Nylon-eating bacteria—part 4: interpretation according to Coded Information System theory

Royal Truman

Three novel enzymes, E-I, E-II, and E-III can hydrolyze amide bonds of side-products from the manufacture of nylon-6. This has been incorrectly interpreted as proof for evolution, meaning descent of all organisms from a common ancestor, since they had not existed before. We evaluate the origin of these enzyme variants with Coded Information System (CIS) theory, which describes logic processing using four refinement components: coded messages, sensors, physical hardware and pre-loaded resources. Since after the completion of Creation Day 6 God rested, the individual organisms, and ecologies produced so far had to be adaptable to new contingencies in real time and across generations. This implies that they were created as open programs based on general and flexible principles and not hard-coded instructions limited to solving individual challenges. The ability to fine-tune enzymes such as E-I, E-II, and E-III to permit catalyzing reactions in a modified chemical context is a natural consequence of an open program design.

In part 1,[1] part 2,[2] and part 3[3] of this series we reviewed the origin of three classes of enzymes, E-I, E-II, and E-III, found in different bacteria which can degrade various synthetic side-products which result from the manufacture of nylon-6.[4] In part 3 we saw that these enzymes probably arose via mutations from a different enzyme. Is this an example of information having arisen for free, *contra* what Dembski[5] and so many others have claimed?

Significance of the origin of enzymes E-I, E-II, and E-III

How significant is the origin of these three enzymes, able to process a slightly different amide group? The precise three-dimensional chemical context of biological amide bonds which are enzymatically hydrolyzed varies greatly (arrangement of the atoms in space, charge distribution, other interfering portions of the molecule, and so on). Very different temperatures and viscosities also affect the local environments dramatically and further increase the challenges amidases[6] face. Not every naturally occurring amidase can hydrolyze every amide, but the ensemble of these enzymes can process all, or virtually all, of the naturally occurring amides found in biochemicals. The individual enzymes needed to process every substrate variant a prokaryote could encounter in the distant future would not have to be present initially on each individual, if a few optimizing mutations would easily provide these modified enzymes later while the population sizes grew, and the modified genes could be shared around.

The chemical context of the amide bonds being degraded in some side-products from nylon-6 manufacture differs but little from natural amides. Thus, obtaining a suitable amidase turns out to be reasonably probable, especially if it only needs to possess limited activity initially.

Anderson and Purdom point out that "a wide range of mutations can be shown to provide a beneficial phenotype to the cell"[7] but also that these mutations "frequently eliminate or reduce pre-existing cellular systems and functions. This has been referred to as antagonistic pleiotropy".

For higher organisms, Dr Borger introduced the idea of front-loaded baranomes—pluripotent, undifferentiated genomes with an intrinsic ability for rapid adaptation and speciation.[8,9] Life was not intended to be static, but adaptable and robust within limits to future challenges. Adaptability is often foolishly claimed to demonstrate evolution theory is true.[10] Evolution assumes all living organisms on earth share a common ancestor. Adaptability does not demonstrate anything of the kind.

Optimization of E-I, E-II, and E-III through selective iteration

Weren't enzymes E-I, E-II, and E-III optimized by natural selection? Again, we must keep in mind what was reported and thus needs explaining.[3] Existing genes were apparently modified in a few key positions, fine-tuning an enzymatic reaction—amide hydrolysis—which was already widespread in nature. Intelligent beings like humans excel in designing guided search algorithms which rely on repeated attempts. A process with suitable constraints is set up, typically conceived around the intuition of iteratively approaching the goal in response to some feedback. Examples include the simplex algorithm to solve linear programming problems,[11] genetic algorithms,[12] the Newton–Raphson method to find roots of equations,[13] and forward and backward chaining in inference engines.[14]

To illustrate adaptive exploratory behaviour, a hunter does not design a specific weapon to target each kind of bird for every environment, but uses a general-purpose one, like a shotgun, able to cover the range of feasible outcomes on an *ad hoc* basis. Feedback after the first shot permits a better subsequent attempt. The number of pellets, amount of gun powder in a shell, the length of the barrel, etc. were optimized in anticipation of a *category of problem* to be solved (hunting birds).

Other examples include the use of a watering can with multiple streams of waters (figure 1) and filters of various sizes to separate stones according to size (filters also have wide application in chemical and biochemical laboratories). Although the outcome may seem in a sense to be random (with respect to the precise results), the equipment and adjustments made as feedback becomes available are not random, revealing that these are guided searches. The randomness of outcomes is deliberately and steadily constrained. Dembski has shown that the guiding informational input necessary to find the correct search algorithm plus parameters cannot be less than the resulting outcome.[15]

Since bacteria play important ecological roles and must recycle countless kinds of substances, their genomes were created to cover a large number and variety of problems, adapting as needed. Their robustness permits them to flourish virtually everywhere on earth where life would be possible, providing the foundation for more complex organisms. Bacteria have been constrained to permit valuable, but not unlimited, variability. The typically low average mutational rates[16] and robustness to change permit viable mutations to occur while avoiding runaway genetic entropy, and the large populations plus short generation times permit a generous number of trials to be made.[17] This is an ideal setup, a problem-solving algorithm. In CIS terms, we can use as a reference state what would happen if the population sizes were dramatically smaller (not enough opportunities for a fortuitous mutation), or if mutation rates were much greater (error cascade results) or much lower (no adaptability results during the needed time frame).[18,19]

A portion of the original bacterial population forced into an environment where survival depends upon being able to process a new nutrient will typically result in a strain which has been degraded with respect to the more robust and general-purpose ancestral one, but it survives. Should the nutritional constraint be removed, the now inferior strain would typically be at a selective disadvantage and die out, permitting a different strain or a more robust and less specialized one to fill the emptied niche.[20] In this manner, by the combination of large populations, short generation times, and a low rate of mutation, short-term fine-tuning can occur while avoiding runaway DNA degradation.

Figure 1. Watering can as an example of a general purpose solution. A single design can be used to water different objects at various times and locations. This is an adaptable design where feedback permits iterative refinement. Evolution has no future, long-term goal and cannot ensure in advance that the necessary instructions and physical components will be integrated into a flexible system. The water can illustrates how for intelligently adaptable systems this is different: water is made available at a suitable location, a sensible number of streams run in parallel, the volume of water and range of variability during attempts make sense, feedback is readily fed into the improvement cycles, and so on.

Coded Information Systems theory to explain biology

CIS theory[18,19,21,22] clarifies how these kinds of designs work by identifying four generic *refinement components*: coded messages, sensors, physical hardware, and pre-loaded resources (which includes the ability to reason).[23] The solution architecture takes tradeoffs and interplay of these informational resources into account. Figure 2 shows a key insight of CIS theory, that first a variety of outcomes must become possible and then the diversity of outcomes is restricted when compared to a reference state lacking the refining component. Goal states are restricted compared to what would have been possible.

To understand Coded Information Systems we recommend determining which kind of sender-receiver design is being examined at a particular level of refinement (figure 2) towards the goal. One version responds mostly *mechanically* to informational resources. The other requires active, mostly *conscious cognitive processing*. CISs are usually hierarchically embedded and both design variants are present in higher organisms. The human mind can decide on a course of action at a higher level which feeds into a cascade of automated subsystems such as mitochondria which generate the necessary energy. It remains to be researched whether it is always possible to clearly separate conceptually active and passive layers of information processing in CISs,[23] such as reports of mind-over-matter.[24]

Once one understands how CISs rely on the hierarchical and integrated interplay of complex resources (one of which must always include coded messages), the pieces begin to fall into place. The theory is quantitative, focusing on functional outcomes and not gene sequence similarities. Each step in the refinement process organizes matter and energy, making its own H_{before}–H_{after} contribution to the total of the CIS.

Since CIS theoreticians believe adaptability and fine-tuning were designed, we predict focused research will show that more than random processes are involved. We anticipate factors will be discovered which help guide change into promising areas especially for important environmental members such as prokaryotes.[25]

CIS theory forces us to look beyond DNA

CIS theory denies that processes such as development and regulation are specified by only the DNA sequences. There is no fully specified blueprint to be found there. This should not surprise us, since this is also true of most activities associated with intelligent behaviour. Our decisions and thoughts are not pre-programmed, nor do we communicate using only coded messages.

An intelligent sender, like a person, anticipates what the receiver already knows or might do when presented with various inputs, taking the immediate context into account. A driving instructor might point leftward, and thereby elicit the correct behaviour for the current situation (turn left at the street light; or adjust for the other car they are too close to; or roll down the window to order food at a drive-in; or admire the sunset). A less abstract gesture, like pushing someone, could anticipate and elicit a wide variety of responses, none of which required agreement to a sender-receiver coding convention nor grammar in advance. Logic and reasoning are pre-loaded resources which intelligent sender-receiver communicators avail themselves of.

Similarly, by knowing in advance the context organisms will face and the natural physical-chemical behaviour of molecules in cellular environments (e.g. diffusion rates of regulators; which biomolecules will interact and how; the presence and wavelength of light) the Creator can ensure intended outcomes (timing, quantity, location) by supplementing only as needed with any of the four refinement components. Most of the intended outcomes are not knowable from analysis of DNA only. In fact, many biologists view DNA as primarily responding to the true informational drivers provided by the cytoplasm. Much of development seems to the atheist to occur by chance interactions,[26] since they overlook the usage of foresight, how existing parts brought together must act, with informational additions provided as needed. Foresight includes knowing which possible solutions would not work, such as when a potential binding factor would interact with wrong DNA sequences throughout the entire genome and thus cannot be used. Evolutionists inevitably overlook the difficulty of creating macro innovation by trial-and-error with natural selection operating on the whole organism level.

Sophisticated Coded Information Systems are adaptable

Modern chess-playing computer programs often confront new positions never seen before yet provide excellent moves (figure 3). This is because the programs are endowed with general-purpose rules instead of hard-coded instructions which respond to each unique move (i.e. a decision tree). Whether new information arises

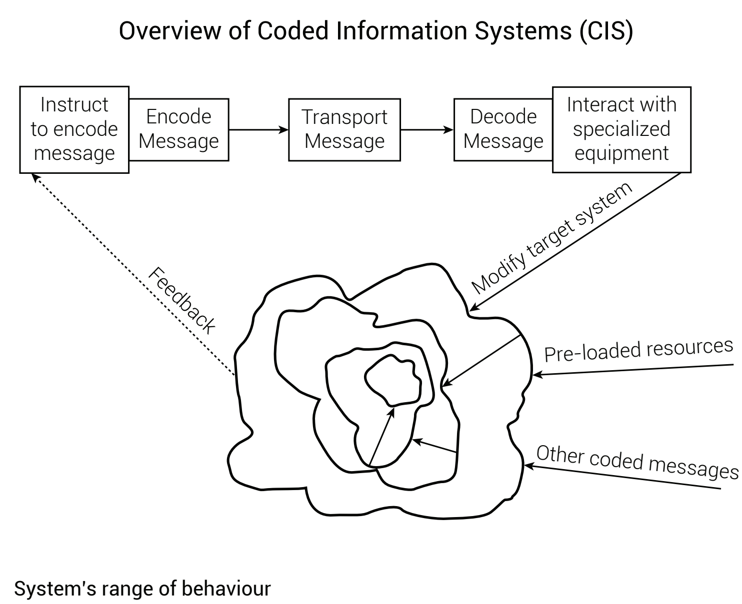

Figure 2. Coded Information Systems sequentially refine behaviour through a series of sequential processes. Each goal-directing refinement step could be influenced through coded messages, sensors, physical hardware, or pre-existing resources. At least one process is guided by coded instructions in order to be classified as a CIS.

in such cases invites discussions on what is meant by 'information', an unprofitable discussion we circumvent by focusing on the concept of Coded Information Systems (CISs). Living organisms reflect the most sophisticated form of CIS: those able to adapt autonomously to new circumstances without requiring new active participation from their designer.

We have good reasons to believe life on earth was conceived to be autonomously adaptable. Genesis 2:2 states that by Day 7 God had finished His creative work and rested, and Genesis 1:31 also states that God saw that all He had made was very good. This would not characterize a biosphere which then fell apart upon cessation of the creative work, in the current and next generations. A biological world acting autonomously in the future—without the need for constant active adjustments—must have built-in features foreseen to adjust to new contingencies. This includes adapting to eventualities during an organism's lifetime and also within new ecological arrangements. Visible benefits may occur within a second, such as rapid reflexive actions (removing a hand from a hot object). A reaction could also take a few seconds to develop (sneezing), up to minutes (vaso-constriction of skin and limb blood vessels when temperature drops), or hours or months (such as resulting from varying hormone levels). These are examples of automated processes involving: 1) receptors, 2) a control centre, and 3) effector machinery.[27]

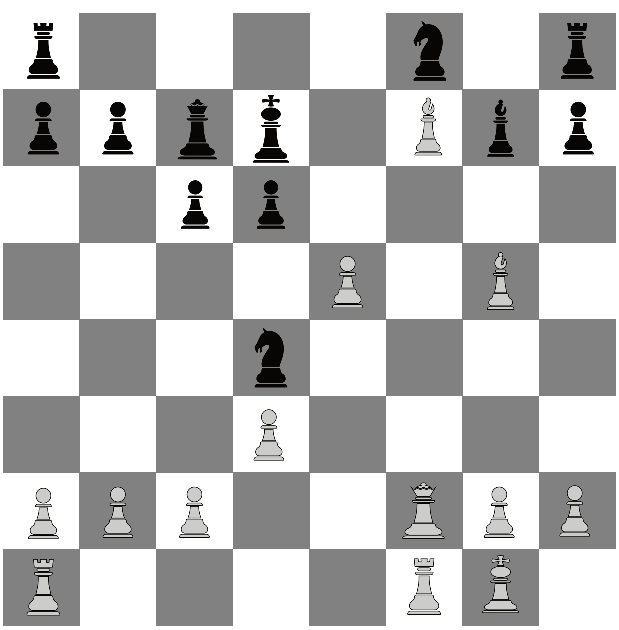

Figure 3. Humans and computer programs can solve problems using broad rules provided in advance. Each unique solution is not hard-coded by the best chess programs for every eventuality (except during the opening moves), and many variants of the above chess problem and countless unrelated other ones can be solved with no need for additional logic-processing resources. (Solution to this problem: 1. Qf5+ Nxf5 2. e6 checkmate).

Open programs are adaptable

Mayr distinguishes between open and closed programs. Instincts and reflexes are examples of 'closed programs'. In 'open programs' such as the capacity to learn languages *information is not rigidly programmed*.[28] Nobel Prize winner Lorenz mentions Mayr's concept of open programs frequently and uses as examples increases in haemoglobin concentration at high altitude and modification of fur thickness with climate changes. He believes these adjustable systems contain more information than closed ones.[29]

A programmed function like X = 2 + 2 has limited value, even though the numbers could be applied to different objects. Used once, one already knows what will result if invoked again. A function like $y = a + b \cdot \log_n(x)$ is more flexible, able to answer a category of questions based on parameter values.

A general-purpose computer subroutine like sub_x($p_1 \ldots p_n$) could also provide additional contextual data not related to the parameters fed in, such as who requested the result, when it was requested, total execution time, and what hardware was used. Such open programs can avail themselves of input from other sources. Multi-purpose programming is more efficient than to create a multitude of individual programs, perhaps with different computer languages and hardware, to deliver all these services.

Biological CISs display anticipatory planning

We introduced above the concept of a sophisticated CIS being adaptable. There is no deterministic instruction book in DNA which pre-specifies every exact eventuality. Oyama wrote in *The Ontogeny of Information*:

> "On the contrary, the more sophisticated the program, the more subtly it responds to its input. A program whose output were completely specified by ('completely controlled by') the program itself would be of limited value."[30]

Living systems are designed to respond to *classes of challenges*. Intelligent beings adjust dynamically with every step they walk, every bite they chew, every time they approach an object. Every eventuality has not been pre-coded on DNA or elsewhere, unlike deterministic computer programs. Processes such as maturation of B-cells; wiring of neurons; the layout of veins; and the location of muscle fibres further emphasize this general truth. The ability to adapt to novel food sources never encountered before, knowable of course to the Creator in advance, is consistent with the Design worldview.

A robust design of CISs requires anticipatory planning adaptability to guide short, middle, and long-term responses to cover within and across generational eventualities. Some changes would only be expressed in the offspring. 'Death', for example of tree leaves, when theologically properly understood is not controversial.[31] Developmental pathways in higher organisms rely often on programmed cell death (apoptosis)[32] for example to eliminate webbing between digits.[33] Surely sperm cells, which would accumulate over multiple mating events, weren't intended to live forever. However, we disagree with Darwin's view that death across all forms of life was necessary to permit overall higher improvement from a single common ancestor.

Adaptations of organisms to new environments can be permanent or temporary, sometimes involving guided genetic modifications fixed in future generations through inheritable epigenetic modifications.[34] Some adjustments require replacing living components within the host organism's lifetime. Long periods of dryness cause spruce trees to sacrifice their 7-year-old needles by cutting off moisture and most nutrition to them, transferring the resources elsewhere in the tree.

Genetically identical organisms can respond to external cues to develop very different morphologies, a phenomenon known as *plasticity*.[35] This could mean variability along a single trait, such as number of red blood cells as a response to altitude (oxygen content), or length of legs on lizards, or multi-trait developmental polymorphism. Examples include colour forms of caterpillars, pupae, and butterflies, winged and non-winged morphs of water striders and plant hoppers, sexual and asexual forms of aphids, and caste systems among social hymenopterans.[36]

These broad and often reversible changes permit many members of the population to respond to environmental changes without requiring mutations. The responses can modify the coordinated expression of many genes. Light absorption by a single photoreceptor in *Arabidopsis* affects up to a third of its genes and defence mechanisms have been shown to change the expression of over 2000 genes. Drought and cold stress are shown to modify the expression of at least 1,300 genes.[37]

Flexible designs, pre-planned to respond to different signals are more sophisticated than multiple dedicated programs, and especially in biology would be more efficient in usage of matter and energy, reproduction, and maintenance. Creation scientists were pleased to learn about overlapping codes,[38] multiple reading frames, translation slippage, alternative splicing, alternative regulation in different tissues, and development stages, plus all the other examples of efficient multi-purpose programming in cells.[39] The latest discoveries reveal that virtually all DNA has informational relevance, involving a larger number of superimposed codes.[40,41] All the evidence confirms that adaptability and regulatory robustness are far more sophisticated than suspected a decade ago.

None of these possibilities were predicted by evolutionary theories. Not only do these discoveries open exciting areas for research by those believing in Design, but also confirm the expectation of brilliant usage of informational principles. The evolutionist is more comfortable with notions like huge amounts of junk DNA and flawed designs which barely work. Without foresight, once a system has been committed to an architectural approach future changes must conform to the built-in constraints.[42]

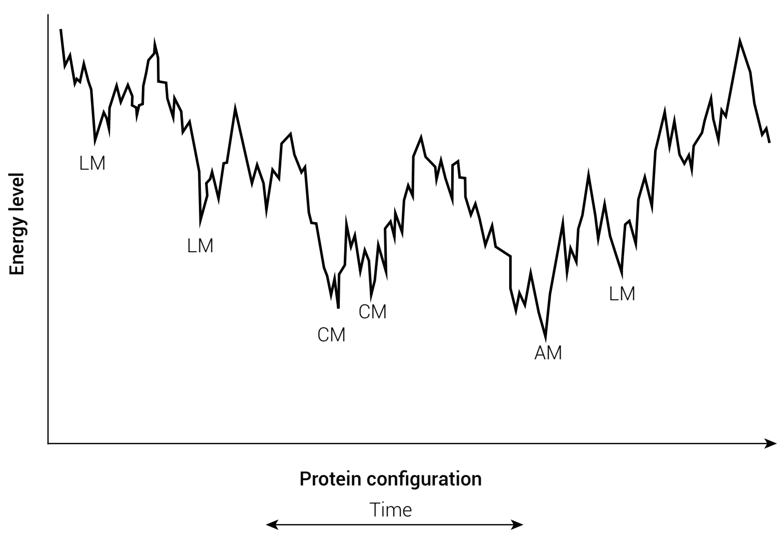

Figure 4. Energy diagram of protein folding showing intermediate, meta-stable states as configurations are explored to find more stable states. The fluid cellular environment, suitable temperature, exclusion of interfering molecules and strong UV light, small changes in energy level for similar configurations (to permit backing out of a false solution), presence of chaperones, availability of salt bridges, sulphide-sulphide bonds and alpha-helices and beta-sheets are some of the resources used by the algorithm to iteratively search for the intended folded state. Being robust to change, mutations in natural proteins will often produce a variant of the folded state optimized for a new environment. LM= Local Minimum; CM = Close to Minimum (as used by conformational switches); AM=Absolute Minimum.

Flawed evolutionary understanding of adaptability

How could examples of adaptability be attributed to Design or evolution? Evolutionary theory has never presupposed, and is incompatible with, the presence of sophisticated anticipatory guidance to protect populations. Unguided evolution, whether neo-Darwinian theory or other evolutionary framework,[43] requires the underlying mechanisms to be naturalistic *in toto*. Explanatory terms like 'canalized development'[44] must be immediately questioned: what is the source of the guidance being provided?

For decades the evolutionary community claimed that random mutations in the protein coding regions of genes plus natural selection explained the origin of virtually all biological features. We are now seeing a massive paradigm shift whereby such point mutations are essentially and correctly recognized as irrelevant for the big picture.[45] However, the new discoveries responsible for complex development and adaptability are being claimed to be unguided evolutionary processes.

In *Arrival of the Fittest*[10] Dr Wagner shows how bacteria can develop novel metabolic paths by accepting genes coding for the necessary enzymes from other bacteria. We view this as a clear example of designed adaptability, an improvement over placing all relevant genes on the same genome initially if not needed at that time and place. The design optimizes from an ecological perspective. Since the output from one enzymatic reaction serves as the substrate for a second one, and its output as raw material for a third one, and so on, then producing the entire path in a new host can occur automatically once the means to easily exchange, add, and eliminate entire genes has been made possible.[46] In many cases only one or two new genes would need to supplement those already present in the host to permit metabolic processing of a different substance.

Change is not the same thing as evolution unless it unambiguously supports the notion of origin of new organisms from a *single* common ancestor. Creating *one* new strain by requiring genes from *two* or more pre-existing strains does not demonstrate this. Useful change is a fundamental and necessary feature of life. Fertilized eggs become mature individuals; from a generalist bacteria population many specialized strains arise, optimized to various niches; and plants show rich varieties in different environments. None of these examples support the grand scheme claimed for evolution.

If the scientific community could agree that information-controlled biological change occurs, often very rapidly, but that there is—at least at this time—no proof the informational guidance arose from purely naturalistic sources, the creation vs evolution conflict would to a large extent dissipate. Discontinuing the habit of attributing miraculous properties to 'evolution'[47] and claiming science explains everything and disproves God's existence, would permit all scientists to concentrate harmoniously on elucidating the fine details of the informational mechanisms involved. CIS theory was developed to provide a more neutral worldview framework for research.

Conclusions

Enzymatic degradation by bacteria of materials generated from the production of nylon-6 is an example of what they have been designed to do: recycle and break down larger biochemicals. This is not an example of information arising for free in nature, and far less answers the question of their origin as Coded Information Systems, including the complex molecular machines needed to create the kinds of macromolecules being degraded.

There is no difficulty for creation scientists in understanding degradation of synthetic substances by bacteria once CIS thinking has been digested (pun intended). In the case of materials resulting from the manufacture of nylon-6, only amide bonds in a slightly different chemical context had to be hydrolyzed, a rather trivial requirement given the huge variety of pre-existing enzymes performing a similar task. But like the movement of a kite which might appear to be random (until one realizes that a string is being intelligently pulled at the right times), deeper analysis of the biological basis which produces changes reveals sources of informative guiding factors.

CIS theory clarifies how biological designs work by identifying four *refinement components*: coded messages, sensors, physical hardware and pre-loaded resources. The solution architecture involves interaction and interplay of these informational resources. The later adaptations to new environments can be temporary or permanent, sometimes involving guided stable genetic modifications.

Intelligent design of individual organisms and ecologies requires that biological Coded Information Systems be able to adjust to needs spanning sub-second to multi-generational time intervals. Like the best information processing designs, biological designs are open programs, able to cope with challenges whose individual solutions were not hard-coded in the instructions. General logic-processing principles are involved which include exchanging genes with other prokaryotes; eliminating genes no longer needed; iterative fine-tuning with the help of feedback towards a useful goal; the use of huge population sizes; short generation times; robustness of protein structures permitting variation;[48] and mutational rates which are neither too high nor too low to permit fine-tuning of enzymes without wreaking havoc on genomes. These are parts of an intelligent algorithm to solve and overcome novel challenges and problems while ensuring collective survival.

References

1. Truman, R., Nylon-eating bacteria—part 1: discovery and significance, *J. Creation* **29**(1):95–102, 2015.
2. Truman, R., Nylon-eating bacteria—part 2: refuting Ohno's frame-shift theory, *J. Creation* **29**(2): 78–85, 2015.
3. Truman, R., Nylon-eating bacteria—part 3: current theory on how the modified genes arose, *J. Creation* **29**(2):106–109, 2015.

4. A Short History of Manufactured Fibers, www.fibersource.com/f-tutor/history.htm.
5. Dembski, W.A., *No Free Lunch: Why Specified Complexity Cannot Be Purchased without Intelligence*, Rowman & Littlefield, Lanham, MD, 2002.
6. Amidases are classified according to the EC scheme under category 3.5.1.4, enzyme.expasy.org/EC/3.5.1.4.
7. Anderson, K.L. and Purdom, G., A creationist perspective of beneficial mutations in bacteria, *Answers in Depth* **4**, 2009, answersingenesis.org/genetics/mutations/a-creationist-perspective-of-beneficial-mutations-in-bacteria/.
8. Borger, P., Evidence for the design of life—part 1: genetic redundancy, *J. Creation* **22**(2):79–84, 2008; creation.com/genetic-redundancy.
9. Borger, P., Evidence for the design of life: part 2—Baranomes, *J. Creation* **22**(3): 68–76, 2008; creation.com/baranomes-and-the-design-of-life.
10. Wagner, A., *Arrival of the Fittest*, Oneworld, London, 2015.
11. Dantzig, G.B., *Linear Programming and Extensions*, Princeton University Press, NJ, 1963.
12. Mitchell, M., *An Introduction to Genetic Algorithms*, A Bradford Book, The MIT Press, Cambridge, MA, 1999.
13. Burden, R.L. and Faires, J.D., *Numerical Analysis*, Brooks/Cole, 9th edn, 2011.
14. Sharma, T., Tiwari, N. and Kelkar, D., Study of difference between forward and backward reasoning, *Int. J. Emerging Tech. and Adv. Eng.* **2**(10):2250–2459, 2012; www.ijetae.com/files/Volume2Issue10/IJETAE_1012_48.pdf.
15. Dembski, W.A., Ewert, W. and Marks, R.J.II, A General Theory of Information Cost Incurred by Successful Search; in: Sanford, J.C. *et al.* (Eds.), *Biological Information: New Perspectives*, Word Scientific, NJ, 2013.
16. Drake, J.W., Charlesworth, B., Charlesworth, D. and Crow, J.F., Rates of spontaneous mutation, *Genetics* **148**(1):1667–1687, 1998.
17. Behe, M.J., *The Edge of Evolution, The Search for the Limits of Darwinism*, Free Press, New York, 2007.
18. Truman, R., Information Theory—part 3: introduction to Coded Information Systems, *J. Creation*, **26**(3):115–119, 2012; creation.com/cis-3.
19. Truman, R., Information Theory—part 4: fundamental theorems of Coded Information Systems theory, *J. Creation*, **27**(1):71–77, 2013; creation.com/cis-4.
20. Wieland, C., Superbugs not super after all, *Creation* **20**(1):10–13, 1997. Purdom, G., Antibiotic Resistance of Bacteria: An Example of Evolution in Action? answersingenesis.org/natural-selection/antibiotic-resistance/antibiotic-resistance-of-bacteria-evolution-in-action/.
21. Truman, R., Information Theory—part 1: overview of key ideas, *J. Creation* **26**(3): 101–106, 2012, creation.com/cis-1.
22. Truman, R., Information —part 2: weaknesses in current conceptual frameworks, *J. Creation* **26**(3):107–114, 2012; creation.com/cis-2.
23. Human and computer languages use grammatical rules which allow the intended meaning to be interpreted. These rules don't need to be re-sent with each communication since the receiver already possess them and knows how to use them. Our minds permit integration with past and present context to infer many things thus simplifying what the sender needs to communicate.
24. Astin, J.A., Shapiro, S.L, Eisenberg, D.M. and Forys, K.L, Mind-Body medicine: state of the science, implications for practice, *J. Am. Board Fam. Med.* **16**(2):131–147, 2003, doi: 10.3122/jabfm.16.2.131
25. To illustrate, we suggest looking at horizontal gene transfer more carefully. Are random pieces of DNA being exchanged, or are the pieces meaningful, for example, such that entire intact genes are transferred which would be operational in the new host? Researchers could look for quality control features guiding how the DNA received gets incorporated into the host genomes. Perhaps duplicates are avoided.
26. Oyama, S., *The Ontogeny of Information: Developmental Systems and Evolution*, Duke University Press, 2000.
27. Levels of oxygen, glucose, mineral ions, pH, temperature, and so on must be regulated to within narrow ranges if an organism is to survive. Martini, F.H., Nath, J.L. and Bartholomew, E.F., Fundamentals of Anatomy & Physiology, 9th edn, Pearson Education, 2012. Relevant portions are available online. See An Introduction to Anatomy and Physiology, Homeostatis and system integration, ©2003 Pearson Education, Inc., wps.aw.com/wps/media/objects/451/462581/CH01/html/ch1_4.html
28. Mayr, E., *This is Biology: The Science of the Living World*, First Harvard University Press, 8th printing, p. 75, 2001.
29. Lorenz, K., *Behind the Mirror: A Search for a Natural History of Human Knowledge*, Mariner Books, New York, 1978.
30. Oyama, ref. 26, p. 132.
31. Cosner, L., 'No death before the Fall'? The importance of the distinction of nephesh chayyah life, creation.com/no-death-before-the-fall. "We don't argue that plants and insects, etc. didn't die before the Fall, and 'what about skin cells' has always been a ridiculous straw man argument: we believe that certain forms of cell death would have had to be programmed at creation, as they are necessary for all multi-cellular life. Broadly speaking, there was no death of vertebrates."
32. Hopkinson-Woolley, J., Hughes, D., Gordon, S. and Martin, P., Macrophage recruitment during limb development and wound healing in the embryonic and foetal mouse, *J. Cell Science* **107**:1159–1167, 1994.
33. Limb development, en.wikipedia.org/wiki/Limb_development.
34. Carey, N., *The Epigenetics Revolution: How Modern Biology is Rewriting Our Understanding of Genetics, Disease and Inheritance*, Icon Books, London, UK, 2012.
35. Junker, R., Die Plastizität der Lebenwesen: Baustein für Makroevolution? (The plasticity of living organisms: buildingblocks for macroevolution), *W+W Special Paper B* **14**(2), August, 2014, www.wort-und-wissen.de/artikel/sp/b-14-2-plastizitaet.pdf.
36. Greene, E., A diet-induced developmental polymorphism in a caterpillar, *Science* **243**(4891):643–646, 1989.
37. Schlichting, C.D. and Smith, H., Phenotypic plasticity: linking molecular mechanism with evolutionary outcomes, *Evol. Ecol.* **16**:189–211, 2002, www.bgu.ac.il/desert_ecology/Novoplansky/Plasticity course 2005-6/Schlichting and Smith.pdf.
38. Trifonov, E.N, Multiple codes of nucleotide sequences, *Bull. Mathematical Biology* **51**:417–432, 1989.
39. Montañez, G., Marks, R.J. II, Fernandez, J. and Sanford, J.C., Multiple Overlapping Genetic Codes Profoundly Reduce the Probability of Beneficial Mutation; in: *Biological Information: New Perspectives*, Sanford, J.C., *et al.* (Eds.), Word Scientific, 2013.
40. Trifonov. E.N., Thirty Years of Multiple Sequence Codes, *Genomics, Proteomics & Bioinformatics* **9**(1–2):1–6, 2011, www.sciencedirect.com/science/article/pii/S1672022911600016.
41. Trifonov, E.N., Second, third, fourth … genetic codes—One spectacular case of code crowding, vimeo.com/81930637
42. For example, Microsoft's DOS operating system was conceived as a single-user system running on isolated hardware. This architectural design does not lend itself to easy improvement for multiple user servers nor to prevent attacks from hackers over the internet. Other operating systems were designed from the beginning with other goals in mind.
43. Gould, J.S., The Structure of Evolutionary Theory, Harvard University Press, 2002. Goldschmidt's Saltation Theory comes to mind and is discussed in this reference.
44. Oyama, ref. 30. The term appears repeatedly in her work and in those she references.
45. Noble, D., Physiology is rocking the foundations of evolutionary biology, *Exp. Physiol.* **98**(8):1235–1243, 2013.
46. Ochman, H., Lawrence, J.G. and Groisman, E.A., Lateral gene transfer and the nature of bacterial innovation, *Nature* **405**:299–304, 2000.
47. Guliuzza, R.J., Darwin's Sacred Imposter: Natural Selection's Idolatrous Trap, www.icr.org/article/darwins-sacred-imposter-natural-selections/
48. Axe, D.D., The case against a Darwinian origin of protein folds, *BIO-Complexity* **1**:1–12, 2010, doi:10.5048/BIO-C.2010.1; bio-complexity.org/ojs/index.php/main/article/view/BIO-C.2010.1/BIO-C.2010.1

Royal Truman *has bachelor's degrees in chemistry and in computer science from State University of New York; an MBA from the University of Michigan (Ann Arbor); a Ph.D. in organic chemistry from Michigan State University; and a two-year post-graduate 'Fortbildung' in bioinformatics from the Universities of Mannheim and Heidelberg. He works in Germany for a European-based multinational.*