

Session 1

Prologue; Chapter 1: Darwin's Nemesis; Chapter 2: The Burgess Bestiary

Prologue

In his 2009 book *Signature in the Cell*, Stephen Meyer argues that the information necessary for the first life is best explained by intelligent design (ID) rather than the blind and unguided mechanisms invoked by theories of chemical evolution. In the prologue to *Darwin's Doubt*, he explains his surprise when critics responded to *Signature in the Cell* by appealing to the creative power of random mutation and natural selection—processes that could not have operated before life began. In 2013, Meyer published *Darwin's Doubt* to answer critics who argue that Darwinian evolution can produce new biological information. In the process, the book explores a mystery that has puzzled biologists since Darwin's time.

Ch. 1

Darwin's Nemesis

Darwin's argument in *Origin of Species* rests upon two pillars: common ancestry and natural selection, where species arise gradually as selection preserves small, step-by-step variations. Darwin recognized that the fossil record did not demonstrate this gradual change. Instead, major groups ("phyla") of complex animals—like shelled brachiopods or multisegmented trilobites—appear suddenly in the fossil record, without evolutionary precursors, in an event that paleontologists today call the Cambrian explosion. Leading contemporaries of Darwin, like Harvard's Louis Agassiz, cited the Cambrian explosion as a challenge to Darwin's theory. Darwin responded by arguing the fossil record must be incomplete, but he nonetheless admitted that the lack of fossil ancestors for the Cambrian animals "may be truly urged as a valid argument against" his theory.

Ch. 2

The Burgess Bestiary

Discovered in 1909 by Smithsonian Institution director Charles Walcott, the fossils of the Burgess Shale in the Canadian Rockies reveal a stunning assortment of animal diversity, including oddball creatures unlike any living phyla. All told, representatives of about twenty of the roughly twenty-six total animal phyla known from the entire fossil record appear abruptly in the Cambrian. This pattern is the opposite of the gradual branching tree predicted by Darwin's theory, where small-scale differences between lower-level taxonomic categories (diversity) should accumulate before the appearance of major differences between higher-level taxonomic categories (disparity). Puzzled by the absence of ancestral fossils in Precambrian rock, Walcott followed Darwin's approach, proposing that the Cambrian explosion was merely an artifact of an incompletely sampled fossil record. Walcott thought the ancestors of the Cambrian animals were waiting to be found in as-of-yet undiscovered strata, but history proved him wrong.

Session 2

Chapter 3: Soft Bodies and Hard Facts; Chapter 4: The *Not* Missing Fossils?

Ch. 3 Soft Bodies and Hard Facts

Another location bearing beautifully preserved Cambrian fossils—including vertebrate fish—was discovered in Chengjiang, China in the 1980s. These finds further confirmed the abrupt appearance of animal body plans in the Cambrian, with the main burst of diversity appearing in less than 5 or 6 million years. Evolutionary scientists have tried to explain this unexpected pattern through the artifact hypothesis, claiming the ancestors of the Cambrian animals were too small, or too soft-bodied to have been preserved as fossils. This argument is contradicted by the existence of numerous fossils of small and soft-bodied organisms from Cambrian and Precambrian strata. Such fossils include bacteria, algae, and tiny sponge embryos—though they aren't the missing ancestors of the Cambrian animals. The artifact hypothesis is also challenged by studies showing that our knowledge of the fossil record is mature enough to conclude that if evolutionary precursors existed, we should have found them.

Ch. 4 The *Not* Missing Fossils?

Evolutionists sometimes attempt to minimize the “explosive” appearance of new animal phyla in the Cambrian fossil record by asserting that the Ediacaran or Vendian fossils of the late Precambrian provide the missing ancestors. However the consensus of paleontologists is that these organisms are ambiguous, enigmatic, and difficult to match to the Cambrian animals. Many have turned out to not be animals at all, and some may not even be fossils. At most, Precambrian fossils (including trace fossils) provide possible ancestors for only four of the twenty-three animal phyla present in the Cambrian. The vast majority of Cambrian animals have no apparent precursors in Precambrian rocks.

Session 3

Chapter 5: The Genes Tell the Story; Chapter 6: The Animal Tree of Life;
Chapter 7: Punk Eek!

Ch. 5 The Genes Tell the Story

After the fossil record failed to produce ancestors of the Cambrian animals, some evolutionary biologists turned to genetic evidence to establish the branching pattern predicted by Darwin's theory. Using "molecular clock" techniques, they propose that by measuring the differences between the genes of living animals and estimating mutation rates, they can establish "deep divergence"—the claim that animals shared common ancestors far back into the Precambrian. Molecular clocks, however, are notoriously unreliable, as different studies give widely varying dates for when those ancestors existed. Some have proposed the common ancestor of animals lived after the Cambrian period, or *prior to the beginning of the universe*—obviously absurd results. These widely divergent results stem from dubious assumptions made by molecular clock studies, such as the constancy of mutation rates or the precise dates of fossils. These discrepancies mean molecular clocks cannot reliably establish deep divergence and resolve the Cambrian enigma.

Ch. 6 The Animal Tree of Life

Biologists also attempt to establish animal evolution by comparing the genetic and anatomical traits of living species to produce phylogenetic trees showing evolutionary relationships. If there is one true history of animal evolution, the evidence should consistently suggest the same tree. But molecule-based trees often conflict with one-another: one gene yields one version of the tree of animal life, and another gene yields an entirely different and conflicting tree. Molecule-based trees also frequently conflict with trees based upon anatomy, and anatomy-based trees often conflict with one another. Such conflicts force evolutionary biologists to appeal to convergent evolution, where the same traits arise independently. This undermines a basic assumption of treebuilding which holds that biological similarity implies inheritance from a common ancestor. Difficulties reconstructing the animal tree of life have caused some biologists to conclude that the animal phyla diverged too abruptly to reveal their evolutionary relationships. Phylogenetic studies have led us right back to where the fossil evidence did: an explosive appearance of diverse animal phyla that contradicts Darwinian predictions.

Ch. 7 Punk Eek!

In the 1970s, paleontologists Stephen Jay Gould and Niles Eldridge proposed a new model of evolution called punctuated equilibrium, where populations experience long periods without change (called stasis), punctuated by short periods of rapid evolution. Hoping to explain why the fossil record lacked transitional forms, they postulated that if evolutionary change took place rapidly, in small populations that were short-lived, then transitional forms

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Punk Eek!
(continued)

would be less likely to become fossilized. Gould and Eldredge also proposed species selection, where interspecies competition would cause some species to dominate over others. Punctuated equilibrium cannot explain the missing precursors to the Cambrian animals for multiple reasons. Species selection eliminates forms, and does not generate new traits. The “top down” pattern of abrupt appearance of the Cambrian animals contradicts the pattern of “bottom up” evolution required by punctuated equilibrium. No genetic mechanism has explained how evolutionary change can occur rapidly. Thus, Cambrian paleontologists James Valentine and Douglas Erwin concluded that punctuated equilibrium cannot explain the origin of new body plans.

Session 4

Chapter 8: The Cambrian Information Explosion;

Chapter 9: Combinatorial Inflation; Chapter 10: The Origin of Genes and Proteins

Ch. 8 The Cambrian Information Explosion

Having established that the Cambrian explosion was real, Meyer considers what is needed to produce the new animal body plans that appeared during that event. Discoveries since Darwin's time reveal that biological traits are determined (at least in part) by genes, which are encoded by sequences of nucleotides in protein-coding stretches of DNA. Building a new body plan requires new organs, which in turn requires new tissues, which requires new cell types, which requires new proteins, which at base requires new genetic information in the form of new nucleotide sequences in DNA. Building a body plan thus requires adding new functional information or specified complexity in DNA—like generating meaningful language or computer codes. It follows then, that the Cambrian explosion was an *information* explosion.

Ch. 9 Combinatorial Inflation

At the Wistar Conference in 1966, MIT professor Murray Eden postulated that mutations will degrade protein function just as randomly changing letters in written language will garble the meaning. Eden's argument challenged neo-Darwinian theory, which holds that random mutations can *improve* protein function, conferring a survival advantage on an organism. As the length of a protein increases, the number of possible combinations of amino acids grows at an exponential rate. This is called "combinatorial inflation." Mutagenesis experiments show that functional amino acid sequences are extremely rare, meaning many mutations must be "just right" in order for them to function. MIT molecular biologist Robert Sauer found that only 1 in 10^{63} sequences of about 100 amino acids in length will yield a functional protein. This suggests long periods of time are necessary for random mutations to "stumble upon" functional protein sequences. But long periods of time were not available during the Cambrian explosion.

Ch. 10 The Origin of Genes and Proteins

Protein scientist Douglas Axe suspected Robert Sauer's research underestimated the rarity of functional protein sequences because it failed to consider simultaneous changes to multiple amino acids. Axe conducted more stringent mutagenesis experiments on enzymes to determine the rarity of amino acid sequences that yield stable protein folds—the smallest, most fundamental unit of structural innovation possible, key to generating macroevolutionary change. Axe's research found that only 1 in 10^{77} sequences of 150 amino acids in length can yield a stable protein fold. Richard Dawkins compares Darwinian evolution to climbing a mountain peak, but Axe's work suggests functional amino acid sequences are so rare in sequence space that random mutation could never successfully find

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The Origin of Genes and Proteins *(continued)*

a peak, and once on a peak, could never leave one peak and successfully find another. Indeed, since only 10^{40} organisms have ever existed on Earth, random mutations could never find even one functional protein fold over life's entire history, much less in the timespan of the Cambrian explosion.

Session 5

Chapter 11: Assume a Gene;

Chapter 12: Complex Adaptations and the Neo-Darwinian Math

Ch. 11

Assume a Gene

Evolutionary attempts to explain the origin of genes typically take a gene, and then seek another gene that is similar (homologous), and then invoke various mutational mechanisms (e.g., duplication, exon shuffling, retropositioning, lateral gene transfer, point mutations, etc.) to explain how those two genes diverged from a hypothetical common ancestor gene. These methods presuppose, rather than demonstrate, that biological similarity is the result of common ancestry, and ignore other possibilities like common design. They frequently presuppose the existence of biological information without explaining its origin. These studies attempt to explain ORFan genes—unique genes with no known homology to other genes—through *de novo* gene origination, which amounts to evolution out of nothing, and gives no explanation for how new information arises. Stories of gene evolution either provide plausible but irrelevant scenarios describing minor genetic changes that fail to account for new protein folds, or promote implausible but relevant scenarios that also fail to produce new folds. At best, gene evolution studies demonstrate where genes have been slightly modified, but offer no mathematical validation nor experimental evidence demonstrating nontrivial gains in biological information.

Ch. 12

Complex Adaptations
and the
Neo-Darwinian Math

Complex adaptations (also called multi-mutation traits) require multiple coordinated mutations before providing any advantage to an organism. Evolving complex adaptations is like playing the lottery: the more time (i.e., number of generations) and opportunities (i.e., number of individuals in a population) available, the greater the likelihood the trait will arise. Michael Behe and David Snoke calculated that in multicellular organisms, population sizes are too small, and too few generations have lived, to produce a complex adaptation requiring only two mutations before providing an advantage. Even Behe's critics calculated that a complex adaptation requiring two or more mutations could not arise in humans within a reasonable timescale. Ann Gauger and Douglas Axe tried to convert one bacterial enzyme into another closely related enzyme, and found that the conversion would require at least seven coordinated mutations. This exceeds a six-mutation-limit Axe established as an upper boundary of what Darwinian evolution could produce, and confirmed that genes and proteins are complex adaptations which cannot be produced by Darwinian mechanisms.

Session 6

Chapter 13: The Origin of Body Plans; Chapter 14: The Epigenetic Revolution

Ch. 13 The Origin of Body Plans

Since events that occur early in development have a greater impact on the body plan than those occurring later, evolutionary biologists have hoped that early-acting mutations might cause large-scale changes and explain the evolution of new body plans. However, changes to early animal development require many other coordinated changes in order to yield beneficial effects. Saturation mutagenesis experiments trying to reverse-engineer fruit fly development found that random changes to developmental genes always resulted in dead larvae. Early in development, signaling molecules interact in a coordinated manner to form circuits or developmental gene regulatory networks (dGRNs) which ensure proper development of cell types that build a body plan. Research shows that mutations which interrupt dGRNs cause embryo death. A dilemma thus arises: the kind of mutations needed for major evolutionary change—beneficial regulatory changes expressed early in development—don't occur; the kind that do occur—viable genetic mutations in DNA generally expressed late in development—don't cause major evolutionary change.

Ch. 14 The Epigenetic Revolution

DNA contains information necessary for building proteins, but biological information is needed at many other levels to generate cell types, tissues, organs, and a body plan. These features often require epigenetic information—heritable biological information that exists outside of DNA. A cytoskeletal array of microtubules determines cell shape and function, but the information for building the array exists apart from the DNA. Patterns of regulatory proteins on the interior surface of an egg are crucial for fruit fly development, but their arrangements are not determined by DNA information. Electromagnetic fields generated by ion gradients across cell membranes are crucial for development, but the field locations are not determined by genetic information. Complex patterns of sugars on cell surfaces influence the arrangements of cell types during development, but this “sugar code” is not determined by DNA. Neo-Darwinism requires that new species form when mutations in DNA produce beneficial variation that is preserved by natural selection. But epigenetic information does not exist within DNA, and thus cannot be produced by changes to DNA. DNA could mutate indefinitely and it would not produce the epigenetic information needed for new animal body plans.

Session 7

Chapter 15: The Post-Darwinian World and Self-Organization; Chapter 16: Other Post-Neo-Darwinian Models; Chapter 17: The Possibility of Intelligent Design

Ch. 15 The Post-Darwinian World and Self-Organization

Challenges to the neo-Darwinian paradigm have caused some theorists to propose “post-Darwinian” models of evolution which invoke strictly unguided, material mechanisms, but reject one (or more) of the three pillars of neo-Darwinism: (1) random mutations cause variation, (2) natural selection preserves variations which enhance survival and reproduction, and (3) favored variations are inherited by offspring. Self-organization, a model advocated by Stuart Kauffman, de-emphasizes random mutation and natural selection by claiming natural laws can spontaneously produce biological form. However, the model presupposes the genetic and epigenetic information necessary for cell differentiation and organization. Stuart Newman proposes dynamical patterning modules to explain how cells self-organize into different patterns to build new body plans, but he presupposes a complex toolkit of mechanisms that allows cells to aggregate, and provides no explanation for how these aggregated cell clusters are arranged into functional tissues, organs, and body plans. Self-organization produces order, not information, and types of order it generates are biologically irrelevant. It cannot explain the specified and complex *information* which generates order in living organisms.

Ch. 16 Other Post-Neo- Darwinian Models

Evolutionary developmental biology (“evo-devo”) rejects the neo-Darwinian view that mutations are random and small-scale, and proposes regulatory mutations can radically reshape body plans. However, the effects cited by evo-devo advocates are small-scale, such as changes to coloration patterns on insect wings. Changes to regulatory *Hox* genes cannot generate new body parts, and are harmful. Proponents of neutral evolution diminish the importance of natural selection, and claim random mutations naturally accumulate to build new complex features. But this model provides no account of the cellular machinery needed for mutations to accumulate, and cannot explain why beneficial mutations should be retained. Neo-Lamarckism claims that heritable changes arise outside of genetic mutations, but the traits influenced by such mechanisms are limited and impermanent. Natural genetic engineering rejects the randomness of mutation for generating variation, and holds that organisms have a natural, preprogrammed capacity to “engineer” themselves. However, this model never accounts for those preprogrammed abilities. Like neo-Darwinism, post-Darwinian models fail to explain the origin of the biological information necessary to build animal body plans.

Ch. 17

The Possibility of Intelligent Design

Intelligent design is another post-Darwinian scientific model which holds that certain features of biology are best explained by the action of a conscious mind—an intelligent agent—as opposed to mindless, material processes like natural selection. ID does not reject “evolution” defined as “change over time” or universal common ancestry, but disputes the claim that life is the result of strictly blind and undirected processes. In claiming that life’s apparent design is *real* design, ID is not a religious theory, and has a longstanding tradition within biology. Design is inferred using the same abductive reasoning employed in other historical sciences, like geology or evolutionary biology, where one infers a prior cause by finding its known effects. If there are features of the Cambrian explosion which are known from experience to be produced by intelligence, and no other cause can explain those features, one may make an inference to the best explanation—intelligent design.

Session 8

Chapter 18: Signs of Design in the Cambrian Explosion; Chapter 19: The Rules of Science; Chapter 20: What's at Stake

Ch. 18 Signs of Design in the Cambrian Explosion

Evolutionary biologists recognize that whatever caused the Cambrian explosion was fundamentally different from evolutionary mechanisms we observe today. ID uses positive arguments, observing that intelligent agency is a cause now in operation that can generate functionally specified digital information, such as software code or written language. ID also uses negative arguments by observing that no known material causes can explain the Cambrian explosion. Neo-Darwinism predicts a bottom-up pattern of appearance, but ID explains the top-down trend in the fossil record where disparity (differences between higher-level taxonomic categories) precedes diversity (differences between lower-level taxonomic categories). Neo-Darwinism cannot explain why similar genes or parts exist in widely disparate organisms, but intelligent agents often reuse functional components in different designs. While neo-Darwinian mechanisms are blind and undirected, our uniform and repeated experience of cause and effect establishes ID as the only known cause capable of generating the complex integrated circuits and large amounts of functionally specified, and hierarchically organized digital (genetic) and structural (epigenetic) information, that rapidly appears in the Cambrian explosion.

Ch. 19 The Rules of Science

Critics often reject ID because they claim it is not science, but ID uses standard methods of historical sciences. ID is testable by comparing its explanatory power with that of competing theories. ID employs the principle of uniformitarianism—the idea that the present is the key to the past—and is based upon our knowledge of the cause and effect structure of the world. ID makes testable predictions that distinguish it from competing theories, such as the successful prediction, confirmed by the ENCODE project, that junk DNA is functional. We need not identify the precise mechanism or details of how a design was implemented to determine that a structure was designed. Philosophers of science lack a consensus definition of science, and generally reject demarcation criteria that distinguish exactly what is, and isn't science. No single demarcation criterion disqualifies ID from being science without also disqualifying other legitimate scientific theories. We should consider ID as science, and follow the evidence wherever it leads.

Ch. 20 What's at Stake

New atheists like Richard Dawkins claim neo-Darwinism shows there is no design in nature, and therefore no God exists. Theistic evolutionists like Francis Collins claim one can believe in God and Darwinism, but provide few details about how God influenced the evolutionary process, or how to reconcile tensions between Darwinian and Judeo-Christian accounts of origins. *Darwin's Doubt* challenges both atheistic and theistic evolutionists

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What's at Stake (continued)

by showing that the neo-Darwinian mechanism fails. Specifically, neo-Darwinism: (1) cannot efficiently search combinatorial sequence space to find rare functional protein sequences, and (2) requires unrealistically long waiting times to generate the information needed for new genes. Neo-Darwinian mechanisms cannot produce new body plans because: (3) early acting developmental mutations are always harmful, and (4) genetic mutations cannot generate the epigenetic information necessary to build an animal. Collins has sought to refute ID by citing the now-defunct concept of junk DNA. But why should we follow his attempt to reconcile traditional Christian theology with Darwinism when Darwinian biology is wrong? As a science, ID does not address religious questions about the identity of the designer, but it opens the possibility that life was purposefully designed by an intelligent person that many would identify as God.