Independent assortment creates new allelic combinations (genetic diversity) for genes on different chromosomes, but is unable to create new allele combinations for genes that are on the same chromosome (linkage). Everything else being equal, if I.A. were the only mechanism capable of creating new combinations of pre-existing alleles, then an organism with fewer small chromosomes would tend to generate diversity more efficiently than an organism with a few large chromosomes.

The term "recombination" is used in several ways by geneticists. The precise meaning of the term is usually understood by the context in which it is used.

The mechanism of crossing-over is a molecular process of recombination that operates during prophase of meiosis I, after homologous pairing (synapsis), and requires the complex cooperation of many enzymes to manipulate the DNA appropriately.

Cis dihybrid (coupling) vs trans dihybrid (repulsion)

A single crossing over event typically involves only 1 chromatid of each homolog.

The frequency of crossing over between any 2 given genes is, to a first approximation, proportional to the physical distance between them. This is the basis of GENETIC MAPPING.

Genetic maps are useful because they allow you to predict the result of genetic crosses.

A "genetic map unit" is defined as the distance sufficient to generate 1% recombinant genotypes among the gametes. This is 1/2 the frequency of the crossing-over events.

The proportionality between the frequency of recombinant genotypes and physical distance between genes fails if genes are far apart (greater than about 10 units) due to multiple crossovers.

Know how to detect linkage vs. independent assortment in a testcross.

Know how to determine the map distance between two linked genes from the results of a 2-point testcross.

Know how to predict the result of a testcross involving two linked genes if given the genetic map.

An interesting feature of linkage analysis in Drosophila is that crossing over is essentially absent during meiosis in males. This includes autosomal as well as X-linked genes. Thus, linkage is complete when genes are passed through males.

If two genes exhibit linkage, it is because they are on the same chromosome. The reverse is not always true. Two genes may be so far apart on their chromosome, and recombination between them so frequent, that they appear to be unlinked (i.e. 50% recombinant genotypes in gametes).

FOCUS ON PROBLEM SOLVING: Using a Genetic Map to Predict the Outcome of a Cross p. 151/ p. 146

This exercise includes coefficient of coincidence (c), which we are not covering. You can ignore the references to coefficient of coincidence and to "observed frequency" of double crossovers. (For us, c = 1.0; and observed frequency = expected frequency.) The odd thing is that in their "Analysis and Solution" they end up ignoring coefficient of coincidence! So, the answer they come up with (30/10,000) is the expected number. With a coefficient of coincidence = 0.2 thrown in they should get 6/10,000. So just ignore the part of the exercise that discusses coefficient of coincidence, which is what they did in the end.
Molecular Mechanisms of Homologous Recombination

The term "recombination" is used broadly, and somewhat loosely; so the meaning will vary with the context. This is not a problem if you are already familiar with genetics, but can be confusing to students. Here we are specifically concerned with "molecular recombination". This means that the sequence or organization of DNA molecules changes as a result of an exchange involving breaking and rejoining at the level of DNA strands. Furthermore, we are dealing with "homologous recombination", which means that the two DNA molecules involved in the exchange have similar or identical base pair sequences (i.e. the DNA substrates are homologous).

Undergraduates ordinarily encounter homologous recombination in the presentation of meiotic crossing over, in which the exchanges are made between chromatids of homologous chromosomes during prophase of Meiosis I, and classical genetic mapping in eukaryotes. In this context, homologous recombination appears to be in the service of creating genetic diversity, and, for geneticists, of mapping genes. But systems of homologous recombination are ubiquitous, and in prokaryotes the mechanism of homologous recombination is often found in contexts where its function is DNA repair.

See p. 275/305 and Fig. 2.12 for a review of the "Synaptonemal Complex"

RECOMBINATION: CLEAVAGE AND REJOINING OF DNA MOLECULES

A simplified version of the Holliday Junction Model (1964) involves:

- ss DNA endonuclease cutting at equivalent positions in strands of the same orientation in the 2 homologous substrate helices
- unwinding of helix to liberate 3’ ends of cut strands (helicase and single-strand-binding protein)
- pairing of single strands with complementary sequence exposed in opposite helix (RecA protein)
- ligation to produce chi structure intermediate (Holliday Junction)
- endonuclease cutting of "virgin" DNA strands within chi structure
- ligation

You should match up these steps with Fig. 13.26

Notice in Fig. 13.265/13.295 the region of "heteroduplex" helix (dark purple strand paired with light purple or red with black) generated by the recombination process.

Here are some better diagrams of the chi structure. You can find more in GOOGLE images.
These are proteins associated with the chi structure.