QCE Biology — Units 3 & 4 Revision Guide

Science Understanding — Syllabus Elaborations and Explanations

Based on Biology 2025 v1.3 General Senior Syllabus

Unit 3: Biodiversity and the interconnectedness of life

Topic 1: Biodiversity and populations

Syllabus Elaboration	Explanation
Describe genetic, species and ecosystem diversity.	Genetic diversity is the variety of alleles/genes within a species or population, giving raw material for adaptation. Species diversity is the variety and abundance of species in an area (richness + evenness). Ecosystem diversity is the variety of habitats, communities and ecological processes across a region. Together these describe biodiversity from the smallest to the largest scale.
Describe the biological species concept and identify its limitations.	A species is a group of organisms that can interbreed in nature and produce fertile offspring, and is reproductively isolated from other such groups. Limitations: it cannot be applied to asexually reproducing organisms, extinct species known only from fossils, or organisms that hybridise; it also cannot be tested for geographically separated populations.
Identify the major taxa in the Linnaean system of biological classification and explain how it is used to classify and name species.	The Linnaean system is hierarchical: Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species. Each level groups organisms by shared characteristics, becoming more specific down the hierarchy. Binomial nomenclature (*Genus + species*) gives every organism a unique, universal two-part name, allowing unambiguous scientific communication worldwide.
Use dichotomous keys to identify and classify organisms.	A dichotomous key is a series of paired (couplet) statements describing contrasting characteristics. At each step the user chooses the statement matching the organism, which leads either to another couplet or to the identification, progressively narrowing down the organism's identity.
Use the Lincoln index (N = M × n/m) to estimate the size of a population.	The Lincoln index is a mark-recapture technique for mobile animals: M = number of individuals marked and released in the first sample, n = total number caught in the second sample, m = number of marked individuals recaptured in the second sample. N = M × n/m estimates total population size.
Determine the diversity of species using measures such as species richness, evenness (relative species abundance), percentage cover, percentage frequency and Simpson's diversity index, SDI = 1 − (∑n(n−1) / N(N−1)).	Species richness = the number of different species present. Evenness = how equally individuals are distributed among species. Percentage cover = the proportion of an area occupied by a species (used for plants). Percentage frequency = the proportion of samples in which a species is present. Simpson's Diversity Index combines richness and evenness into one value between 0 and 1 — the closer to 1, the greater the diversity.
Describe how sampling can be used to investigate the species diversity of a given area, considering the most appropriate sampling method (random, systematic, stratified), sampling technique (quadrats, line transect, belt transect, capture–recapture), strategies to minimise bias, and measure/s of diversity.	Random sampling uses random-number generators to avoid bias in quadrat placement. Systematic sampling takes measurements at regular fixed intervals (e.g. along a transect). Stratified sampling divides the area into distinct sub-habitats and samples each proportionally. Techniques include quadrats (area sampling), line transects (recording species intersecting a line across a gradient), belt transects (a strip transect giving more coverage), and capture–recapture (for mobile animals). Bias is minimised by using an adequate number/size of samples, randomisation, consistent counting criteria and calibrated equipment.

Syllabus Elaboration	Explanation
Explain that ecosystems are composed of varied habitats, including microhabitats, which may impact the distribution of species (e.g. uniform, random or clumped), and therefore the validity and reliability of different sampling methods/techniques.	Microhabitats create localised variation in conditions, so species may be distributed uniformly, randomly, or in clumps rather than evenly across an ecosystem. This spatial pattern affects which sampling method/technique will give valid and reliable results — e.g. clumped distributions require more or stratified samples to avoid under- or over-representing a species.
Interpret data from an experiment investigating how abiotic factors affect the distribution, abundance and/or biodiversity of species in an ecosystem.	This involves analysing trends, correlations or patterns between measured abiotic variables (e.g. light, moisture, pH, temperature) and species distribution, abundance or biodiversity data to draw evidence-based conclusions about environmental influence on species.
Interpret data to classify and name ecosystems using Specht's classification system and the Holdridge life zone classification scheme.	Specht's classification categorises Australian vegetation communities by dominant growth form (e.g. trees, shrubs) and percentage foliage cover (e.g. forest, woodland, open-forest, scrub, heath). The Holdridge life zone scheme classifies world ecosystems/biomes based on biotemperature, average annual precipitation and potential evapotranspiration ratio.
Identify and explain different modes of population growth, including exponential growth (J-curve) and logistic growth (S-curve).	Exponential growth occurs when resources are unlimited; the population grows at an ever-increasing rate, producing a J-shaped curve. Logistic growth occurs when resources are limited; growth slows as the population approaches the environment's carrying capacity (K), producing an S-shaped curve that plateaus.
Compare the reproductive strategies and growth curves of K- and r-strategists.	r-strategists produce many small offspring with little parental care, mature quickly and have short lifespans; they are effective colonisers of unstable/unpredictable environments and typically show exponential (J-curve) growth. K-strategists produce fewer, larger offspring with greater parental investment, mature slowly and live longer; they are favoured in stable environments near carrying capacity and typically show logistic (S-curve) growth.
Calculate population growth rate and change using birth, death, immigration and emigration data.	Population change = (births + immigrants) − (deaths + emigrants). This value, calculated over a set time period, gives the population growth rate and shows whether a population is increasing, decreasing or stable.

Topic 2: Functioning ecosystems and succession

Syllabus Elaboration	Explanation
Explain the transfer and transformation of energy as it flows through the biotic components of an ecosystem, including the conversion of light into chemical energy, production of biomass and its interactions with components of the carbon cycle, and loss of energy as heat.	Producers convert light energy into chemical energy (stored in glucose) via photosynthesis. This energy is incorporated into biomass, linking energy flow to the carbon cycle as carbon is fixed into organic molecules and later released via respiration/decomposition. At each transfer between organisms/trophic levels, energy is lost as heat (a consequence of the second law of thermodynamics), so energy flow through an ecosystem is one-directional and progressively diminishes.
Analyse food chains, energy flow diagrams and ecological pyramids to determine efficiencies of energy and biomass transfer, gross and net productivity, and loss of energy through radiation, reflection and absorption.	Energy pyramids show the reduction in available energy at each trophic level (typically ~10% transfer efficiency). Gross primary productivity (GPP) is the total energy captured by producers; net primary productivity (NPP) is GPP minus the energy used in respiration, representing energy available to consumers. Additional energy losses occur through radiation and reflection of light (not absorbed by producers) and inefficiencies in absorption/digestion.
Describe the transfer and transformation of matter (water, carbon, nitrogen) as it cycles through ecosystems.	The water cycle moves water between reservoirs via evaporation, transpiration, condensation, precipitation and run-off. The carbon cycle moves carbon via photosynthesis (fixation), respiration, decomposition and combustion. The nitrogen cycle moves nitrogen via fixation (by bacteria or lightning), nitrification, assimilation by

Syllabus Elaboration	Explanation
	producers, and denitrification back to the atmosphere. These cycles link biotic organisms and the abiotic environment.
Explain the following species interactions: predation, competition, mutualism, commensalism and parasitism.	Predation (+/−): the predator benefits, the prey is harmed (killed and consumed). Competition (−/−): both species are harmed as they compete for the same limited resource. Mutualism (+/+): both species benefit. Commensalism (+/0): one species benefits, the other is unaffected. Parasitism (+/−): the parasite benefits (often without killing quickly), the host is harmed.
Describe the concept of an ecological niche.	An ecological niche is the functional role and position a species occupies within its ecosystem — including its habitat, resource use, interactions with other species, and how it obtains what it needs to survive and reproduce.
Explain the competitive exclusion principle.	Two species that compete for exactly the same limiting resource within the same niche cannot coexist indefinitely in the same habitat — one species will out-compete and exclude the other, or the species will evolve to occupy slightly different niches (niche differentiation).
Explain the critical role that keystone species play in maintaining the structure of a community.	A keystone species has an effect on community structure that is disproportionately large relative to its abundance. Its presence maintains the balance, structure and diversity of the ecosystem; its removal can cause dramatic, cascading changes or even ecosystem collapse.
Analyse ecological data (e.g. food webs, population data) to identify keystone species, infer species interactions, and predict the outcomes of removing species from an ecosystem.	Keystone species can be identified from food-web connectivity and the scale of impact their removal would have. Species interactions can be inferred from patterns such as correlated changes in abundance data. Modelling the removal of a species from a food web allows prediction of trophic cascades and flow-on effects on other populations.
Explain how overexploitation, habitat destruction, monocultures and pollution affect community structure and ecosystem functioning.	Overexploitation (excessive harvesting/hunting) depletes populations faster than they can replace themselves. Habitat destruction removes the resources and niches species depend on. Monocultures reduce biodiversity and genetic diversity, increasing vulnerability to pests, disease and environmental change. Pollution introduces toxins or excess nutrients (e.g. eutrophication), harming organisms and disrupting ecosystem processes. All of these reduce ecosystem resilience and biodiversity.
Explain how the carrying capacity of an ecosystem can be impacted by changes to biotic and abiotic factors, including climatic events.	Carrying capacity (K) is the maximum population size an environment can sustainably support. It can rise or fall due to biotic factors (e.g. changes in predators, disease, competitors, food availability) and abiotic factors (e.g. droughts, floods, fires or other climatic events) that alter the availability of resources such as food, water and shelter.
Describe the process of ecological succession.	Ecological succession is the predictable, directional and gradual change in the composition of a community of species over time, occurring in a habitat that is newly formed or has been disturbed, progressing towards a relatively stable climax community.
Distinguish between primary and secondary succession.	Primary succession begins on bare substrate that has never previously supported life and has no soil (e.g. new volcanic rock, retreated glacier). Secondary succession occurs after a disturbance (e.g. fire, farming) where soil and some organisms/seeds remain, allowing recovery to occur more rapidly.
Identify the features of pioneer species that make them effective colonisers.	Pioneer species typically disperse widely and reproduce rapidly, tolerate harsh abiotic conditions (e.g. poor soil, extreme temperature/light), and are often able to modify the environment (e.g. nitrogen-fixing plants improving soil) to make it more suitable for later-successional species.

Syllabus Elaboration	Explanation
Explain successional changes, with reference to species interactions, abiotic factors, K- and r-selected species, biodiversity and biomass.	Over the course of succession, r-selected pioneer species are gradually replaced by K-selected species as conditions stabilise. Species interactions intensify (e.g. increased competition) as the community becomes more complex. Abiotic conditions such as soil depth, nutrient availability and shade change as succession proceeds. Biodiversity and biomass generally increase through the seral stages, typically peaking as the community approaches a climax community.
Interpret ecological data to compare ecosystems across spatial and temporal scales.	This involves comparing data such as biodiversity indices, species composition, or succession stage between different locations (spatial comparison) or the same location at different points in time (temporal comparison) to draw conclusions about ecosystem change, health or the influence of human activity.

Unit 4: Heredity and continuity of life

Topic 1: Genetics and heredity

Syllabus Elaboration	Explanation
Describe the structure and function of DNA, genes and chromosomes in prokaryotes and eukaryotes, including helical structure, nucleotide composition (nitrogenous base + sugar + phosphate), complementary base pairing, hydrogen bonds; introns and exons, promoter region; homologous chromosomes (sister chromatids, centromeres, telomeres, gene loci, alleles), role of histones; circular chromosomes (prokaryotes, mitochondria, chloroplasts) and plasmids.	DNA is a double helix made of nucleotides (a nitrogenous base + deoxyribose sugar + phosphate group), with complementary base pairing (A–T, G–C) held together by hydrogen bonds. Genes contain exons (coding regions) and introns (non-coding regions removed before translation), plus a promoter region where transcription begins. Homologous chromosomes are matched pairs carrying genes at the same loci (positions), each made of two sister chromatids joined at a centromere and capped by telomeres; alleles are alternative versions of a gene at a locus; DNA wraps around histone proteins for packaging. Prokaryotes, as well as mitochondria and chloroplasts (reflecting their endosymbiotic origin), have circular chromosomes; prokaryotes may also carry small circular plasmids.
Describe the process of DNA replication with reference to helicase, DNA polymerase and the joining of Okazaki fragments.	Helicase unwinds and separates the DNA double helix by breaking hydrogen bonds between base pairs. DNA polymerase then synthesises new complementary strands by adding nucleotides to each template strand. Because DNA polymerase only works in one direction, the leading strand is synthesised continuously while the lagging strand is made in short Okazaki fragments, which are joined together by DNA ligase.
Explain how errors in DNA replication and damage by physical/chemical factors in the environment can lead to point and frameshift mutations.	Point mutations arise when a single base is incorrectly incorporated, substituted, or altered by mutagens (e.g. UV radiation, chemicals), changing only one base pair. Frameshift mutations occur when bases are inserted or deleted (not in multiples of three), shifting the reading frame for every codon downstream of the mutation, which usually has a much larger effect on the resulting protein.
Describe the process of meiosis and explain how crossing over, independent assortment and random fertilisation produce variation in the genotypes of offspring.	Meiosis is two successive divisions that reduce a diploid cell to four haploid gametes. Crossing over during prophase I exchanges DNA segments between homologous chromosomes, creating new allele combinations. Independent assortment during metaphase I randomly orients homologous chromosome pairs, so maternal and paternal chromosomes are distributed randomly into gametes. Random fertilisation then combines gametes from two parents unpredictably. Together, these three processes generate the genetic variation seen among offspring.
Compare spermatogenesis and oogenesis.	Spermatogenesis produces four equally sized, small, motile sperm from each primary spermatocyte, continuously from puberty onward. Oogenesis produces only one large, viable ovum per primary oocyte (with the other three becoming small polar bodies that degenerate), occurring cyclically and with meiosis arrested at certain stages until later triggered by hormonal changes or fertilisation.
Explain how errors in meiosis can lead to chromosomal abnormalities such as insertions, deletions, duplications, inversions, translocations and aneuploidy.	Nondisjunction (failure of chromosomes/chromatids to separate properly) results in aneuploidy — gametes with an abnormal number of chromosomes (e.g. trisomy, monosomy). Errors during crossing over or chromosome breakage can cause structural abnormalities: insertions (extra segment added), deletions (segment lost), duplications (segment repeated), inversions (segment reversed), and translocations (segment moves to a non-homologous chromosome) — all of which can disrupt normal gene function or dosage.

Syllabus Elaboration	Explanation
Identify ploidy changes within a human karyotype to predict a genetic disorder.	A karyotype is an image of an individual's chromosomes arranged in matched, numbered pairs by size and banding pattern. Counting the number of chromosomes present in each pair allows identification of ploidy abnormalities (e.g. an extra chromosome 21, indicating trisomy 21/Down syndrome), which can be used to predict associated genetic disorders.
Explain the process of protein synthesis in terms of transcription of a gene into messenger RNA in the nucleus, RNA processing (5' cap, RNA splicing, poly-A tail), and translation of mRNA into an amino acid sequence at the ribosome, referring to transfer RNA, codons and anticodons.	Transcription: RNA polymerase binds the promoter and synthesises a complementary pre-mRNA strand from the DNA template in the nucleus. RNA processing: a 5' cap and poly-A tail are added to protect the mRNA and aid export/translation, and splicing removes introns, joining exons together to form mature mRNA. Translation: the mRNA moves to a ribosome in the cytoplasm, where transfer RNA molecules bring specific amino acids, matching their anticodon to each mRNA codon (a triplet of bases), building the amino acid sequence (polypeptide) in order.
Determine the effect of point and frameshift mutations on polypeptides using the genetic code.	Using a codon table, a point mutation may be silent (codon still codes for the same amino acid), missense (codes for a different amino acid, potentially altering protein function) or nonsense (creates a premature stop codon, truncating the protein). A frameshift mutation alters every codon downstream of the mutation site, typically producing a completely different and non-functional amino acid sequence.
Explain how gene expression is regulated in response to environmental signals and to allow for cell differentiation, including chemical tags that affect chromatin structure (heterochromatin vs. euchromatin) and proteins that bind to the promoter region of a gene (transcription factors).	Chemical tags (e.g. methylation, acetylation) alter how tightly DNA is packaged: heterochromatin is tightly coiled and its genes are largely inaccessible/'switched off', while euchromatin is loosely packed and accessible for transcription/'switched on'. Transcription factors are proteins that bind to a gene's promoter region, enhancing or blocking RNA polymerase binding, thereby turning genes on or off in response to environmental or developmental signals — this regulation underlies how different cell types differentiate despite sharing the same DNA.
Explain how genes from the HOX transcription factor family regulate morphology.	HOX genes are a family of transcription factor genes that control the body plan and identity of body segments during embryonic development, by switching on/off other genes that determine structures such as limb placement — mutations in HOX genes can cause major changes in body morphology.
Describe dominant, recessive, autosomal, sex-linked, polygenic and multiple-allele inheritance.	Dominant alleles are expressed in the phenotype even when only one copy is present (heterozygous); recessive alleles are only expressed when present in two copies (homozygous). Autosomal genes are located on non-sex chromosomes, inherited equally regardless of sex; sex-linked genes are located on the X or Y chromosome, producing different inheritance patterns in males and females. Polygenic traits are controlled by multiple genes, producing continuous variation (e.g. height, skin colour). Multiple-allele traits have more than two allele variants present in the population, though an individual still only carries two (e.g. ABO blood groups).
Infer patterns of inheritance and predict frequencies of genotypes and phenotypes from genetic data, including histograms (polygenic inheritance), pedigrees (dominant/recessive, autosomal/sex-linked) and Punnett squares (dominant/recessive, autosomal/sex-linked and multiple-allele inheritance).	Histograms showing a continuous, bell-shaped distribution of a trait indicate polygenic inheritance. Pedigrees trace a trait through generations of a family and can be analysed to determine whether inheritance is dominant/recessive and autosomal/sex-linked, based on patterns of affected individuals. Punnett squares use parental genotypes to predict the ratios of genotypes and phenotypes in offspring for dominant/recessive, sex-linked and multiple-allele crosses.
Describe the process of making recombinant DNA, including the role of restriction enzymes, plasmids and DNA ligase.	Restriction enzymes cut DNA at specific recognition sequences, producing 'sticky' or blunt ends. The same restriction enzyme is used to cut both a plasmid vector and the DNA containing the gene of

Syllabus Elaboration	Explanation
	interest, so their cut ends are complementary. DNA ligase then joins (splices) the gene of interest into the plasmid, creating a single recombinant DNA molecule that can be inserted into a host cell.
Describe how PCR and gel electrophoresis are used in DNA profiling and explain how differences in DNA allow for characteristic banding patterns.	PCR (polymerase chain reaction) amplifies specific regions of DNA (such as short tandem repeats) using primers, Taq polymerase and repeated cycles of heating and cooling, producing millions of copies. Gel electrophoresis then separates the amplified DNA fragments by size using an electric current, with smaller fragments travelling further through the gel. Because individuals have differing numbers of repeats at these regions, this produces a unique banding pattern that can be used to profile/identify a person.
Interpret DNA profiles from gel electrophoresis.	This involves comparing the number and position of bands between DNA samples (e.g. a suspect's DNA and crime-scene DNA, or between potential relatives) to determine whether profiles match, exclude an individual, or indicate a biological relationship.

Topic 2: Continuity of life on Earth

Syllabus Elaboration	Explanation
Distinguish between microevolution and macroevolution.	Microevolution refers to small-scale changes in allele frequencies within a population from one generation to the next. Macroevolution refers to large-scale evolutionary patterns occurring above the species level over long timescales, such as speciation and extinction, which result from the accumulation of microevolutionary changes.
Explain microevolutionary change through the main processes of mutation, gene flow and genetic drift.	Mutation introduces new alleles into a population, providing the raw material for variation. Gene flow is the movement of alleles between populations through migration and interbreeding, altering allele frequencies. Genetic drift is the random change in allele frequency due to chance events, with especially strong effects in small populations (e.g. through founder effects or population bottlenecks).
Explain natural selection and identify the three main types of phenotypic selection: stabilising, directional and disruptive.	Natural selection is the differential survival and reproduction of individuals based on heritable traits that affect their fitness in a given environment. Stabilising selection favours intermediate phenotypes and reduces variation. Directional selection favours one phenotypic extreme, shifting the population's average trait value over time. Disruptive selection favours both phenotypic extremes over the intermediate form, increasing variation and potentially driving speciation.
Calculate allele frequencies from genotype data.	Allele frequency is the proportion of a particular allele among all alleles for that gene in a population, calculated by counting alleles from genotype data (e.g. using Hardy–Weinberg principles, where p and q represent the frequencies of two alleles and $p + q = 1$).
Analyse data to determine the effect of a selection pressure on a population, recognising that selection for an allele can be positive or negative.	This involves comparing trait or allele frequency data before and after an environmental change or selection pressure to determine whether the pressure is increasing (positive selection) or decreasing (negative selection) the frequency of a particular allele or trait in the population.
Describe how macroevolutionary changes result from the accumulation of microevolutionary changes using examples of divergent, convergent, parallel and coevolution.	Divergent evolution occurs when related species with a common ancestor accumulate different traits over time due to differing environments/selection pressures. Convergent evolution occurs when unrelated species independently evolve similar traits due to similar environmental pressures. Parallel evolution occurs when related species evolve in similar ways independently after diverging. Coevolution occurs when two interacting species (e.g. predator–prey,

Syllabus Elaboration	Explanation
	plant–pollinator) reciprocally influence each other's evolution over time.
Explain how geographic, temporal and spatial isolation influence gene flow and may lead to allopatric, sympatric and parapatric speciation.	Geographic isolation (a physical barrier separating populations) prevents gene flow and can lead to allopatric speciation. Speciation without a physical barrier — for example through behavioural, temporal or habitat differences within the same area — is sympatric speciation. Partial geographic separation with limited but not fully blocked gene flow along a contact zone is parapatric speciation. In all cases, reduced gene flow allows populations to accumulate independent genetic differences until they become reproductively isolated.
Explain why populations with reduced genetic diversity face increased risk of extinction.	With less genetic variation, there is less raw material for natural selection to act on, reducing a population's ability to adapt to environmental change, disease or new predators/competitors. Reduced genetic diversity can also lead to inbreeding depression, lowering fitness and survival, all of which increase the population's vulnerability to extinction.
Explain how comparative genomics provides evidence for the theory of evolution and how conserved sequences can be used to date divergence.	Comparing DNA and protein sequences between species reveals similarities that indicate shared evolutionary ancestry — the more similar the sequences, the more closely related the species are likely to be. Highly conserved sequences (which mutate slowly because they are essential for survival) can be used, along with an estimated/molecular-clock mutation rate, to estimate how long ago two lineages diverged from a common ancestor.
Infer species relatedness from cladograms, phylograms and molecular sequence data.	Cladograms are branching diagrams showing hypothesised evolutionary relationships and the order in which lineages diverged, based on shared derived characteristics. Phylograms are similar but also show branch lengths representing the relative amount of evolutionary change or time. Molecular sequence data (DNA/protein similarity) is used to construct and interpret both types of diagrams to infer how closely related different species are.
Determine episodes of evolutionary radiation and mass extinctions from an evolutionary timescale of life on Earth (approximately 3.5 billion years).	By examining the fossil record and geological timescale, periods of evolutionary/adaptive radiation can be identified — times of rapid diversification into many new species, often following the opening up of ecological niches (e.g. after a mass extinction). Mass extinction events (e.g. the Permian and Cretaceous extinctions) are identified by rapid, large-scale losses of biodiversity recorded in the fossil record.