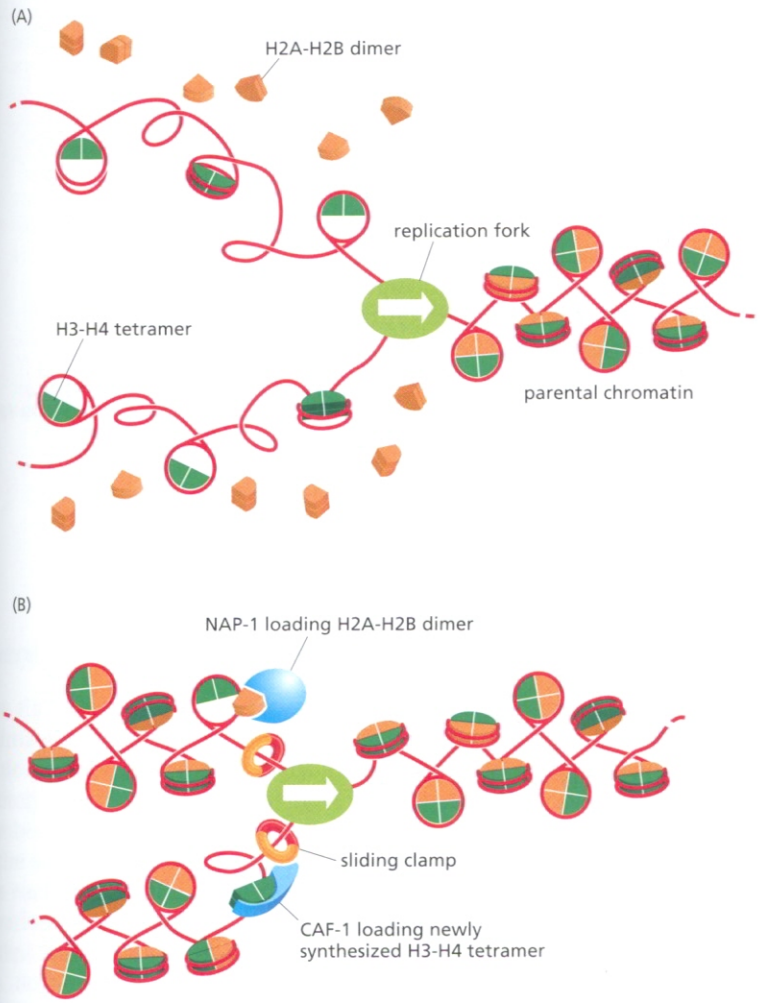

Figure 5–38 Distribution of parental and newly synthesized histones behind a eucaryotic replication fork. (A) The distribution of parental H3-H4 tetramers to the daughter DNA molecules is apparently random, with roughly equal numbers inherited by each daughter. In contrast, H2A-H2B dimers are released from the DNA as the replication fork passes. (B) Histone chaperones (NAP1 and CAF1) restore the full complement of histones to daughter molecules. Although some daughter nucleosomes contain only parental histones or only newly synthesized histones, most are hybrids of old and new. (Adapted from J.D. Watson et al., Molecular Biology of the Gene, 5th ed. Cold Spring Harbor: Cold Spring Harbor Laboratory Press, 2004.)

Once the nucleosome assembly behind a replication fork has been completed, the parental patterns of H3-H4 modification can be reinforced through histone modification enzymes in reader–writer complexes that recognize the same type of modification they create (**Figure 5–39**).

The faithful duplication of patterns of histone modification may be responsible for many examples of *epigenetic inheritance*, in which a heritable change in a cell's phenotype occurs without a change in the nucleotide sequence of DNA. We shall revisit the topic of epigenetics in Chapter 7 when we consider how decisions made by a cell are "remembered" by its progeny cells many generations later.

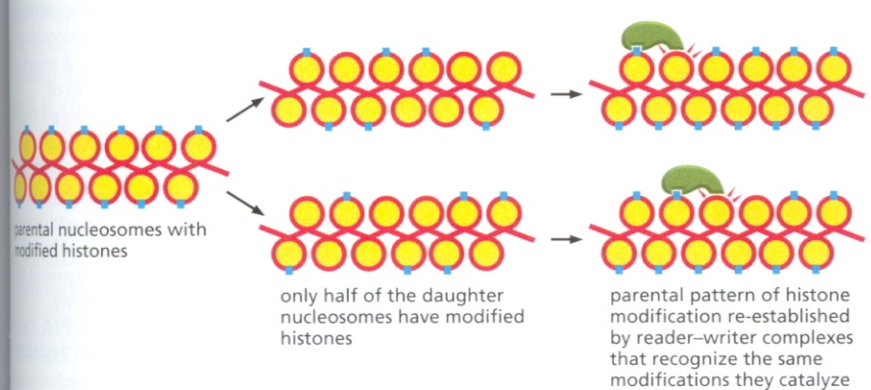

Figure 5–39 Strategy through which parental patterns of histone H3 and H4 modification can be inherited by daughter chromosomes. Although it is unlikely that this mechanism applies to all histone modifications, it does pertain to some (see Figure 4–51). For example, a number of histone methylase complexes specifically recognize N-terminal histone tails that have been previously methylated at the same site that the methylase modifies.