Week 1

- Cells as the structural and functional units of life
  - Cells are the most basic unit of life
  - In all cells
    - Hereditary information is stored as DNA
    - DNA is replicated by template-directed polymerisation
    - Sections of DNA are transcribed into RNA
    - Proteins are used as catalysts
    - Proteins are produced by translation of RNA
    - Basic mechanism of translation is the same
- The universal nature of genetic information and its mode of expression
  - Genetic information is stored in DNA
  - DNA is transcribed into RNA for protein synthesis using complimentary base pairing (A=T, C=G)
  - DNA can be switched 'on' and 'off' in response to environmental conditions
  - Controls cell growth, function and reproduction
- The quantities of DNA required for cell function
  - Much of the DNA in a cell is 'silent' or 'noncoding'
  - Humans have approx. 20,000-25,000 protein coding genes
- The organisation of DNA into functional units – genes
  - DNA is sorted into 'genes' which code for a particular protein
  - Genes contain coding (exons) and noncoding (introns) areas of DNA
- Describe the primary and secondary structure of both DNA and RNA
  - Bases consist of:
    - Sugar (deoxyribose in DNA and ribose in RNA)
    - Phosphate groups
    - Nitrogenous base
  - Nitrogenous bases can be:
    - Purines – double carbon/nitrogen ring (A and G)
    - Pyrimidines – single carbon/nitrogen ring (T, C and U)
  - Primary
    - Sugar-phosphate backbone
    - Linear sequence of bases in hydrophobic single strand
    - Strand has orientation (5' to 3')
  - Secondary
    - Nitrogenous bases form hydrogen bonds (A-T forms 2, G-C forms 3)
    - Strands form antiparallel
  - Tertiary
    - Double helix
- Recognise how DNA can act as a template
  - Complimentary base pairing allows DNA to act as a template for transcription
- Begin to recognise the implications structure has on function, especially as it relates to DNA replication and expression
  - Complementary strands of DNA encode two copies of the gene, and thus can be used for replication and repair

- Recognise that physical properties are the consequence of structure
    - Structural features
        - Double stranded helix
        - Hydrogen bonding maintains helix
        - Complimentary base pairing
        - Long length and thin diameter
        - Acidity due to negatively charged phosphates
- Understand the structural basis of DNA's:
    - Solubility
        - Polyanionic due to the high phosphate content
        - Soluble in aqueous/low salt condition
        - Insoluble in alcohols
    - Viscosity
        - Long, rigid, rod shape
        - Large hydrodynamic volume (attracts large shell of water from phosphate groups)
        - Disruption of hydrogen bonding decreases viscosity
        - Mechanical shearing decreases viscosity
    - UV absorption
        - Nitrogenous bases strongly absorb UV at 260nm
        - Double helix shield bases
        - Can be used to measure concentration
    - Acidity
        - Acidic due to negative phosphates
    - Denaturation
        - High temperature and pH extremes interrupt hydrogen bonding
        - When denatured, viscosity decreases and UV absorption increases
    - Renaturation
        - Renatures easily because of complimentary base pairing
- Understand the process of hybridisation between nucleic acids and the technical use of probes
    - Hybrid molecules can form when species have complimentary sequences
    - Two DNA species are heated, mixed and cooled
    - Allows probing to determine sequences
- Describe the behaviour of DNA molecules during gel electrophoresis
    - Move towards positive pole because of negative phosphate groups
    - Smaller fragments move faster/go further
    - Supercoiled goes fastest, then linear, then circular

Week 2

- Describe the role of restriction endonucleases in nature and in the laboratory
    - Restriction endonucleases are used by bacteria to protect their cells (cut viral DNA when it enters their cells)
    - They cut very specific places and thus generate a reproducible set of fragments
    - Used in labs to analyse DNA

    - Bacteria protect their own DNA from being cut up by methylating the area where the endonuclease would cut, thus rendering it unrecognisable
    - Restriction sites are between 4-8 bases long, and normally palindromic
- Describe the use of Southern blotting to detect specific DNA sequences
    - DNA is fragmented using restriction endonucleases
    - Run through electrophoresis
    - Denatured and hybridised with probes
    - Sequences are then detected using autoradiography or fluorescence
- Describe the principles of DNA sequencing using the 'dideoxy method'
    - Sequence is run on acrylamide gel
    - Bases organised into separate columns
    - First base moves the furthest
- Have some appreciation of the scientific and social value of the Human Genome Project
    - Diagnostics
    - Evolutionary studies
    - Population genetics
    - Genome organisation
    - Identify gene functions
    - Product development
- Describe the basic process of transcription
    - Directed by complimentary base pairing
    - Selected regions on one strand act as a template
    - RNA polymerase runs along the strand and connect matching base pairs
    - In prokaryotes
        - Enhancer, promoter and RNA polymerase bind to strand
        - Loop activation intermediate forms
        - Forms polycistronic mRNAs (multiple proteins coded for on the same gene)
    - In eukaryotes
        - Gene interruption and chromatin structure interrupt transcription
        - Requires promoter and transcription factors
- Understand the selective and variable nature of gene expression
    - Exons (coding) and introns (non-coding)
    - Introns cut out of RNA in nucleus before transport to cytoplasm
- Describe eukaryotic gene structure
    - Genes on chromosomes
    - Separated by coding and non-coding
- Understand the impact that eukaryotic gene structure and cellular organisation has on transcription
    - Nucleus means that transcription and translation can't be simultaneous
    - Introns and exons mean that RNA must be processed further before translation