

**Problem 1.10** (a) For a suitable map, either photocopy a suitable page from an atlas, or download: [https://www.cia.gov/library/publications/the-world-factbook/reference\\_maps/pdf/north\\_america.pdf](https://www.cia.gov/library/publications/the-world-factbook/reference_maps/pdf/north_america.pdf)

Or see <http://nmviewogc.cr.usgs.gov/viewer.htm> for an interactive map on which you can move the mouse and see the latitude and longitude values reported. (b) Find the most similar sequences and see where that sample originated, on the map from part (a). (c) This is also a question of detecting sequence similarity and appealing to the map. (d) 1 sequence change required about 80000 years. (e) Consider geological data collecting, to describe palaeoclimates; and sequencing of nuclear DNA. (f) You must present data that show that the population in question is reproductively isolated, and contains unique genetic features.

**Problem 1.11** Crucial points here involve minimizing cruelty to animals; in particular, eliminating suffering by animals that cannot be justified by the results of using them in experiments.