

4.3 Topic 1: Describing biodiversity

In this topic, students will:

Subject matter	Guidance
<p>Biodiversity</p> <ul style="list-style-type: none"> • <u>recognise</u> that biodiversity includes the diversity of species and ecosystems • <u>determine</u> diversity of species using measures such as species richness, evenness (relative species abundance), percentage cover, percentage frequency and Simpson's diversity index • use species diversity indices, species interactions (predation, competition, symbiosis, disease) and abiotic factors (climate, substrate, size/depth of area) to <u>compare</u> ecosystems across spatial and temporal scales • <u>explain</u> how environmental factors limit the distribution and abundance of species in an ecosystem. • Mandatory practical: Determine species diversity of a group of organisms based on a given index. 	<ul style="list-style-type: none"> • Notional time: 9 hours • <u>Use</u> local context throughout the unit to develop the content objectives. • Diversity indices and measurements should be supported through <u>fieldwork</u> and based on classification. Measures of biodiversity, i.e. species richness (S) and Simpson's diversity index (D) should be used where applicable. • Formula: The formula used to quantify biodiversity of a habitat is Simpson's diversity index (SDI), shown as: $SDI = 1 - \left(\frac{\sum n(n-1)}{N(N-1)} \right)$ <i>where:</i> <i>N = total number of organisms of all species</i> <i>n = number of organisms of one species</i> • Manipulative skill: Use <u>appropriate</u> technology, such as data loggers, chemical tests, turbidity tubes and other equipment to measure factors. • Suggested practical: Measure abiotic factors in the classroom using field samples (e.g. pH, nitrogen nutrients, salinity, carbonates, turbidity). • Suggested practical: Measure abiotic factors in the field (e.g. dissolved oxygen, light, temperature, wind speed, infiltration rate).
<p>Classification processes</p> <ul style="list-style-type: none"> • <u>recognise</u> that biological classification can be hierarchical and based on different levels of similarity of physical features, methods of reproduction and molecular sequences • <u>describe</u> the classification systems for <ul style="list-style-type: none"> – similarity of physical features (the Linnaean system) – methods of reproduction (asexual, sexual — K and r selection) – molecular sequences (molecular phylogeny — also called cladistics) • <u>define</u> the term <u>clade</u> • <u>recall</u> that common assumptions of cladistics include a common ancestry, bifurcation and physical change 	<ul style="list-style-type: none"> • Notional time: 12 hours • Students should <u>understand</u> that the concept of classification is directly related to the purpose for which the <u>data</u> will be used. • Students should <u>recognise</u> that the Linnaean system does not rely solely on physical features for classification. • Classification should be supported by the analysis of field data. • Students should recognise that conserved sequences (e.g. mitochondrial DNA) are assumed to accumulate mutations at a constant rate over time and, therefore, provide a method for dating divergence. • <u>Identification</u> of applications of molecular phylogeny (DNA barcoding and

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<ul style="list-style-type: none"> • <u>interpret</u> cladograms to <u>infer</u> the evolutionary relatedness between groups of organisms • <u>analyse data</u> from molecular sequences to infer species evolutionary relatedness • recognise the need for multiple definitions of species • <u>identify</u> one example of an interspecific hybrid that does not produce fertile offspring (e.g. mule, <i>Equus mulus</i>) • <u>explain</u> the classification of organisms according to the following species interactions: predation, competition, symbiosis and disease • <u>understand</u> that ecosystems are composed of varied habitats (microhabitat to ecoregion) • interpret data to <u>classify</u> and name an ecosystem • explain how the process of classifying ecosystems is an important step towards effective ecosystem management (consider old-growth forests, productive soils and coral reefs) • describe the process of stratified sampling in terms of <ul style="list-style-type: none"> – purpose (estimating population, density, distribution, environmental gradients and profiles, zonation, stratification) – site selection – choice of ecological surveying technique (quadrats, transects) – minimising bias (size and number of samples, random-number generators, counting criteria, calibrating equipment and noting associated precision) – methods of data presentation and analysis. • Mandatory practical: <u>Use</u> the process of stratified sampling to <u>collect</u> and analyse primary biotic and abiotic field data to classify an ecosystem. 	<p>genetic testing) should be linked to understanding of subject matter in Unit 4.</p> <ul style="list-style-type: none"> • Refer to the glossary for a definition of <u>clade</u>. • Students should be familiar with the <u>limitations</u> of different definitions of species, e.g. biological species concept and phylogenetic species concept. • Classification of ecosystems could be based on the Holdridge life zone classification scheme, Specht's classification system, ANAE classification system or EUNIS habitat classification system.
<p>Science as a Human Endeavour (SHE)</p> <ul style="list-style-type: none"> • SHE subject matter will not be assessed on the external examination but could be used in the development of claims and research questions for a research investigation. 	<ul style="list-style-type: none"> • Technology as a tool to measure, analyse and monitor biodiversity: Advances in remote sensing radar imagery and satellite tracking in real time have enabled scientists to measure and monitor populations, and play a significant role in surveying and monitoring large or inaccessible ecosystems. • International biodiversity protection: International agreements about biodiversity protection, such as the World Heritage Convention, are based on the premise that local, regional and international biodiversity represent a global resource, vital for human survival, that should be maintained for future generations.

Subject matter	Guidance
	<ul style="list-style-type: none"> • Biodiversity targets: Setting agreed biodiversity targets is required to achieve positive international action towards biodiversity conservation by reducing the rate of biodiversity loss at global, regional and national levels.

4.4 Topic 2: Ecosystem dynamics

In this topic, students will:

Subject matter	Guidance
<p>Functioning ecosystems</p> <ul style="list-style-type: none"> • <u>sequence</u> and <u>explain</u> the transfer and transformation of solar energy into biomass as it flows through biotic components of an ecosystem, including <ul style="list-style-type: none"> – converting light to chemical energy – producing biomass and interacting with components of the carbon cycle • <u>analyse</u> and <u>calculate</u> energy transfer (food chains, webs and pyramids) and transformations within ecosystems, including <ul style="list-style-type: none"> – loss of energy through radiation, reflection and absorption – efficiencies of energy transfer from one trophic level to another – biomass • <u>construct</u> and analyse simple energy-flow diagrams illustrating the movement of energy through ecosystems, including the productivity (gross and net) of the various trophic levels • <u>describe</u> the transfer and transformation of matter as it cycles through ecosystems (water, carbon and nitrogen) • <u>define ecological niche</u> in terms of habitat, feeding relationships and interactions with other species • <u>understand</u> the competitive exclusion principle • analyse data to <u>identify</u> species (including microorganisms) or populations occupying an ecological niche • define <u>keystone species</u> and understand the critical role they play in maintaining the structure of a community • analyse data (from an Australian ecosystem) to identify a keystone species and <u>predict</u> the outcomes of removing the species from an ecosystem. 	<ul style="list-style-type: none"> • Notional time: 12 hours • Energy transfers through ecosystems should be <u>demonstrated</u> using food chains, webs and pyramids. • A detailed description and <u>understanding</u> of the multiple biochemical steps in photosynthesis and respiration (from Unit 1) is not required. Gross inputs and outputs are required. • Interactions between the biotic and abiotic components of the ecosystem should be represented through food webs, biomass pyramids, the water cycle and biogeochemical cycles — carbon and nitrogen. • <u>Fieldwork</u> should be used to <u>develop</u> scientific skills and <u>collect data</u>, as well as to develop student <u>understanding</u> of <u>concepts</u>, especially abiotic–biotic <u>relationships</u> and biotic–biotic relationships. • Refer to the glossary for a definition of <u>ecological niche</u> and <u>keystone species</u>. • Suggested practical: Study the abundance of each trophic level in a simple food chain. • Suggested practical: Measure the wet biomass of producer samples. • Suggested practical: <u>Test</u> the competitive exclusion principle hypothesis by studying vertical zonation on a tree. • Suggested practical: Carry out a longitudinal study of a keystone species and <u>relevant</u> ecological interactions.

Subject matter	Guidance
<p>Population ecology</p> <ul style="list-style-type: none"> • <u>define</u> the term <u>carrying capacity</u> • <u>explain</u> why the carrying capacity of a population is determined by limiting factors (biotic and abiotic) • <u>calculate</u> population growth rate and change (using birth, death, immigration and emigration data) • <u>use</u> the Lincoln Index to estimate population size from secondary or primary data • <u>analyse</u> population growth data to <u>determine</u> the mode (exponential growth J-curve, logistic growth S-curve) of population growth • <u>discuss</u> the effect of changes within population-limiting factors on the carrying capacity of the ecosystem. 	<ul style="list-style-type: none"> • Notional time: 4 hours • Refer to the glossary for a definition of <u>carrying capacity</u>. • Limiting factors of population growth should include <ul style="list-style-type: none"> – biotic factors — competition for resources, predation and disease – abiotic factors — space, availability of nutrients, pollution, natural disasters, extreme climatic events (drought, cyclones, global temperature change). • Formula: The formula for estimation of population size by the capture–recapture measure is the Lincoln index, shown as: $N = \frac{M \times n}{m}$ <p>where:</p> <p><i>M</i> = number of individuals caught, marked and released initially <i>n</i> = number of individuals caught on second sampling <i>m</i> = number of individuals recaptured that were marked</p> • Suggested practical: <u>Conduct</u> an abundance and distribution study, including abiotic and biotic factors. • Suggested practical: Measure the population of microorganisms in Petri dishes to observe carrying capacity.
<p>Changing ecosystems</p> <ul style="list-style-type: none"> • <u>explain</u> the <u>concept</u> of ecological succession (refer to pioneer and climax communities and seres) • <u>differentiate</u> between the two main modes of succession: primary and secondary • <u>identify</u> the features of pioneer species (ability to fixate nitrogen, tolerance to extreme conditions, rapid germination of seeds, ability to photosynthesise) that make them <u>effective</u> colonisers • <u>analyse data</u> from the fossil record to observe past ecosystems and changes in biotic and abiotic components • analyse ecological data to <u>predict</u> temporal and spatial successional changes • predict the impact of human activity on the reduction of biodiversity and on the magnitude, duration and speed of ecosystem change. • Mandatory practical: <u>Select</u> and <u>appraise</u> an ecological surveying technique 	<ul style="list-style-type: none"> • Notional time: 8 hours • Predictions of succession could be based on r-selected species versus K-selected species, biodiversity, biomass, or changes in biotic and abiotic interactions. • Human activities could include overexploitation, habitat destruction, monocultures or pollution.

Subject matter	Guidance
<p>to analyse species diversity between two spatially variant ecosystems of the same classification (e.g. a disturbed and undisturbed dry sclerophyll forest).</p>	
<p>Science as a Human Endeavour (SHE)</p> <ul style="list-style-type: none"> • SHE subject matter will not be assessed on the external examination but could be used in the development of claims and research questions for a research investigation. 	<ul style="list-style-type: none"> • Aboriginal knowledge and Torres Strait Islander knowledge of ecosystem interactions and change: Aboriginal communities and Torres Strait Islander communities have knowledge of environmental change and interactions between abiotic and biotic elements of ecosystems in their local contexts. This can provide valuable data for understanding ecosystem dynamics, which can complement practices in conservation areas. • Marine reserves: Scientific knowledge based on local data collection and analysis, computer simulation of future scenarios and analysis of analogous scenarios is required to analyse the unique factors that affect marine ecosystems to classify areas and predict the likelihood that the reserve will successfully protect marine biodiversity. • Keystone species and conservation: Keystone species can be more effective as a conservation strategy to maintain complex ecosystem dynamics compared with other strategies such as conservation of flagship species and umbrella species.

5.3 Topic 1: DNA, genes and the continuity of life

In this topic, students will:

Subject matter	Guidance
<p>DNA structure and replication</p> <ul style="list-style-type: none"> • <u>understand</u> that deoxyribonucleic acid (DNA) is a double-stranded molecule that occurs bound to proteins (histones) in chromosomes in the nucleus, and as unbound circular DNA in the cytosol of prokaryotes, and in the mitochondria and chloroplasts of eukaryotic cells • <u>recall</u> the structure of DNA, including <ul style="list-style-type: none"> – nucleotide composition – complementary base pairing – weak, base-specific hydrogen bonds between DNA strands • <u>explain</u> the role of helicase (in terms of unwinding the double helix and separation of the strands) and DNA polymerase (in terms of formation of the new complementary strands) in the process of DNA replication. Reference should be made to the direction of replication. 	<ul style="list-style-type: none"> • Notional time: 5 hours • <u>Identification</u> and <u>use</u> of chemical formulas are not required for <u>recalling</u> the components in DNA structure. Students should be able to use a schematic model identifying nucleotides (nitrogenous base + phosphate + sugar) and the associated hydrogen bonds. • Specific numbers of hydrogen bonds and reference to purines and pyrimidines are not required for the description of hydrogen bonding in DNA. • Reference to DNA polymerase I and II is not required in the explanation of DNA replication. • Suggested practical: Extract DNA from strawberries, kiwifruit or wheat germ. • SHE: <u>Understand</u> the development of the double-helix model through the contributions of James Watson, Francis Crick and Rosalind Franklin.
<p>Cellular replication and variation</p> <ul style="list-style-type: none"> • within the process of meiosis I and II <ul style="list-style-type: none"> – <u>recognise</u> the role of homologous chromosomes – <u>describe</u> the processes of crossing over and recombination and <u>demonstrate</u> how they contribute to genetic variation – <u>compare</u> and <u>contrast</u> the process of spermatogenesis and oogenesis (with reference to haploid and diploid cells). • demonstrate how the process of independent assortment and random fertilisation alter the variations in the genotype of offspring. 	<ul style="list-style-type: none"> • Notional time: 5 hours (time allocation should consider a SHE) • SHE: <u>Discuss</u> implications of genetic screening technologies, such as preimplantation genetic diagnosis and CRISPR, on reproductive technologies.

Subject matter	Guidance
<p>Gene expression</p> <ul style="list-style-type: none"> • <u>define</u> the terms <i>genome</i> and <i>gene</i> • <u>understand</u> that genes include 'coding' (exons) and 'noncoding' DNA (which includes a variety of transcribed proteins: functional RNA (i.e. tRNA), centromeres, telomeres and introns. <u>Recognise</u> that many functions of 'noncoding' DNA are yet to be determined) • <u>explain</u> the process of protein synthesis in terms of <ul style="list-style-type: none"> – transcription of a gene into messenger RNA in the nucleus – translation of mRNA into an amino acid sequence at the ribosome (refer to transfer RNA, codons and anticodons) • recognise that the purpose of gene expression is to <u>synthesise</u> a functional gene product (protein or functional RNA); that the process can be regulated and is used by all known life • <u>identify</u> that there are factors that regulate the phenotypic expression of genes <ul style="list-style-type: none"> – during transcription and translation (proteins that bind to specific DNA sequences) – through the products of other genes – via environmental exposure (consider the twin methodology in epigenetic studies) • recognise that differential gene expression, controlled by transcription factors, regulates cell differentiation for tissue formation and morphology • <u>recall</u> an example of a transcription factor gene that regulates morphology (HOX transcription factor family) and cell differentiation (sex-determining region Y). 	<ul style="list-style-type: none"> • Notional time: 6 hours • Refer to glossary for definitions of <i>genome</i> and <i>gene</i>. • The term <i>junk DNA</i> is misleading and should not be used in reference to 'noncoding' DNA. • When <u>identifying</u> transcription factors in the regulation of gene expression, reference to operators, promoters, regulators, enhancers, silencers, insulators, TATA boxes, polyadenylation and DNA methylation is not required. • Students should <u>recognise</u> gene expression in the context of an example. They are not required to <u>explain</u> or <u>describe</u> the mechanisms of this process.

Subject matter	Guidance
<p>Mutations</p> <ul style="list-style-type: none"> • <u>identify</u> how mutations in genes and chromosomes can result from errors in <ul style="list-style-type: none"> – DNA replication (point and frameshift mutation) – cell division (non-disjunction) – damage by mutagens (physical, including UV radiation, ionising radiation and heat and chemical) • <u>explain</u> how non-disjunction leads to aneuploidy • <u>use</u> a human karyotype to identify ploidy changes and <u>predict</u> a genetic disorder from given data • <u>describe</u> how inherited mutations can alter the variations in the genotype of offspring. 	<ul style="list-style-type: none"> • Notional time: 3 hours • Students are not required to <u>identify</u> the effects of mutations (i.e. silent, missense, nonsense). • <u>Recall</u> of specific chemical mutagens is not required. Rather, an <u>understanding</u> should be developed that a large number of chemical mutagens are carcinogenic and interact directly with DNA. • Examples of aneuploidy could include trisomy 21.
<p>Inheritance</p> <ul style="list-style-type: none"> • <u>predict</u> frequencies of genotypes and phenotypes using <u>data</u> from probability models (including frequency histograms and Punnett squares) and by taking into consideration <u>patterns</u> of inheritance for the following types of alleles: autosomal dominant, sex linked and multiple • <u>define</u> <u>polygenic inheritance</u> and predict frequencies of genotypes and phenotypes for using three of the possible alleles. 	<ul style="list-style-type: none"> • Notional time: 3 hours • Refer to the glossary for a definition of <u>polygenic inheritance</u>. • <u>Multiple allele inheritance</u> refers to situations where there are more than two alleles considered, i.e. incomplete and co-dominance situations. • Examples for patterns of inheritance could include haemophilia (sex linked) and ABO blood types (multiple), grain colour in wheat (polygenic).
<p>Biotechnology</p> <ul style="list-style-type: none"> • <u>describe</u> the process of making recombinant DNA <ul style="list-style-type: none"> – isolation of DNA, cutting of DNA (restriction enzymes) – insertion of DNA fragment (plasmid vector) – joining of DNA (DNA ligase) – amplification of recombinant DNA (bacterial transformation) • <u>recognise</u> the applications of DNA sequencing to map species' genomes and DNA profiling to <u>identify</u> unique genetic information • <u>explain</u> the purpose of polymerase chain reaction (PCR) and gel electrophoresis • <u>appraise data</u> from an outcome of a current genetic biotechnology technique to <u>determine</u> its success rate. 	<ul style="list-style-type: none"> • Notional time: 8 hours • Examples for species genome mapping could include the Human Genome Project. The BLAST database could be used to <u>develop understanding</u> of bioinformatics. • Suggested practical: Perform a bacterial transformation. • Suggested practical: <u>Interpret</u> DNA profiles from gel electrophoresis (either laboratory or computer simulation based). • Examples of current biotechnology techniques could include gel electrophoresis, PCR or CRISPR-based technologies. • <u>Data</u> for appraisal could be from DNA banding, frequency of DNA fragments, effectiveness of restriction enzymes, location of a gene or gene expression. This could be supported with a practical. • SHE: <u>Analyse</u> the implications of DNA profiling for individuals.

Subject matter	Guidance
<p>Science as a Human Endeavour (SHE)</p> <ul style="list-style-type: none"> • SHE subject matter will not be assessed on the external examination but could be used in the development of claims and research questions for the research investigation. 	<ul style="list-style-type: none"> • Bioinformatics: Bioinformatics can be used to analyse the relationships in biological data, such as amino acid sequences or nucleotide sequences (e.g. the Human Genome Project). • A \$1000 genome: Low-cost genome sequencing can be used to enable people to identify whether they have gene variants associated with genetic diseases. • Genetically modified organisms: Transgenic organisms have potential for advancement in agriculture and pharmaceuticals.

5.4 Topic 2: Continuity of life on Earth

In this topic, students will:

Subject matter	Guidance
<p>Evolution</p> <ul style="list-style-type: none"> • <u>define</u> the terms <i>evolution</i>, <i>microevolution</i> and <i>macroevolution</i> • <u>determine</u> episodes of evolutionary radiation and mass extinctions from an evolutionary timescale of life on Earth (approximately 3.5 billion years) • <u>interpret data</u> (i.e. degree of DNA similarity) to reveal phylogenetic relationships with an <u>understanding</u> that comparative genomics involves the comparison of genomic features to provide <u>evidence</u> for the theory of evolution. 	<ul style="list-style-type: none"> • Notional time: 3 hours • Refer to the glossary for definitions of <i>evolution</i>, <i>microevolution</i> and <i>macroevolution</i>. • Evolutionary radiation refers to an increase in taxonomic diversity or morphological disparity.
<p>Natural selection and microevolution</p> <ul style="list-style-type: none"> • <u>recognise</u> natural selection occurs when the pressures of environmental selection confer a selective advantage on a specific phenotype to enhance its survival (viability) and reproduction (fecundity) • <u>identify</u> that the selection of allele frequency in a gene pool can be positive or negative • <u>interpret data</u> and <u>describe</u> the three main types of phenotypic selection: stabilising, directional and disruptive • <u>explain</u> microevolutionary change through the main processes of mutation, gene flow and genetic drift. • Mandatory practical: <u>Analyse</u> genotypic changes for a selective pressure in a gene pool (modelling can be based on laboratory work or computer simulation). 	<ul style="list-style-type: none"> • Notional time: 6 hours • Examples of natural selection could include beak size in the Galapagos finches, antibiotic resistance or insecticide resistance. • <u>Recognise</u> that mutation is the ultimate source of genetic variation, as it introduces new alleles to a population (syllabus link to Unit 4, Topic 1).

Subject matter	Guidance
<p>Speciation and macroevolution</p> <ul style="list-style-type: none"> • <u>recall</u> that speciation and macroevolutionary changes result from an accumulation of microevolutionary changes over time • <u>identify</u> that diversification between species can follow one of four patterns: divergent, convergent, parallel and coevolution • <u>describe</u> the modes of speciation: allopatric, sympatric, parapatric • <u>understand</u> that the different mechanisms of isolation — geographic (including environmental disasters, habitat fragmentation), reproductive, spatial, and temporal — influence gene flow • <u>explain</u> how populations with reduced genetic diversity (i.e. those affected by population bottlenecks) face an increased risk of extinction • <u>interpret</u> gene flow and allele frequency <u>data</u> from different populations in order to <u>determine</u> speciation. 	<ul style="list-style-type: none"> • Notional time: 6 hours. • Habitat fragmentation should be referred to in terms of natural and human causes. • Populations with reduced genetic diversity should be linked to subject matter in Unit 3. • Students should be able to <u>determine</u> the modes of speciation from <u>interpretation of data</u>.
<p>Science as a Human Endeavour (SHE)</p> <ul style="list-style-type: none"> • SHE subject matter will not be assessed on the external examination but could be used in the development of claims and research questions for the research investigation. 	<ul style="list-style-type: none"> • Evidence for evolution: Technological developments in the fields of comparative genomics, comparative biochemistry and bioinformatics enable identification of further evidence for evolutionary relationships. • Human evolution — are we still evolving? Human evolution is still occurring (particularly in Western societies) after the significant cultural events of the Industrial Revolution and the introduction of agriculture, modern medicine and mass transportation. • Unsustainable population size and reserve area: Calculating minimum reserve sizes for a target conservation species should consider the viability of a single large reserve vs. a number of smaller reserves that are connected by 'green corridors'.