

## **Bits and Particles: Information and Machines Sufficient to Infer an Intelligent Designer**

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### **Stories**

*We live in the Age of Science. Scientism is our world view, our mythic story about who we are, where we came from, and where we are going. As such, scientists are our preeminent storytellers, the myth-makers of our epoch.<sup>1</sup>—Michael Shermer*

It's the end of the story, and—after many adventures turning back stampeding cattle, fighting villains, and rescuing helpless children—our cowboy hero canters on his faithful horse toward a small log cabin. At the cabin door a raven-haired beauty watches his approach. A warm smile spreads across her face and green eyes sparkle in evening sunlight. Above the rider a light begins to glow, growing rapidly brighter until, in a blinding flash, a small meteor vaporizes horse and rider, leaving only a crater and a wisp of smoke near the cabin door.

Most people find the culmination of this story unsatisfying. They want the cowboy and beauty to ride off into the sunset and blissful domestic life together. Heroes should live long prosperous lives, but in reality that does not always happen. Real stories frequently end in tragedy. Sometimes villains end up with peaceful, affluent lives and real heroes are left, like Jeremiah, asking why the wicked prosper.<sup>2</sup> The stories we like reflect what we want, but reality is not always so kind. To a large degree science involves constructing stories about the way reality is. When doing this, it is always tempting to construct these stories in a way that reflects more our wishes about reality than the way things actually are.

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<sup>1</sup> M. Shermer, "Darwin's Duomo and Gould's Pinnacle." *E-skeptic* for April 14, 2002.

<sup>2</sup> Jeremiah 12:1

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Stories have tremendous power to explain reality and have been used for this purpose in all cultures and by proponents of all worldviews. The way reality is viewed can be subdivided into two major categories reflecting the worldviews from which they spring: views that exclude supernatural influence on the material world and views that welcome involvement of the supernatural. For convenience, belief that the material world is all that exists and natural laws account for all of reality may be called either materialism or naturalism, while belief that reality transcends nature may be called supernaturalism. In modern Western culture, the story of evolution is used as a way of explaining reality while excluding God from involvement in the material world. The word evolution is loaded with much baggage, so it requires careful definition. In this case, the story of evolution means that matter, associating together by chance and obeying natural laws, resulted in the universe and life; in short, all of reality. The explanatory power of this story is strongly promoted by a small intelligentsia and is not a new phenomenon. The Roman poet and popularizer of Epicurean philosophy Titus Lucretius Carus eloquently outlined this story of evolution c. 55 BC:

The atoms did not intend to intelligently place themselves in orderly arrangement, nor did they negotiate the motions they would have, but many atoms struck each other in numerous ways, carried along by their own momentum from infinitely long ago to the present. Moving and meeting in numerous ways, all combinations were tried which could be tried, and it was from this process over huge space and vast time that these combining and recombining atoms eventually produced great things, including the earth, sea, and sky, and the generation of living creatures.<sup>3</sup>

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<sup>3</sup> This is my own translation of the original Latin as printed in Titus Lucretius Carus, circa 55 B.C., *De Rerum Natura*, Book 5, lines 416-31. *Lucretius: On the Nature of Things*, trans. W. H. D. Rouse, rev. Martin F. Smith (Cambridge, MA: Harvard UP, 1992). The Latin text is reproduced below:

416 Sed quibus ille modis coniectus materiai  
417 fundarit terram et caelum pontique profunda,  
418 solis sunai cursus, ex ordine ponam.  
419 nam certe neque consilio primordia rerum  
420 ordine se suo quaeque sagaci mente locarunt  
421 nec quos quaeque darent motus pepigere profecto,  
422 sed quia multa modis multis primordial rerum  
423 ex infinito iam tempore percita plagis  
424 ponderibusque suis consuerunt concita ferri  
425 omnimodique coire atque omnia pertemptare,  
426 quacumque inter se possent congressa creare,  
427 propterea fit uti magnum volgata per aevom,  
428 omne genus coetus et mortus experiundo,  
429 tandem convenient ea quae convecta repente  
430 magnarum rerum fiut exordia saepe,

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To be sure that his readers understood that everything, including the living creatures, resulted from natural and not supernatural causes, Lucretius explicitly stated this several times in his epic philosophical poem *De Rerum Natura*: “Nature can be seen to be free of overlords. Everything she does is completely by herself, without help from gods.”<sup>4</sup>

In its modern iteration, both scientists and theologians have acknowledged the explanatory power of evolution. For example, in a recent open letter to British Prime Minister Tony Blair condemning questioning of evolution in schools, a group of church leaders and scientists wrote, “Evolution is a scientific theory of great explanatory power, able to account for a wide range of phenomena in a number of disciplines.”<sup>5</sup>

But the evolution story is not unique in its explanatory power. Bible-believing Christians also have a story with power to explain the origin of life. This story invokes a supernatural intelligent cause for the origin of life and interaction of the Creator God with nature and humanity throughout the course of earth history. The explanatory power of this story runs deep and broad, providing a framework for understanding the origin of life, nature, man’s current condition, and future salvation. This gospel story has become the single most widely held view of reality.<sup>6</sup> Some might attribute this to wishful thinking—after all, the creation/salvation story has a very happy ending for believers. But the saga

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431 terrain maris et caeli generisque animantium.

<sup>4</sup> My own translation from the same source as above. Book 2, lines 190-192:

190 Natura videtur

191 Libera continuo, dominis privata superbis,

192 ipsa sua per se sponte omnia dis agere espers.

<sup>5</sup> This open letter was dated March 22, 2002, and signed by the following Church leaders and scientists: The Rt Revd Richard Harries, Bishop of Oxford; Sir David Attenborough FRS; The Rt Revd Christopher Herbert, Bishop of St Albans; Lord May of Oxford, President of the Royal Society; Professor John Enderby FRS, Physical Secretary, Royal Society; The Rt Revd John Oliver, Bishop of Hereford; The Rt Revd Mark Santer, Bishop of Birmingham; Sir Neil Chalmers, Director, Natural History Museum; The Rt Revd Thomas Butler, Bishop of Southwark; Sir Martin Rees FRS, Astronomer Royal; The Rt Revd Kenneth Stevenson, Bishop of Portsmouth; Professor Patrick Bateson FRS, Biological Secretary, Royal Society; The Rt Revd Crispian Hollis, Roman Catholic Bishop of Portsmouth; Sir Richard Southwood FRS, Past Biological Secretary, Royal Society; Sir Francis Graham-Smith FRS, Past Physical Secretary, Royal Society; Professor Richard Dawkins FRS.

<sup>6</sup> According to Adherents.Com (<http://www.adherents.com/>), approximately 2 billion people are Christians, making up 33 % of humanity. When Christians are combined with Muslims (1.3 billion, 22 %), who share a similar view of life’s origin, this group constitutes a simple majority of people living today. Even compensating for liberal traditions that may not subscribe to specific scriptural claims, it seems reasonable to suggest that creation is still the single most widely held view. Other religions, e.g., the 14 million adherents of Judaism, also hold to the creation tradition. In contrast, approximately 840 million (14 %) non-religious individuals—agnostics, secular humanists, and atheists—are currently living.

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of human history from creation to fall to redemption is not simply another “just so” story,<sup>7</sup> but the product of God’s revelation to mankind.

Because both creation and evolution provide explanations of reality, both can be checked to one degree or another against nature. The scientific method has proven to be a powerful tool for studying nature, resulting in numerous benefits to humanity. Science has proven its practical worth and, as a consequence, is held in high regard. Unfortunately, the authority of science has occasionally been hijacked to promote one worldview over another. Science may serve as a check when evaluating the credibility of stories that make claims about reality, but when doing this, the tentative nature of good science can never be ignored. Scientists do not reason from authority, but rather from empirical investigation of nature. When what some scientists extrapolate from discoveries made using the scientific method is interpreted as authoritative, confused understandings of nature can result. For example, the Bishop of Oxford recently responded with the following to critics of a radio broadcast he made condemning schools that teach creation along with evolution as part of their science curriculum:

The evidence for evolution is in general so overwhelming, in all sorts of overlapping areas of science, that the literalist creationist is forced to postulate a God who deliberately faked it in order to deceive us (tempt us?) into thinking that evolution happened. To the true believer, isn't it an insult to God to suggest that He is a charlatan, a faker? And isn't literalist creationism therefore a form of blasphemy?<sup>8</sup>

Interestingly, these words are not actually the Bishop’s: Richard Dawkins, Britain’s leading atheist, penned them at the Bishop’s request. While the Bishop of Oxford is perhaps to be commended for recruiting Richard Dawkins to bravely defend God against charges of charlatanism, both are confused about the evidence science provides. The evidence for evolution is not overwhelming, and it is not blasphemy to acknowledge God as the Creator.<sup>9</sup>

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<sup>7</sup> Rudyard Kipling wrote a collection of stories for his daughter that was published in 1902 as a volume entitled *Just So Stories*. In this collection of fanciful tales he explains how the camel got his hump as a result of saying “Humph” when asked to work. Similarly fanciful tales describe how the leopard got its spots, the whale got its throat, and so on. While just so stories provide explanations of the origin of things in nature, they have no basis in historical reality.

<sup>8</sup> The quoted material was sent out under the imprimatur of the Rt. Rev. Richard Harries, Bishop of Oxford. In a private communication with the Bishop’s office, the following reference was given: Richard Dawkins (2002) Unpublished letter to the Bishop of Oxford.

<sup>9</sup> Blasphemy is the act of putting one’s self in the place of God or in some way showing contempt or irreverence to God or some sacred thing. It is hard to understand why Dawkins chose this word, other than for its pejorative power. Whether God is a charlatan or not, assigning his creative power to the material world that He created clearly can be rightly defined as a form of blasphemy.

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**Logic**

*"Facts are meaningless. You could use facts to prove anything that's even remotely true!"<sup>10</sup> –Homer Simpson*

The logical foundation of science cannot be overemphasized if scientific evidence is to be viewed appropriately. Two types of reasoning are utilized in the scientific method. The first is inductive reasoning, in which theories that make sense of the information at hand are logically inferred from data. The theories that data suggest to individual scientists may be strongly influenced by beliefs that lie well outside the realm of empirical science. In addition, data can be picked and chosen to support any theory. Due to these two factors, inductive reasoning alone can be very misleading. For example, the theory that all humans are male can be supported by a data set of close to three billion men, but this does not make the theory true.

Deductive reasoning involves drawing logical testable hypotheses from theories previously generated using inductive reasoning. Logically reasoning from the "all humans are men" theory, residents of the Sisters of Mercy Convent in Auburn, California, must all be men. This hypothesis can be tested by traveling to Auburn and checking to see if the Sisters of Mercy are actually men. Based on the empirical outcome of this test, the theory that all humans are men would be disproved and could be removed from the list of possible ideas about the nature of humanity.

A single exception to the predictions of a theory is generally not enough to invalidate it. In the words of Karl Popper:

We say that a theory is falsified only if we have accepted basic statements which contradict it. This condition is necessary but not sufficient; for we have seen that non-reproducible single occurrences are of no significance to science. Thus a few stray basic statements contradicting a theory will hardly induce us to reject it as falsified.<sup>11</sup>

The very fact that science, as defined by Popper, must be falsifiable emphasizes the tentative nature of this endeavor. But a single anomalous datum or a few deviations from the predictions of a theory are not enough to cause its rejection. Falsification of theories requires significant deviations from what the theory predicts. As a consequence of this, ideas in science tend to change either slowly or rapidly, but not at a steady rate. The evolving concept of normal human body temperature illustrates gradual changes in understanding. Physicians and mothers once universally believed that 37°C (98.6°F) was the normal healthy human body temperature. Careful measurement, though, has revealed

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<sup>10</sup> This quote appears in many places on the internet and in print. <http://www.gdargaud.net/Humor/QuotesScience.html>

<sup>11</sup> Popper KR. 1968. *The Logic of Scientific Discovery*. Harper and Row, New York, 87.

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that healthy humans vary in temperature depending on the time of day, gender, age, and where on the body temperature is measured.<sup>12</sup> 37°C represents neither a mean nor mode of body temperatures measured orally or anally in healthy humans. Thus the old idea of a single ideal temperature has been modified to recognize a range of normal temperatures.

It is only when a large data set contradicts a theory that it should rightly be rejected in a Kuhnian paradigm shift.<sup>13</sup> A recent example of this is early termination of the Heart and Estrogen/progestin Replacement Study (HERS).<sup>14</sup> Much evidence was necessary to convince authors of the study that Hormone Replacement Therapy (HRT) does more harm than good. The study was continued for almost 3 years after an initial analysis of data indicated that HRT does little to protect against coronary heart disease, one of the main reasons for postmenopausal women to take hormones. To reject the theory that replacing estrogens after menopause would improve the health of women, significant evidence was necessary, evidence both indicating the expected therapeutic benefit does not occur and evidence indicating increased risk of problems due to blood clotting and cancer. In short, significant evidence was necessary to overwhelm the wish that the HRT story would have a positive ending with happier, healthier aging women.

#### Necessary or Sufficient?

*He holds a plainly false opinion who says that it makes no difference to the truth of faith what someone's opinions about creation are so long as he holds the right opinion about God . . . because an error about creation flows back into a false opinion about God.*<sup>15</sup> –St. Thomas Aquinas

When Richard Dawkins, writing for the Bishop of Oxford, refers to “overwhelming” evidence, a naive reader could be excused for thinking that scientists have evidence sufficient to confirm the evolution story and falsify other potential causes for life. In reality, the “overwhelming” evidence for evolution can only overwhelm those who don’t understand that some evidence consistent with a theory does not prove that theory true. For example, apparent close similarities

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<sup>12</sup> Mackowiak PA, Wasserman SS, Levine MM. 1992. A critical appraisal of 98.6°F, the upper limit of the normal body temperature, and other legacies of Carl Reinhold August Wunderlich. *Journal of the American Medical Association* 268(12):1578-1580. And Hirschmann JV. 1992. Normal Body Temperature. *Journal of the American Medical Association* 267(3):414.

<sup>13</sup> Thomas Kuhn suggested that changes in scientific thought occur suddenly when the current paradigm collapses under the weight of contrary evidence and is replaced by a new paradigm. He outlined this idea in: Kuhn TS. 1996. *The Structure of Scientific Revolutions* 3rd edition University of Chicago Press, Chicago.

<sup>14</sup> Petitti DB. 2002 Hormone replacement therapy for prevention: more evidence, more pessimism. *Journal of the American Medical Association* 288(1):99-101.

<sup>15</sup> St. Thomas Aquinas, *Summa Contra Gentiles*, 2.3

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between ape and human DNA is evidence consistent with the theory that humans and apes share a common ancestor. This evidence and other similarities between apes and humans at best adds to the data set from which one can inductively reason to common ancestry, but it is not sufficient to prove common ancestry true, just as collecting billions of men is not sufficient evidence to prove all humans are men. Similarities between organisms are, in the parlance of philosophers, necessary causes when reasoning to common ancestry, but not sufficient causes for one to conclude that common ancestry is true. In other words, similarities must be present if the theory of evolution from common ancestors is to be true, but they are not sufficient to prove it.

The logical difference between sufficient and necessary causes can be illustrated by imagining a hypothetical charge of plagiarism brought by novelist Tom Clancy against the estate of Mark Twain. The central complaint in the suit is that Twain stole Clancy's *The Hunt for Red October* and used it for his novel *A Connecticut Yankee in King Arthur's Court*. The "overwhelming" evidence that Twain used Clancy's material could include the fact that almost all the words used in Twain's book are identical to those used in Clancy's. Literally hundreds of words are identical. It would not be surprising if several sentences were essentially identical. The problem is that while using the same words is *necessarily* true if Twain stole Clancy's work, *sufficient* evidence exists to exonerate Twain; he died before Clancy was born.

The story of creation and salvation outlined in Scripture is, like the evolution story, ancient and unprovable using the scientific method. Huge data sets can be collected as evidence consistent with either account, much of it necessarily true if the stories truly reflect reality, but ultimately marshalling data is insufficient to definitively show one or the other to be true. However, evidence may be sought that is not consistent with one of the theories. In other words, it should be possible to use deductive reasoning to eliminate the possibility of either creationism or evolutionism. In fact, proponents of both naturalism and supernaturalism have attempted this. Quoting again from Lucretius:

The nature of the universe confirms it cannot have been created for us  
by divine power: it has so many faults.<sup>16</sup>

This argument from imperfection has been recycled in many different forms. For example, Stephen J. Gould wrote an entire book, *The Panda's Thumb*, in which he claimed, "Imperfection carries the day for evolution."<sup>17</sup> The problem is that this argument is simply a debating tactic in which definitions are contorted to ensure the victory of one point of view. In this particular iteration, a

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<sup>16</sup> Lucretius, book 2, lines 180, 181: Nequaquam nobis divinitus esse creatam naturam mundi: tanta stat praedita culpa.

<sup>17</sup> Gould SJ. 1980 *The Panda's Thumb: More Reflections on Natural History*. W. W. Norton, New York. p 37.

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very specific view of the Creator is required in which He may do nothing that in the writer's opinion is not optimal. In addition, the assumption is made that we are in a good position to make adequate judgments about what is perfectly designed and what is not. The history of science lays out a long series of "imperfections" that upon closer examination turned out to be brilliantly functional. Scientists declared them useless before exerting the effort to understand them. Vestigial organs, once thought to be remnants of organs useful in the evolutionary past, but not the present, have now been thoroughly discredited as evidence of evolution. As Scadding noted, "Since it is not possible to unambiguously identify useless structures, and since the structure of the argument used is not scientifically valid, I conclude that 'vestigial organs' provide no special evidence for the theory of evolution."<sup>18</sup> More recently, "junk DNA" has been presented and discredited as molecular evidence of evolution.<sup>19</sup> Declaring parts of organisms to be functionless and thus vestiges of the evolutionary past amounts to no more than an argument from ignorance in which ignorance of function is used as evidence of lack of function. This is true whether the old argument about vestigial organs is used or the more recent molecular argument about "junk DNA."

In general, arguments about what data support evolution versus what data are more consistent with creation do not change in any profound way when transitioning from the macroscopic to molecular levels. What does change is that appeals to unknown or complex ill-defined processes are harder to make at the molecular level. This is because laws governing behavior of molecules and atoms from which they are composed are well understood. Understanding the chemical workings of cells precludes them from being treated as "black boxes," as Michael Behe calls them,<sup>20</sup> in which unknown processes somehow produce known outcomes by unknown means. Unaware of the complex machinery inside cells, Darwin's contemporary and enthusiastic supporter Ernst Haeckel wrote:

The Monera [bacteria] . . . which consist only of this primitive protoplasm, and which arise by spontaneous generation from these inorganic nitrocarbonates, may thus have entered upon the same course of evolution on many other planets . . .

We now know that the "inorganic nitrocarbonates" within cells are not accurately described in the term "primitive protoplasm." There is no substance in cells or outside of cells that spontaneously comes together to make bacteria and then all the other life forms we know today. We understand to a greater degree

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<sup>18</sup> Scadding SR. 1981. Do "Vestigial Organs" Provide Evidence for Evolution? *Evolutionary Theory*, 5:173-176.

<sup>19</sup> For a review of the way "junk DNA" has been used as evidence of evolution, see: Standish, TG. 2002. Rushing to Judgment: Functionality in non-coding or "junk" DNA. *Origins* 53:7-30.

<sup>20</sup> Behe, MJ. *Darwin's Black Box: The Biochemical Challenge to Evolution*. Free Press, New York.

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with each passing day what the molecular machinery within cells is and what it does. The more cells, the fundamental building blocks of all life, are studied, the more complex and elegant they appear to be. No wonder Nobel laureate and dedicated materialist Francis Crick once wrote, "Biologists must constantly keep in mind that what they see was not designed, but rather evolved."<sup>21</sup>

**Inferring an Intelligent Cause**

*I said I thought it no more likely that I should be right in nearly all points, than that I should toss up a penny and get heads twenty times running.*<sup>22</sup> –Charles Darwin

Within cells two lines of evidence strongly point to origin through the creative act of an intelligent being rather than chance coupled with the forces of nature. The first is the information content of cells; the second is the way molecular machines which do the cell's work are constructed. Even the simplest cells contain incredible amounts of meaningfully functional information. Certain molecules in cells, specifically the nucleic acids, function as libraries of information. Complex mechanisms exist to retrieve that information and translate the DNA "blue print" into protein machines. William Dembski has written extensively about the nature of information, particularly biological information, and how intelligence can be rigorously inferred when information is present.<sup>23</sup> This is not a difficult inference to understand: information is a product of intelligence, and thus intelligence can be inferred from the presence of information.

The metaphors of a code, cipher, or written language may not be perfect when referring to information stored in DNA, but they provide a logical inference to the intelligent cause behind the information DNA encodes and the mechanism through which it is stored. The chemical nucleotide "letters" of the genetic code are specifically arranged in DNA sequences to store information defining the primary structure, the amino acid sequence, of proteins. Other information is also stored by specific sequential arrangement of nucleotides. This information includes where and when specific proteins should be produced. Just as printed words have no intrinsic meaning in the absence of an intelligent mind,

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<sup>21</sup> Crick FHC. 1988. *What Mad Pursuit: A Personal View of Scientific Discovery*. Penguin, London: p 138.

<sup>22</sup> Darwin, CR. Letter to Charles Lyell December 12, 1859 in Darwin F. ed. 1959. *The Life and Letters of Charles Darwin: Including an Autobiographical Chapter* Vol. II. Basic Books, New York. p36.

<sup>23</sup> For examples of Dembski's writings on information and the design inference, see: Dembski, WA. 1999. *Intelligent Design: The Bridge Between Science and Theology*. Intervarsity Press, Downers Grove, Illinois; Dembski, WA. 1998. *The Design Inference: Eliminating Chance Through Small Probabilities (Cambridge Studies in Probability, Induction and Decision Theory)*. Cambridge University Press, New York; Dembski, WA. 2001. *Signs of Intelligence: Understanding Intelligent Design*. Brazos Press, Grand Rapids, Michigan; Dembski, WA. 2001. *No Free Lunch: Why Specified Complexity Cannot Be Purchased Without Intelligence*. Rowman & Littlefield, Lanham, Maryland.

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information in DNA has no meaning if it does not interact with numerous protein and RNA molecules.

As is the case with letters of the alphabet, there are no known natural laws that produce specific nucleotide sequences defining useful proteins. In the absence of already existing information-rich sequences, newly formed DNA is gibberish with no functional information value. An intelligent designer may order nucleotides as meaningful sequences, just as an intelligent writer may arrange letters to have meaning, but natural laws or chance will not produce meaningful sequences. To be fair to evolutionary theory, it is important to emphasize that it does not claim natural laws or chance sequence arrangements alone account for information stored in DNA. Current evolutionary theory claims that the law-like behavior of natural selection, selecting sequences most efficiently passed on to the next generation, coupled with chance mutations in DNA sequences producing variability in organisms, is a two-part mechanism which produced life as we know it. The catch is that to be selected, a sequence must first have meaning. In the absence of a natural law that generates information in DNA sequences, the question then becomes: What are the odds that chance alone can produce meaningful sequences upon which natural selection can act?

Aside from DNA, cells may also contain information in the way chemicals are spatially distributed within them. For example, the endoplasmic reticulum is an organelle that is active in production of new membrane. To achieve this function it must contain specific proteins on its surface that signal for production and transport across the membrane of proteins which will become part of the growing membrane or will be contained in membrane bound vesicles which bud off the endoplasmic reticulum and travel to other parts of the cell. Clearly, those proteins that function in moving new proteins into or across the membrane are also proteins that themselves must be produced and inserted into the membrane before more membrane can be made. Thus, these proteins present a hen-and-egg type situation: Proteins in the membrane that allow proteins to be inserted into the membrane must be present before new membrane containing these proteins can be made. Thus, fully formed membrane must be present before fully formed membrane can be made. As a consequence of this, functional membranes must be passed on to offspring just as a complete set of genetic information in the form of DNA must be passed on. DNA alone cannot mediate the *de novo* construction of new endoplasmic reticulum membrane. Additional examples of information other than that coded in DNA may also exist in cells.

#### **Endothelin-1: An Information-rich Example**

*The irony of the whole wretched thing is this: In the SETI quest we are looking for evidence of something that is artificial - a signal. Yet when we look at the natural world, we won't accept that the engi-*

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*neering that's there, and the information that's there in the universe,  
is artificial.*<sup>24</sup>—Frank Stootman, Director of SETI Australia

The presence of information in cells along with machine-like protein complexes can best be understood when looking at specific examples, of which there are many. One relatively simple example is the coding and production of the endothelins. These small proteins are potent vasoconstrictors and have also been shown to play several other important physiological roles.<sup>25</sup> At the molecular level, endothelin proteins function by binding very specifically to receptors located on the surface of cells. When endothelin binds in a lock-and-key-like manner with its receptor, the receptor changes shape. This change in receptor shape signals “G” proteins within cells, and these proteins then transmit the signal on to other proteins in a cascade of events, which ultimately causes contraction of smooth muscle cells within blood vessels. Without receptors and the rest of the proteins involved in transmitting the signal inside cells, endothelins would have no impact. Clearly the receptors recognize endothelins with great precision, as vasoconstriction in response to other molecules would very likely be disastrous.

Information coding for construction of endothelin proteins is contained in DNA genes. The gene for human preproendothelin-1 (preproET-1) is found on the short arm of chromosome 6.<sup>26</sup> It is the protein product of this gene, diagrammed in Figure 1, from which endothelin-1 will be made (several other endothelins are coded for elsewhere). The final product of the endothelin-1 gene is only 21 amino acids long. Coded for in DNA, these 21 amino acids represent only 63 nucleotides, which in terms of functional information content can be represented as 17 bits.<sup>27</sup> This does not seem like a large amount of information, and may well be a conservative estimate,<sup>28</sup> but it serves the purpose of allowing comparison with the information content of larger stretches of DNA.

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<sup>24</sup> Frank Stootman, Director of SETI Australia quoted in: Linnell G. 1999. Heaven Only Knows. *The Bulletin* 117(6181):34.

<sup>25</sup> The following is an excellent review of the biology and clinical importance of endothelins: Hunley TE, Kon V. 2001. Update on endothelins-biology and clinical implications. *Pediatric Nephrology* 16:752-762.

<sup>26</sup> GenBank accession number J05008. Inoue A, Yanagisawa M, Takuwa Y, Mitsui Y, Kobayashi M, Masaki T. 1989. The human preproendothelin-1 gene: Complete nucleotide sequence and regulation of expression. *The Journal of Biological Chemistry* 264(25):14954-14959.

<sup>27</sup> The term “bits” used here has the same meaning as the bits of information processed by computers. Eight bits are equivalent to one byte.

<sup>28</sup> Shannon (Shannon CE. 1948. A mathematical theory of communication. *Bell System Technical Journal*, vol. 27, pp. 379-423 and 623-656) proposed information (H) in bits per symbol is described by  $H = -\sum p_i \log_2 p_i$ , where  $p_i$  is the probability of the  $i$ th configuration and K is an arbitrary constant. If we assume the probability of each symbol is approximately equal, and if we set  $K = 1$ , then H simplifies to  $\log_2 N$ . Solving this equation for H yields theoretical maximal information content for a sequence with possible combinations N. But nucleic acid sequences representing amino acid sequences in proteins represent a special problem because information contained in a sequence

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Information is intuitively associated with intelligence and is not known to be the product of natural laws. For example, natural processes in space produce a wide range of radio waves that can be detected using radio telescopes. The Search for Extra Terrestrial Intelligence (SETI)<sup>29</sup> scans these radio waves from outer space looking for information carrying signals. If information were found in these radio signals, it would serve as *prima facie* evidence of an intelligent cause: Intelligent space aliens sending information-rich radio signals.

Sometimes information is confused with highly ordered phenomena. Natural laws readily produce simple repeating patterns like those found in crystals, but crystals are not good repositories of information, as the same pattern of atoms repeated over and over again has very little capacity to store information. The kind of information stored in DNA coding for endothelin-1 is very ordered, yet also complex, not simply the same short sequence repeated many times. But, as already mentioned, the information contained in the endothelin-1 protein is small, only 17 bits. If DNA of random sequence was produced and then scanned for a sequence coding for this protein, it would be expected to occur  $1/2^{1730}$  or 0.0008 % of the time. That is a small number, but not so impossibly small that it could not have happened by chance. In the 3 billion base human genome, assuming a random sequence of nucleotides, sequences for functional endothelin-1 would be expected to appear 22,888 times. To give the appearance of design, the endothelin-1 gene would have to contain significantly more information than just that coding for the 21 amino acid mature protein, and this is the case.

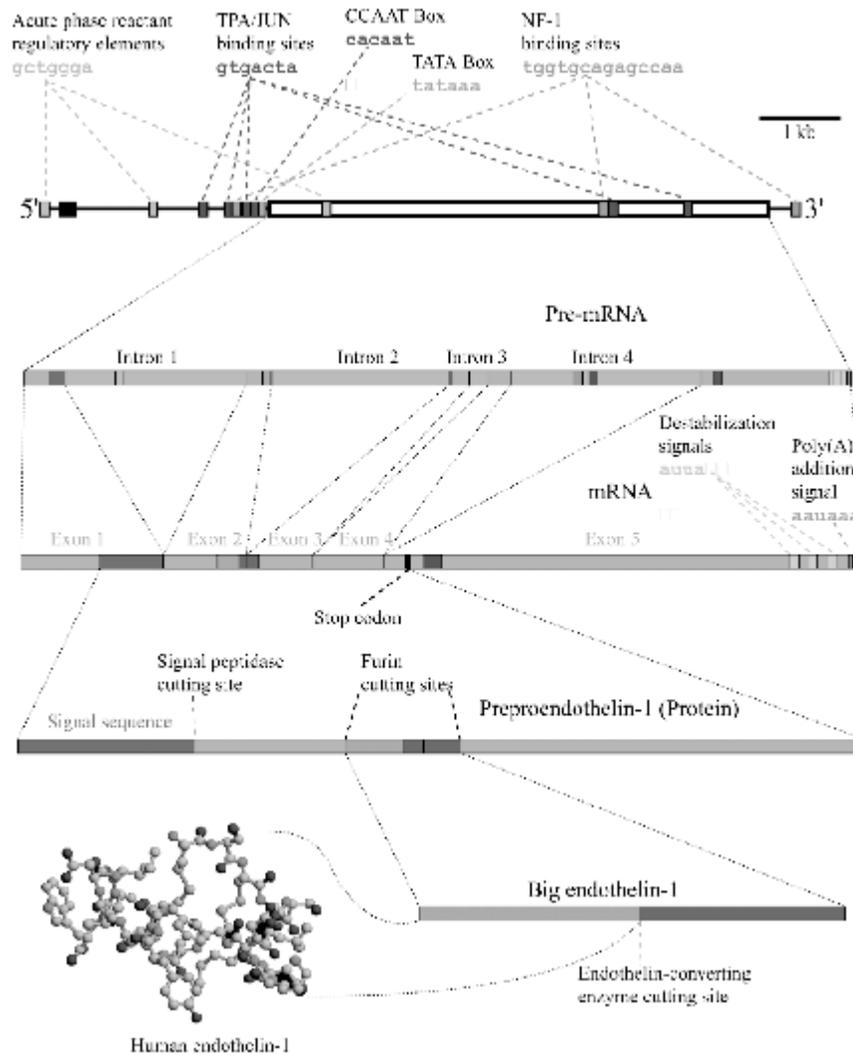
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must fall within a functional range. Functionality of proteins is determined in a large degree by the amino acid sequence; not all sequences are equally “meaningful” for a given function. Durston (personal communication, 2002) has symbolized this functional information as  $I_f = H - H_f$ . Inserting values for  $H$ ,  $I_f = \log_2 N - \log_2 N_f$  which simplifies to  $I_f = -\log_2(N_f/N)$ . Accurate determination of the range within which a protein remains functional,  $N_f$ , is almost impossible without checking each of the possible sequence combinations. The rough and very conservative estimate given here is based on Taylor et al. (Taylor SV, Walter KU, Kast P, Hilvert D. 2001. Searching sequence space for protein catalysts. Proc. Natl. Acad. Sci. USA. 98 (19):10596–10601), in which it was demonstrated that generation of a moderately active 95 amino acid enzyme would require a library of  $5 \times 10^{23}$  members, thus  $N_f/N = 2 \times 10^{-24}$ , so  $I_f = 79$  bits for this protein, or 79 bits/[3 nucleotides/amino acid]x95 amino acids]=0.28 bits per nucleotide. Assuming this to be a reasonable estimate for all proteins (acknowledging the scarcity of relevant empirical data at present), the information content of the 21 amino acid (63 nucleotide) endothelin-1 is 63 nucleotides x 0.28 bits/nucleotide=17.64 bits. Seventeen bits was used in this discussion to be as conservative as possible.

<sup>29</sup> <http://www.seti-inst.edu/>

<sup>30</sup> A bit represents a binary state of either 1 or 0; thus, as there are two states, the probability of a specific number of bits of information is equal to the inverse of 2 raised to the number of bits.

**Figure 1**  
The Human Endothelin-1 Gene



The human endothelin-1 gene is located on the short arm of chromosome 6 and covers approximately 8,000 nucleotides. The top of this figure shows the whole gene, while lower layers deal with specific sections involved with the expression of the gene, each of which is progressively smaller, until the molecular structure of the 21 amino acid endothelin-1 final product is shown in the lower left-hand corner.

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**Information Controlling Gene Expression**

*To the powerful theories of chemistry and physics must be added a late arrival: a theory of information. Nature must be interpreted as matter, energy, and information.*<sup>31</sup> –Jeremy Campbell

As a potent vasoconstrictor, endothelin-1 is both a very useful protein and at the same time an extremely dangerous one. Without appropriate vasoconstriction, blood would not be distributed appropriately, and thus death or severe impairment would result. Excessive vasoconstriction would have a similar effect. Thus much of the information contained in the endothelin-1 gene is there not only for dictating the primary amino acid sequence of the protein, but also for the purpose of controlling expression and activity of the gene product. Step one in controlling gene expression is at the point of transcribing the gene as an RNA copy of the DNA master. This control is achieved by a complex system of proteins that interact with signals encoded in DNA. These signals are not yet fully understood, but some of them are indicated at the top of Figure 1. Acute phase reactant regulatory elements with the nucleotide sequence CTGGGA<sup>32</sup> signal that the endothelin-1 gene should be transcribed during acute physical stress. Other sequences that are known to interact with proteins regulating transcription are the TPA/JUN and NF-1 binding sites. More as yet uncharacterized signals encoded both within and outside the transcribed part of the gene are likely to be present, as levels of the RNA transcript of this gene are known to be regulated by thrombin, angiotensin II, vasopressin, transforming growth factor- $\beta$ ,  $\text{Ca}^{2+}$  ionophores, and hemodynamical shear stress.<sup>33</sup> Thus it is evident that information independent of the actual amino acid sequence of the protein is coded in the DNA.

Another form of information is represented by two sequences that lie just upstream of the transcription start site. These sequences, CACAAT and TA-TAAA, provide very specific information to the RNA polymerase II complex that copies the DNA as an RNA transcript. The first sequence, CACAAT, starting 97 nucleotides prior to the start of the RNA transcript, plays a major role in determining how swiftly RNA copies of the gene will be produced. The TATAA

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<sup>31</sup> Campbell J. 1982. *Grammatical Man: Information, Entropy, Language and Life*. Penguin Books: Harmondsworth, Middlesex UK, 1984, reprint, p.16

<sup>32</sup> Four different nucleotides are used to code information in DNA, much as 26 letters are used to code information in written English. The only difference between the four different nucleotides is a nitrogen-containing base that is part of each one. The four bases are adenine, cytosine, guanine and thymine, each of which is commonly symbolized using the first letter of its name. Thus, sequences of nucleotides are represented using the letters A, C, G, and T. The sequence CTGGGA symbolizes a sequence of nucleotides with bases cytosine, thymine, guanine, guanine, guanine and adenine in that order.

<sup>33</sup>Inoue A, Yanagisawa M, Takuwa Y, Mitsui Y, Kobayashi M, and Masaki T. 1989. The human preproendothelin-1 gene: Complete nucleotide sequence and regulation of expression. *Journal of Biological Chemistry* 264(25):14954-14959.

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sequence starting 30 nucleotides upstream from the transcription start site gives very precise information about where to start transcribing the DNA.<sup>34</sup>

**Information About Processing mRNA**

*I can hardly imagine to myself a more distinguishing mark, and, consequently, a more certain proof of design, than preparation, i.e. the providing of things beforehand, which are not to be used until a considerable time afterwards, for this implies a contemplation of the future, which belongs only to intelligence. –William Paley*

The RNA transcript includes some of the sequences mentioned earlier that are known to play a role in determining when to turn on transcription of the endothelin-1 gene, but also contains additional information. One important set of information delineates junctions between exons and introns. Exons contain sequence information that determines the protein sequence, while introns fall between exons and must be removed before the information encoded in nucleotide bases can be translated into protein. Thus, if functional proteins are to be made, accurate delineation is necessary of introns to be cut out and exons to be spliced together. Aside from cutting signals at each end, introns contain additional sequences clearly marking them as introns.

At the 3' end (the right-hand end in Figure 1) of the RNA transcript is a sequence signaling for addition of adenine nucleotides. Once these nucleotides are added, introns are removed, and a cap is placed on the 5' end of the RNA transcript, it is officially known as mRNA. Now it is ready for export from the nucleus to the cytoplasm where the protein, based on information encoded in the mRNA, will be produced. To arrive at this point, many different kinds of information were required: Information about when to produce the RNA, how many copies to make, where to start (and stop) making it, what parts to remove or retain, and where to add adenosine nucleotides.

Another interesting set of signals lies at the 3' end of endothelin-1 mRNA. Three AUUA destabilization signals in this region, each approximately 9 bases apart, signal for destruction of the mRNA following translation. These signals turn the mRNA into something like the self-destructing messages sent to spies in movies and television shows produced during the 1960s. Once the message is read, it is destroyed so that it can't be read again. This is a vital feature of the endothelin-1 mRNA that allows very tight control of endothelin-1 production. Stray copies of mRNA do not linger around to be translated in an uncontrolled manner.

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<sup>34</sup> Lewin B. 1997. *Genes VI*. Oxford University Press, New York.

## STANDISH: BITS AND PARTICLES

### Information Encoding the Protein

*... the natural selection of a meaningful minority of changes in DNA generates spectacularly complex structures, which seem in retrospect—but only in retrospect—to be the result of an intelligent plan.<sup>35</sup>*  
—Robert Pollack

The protein encoded on endothelin-1 mRNA is not just the 21 amino acid mature product. Endothelin-1 starts out as a 212 amino acid protein called preproendothelin-1. Assuming that each amino acid on average represents the same amount of information as those in the mature endothelin-1 protein, the part of endothelin-1 mRNA encoding the protein represents 178 bits. This much information is readily produced as a result of intelligent causes, but is not known to result from physical or chemical laws. Repeating the logic used to argue that the 21 amino acid mature endothelin-1 protein is not necessarily remarkable and may be produced by chance, the probability of stringing together the nucleotides to code for a functional preproendothelin-1 is  $2.6 \times 10^{-54}$ .<sup>36</sup> This is a very small number and would not be expected to happen as a result of chance processes. A sequence coding for a functional preproendothelin-1 would be expected to occur once in a random string of  $3.8 \times 10^{53}$  nucleotides.<sup>37</sup> This random string would have a mass close to that of the sun<sup>38</sup> and would stretch an unimaginable one hundred thousand trillion trillion light years in length.<sup>39</sup>

It is important to remember that any randomly generated string of nucleic acids long enough to code for 212 amino acid preproendothelin-1 has the theoretical capacity to store more information than is present in the actual 636 nucleotides that encode it. But this is information defined in a very generic way. The kind of information that is stored in the endothelin-1 gene, functional information, constitutes only a very small part of the possible generic information that could be stored. Imagine a situation where the fabled Swiss archer William Tell is going to shoot an arrow through an apple balanced on the head of his son. Most people would be impressed by his skill if he were able to hit the apple from 50 paces away. This would be an even more impressive feat if it could be repeated several or many times. Now imagine the outcome if Mrs. Tell was provided with the bow, blindfolded, and then asked to shoot the apple. Anyone within range of the arrow would be well advised to take cover. Any spot that

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<sup>35</sup> Pollack R. 1995. *Signs Of Life: The Language And Meanings Of DNA*. Mariner Books, Boston p. 38.

<sup>36</sup>  $1/2^{178}$

<sup>37</sup> The probability of stringing together the nucleotides to code for a functional preproendothelin-1 =  $2.6 \times 10^{-54}$ , divided into one.

<sup>38</sup> The average molecular weight of a nucleotide is approximately 337g/mol, thus:  $(3.8 \times 10^{53} \text{ nucleotides}) \times (337 \text{ g/mol}) \times (1 \text{ mol} / 6.02 \times 10^{23} \text{ nucleotides}) \times (1 \text{ kg} / 1,000 \text{ g}) = 2.1 \times 10^{29}$  which is on the order of  $1.99 \times 10^{30}$ , the mass of the sun.

<sup>39</sup>  $(3.8 \times 10^{53} \text{ nucleotides}) \times (0.338 \text{ nm/nucleotide}) \times (10^{-9} \text{ m/nm}) \times (1.06 \times 10^{16} \text{ light years/m}) = 1.36 \times 10^{28}$  light years.

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Mrs. Tell's arrow hits is just as improbable as the apple, but skill is evident, intelligent handling of the bow and arrow, only when the apple is hit, not when it misses and hits something else. The incredible thing about information stored in DNA is not that there is potential for great quantities of information to be stored, but that the information is functional; it has meaning in terms of real proteins that make living things function to useful ends.

When we see William Tell hit the apple every time, we are impressed that a master is at the bow. When we see that the "apple" is hit every time in terms of information stored in DNA, we can be equally impressed that a Master played a hand in its production. This is particularly so when we consider the child on whose head the apple rests. If William Tell could only get the arrow within a meter of the apple, an impressive feat at 50 paces, observers would most likely sign with relief if the arrow went high, but be horrified should the arrow hit below the apple. Biological information must frequently be extremely accurate, as even slight deviations can result in dire consequences. In other words, having William Tell supplying the blindfolded Mrs. Tell with arrows and hints—something like the children's game of hot and cold—as she shot arrows closer to or further away from the apple would do little to avert disaster. In fact, it would be much better to have Mrs. Tell shooting arrows randomly than close to the apple. As previously mentioned, to be selected, a sequence must be functional, but the case of endothelin-1 illustrates why all the control information must be in place before the protein can be functional. Near misses, the protein produced in an uncontrolled manner, stand a high chance of being detrimental and thus being selected against. In the case of at least some proteins, selection may very well be against near misses.

The best alternative to design as the cause of functional information in the endothelin-1 gene is mutation, generating variation in DNA sequences, coupled with natural selection. The problem with invoking mutation and natural selection is that nature has not been shown to skillfully generate functional information, particularly when that information is tightly constrained. The kind of functional information commonly found in DNA is an example of what Dembski has called specified complexity.<sup>40</sup> Dembski has proposed an explanatory filter (Figure 2) outlining how this type of complexity is recognized and the inference from it to design. One might infer an intelligent cause behind the production of radio waves encoding information (as SETI hopes to do), or hieroglyphics on an obelisk in the Egyptian desert. The author of information may not be known, and the exact meaning of the information may not be known, but the presence of information is a reliable indicator of an intelligent cause.

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<sup>40</sup> For a brief discussion of specified complexity, see: Dembski WA. 1998. Redefining science. p 93-112 in *Mere Creation*. WA Dembski ed. InterVarsity Press, Downers Grove, Illinois.

## STANDISH: BITS AND PARTICLES

### The Genetic Code

*Our conclusion is based on two facts that we would think would be entirely uncontroversial: language shows signs of complex design for the communication of propositional structures, and the only explanation for the origin of organs with complex design is the process of natural selection.<sup>41</sup> –Steven Pinker and Paul Bloom*

The molecular machines from which cells are made represent another kind of meaningfully specified complexity. An example of this kind of machine can be illustrated by following production of endothelin-1 beyond export of mRNA from the nucleus. After transcription from the DNA gene and processing to remove introns, the endothelin-1 mRNA travels out of the nucleus to the cytoplasm. Here the small subunit of protein factories called ribosomes recognize the 5' end of the mRNA and slide along the mRNA until they encounter a start codon. This codon, which always codes for the amino acid methionine, can be thought of as the capitalized word at the beginning of a sentence. Codons are groups of three nucleotides strung together in sequence on mRNA, each of which represents a specific amino acid. The job of ribosomes is to translate the meaning of each codon to that of the amino acid it codes for. As already mentioned, the first codon in any gene is one that codes for methionine. In human preproendothelin-1 the next codon, GAU,<sup>42</sup> codes for aspartic acid, then UAU for tyrosine, and so on for another 209 codons (627 nucleotides), representing a specific sequence of 209 amino acids. The codon following the last one coding for an amino acid is a stop codon, UGA. This codon acts like the period at the end of a sentence, telling ribosomes that they have reached the end of the part of an mRNA that codes for the protein.

The genetic code is another example of apparent design at the molecular level. Because of the way amino acid meanings are assigned to codons in the genetic code, the impact of mutations is minimized. A specific example involves the impact of changes to the middle base of the three-base codon. If the mutation is of the most common type, called a transition,<sup>43</sup> slightly over half the time the chemical class of the amino acid specified in the new codon will be in the same chemical class as the one coded for by the original codon prior to mutation. Thus, slight changes in the DNA sequence coding for a gene are less likely to have a deleterious impact on the gene's meaning than they would if codons had

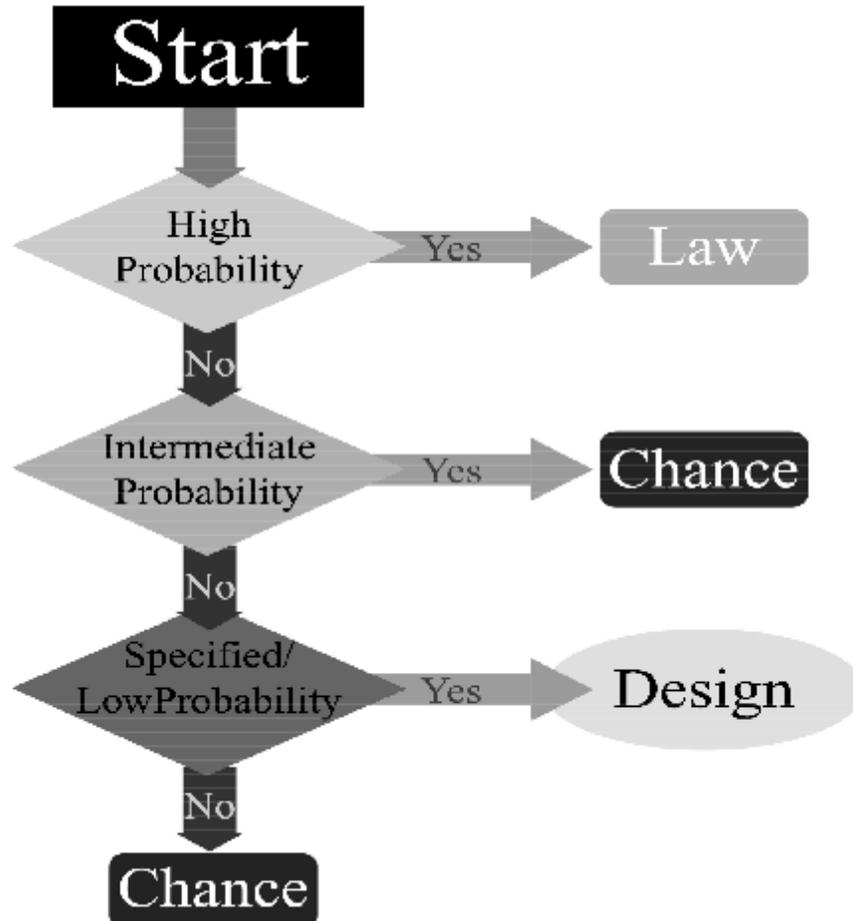
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<sup>41</sup> Pinker S, Bloom P. 1990. Natural language and natural selection. *Behavioral and Brain Sciences* 13 (4): 707-784.

<sup>42</sup> In the nucleotides used to make RNA, a very slightly different base called uracil is used instead of the thymine used in DNA. Thus, wherever the symbol T would be used to represent thymine in DNA, U is substituted in RNA.

<sup>43</sup> Transitions involve changing from one purine to another, for example, from an adenine to a guanine, or a pyrimidine to another pyrimidine. Transversions, for example, from pyrimidine to purine, or vice versa, are generally more serious, but are also more easily detected and repaired; thus they are less commonly observed.

Figure 2  
William Dembski's Explanatory Filter



Dembski's filter provides an algorithm for determining whether design can be inferred from an object or event. The three nodes proceeding from top to bottom represent questions to be addressed with yes or no answers. Events or objects that are highly probable, like stones falling to the ground when dropped or salt forming crystals, can be attributed to physical laws. Events equivalent to flipping a coin and getting heads 5 or ten times in a row are improbable, but not so improbable that chance can be ruled out as the cause. Highly improbable events or objects that also represent specified outcomes, for example, William Tell hitting the apple as opposed to his son, suggest design. Low probability alone is not sufficient to infer design; specification is also necessary.<sup>44</sup>

<sup>44</sup> Dembski, WA. 1998. "Redesigning Science" pp 93-112 in *Mere Creation: Science, Faith and Intelligent Design*. InterVarsity Press, Downers Grove, IL p 99.

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been assigned meanings randomly.<sup>45</sup> This is only one of several possible examples of the brilliant matching of codons with amino acid meanings in which nature “hits the apple.” Four theories may explain why the genetic code is so good: 1) luck, 2) coevolution, in which the genetic code evolved as new metabolic pathways for amino acid synthesis evolved, 3) the code started sub-optimally and evolved to its current optimum, and 4) the code was created by a very intelligent designer.

Luck in getting the optimal genetic code now used in cells would be something like the blindfolded Mrs. Tell shooting an arrow from the other side of the universe and hitting the apple on her son’s head.<sup>46</sup> Coevolution is a complicated and vague idea that has been discredited.<sup>47</sup> This leaves two theories for serious consideration: 1) Evolution from sub-optimal to the current very good code and 2) brilliant design of the genetic code when life was created.

The impossibility of evolving from one genetic code to another is illustrated by a conversation between Alice and Humpty Dumpty in British mathematician and novelist Lewis Carol’s book *Through the Looking Glass*. Alice can’t understand what Humpty Dumpty is saying. The root of her confusion is summed up in the following: “‘When I use a word,’ Humpty Dumpty said in rather a scornful tone, ‘it means just what I choose it to mean—neither more nor less.’” For information to be communicated, both the sender and recipient must agree on the meaning of the symbols used, be they sounds, words, radio waves, or any other medium. If the sender of a signal suddenly decides to change the meaning of the signal without informing the recipient, either the wrong signal will be received, or no signal will be received. The ribosome and the molecules that work with it to translate RNA codons, the genetic signal, into proteins constitute a breathtaking information processing system, but if it or its helper molecules somehow changes the meaning of one codon to another, the genetic signal will be garbled. Instead of the proteins specified in DNA genes, far less functional, in

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<sup>45</sup> During the Nature of Nature conference held at Baylor University during 2000, eminent evolutionist Simon Conway-Morris summed up the genetic code in the following words: “The genetic code is not very good.” And then, following a long pause for effect, “It is absolutely fantastic.” He was specifically referring to the work of Freeland and Hurst, who demonstrated the incredible optimization of the genetic code. Freeland SJ, Knight RD, Landweber LF, Hurst LD. 2000. Early fixation of an optimal genetic code. *Molecular Biology and Evolution* 17(4):511-8. Also, Freeland SJ, Hurst LD. 1998. The genetic code is one in a million. *Journal of Molecular Evolution* 47(3):238-48.

<sup>46</sup> As each codon is 3 nucleotides long and there are 4 bases (A, C, G and T)  $4^3=64$  codons are possible. These 64 codons code for 20 amino acids and stop for a total of 21 meanings. The total possible combinations of codons and meanings is thus  $21^{64}=4.2 \times 10^{84}$ . This number is higher than some estimates of the number of particles in the universe. The probability of getting the genetic code we have assuming it was randomly generated is thus  $(1/21)^{64}=2.4 \times 10^{-85}$ , a number so small that it is virtually zero.

<sup>47</sup> Ronneberg TA, Landweber LF, Freeland SJ. 2000. Testing a biosynthetic theory of the genetic code: fact or artifact? *Proceedings of the National Academy of Sciences, USA*. 97(25):13690-5.

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many cases functionless, proteins will be produced. Changing the genetic language will lead to certain death of any organism that tries it.<sup>48</sup> The theory that evolution of the genetic code accounts for the current apparently optimal code must thus be viewed skeptically, as evolution of the genetic code appears to be a recipe for certain disaster

Theory 4, that the genetic code was intelligently designed, is consistent with two observations, the first that the genetic code is very good, the second that certain small variations in the genetic code are known. If mutation and selection do not present a realistic path to optimization and variation in the genetic code, intelligent design does. Variation in the genetic code is evidence consistent with a polyphyletic origin of life, that life began as many different ancestors rather than the single common ancestor (monophyletic origin) suggested by Darwinism. In short, the optimal genetic code is not well accounted for by the neodarwinian mutation selection mechanism, and slight variation in the code is inconsistent with the Darwinian belief in common descent of all life from a single ancestor.

### **Molecular Machines**

*Biology is the study of complicated things that give the appearance of having been designed for a purpose. —Richard Dawkins*

The ribosome, where information encoded in mRNA is translated into proteins, is not yet completely understood. For the purposes of this discussion we will avoid the details of its workings and look at a molecular machine with which it is associated. As the information in preproendothelin-1 mRNA is translated into a string of amino acids, the growing protein begins to exit the ribosome. Here it encounters the Swiss Army knife of the molecular machine world—Signal Recognition Particle (SRP). SRP has been described as a “remarkable cellular machine,”<sup>49</sup> and like a Swiss Army knife, SRP contains multiple protein and RNA tools, each designed to fulfill a specific function; each tool plays a vital roll in the greater purpose of the machine.

In eukaryotic cells<sup>50</sup> proteins destined for export, like endothelin-1, are inserted into the endomembrane system as a first step in the secretory pathway.

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<sup>48</sup> It is true that certain strains of *E. coli* have been developed which have specific changes in the genetic code. These bacteria are extremely delicate and require intense careful maintenance to survive. This is something they can only do under laboratory conditions with lots of human help. For an example, see Rogers MJ, Adachi T, Inokuchi H, Söll D. 1992. Switching tRNA<sup>Gln</sup> identity from glutamine to tryptophan. *Proceedings of the National Academy of Sciences, USA.* 89:3463-3467.

<sup>49</sup> Keenan RJ, Freymann DM, Stroud RM, Walter P. 2001. The signal recognition particle. *Annual Review of Biochemistry* 70:755-75.

<sup>50</sup> Two fundamentally different kinds of cells are recognized. Eukaryotic cells have a nucleus in which the genetic material is sequestered, separated from the rest of the cell by a nuclear membrane.

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Here they are processed and distributed to membrane-bound vesicles that fuse with the cell membrane, releasing their contents outside the cell. Signals encoded into proteins destined for export serve like zip codes on letters as they pass through the cell's intricate sorting and packaging system. The first step in this sorting process occurs as the protein is being produced via translation of the mRNA in ribosomes.

The first 17 amino acids<sup>51</sup> of preproendothelin-1 constitute a "signal peptide"<sup>52</sup> to which SRP binds in a very clever way. The signal peptide binding site is very selective about which proteins it will bind and at the same time recognizes a wide variety of different signal sequences. This flexibly selective system will accept many different signal sequences that start with a series of basic amino acids followed by uncharged amino acids. This is achieved by an elegant mechanism in which a protein called SRP54 forms a groove lined with methionine amino acids. Methionine side chains provide a flexible hydrophobic surface for interaction with other hydrophobic nonpolar amino acids in the signal sequence. The SRP54 protein also binds with the RNA component of SRP, and it is the negatively charged phosphate groups of the RNA that provide a binding site for positively charged basic amino acids at the end of the signal sequence. So, to achieve signal peptide binding that is both flexible and selective, SRP utilizes both protein and RNA components.

Not only must preproendothelin-1 be transported to the right place in the cell, but it must also arrive in a form that is capable of crossing the endoplasmic reticulum membrane at a place on the membrane where passage across is possible. If preproendothelin-1 arrived already folded into a globular shape, as proteins tend to do spontaneously, it could not cross the membrane. In an elegant solution to this problem, when the first part of preproendothelin-1 is recognized as a signal sequence, SRP switches off further production of the protein until the complex of partially produced protein, SRP, ribosome and mRNA are transported as a unit to the endoplasmic reticulum. Once this translation complex arrives at the endoplasmic reticulum, SRP ensures that it is handed off to the correct set of pore-forming proteins embedded in the membrane. This protein pore complex contains a component that both recognizes the SRP and is recognized by the SRP. Once recognition is achieved, both SRP and the protein that recognizes it change in shape, releasing the translation complex to the custody of the pore-forming proteins through which preproendothelin-1 is threaded as the ribosome resumes protein production.

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The other kind of cell is found in bacteria. These cells lack a nucleus and are commonly referred to by the unfortunately prejudicial term "prokaryotic."

<sup>51</sup> Fabbrini MS, Valsasina B, Nitti G, Benatti L, Vitale A. 1991. The signal peptide of human preproendothelin-1. *FEBS (Federation of European Biochemical Societies)* 286(1,2):91-94.

<sup>52</sup> Amino acids are linked together by a specific kind of covalent bond called a peptide bond. Thus, short chains of amino acids are sometimes simply referred to as "peptides," while long chains are called "polypeptides." Proteins may be made up of one or more polypeptide chains.

### **Processing Preproendothelin-1**

*At first sight the biological sector seems full of purpose. Organisms are built as if purposefully designed, and work as if in purposeful pursuit of a conscious aim. But the truth lies in those two words 'as if'. As the genius of Darwin showed, the purpose is only an apparent one.<sup>53</sup> –Julian Huxley*

Once inside the endoplasmic reticulum, the signal sequence is cut from preproendothelin-1, leaving a protein 195 amino acids long. This task is done by a signal peptidase enzyme that recognizes specific information in the protein telling where the signal sequence ends and the rest of the protein begins. Much of the remaining protein may be involved with ensuring preproendothelin-1 is routed correctly through the secretory pathway.

Before endothelin-1 is released outside the cell, 35 more amino acids are cut off one end and 122 off the other, leaving a 38 amino acid protein called “big endothelin-1.” Repeating the pattern already noted for the signal sequence, vital information about where the cuts should be done is contained in the protein. The best evidence indicates that furin-like enzymes, possibly furin itself, are the machines that both recognize the cutting site and make the cut.<sup>54</sup> Furin is a very busy enzyme involved with processing many proteins in addition to endothelin-1. The signal for furin cutting is fairly simple: two arginine amino acids separated by any two other amino acids. At both cutting sites endothelin-1 uses the sequence arginine-serine-lysine-arginine.

The interesting thing about this signal is that it is simple enough that in random sequences of amino acids it would appear once every 400 amino acids.<sup>55</sup> The design challenge with information of this type is exactly the opposite of the challenge of hitting a small target. If a signal to cut a protein appears in the wrong position, the resulting cut could very well destroy protein function. The furin cutting signal can be thought of as the side of a barn that the blindfolded Mrs. Tell, standing only a few paces away, is trying to miss rather than hit with an arrow. A skilled marksman with his eyes open would have no trouble missing even a large target. Using the same reasoning, a skilled designer could easily ensure that the furin cutting signal did not appear in the wrong place. Avoiding

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<sup>53</sup> Huxley JS. 1953. *Evolution in Action*. Penguin: Harmondsworth, Middlesex UK, 1963, reprint, p.16.

<sup>54</sup> Kido T, Sawamura T, Masaki T. 1998. The processing pathway of endothelin-1 production. *Journal of Cardiovascular Pharmacology* 31(Suppliment 1):S13-S15.

<sup>55</sup> Twenty amino acids are commonly used to construct proteins. Assuming that any position in a random sequence of amino acids has one chance in twenty of getting arginine, the probability of getting arginine in position 1 is 1/20 and the probability in position 4 is 1/20. Thus, the net probability is  $(1/20)^2=1/400$ .

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an inappropriately placed cutting signal within the relatively short 40 amino acid big endothelin-1 may be attributable to luck, but avoiding it in all proteins that furin plays a role in processing is suggestive of design.

Another factor suggestive of design is the way in which cutting signals are presented in the three dimensional structure of preproendothelin-1. To act, the signal must be accessible to furin, and this is by no means guaranteed in proteins. As mentioned earlier, proteins tend to spontaneously fold into globular structures, and a signal buried somewhere deep within the protein would not be available to signal for cutting. Thus, systems must be in place to either ensure that the protein does not fold, or alternatively that it folds in a way that ensures the signal is available. Proteins called heat shock proteins and chaperons are known to assist with folding of many other proteins, but their exact role, if any, in the folding of endothelin-1 has not yet been elucidated.

The 38-amino-acid-long big endothelin-1 is released from cells. In this form, endothelin-1 has essentially no biological action, and this is important. Endothelin-1, as a potent inducer of vasoconstriction, is an extremely dangerous molecule. Like nitroglycerine, the body does not want it to go off in the wrong place or at the wrong time. Big endothelin-1 is a safe form of endothelin-1, just as dynamite is a safe form of nitroglycerine. The trigger that then converts this endothelin-1 to its 21 amino acid active form is an enzyme called Endothelin Converting Enzyme-1a (ECE-1a). Information is encoded first in DNA, then amino acids of big endothelin-1 signal the cutting site for ECE-1a to produce endothelin-1.<sup>56</sup>

The part of big endothelin-1 that is cut away by ECE-1a then curves around endothelin-1 in such a way that endothelin-1 is protected from interacting with receptor proteins on the surface of smooth muscle cells in blood vessels.<sup>57</sup> This system is elegantly flexible and yet precise. Multiple components are involved in activation of endothelin-1 and transmission of the signal it conveys into the action of vasoconstriction. ECE-1a is a membrane bound protein that may be present close to the site of action of endothelin-1. Big endothelin-1 is converted to active endothelin-1 only where it is needed. Because of this, receptors in other parts of the body will not be exposed to endothelin-1, and it will not cause vasoconstriction where it is not needed or wanted. Each step along the pathway from initial DNA gene transcription to endothelin-1 receptor binding provides a potential control site allowing extremely delicate management of this very small, very potent protein.

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<sup>56</sup> Brooks C, Ergul A. 1998. Identification of amino acid residues in the C-terminal tail of big endothelin-1 involved in processing to endothelin-1. *Journal of Molecular Endocrinology* 21:307-315.

<sup>57</sup> Peto H, Corder R, Janes RW, Wallace BA. 1996. A molecular model for human Big-Endothelin-1 (Big ET-1). *FEBS (Federation of European Biochemical Societies) Letters* 394:191-195.

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Despite its small size, endothelin-1 is a good example of the ways information may be stored in biological molecules. Classes of information in the endothelin-1 gene include signals controlling transcription, signals controlling removal of introns, signals controlling how many times the mRNA can be translated, information encoding the protein sequence of preproendothelin-1 within which information about where to translate the protein is encoded, information about where to deliver the protein, and signals controlling when the protein is activated to its active form. Endothelin-1 draws our attention to the remarkable amount of information that may be stored even for a very small protein. From the presence of information it is reasonable to infer design. Thus, the endothelin-1 gene, along with thousands of others, suggests an intelligent cause rather than an origin due to natural forces or laws. But this is only part of the bigger picture suggesting intelligent causes behind the molecules that make up cells.

### **Signal Recognition Particle**

*But now hath God set the members every one of them in the body, as it hath pleased him. And if they were all one member, where were the body?*<sup>58</sup> –The Apostle Paul

During its production, endothelin-1 is processed in one way or another by several machine-like proteins, including enzymes that cut away various parts of the protein after their function has been completed, but before they are a hindrance to the ultimate purpose of the protein. One of the most spectacular machines is SRP. Machines, like information, are typically the product of intelligent creators, not natural laws. SRP is a particularly interesting machine, as one version or another of it is found in every known living thing.<sup>59</sup>

Because all organisms appear to have SRP, it has been suggested that it was inherited from a single common ancestor shared by all organisms. The simplest known version of SRP is found in bacteria, where it is composed of a single large protein and a relatively small RNA molecule. Reasoning from the Darwinian assumption of common ancestry, phylogenetic trees have been constructed based on variation in the sequence of amino acids in SRP proteins. The SRP provides data suggesting a “universal tree of life” that contradicts data generated from other ubiquitous proteins.<sup>60</sup> In other words, different proteins suggest different phylogenetic trees.

To one degree or another, molecular data indicating no single logically consistent tree of life can be explained away by invoking *ad hoc* explanations. These may include differing rates of evolution between genes and biological

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<sup>58</sup> 1 Corinthians 12:18, 19

<sup>59</sup> Lütcke H. 1995. Signal recognition particle (SRP), a ubiquitous initiator of protein translocation. *European Journal of Biochemistry* 228:531-550. Also see Keenan et al cited in XL.

<sup>60</sup> Philippe H, Forterre P. 1999. The rooting of the universal tree of life is not reliable. *Journal of Molecular Evolution* 49:509-523.

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groups or the increasingly popular Lateral Gene Transfer (LGT). In a few exceptional cases, passing off deviations from what common descent would predict may be reasonable, but molecular data increasingly forces the question of how much data counter to the theory of common descent is needed before its general acceptance should be reevaluated. For example, it has been suggested that about 40 genes have moved into the human genome directly from bacteria rather than passing through millions of ancestors prior to the evolution of *Homo sapiens*.<sup>61</sup> This seems incredible.

Discovery of large numbers of genes that appear where they are not expected to be on the basis of common descent has led some prominent thinkers to abandon the idea that all life came from a single organism. In her most recent book, Lynn Margulis and her son, Dorian Sagan, claim, “We show here that the major source of inherited variation is not random mutation. Rather the important transmitted variation that leads to evolutionary novelty comes from the acquisition of genomes.”<sup>62</sup> Essentially, what Margulis and Sagan are saying is that there is no single common ancestor, but rather all organisms are chimeras made up of more than one simpler organism. Carl Woese and others have expressed similar ideas.<sup>63</sup> At the molecular level, organisms do not appear to have descended from a single common ancestor with the family histories of different groups following single slowly branching trajectories until they reached their present state. When design is arbitrarily eliminated from consideration, molecular data suggests a complicated story of life best represented by a bush with many interconnecting twigs, rather than a tree with a single trunk and gradually branching taxonomic groups. If design is not forbidden before the data is considered, molecular data is consistent with the idea of a Designer who combined standard parts—genes—in novel ways to create different kinds of organisms.

One of the most startling things about SRP is that its components seem to be interchangeable between very different organisms. The SRP proteins from human cells, which by themselves show no activity, will form fully functional SRPs when combined with the RNA component of SRP from *Xenopus laevis* (frogs) or *Drosophila melanogaster* (fruit flies).<sup>64</sup> Equally startling, when components of *Canis familiaris* (dog) SRPs are reconstituted with one of the major

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<sup>61</sup> Salzberg SL, White O, Peterson J, Eisen JA. 2001. Microbial genes in the human genome: Lateral transfer or gene loss? *Science* 292:1903-1906. And Andersson JO, Doolittle WF, Nesbø CL. 2001. Are there bugs in our genome? *Science* 292:1848-1850.

<sup>62</sup> Margulis L, Sagan D. 2002. *Acquiring Genomes: A Theory of the Origins of Species*. Basic Books, New York. p12

<sup>63</sup> Woese, CR. 2002. On the evolution of cells. *Proceedings of the National Academy of Sciences USA*. 99(13):8742-8747. Sapp J. 1994. *Evolution by Association: A History of Symbiosis*. Oxford University Press, New York. Williamson DI. 2001. Larval transfer and the origin of larvae. *Zoological Journal of the Linnean Society* 131:111-122. Williamson DI. 1992. *Larvae and Evolution: Toward a New Zoology*. Chapman and Hall, New York. And many others.

<sup>64</sup> Walter P, Blobel G. 1983. Disassembly and reconstitution of signal recognition particle. *Cell* 34:525-533.

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components replaced by the single large protein from the bacteria *Escherichia coli* SRP, an SRP results functional in all respects except for binding to the endoplasmic reticulum receptor.<sup>65</sup> The same dog SRP protein replaced by the *E. coli* protein can in turn bind to the RNA portion of *E. coli* SRP.<sup>66</sup> The amazing thing about these proteins, called SRP54 in mammals and Ffh in *E. coli*, is that they only share 38 % amino acid identity, and yet their three-dimensional structures contain similar structural elements.<sup>67</sup> In addition, dramatic differences exist between dog and *E. coli* SRP RNA.<sup>68</sup> That both proteins and both RNAs would have evolved so dramatically in sequence in such radically different organisms and yet remained so similar in structure and function beggars the imagination. Invoking some kind of design teleology is consistent with what is known. Random mutation coupled with selection seems like a very unlikely explanation.

### Conclusions

*Darwin convinced the world of the historical fact of evolution. This we owe him. What more need we ask? He was the apostle who converted the Christians, or a large body of them. Did he not devote almost all his life to this tremendous task? And was he not as successful in this mission in partibus fidelium [in the land of the faithful] as any apostle has ever been?*<sup>69</sup> –Cyril Darlington

Living systems are full of amazing machines. At the macro level the heart pumps blood, the kidneys filter it, the diaphragm acts as a bellows to pump air into the lungs, and so on. Charles Darwin recognized that natural selection was not adequate to create any one of these machines in a single step. Instead, he suggested:

If it could be demonstrated that any complex organ existed, which could not possibly have been formed by numerous, successive, slight modifications, my theory would absolutely break down.<sup>70</sup>

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<sup>65</sup> Bernstein HD, Zopf D, Freymann DM, Walter P. 1993. Functional substitution of the signal recognition particle 54-kDa subunit by its *Escherichia coli* homolog. Proceedings of the National Academy of Sciences USA. 90:5229-5233.

<sup>66</sup> Romisch K, Webb J, Lingelbach K, Gausepohl H, Dobberstein B. The 54-kD protein of signal recognition particle contains a methionine-rich RNA binding domain. Journal of Cell Biology 111:1793-1802. And Zopf D, Bernstein HD, Johnson AE, Walter P. 1990. The methionine-rich domain of the 54 kd protein subunit of the signal recognition particle contains an RNA binding site and can be crosslinked to a signal sequence. EMBO Journal 9(13):4511-4517.

<sup>67</sup> Bernstein HD, Poritz MA, Strub K, Hoben PJ, Brenner S, Walter P. Model for signal sequence recognition from amino-acid sequence of 54K subunit of signal recognition particle. Nature 340:482-486.

<sup>68</sup> Larson N, Zwieb C. 1991. SRP-RNA sequence alignment and secondary structure. Nucleic Acids Research 19(2):209-215. And Zwieb C. 2002. Personal communication.

<sup>69</sup> Darlington CD. 1959. *Darwin's Place in History*. Basil Blackwell, Oxford p.59.

<sup>70</sup> Darwin CR. 1958. *The Origin of Species by Means of Natural Selection or the Preservation of Favoured Races in the Struggle for Life*. Penguin Books, New York p 171.

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While laying the burden of essentially proving a negative on those who disagreed with his theory, Darwin recognized the necessity of effecting change in small steps; a principle stated repeatedly in *The Origin of Species*: “Any change in function, which can be effected by insensibly small steps, is within the power of natural selection.”<sup>71</sup> Darwin used the eye to illustrate how change might be effected using what appeared to him to be small steps as eyes evolved from light detecting spots to fully formed camera type eyes of the kind seen in humans and octopuses. The problem was that Darwin was ignorant of the mechanisms within cells that allow eyes to work. Molecular biology has shown that organisms are not only made up of machines at the macroscopic level. The cells from which organs are made contain numerous machines as well. SRP demonstrates that these machines perform complex functions. Intelligent humans can design complicated machines. Along with information, machines—whether they be boomerangs, stone tools, cars or aircraft—are readily recognized as products of intelligence.

Michael Behe has argued convincingly that some molecular machines are irreducibly complex.<sup>72</sup> In other words, there is a point at which no more parts can be removed before the machine no longer works. Imagine removing parts from the engine of a car. It may be possible to remove some of the bolts or the air filter and still have an engine that, under ideal conditions, will run. However, there are some parts that cannot be removed without destroying the function of the engine. For example, removing the crankshaft may turn the engine into an effective anchor, but the function as an engine will no longer exist. Molecular machines can behave in exactly the same way. SRP demonstrates this. Some parts can be removed, making it less effective at moving proteins to the endoplasmic reticulum surface, but removal of other parts completely destroys the function. None of the six proteins and single RNA molecule that make up the mammalian SRP has any known function other than its role within the SRP. However, simpler SRP complexes are known.

The bacterial *E. coli* SRP, as noted earlier, is composed of an RNA molecule much shorter than the one found in mammals. In addition, instead of six proteins, *E. coli* only uses one (Ffh). This less complex SRP may not do some of the things mammalian SRP does, but it can still bind to signal sequences, transport the protein to a membrane (the cell membrane in the case of *E. coli*), bind to a membrane bound receptor—thus ensuring the protein is at a pore where it can be released outside the cell—then let go of the protein, then repeat the cycle. To achieve this, both parts of the *E. coli* SRP are needed: the RNA and the protein.

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<sup>71</sup> Darwin CR. 1958. *The Origin of Species by Means of Natural Selection or the Preservation of Favoured Races in the Struggle for Life*. Penguin Books, New York p 422.

<sup>72</sup> Behe M. 1996. *Darwin's Black Box: The Biochemical Challenge to Evolution*. Free Press, NY.

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On the surface it looks like a relatively simple irreducibly complex machine. How simple it is in absolute terms is a matter of judgment.

Another factor to take into consideration is that SRP is irrelevant unless two things are present: 1) A signal sequence on the proteins it is to recognize and mediate the transport of and 2) a receptor on the surface of the membrane it is to transport them to. In other words, the SRP is part of a much larger system. Because of its machinelike qualities, SRP appears to be designed. Because it is part of a much larger system with a teleological objective—export of proteins from the cell and insertion of proteins into membranes—presence of SRP suggests that this system has elements of design in it. Endothelin-1, because of its signal sequence designed to interact with SRP as well as the information content of the gene that codes for it, also suggests design.

The two examples given in this paper, information in endothelin-1 and machine-like SRP, do not compel belief that every system of the cell is designed or that every organism composed of cells is designed. However, what is known about organisms at the molecular level is consistent with the creation/salvation story contained in Scripture in which a benevolent Creator seeks to save his creation currently suffering under the curse of sin.

### **No Miracles**

*By coupling undirected purposeless variation to the blind, uncaring process of natural selection, Darwin made theological or spiritual explanations of the life processes superfluous.<sup>73</sup> –Douglas Futuyma*

The car engine example demonstrates that irreducibly complex machines can be a product of human intelligence. What has not been demonstrated is that natural forces, unguided by intelligence, can produce machines of this sort. The short steps Darwin suggested are not adequate to account for machines with multiple parts coming together with no precursors. The evolution story may be salvaged with appeals to unknown or hypothetical functions for individual components—like using the engine block as an anchor—but these functions are beyond the scope of empirical science and thus become simple articles of faith. Multiple parts appearing at the same time and interacting with each other in precise and complex ways—what Dembski would call highly specified ways—is not a little step: it is a miracle.

“I would give nothing for the theory of natural selection, if it requires miraculous additions at any one stage of descent.”<sup>74</sup> Darwin used these words in a letter to Charles Lyell shortly after publication of the *Origin of Species*. Darwin

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<sup>73</sup> Futuyma D. 1986. *Evolutionary Biology*, 2nd ed. Sinauer Associates Inc. Sunderland, MA. p. 2.

<sup>74</sup> Darwin, CR. Letter to Charles Lyell October 11 1859 in Darwin F. ed. 1959. *The Life and Letters of Charles Darwin: Including an Autobiographical Chapter* Vol. II. Basic Books, New York. p. 7.

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set up an arbitrary rule in his creation story—no miracles allowed—revealing a dogmatic commitment to materialism. There is nothing very logical about this precondition on how species may come into existence. In fact, the mechanism of mutation and selection as formulated in the modern evolutionary synthesis does not in any way logically exclude the existence of miracles or a role for miracles in the creation of species. What biology does show, at the molecular and every other level, is that natural selection does not adequately explain all of nature. In addition, the monophyletic origin of life suggested by Darwinism is not consistent with molecular data unless special miracles are allowed, like lateral gene transport, an evolving genetic code, and simultaneous appearance of parts engineered to very fine specifications to fit together into complex molecular machines.

The story of the origin of life and its development until the present is clearly a long and complex one in which natural forces have played a major role; however, the explanatory power of stories that only invoke natural causes is not sufficient to account for what is observed in nature. Design is logically inferred from at least some of the data, particularly that data dealing with life at the molecular level. Molecular data does not tell us who the Designer is, but it is sufficient to tell us that He exists. Like Moses asking God's name,<sup>75</sup> nature gives a clear answer, "I Am."

The molecules of life suggest no need for Christians to become sycophants to materialistic philosophy posing as science. On the contrary, science liberated from the artificial constraints of materialism provides an elegant mechanism for study of the creation and logically points to a wonderful Creator. In the words of Johan Kepler, "To God there are, in the whole material world, material laws, figures and relations of special excellency and of the most appropriate order . . . Those laws are within the grasp of the human mind; God wanted us to recognize them by creating us after his own image so that we could share his own thoughts."<sup>76</sup>

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<sup>75</sup> Exodus 3:14

<sup>76</sup> Kepler, J. (1599). Letter to Herwart von Hohenburg reprinted in *Johannes Kepler: Life and Letters*. Carola Baumgardt, 1951. Philosophical Library, New York. p 50.