Chapters 1-5 basically review of principles and information that you got in earlier courses- Read them at your leisure

Concentrate on the following sections:

Chapter 1  p. 9-11 Gene linkage/Crossing over
           p. 12 Chromosome mapping
           p. 15 Origins of genetic variability through mutations

Chapter 2  p. 31-36 Central Dogma

Chapter 3  p. 45-53 Weak Bonds in Biological Systems

Chapter 5  p. 69-71 (at bottom) Higher order structures
           p. 84-87 Weak bonds correctly position
To start out we will do some fundamental review

Structure of DNA

A-T base pairs, 2 H bonds and 11.1 angstroms apart

G-C base pairs, 3 H bonds and 10.8 angstroms apart

Major groove - site of most protein-DNA interactions (see later)

Minor groove - site of a few specialized protein-DNA interactions

Fig. 6.1
### Table 6-1 Adenine and Related Compounds

<table>
<thead>
<tr>
<th></th>
<th>Base Adenine</th>
<th>Nucleoside 2′-deoxyadenosine</th>
<th>Nucleotide 2′-deoxyadenosine 5′-phosphate</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Structure</strong></td>
<td><img src="image" alt="Adenine Structure" /></td>
<td><img src="image" alt="Deoxyadenosine Structure" /></td>
<td><img src="image" alt="Nucleotide Structure" /></td>
</tr>
<tr>
<td><strong>Molecular weight</strong></td>
<td>135.1 (Daltons)</td>
<td>251.2</td>
<td>331.2</td>
</tr>
</tbody>
</table>

Molecular weight of a base pair (2 nucleotides) on average = 660 daltons
Nucleotide synthesis

Dehydration

Fig. 6.2
Base pairing of Nucleotides - the H bonds

Individually these are weak; together they are strong and help maintain a stable structure

Fig. 6.3
Base tautomerization

Fig. 6.5
G:C vs A:T base pairs
A:C cannot normally base pair

Fig. 6.7
Base flipping

This is done by a number of processing enzymes, such as methylases; it does not seriously destabilize the double helix. It is actually used to “examine” the DNA base for potential interactions.
Major and Minor Groove Chemistry

Major groove is richer in chemical information than minor groove, therefore it is more likely to be important in protein-DNA interactions.

A = H bond acceptor

D = H bond donor

M = Methyl group

H = non polar Hydrogen

Fig. 6.10
Helices can be oriented in two directions

A-, B-, C-, D, E, X-DNA

Z-DNA (possibly D-DNA)

Fig. 6.9
A - form – the primary conformation of RNA:RNA interactions, as well as RNA:DNA hybrids

B – form – the classical “Watson-Crick” conformation, the most common form of most DNA in cells

C – form – a rarely seen derivative of B-DNA that forms in conditions of lower hydration, it is less compact than B-DNA; can form under binding by certain ionic substances such as amines

D – form – a rarely seen conformation of B-DNA that also forms in conditions of dehydration, especially involving poly(dA-dT) fibers; forms experimentally

E – form – derivative of B-DNA, little idea of structure or identity

X – form – a derivative of D-DNA (poly[dA-dT] and [dT-dA]4); destabilized by regions of GC; forms experimentally

Z – form- left handed helix, forms in local regions of high salt involving GC rich sequences, implicated in regulation
Three forms of DNA

Fig. 6.11
Local environment and adjacent bases affect Watson-Crick base pairing

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Fig. 6.12
Right handed helix (purines always \textit{anti} conformation)

Left handed helix (purine G always \textit{syn} conformation)
<table>
<thead>
<tr>
<th>Overall proportions</th>
<th>A</th>
<th>B</th>
<th>Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rise per base pair</td>
<td>2.3 Å</td>
<td>3.32 Å</td>
<td>3.8 Å</td>
</tr>
<tr>
<td>Helix-packing diameter</td>
<td>25.5 Å</td>
<td>23.7 Å</td>
<td>18.4 Å</td>
</tr>
<tr>
<td>Helix rotation sense</td>
<td>Right-handed</td>
<td>Right-handed</td>
<td>Left-handed</td>
</tr>
<tr>
<td>Base pairs per helix repeat</td>
<td>1</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Base pairs per turn of helix</td>
<td>~11</td>
<td>~10</td>
<td>12</td>
</tr>
<tr>
<td>Rotation per base pair</td>
<td>33.6°</td>
<td>35.9°</td>
<td>-60° per 2 bp</td>
</tr>
<tr>
<td>Pitch per turn of helix</td>
<td>24.6 Å</td>
<td>33.2 Å</td>
<td>45.6 Å</td>
</tr>
<tr>
<td>Tilt of base normals to helix axis</td>
<td>+19°</td>
<td>-1.2°</td>
<td>-9°</td>
</tr>
<tr>
<td>Base-pair mean propeller twist</td>
<td>+18°</td>
<td>+16°</td>
<td>~0°</td>
</tr>
<tr>
<td>Helix axis location</td>
<td>Major groove</td>
<td>Through base pairs</td>
<td>Minor groove</td>
</tr>
<tr>
<td>Major-groove proportions</td>
<td>Extremely narrow but very deep</td>
<td>Wide and of intermediate depth</td>
<td>Flattened out on helix surface</td>
</tr>
<tr>
<td>Minor-groove proportions</td>
<td>Very broad but shallow</td>
<td>Narrow and of intermediate depth</td>
<td>Extremely narrow but very deep</td>
</tr>
<tr>
<td>Glycosyl-bond conformation</td>
<td>anti</td>
<td>anti</td>
<td>anti at C, syn at G</td>
</tr>
</tbody>
</table>