

Grand Designs and Facile Analogies

Matt Young

Department of Physics
Colorado School of Mines
Golden, Colorado 80401

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Though analogy is often misleading, it is often the least misleading thing we have.

— SAMUEL BUTLER

Much of what we know or think we know, it seems to me, is based on analogy. When we describe a gas as a collection of colliding billiard balls, our model is based on an analogy. When we think of a gene as fighting for its survival against other genes, our model is based on an analogy. When we ask whether a photon is a wave or a particle, however, our analogy breaks down, because the photon has both wave and particle properties.

It is thus necessary to use analogy judiciously.

The neocreationists Michael Behe (1996) and William Dembski (1999, 2002) do no such thing with their analogies of the mousetrap and the archer. (Perakh, 2001) Behe especially expects his analogy to bear the heavy burden of illustrating his point. If the analogy fails, then the entire argument is likely to fail. Dembski, likewise, leans heavily on a flawed analogy and covers up its failure with mathematical notation and invented jargon.

Behe's Opaque Box

Behe, a biochemist, argues that his own field is somehow more fundamental than all others. He notes that biochemistry is extremely complicated and points to some systems that are so complicated that they are *irreducibly complex*.

Irreducible complexity. According to Behe, a system is irreducibly complex if it includes three or more parts that are crucial to its operation. The system may have many more than three parts, but at least three of those parts are crucial. An irreducibly complex system will not just function poorly without one of its parts; it will not function at all.

Behe has found several biochemical systems that he claims are irreducibly complex. Such systems, argues Behe, cannot have evolved gradually, by slight modifications, because they will not work at all if one of their crucial parts is missing. I do not want to discuss Behe's claim in detail; rather, I want to concentrate on his analogy of the mousetrap.

Behe uses the common mousetrap to exemplify a system that, he claims, is irreducibly complex. Figure 1, left, shows a mousetrap, which includes a hammer, a spring, a pin (which passes through the center of the spring), a latch, a bar, a platform, and a handful of other parts such as staples. The bait, which is not crucial to the operation of the trap, is not shown. The bar is used to hold the hammer in place and is in turn held in place by the latch. When the mouse takes the bait, he dislodges the bar and frees the hammer, which is driven by the spring and snaps closed, with unfortunate consequences for the mouse.

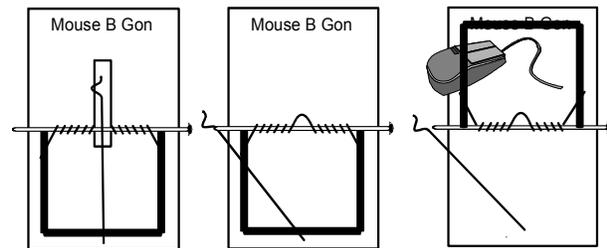


Figure 1. Left, a mousetrap with the conventional latching mechanism. Center, with the latch removed. Right, the mousetrap still functions.

Behe claims that the mousetrap is irreducibly complex, that is, that it cannot function without all of its parts. The statement is entirely wrong. I have acquired a mousetrap and removed the latch. In the mousetrap I used, it was a simple matter to wedge the bar under the pin in such a way that it was barely stable, as shown in Figure 1, center. No bending or filing was necessary. If the mouse dislodged the bar from the left side of the trap, he probably got away with a good scare. But if he dislodged the bar from the right (platform) side, he was probably caught. Thus, the reduced mousetrap is not nearly as good as the original trap, but it still works.

My mousetrap has seven parts, not counting staples. Could Behe merely have counted wrong, and is the mousetrap with six parts irreducibly complex? No. John McDonald (2000) has shown that the trap can be reduced successively to fewer and fewer parts, until only the spring remains. Dembski (2002) has criticized McDonald's approach, claiming that McDonald has modified some parts as he has removed others.

Irreducible complexity, to Dembski, means that a given part has to be removed with no changes to any of the others. And that points out exactly what is wrong with the concept of irreducible complexity.

In biology, parts that were used for one purpose may be coopted, altered, and used for another purpose. A well known example is the development of the mammalian ear from reptilian jaw bones. Specifically, Gould (1993) gives good evidence that bones that originally supported the gills of a fish evolved first into a brace for holding the jaw to the skull and then into the bones in the inner ear of mammals.

Those jaw bones did not just suddenly one day re-form themselves and decide to become ear bones; because mammals did not need unhinging jaws, the jaw bones gradually changed their shape and their function until they became the bones of the inner ear. They evolved into the ear bones in part because snakes are not wholly deaf but rather can hear by sensing vibrations in precisely those bones. The ear is today irreducibly complex, but once it was not. You might, however, be fooled into thinking that the ear could not have evolved if you did not know exactly how it originated.

Blueprints versus recipes. What is the difference between a mouse and a mousetrap? Or more precisely, how do mice propagate, and how do mousetraps propagate? (Young, 2001a)

Table 1. How mice differ from mousetraps

Mousetraps propagate by <i>blueprints</i>	Mice propagate by <i>recipes</i> , not blueprints
<i>Exact</i> specifications Errors do not propagate	<i>Inexact</i> specifications Errors propagate
<i>Finite</i> changes, if any	<i>Small</i> or infinitesimal changes
All mousetraps of given generation identical	All mice of given generation different

Mousetraps propagate (are propagated, really) by blueprints, or exact specifications (Table 1). Each mousetrap in a given generation is nominally identical to each other mousetrap. If there are differences among the mousetraps, they are usually not functional, and they do not propagate to the next generation. Changes from one generation to the next, however, may be very significant, as when the designer triples the strength of the spring or doubles the size of the trap and calls it a rat trap.

The genome, by contrast, is a recipe, not a blueprint. The genome tells the mouse to have hair, for example, but it does not specify where each hair is located, precisely as the recipe tells the cake to have bubbles but does not specify the location of each bubble. Additionally, the specifications of each mouse differ from those of each other mouse because they have slightly different genomes. Thus, we could expect a mouse to evolve from a protomouse by a succession of small changes, whereas we can never expect a mousetrap to evolve from a prototrap.

This is so because the mousetrap is specified by a blueprint, the mouse by a recipe. If improvements are made to a mousetrap, they need not be small. It is therefore no criticism of McDonald to argue, as Dembski does, that McDonald cannot reverse-engineer a complex mousetrap by building it up from his simpler examples. It is Behe, not McDonald, who has erred in using the mousetrap as an analog of an evolving organism—in part because the mousetrap is made from a blueprint, not a recipe.

Half a flagellum. Behe argues that an irreducibly complex system cannot evolve by small changes. His preferred example is the flagellum, and he asks, in essence, “What is half a flagellum?” A flagellum without its whiplike tail or without its power source or its bearing cannot work. Behe cannot imagine how each part could have evolved in concert with the others, so he decides it could not have happened. In this respect, he echoes the smug self-confidence of the creationist who asks, “What good is half an eye?” An eye, according to the creationist, has to be perfect or it has no value whatsoever.

This logic is easily debunked: (Young, 2001b) As any near-sighted person will tell you, an eye does not have to be perfect in order to have value. An eye does not even have to project an image to have value. Indeed, the simplest eye, a light-sensitive spot, gives a primitive creature warning of an approaching predator. A sophisticated computer simulation has shown

how an eye capable of casting an image can evolve gradually, possibly within a few hundred thousand years, from such a simple eye spot, through a somewhat directional eye pit, to a spherical eye that cannot change focus, and finally to an eye complete with a cornea and a lens. (Nilsson and Pelger, 1994)

Because the eye is composed of soft tissue, we do not have fossil evidence of the evolution of eyes in this way. Nevertheless, every step that appears in the simulation is represented in some animal known today. The inference that eyes evolved as suggested in the simulation is therefore supported by hard evidence.

The eye is not irreducibly complex. You can take away the lens or the cones, for example, and still have useful if impaired vision. Nevertheless, the eye was used for years as an example of a system that was too complicated to have evolved gradually. It is not, and neither is the flagellum. (Stevens, 1998; Cavalier-Smith, 1997)

Emergence. The physical world can be thought of as a series of levels, each underlain by a lower level but largely isolated from that level. Thus, the viscosity of water can be explained in terms of molecular physics, but you do not have to understand molecular physics to appreciate viscosity and indeed to study it. Viscosity is an example of an *emergent property*, a property that, in this case, appears only when we assemble a large number of water molecules under certain conditions of pressure and temperature.

Emergent properties are the result of self-organization and force reality into a series of levels: biochemical, organelle (an “organ” within a cell), cell, organ, organism, ..., for example. No one level is more fundamental than any other. Neither liquid water nor isolated water molecules is any more fundamental than the other. Rather, each level is an alternate way of looking at reality. Viscosity does you no good if you are interested in the spectroscopy of water vapor, whereas spectroscopy does you no good if you are interested in viscosity.

Creationism has failed at the level of the organism. We understand in enough detail how an eye might have evolved to say with certainty that the creationist’s argument is no longer cogent. That argument is sometimes called a *God-of-the-gaps* argument: A gap in our understanding is seen as evidence for a divine creator.

Aware that the half-an-eye argument has failed, Behe has developed the half-a-flagellum argument. He has dressed it up with a rigorous-sounding term: irreducible complexity. But it is still the half-an-eye argument. Terminology apart, Behe’s argument is pure God-of-the-gaps. If we do not know today how a flagellum could have evolved from simpler systems, then we never will. If we do, then the Behe of the day will surely slither down another level and find an argument at the level of, say, physics, rather than biochemistry.

All that based on the flawed analogy of the mousetrap.

Dembski's Arrow

William Dembski (1999) invites us to consider an archer who shoots at a target on a wall. If the archer shoots randomly and then paints a target around every arrow, says Dembski, we may infer nothing about the targets or the archer. On the other hand, if the archer consistently hits a target that is already in place, we may infer that he is a good archer. His hitting the target represents what Dembski calls a pattern, and we may infer design in the sense that the arrow is purposefully, not accidentally, centered in the target.

Using the archer as an analogy, Dembski notes that, in biology, we find genes that are highly improbable, yet not exactly random. That is, the genes contain information; their bases are not arranged arbitrarily. Dembski calls such improbable but nonrandom genes *complex* because they are improbable and *specified* because they are not random. A gene or other entity that is specified and complex enough displays *specified complexity*. Arrows sticking out of targets that have been painted around them are complex but not specified; arrows sticking out of a target that has been placed in advance are specified.

According to Dembski, natural processes cannot evolve complexity in excess of a certain number of bits, that is, cannot evolve specified complexity. His claim is not correct. We can easily see how specified complexity can be derived by purely natural means, for example, by genes duplicating or by organisms incorporating the genes of other organisms. In either case, an organism whose genome has less than the putative upper limit, 500 bits, can in a single stroke exceed the upper limit, as when an organism with a 400-bit genome incorporates another with a 300-bit genome. (Young, 2002) Here I want to concentrate, not on the 500-bit limit, but on the arrow analogy and its pitfalls.

Many targets. Consider a biological compound such as chlorophyll. Chlorophyll provides energy to plant cells, and most (but not all) of life on earth either directly or indirectly depends for its existence on chlorophyll. The gene that codes for chlorophyll has a certain number N of bits of information. Dembski would calculate the probability of that gene's assembling itself by assuming that each bit has a 50 % probability of being either 0 or 1. (Wein, 2002) As I noted earlier, (Young, 1998) in connection with a book by Gerald Schroeder, such calculations are flawed by the assumption of independent probabilities, that is, by the assumption that each bit is independent of each other bit. Additionally, they assume that the gene in question has a fixed length and that the information in the gene has been selected by random sampling, whereas most biologists would argue that the gene developed over time from less complex genes.

But Dembski makes a more fundamental error: He calculates the probability of occurrence of a specific gene and also considers genes that are homologous with that gene (it's not chlorophyll but rather a gene called T-urf13). In other words, he calculates the probability of a specific gene and only those genes that are closely related to that gene. In terms of the archer analogy, Dembski is saying that the target is not a point but is a little fuzzy. Nevertheless, calculating the probability of a specific gene or genes is the wrong calculation, and the error is exemplified in Dembski's archer analogy.*

Let us do a Dembski style analysis using the example of chlorophyll. According to the *Encyclopedia Britannica*, there are at least 5 different kinds of chlorophyll. There may be

potentially many more that have never evolved. Thus, as shown in Figure 2, the archer is not shooting at a single, specific target on the wall, but at a wall that may contain a very large number of targets, any one of which will count as a bull's-eye. Dembski should have considered the probability that the archer would have hit any one of a great number of targets, not just one target.

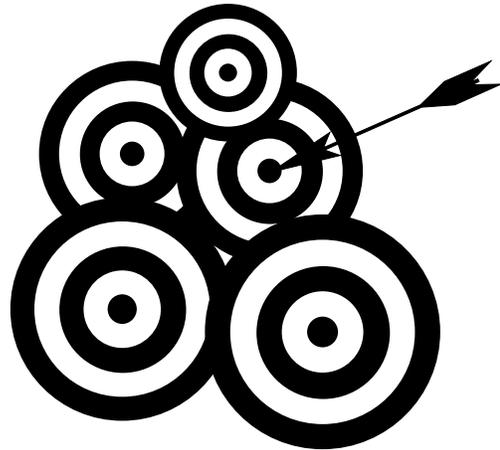


Figure 2. Bull's eye!

Chlorophyll, moreover, is not necessary for life. We know of bacteria that derive energy from the sun but use bacteriorhodopsin in place of chlorophyll. Other bacteria derive their energy from chemosynthesis rather than photosynthesis and do not need light at all. If we are interested in knowing whether life was designed, then we have to calculate the probability that any energy-supplying mechanism will evolve, not just chlorophyll. Thus, photosynthesis, chemosynthesis, and all their variants must show up as targets on the wall, as well as other perhaps wholly unknown mechanisms for providing energy to a cell, as suggested in Figure 3.

I do not think Dembski is arguing that life takes a single shot at a target and either hits it or not; he knows very well that complexity was not born instantaneously. The target is a distant target, and the path is tortuous. But by using his archer analogy, Dembski implies that life is very improbable, and the target impossible to hit by accident. They may or may not be: There are more galaxies in the known universe than there are stars in our galaxy. Life has arguably had a great many opportunities to evolve. That it evolved complexity here is no doubt improbable; that it evolved complexity somewhere is very possibly not.

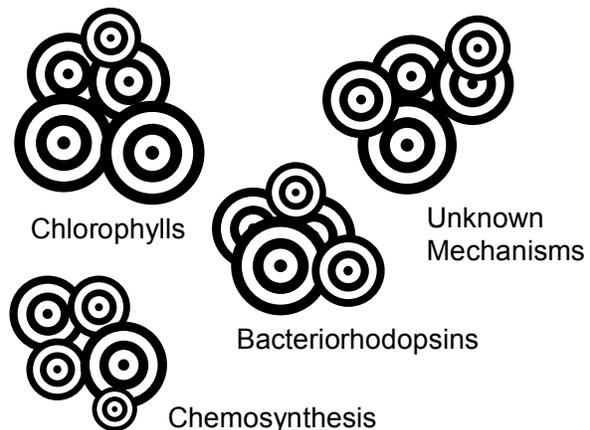


Figure 3. What Dembski's wall really looks like.

In terms that Dembski knows very well, his *rejection region* should have included many more possibilities than just a handful of homologous genes. In my example, the rejection region should have included a set of targets for chlorophyll, a set for bacteriorhodopsins, a set for chemosynthesis, and so on—on every planet in the universe. Now, it is entirely possible that even such an extended rejection region will yield a very low net probability, but Dembski has shown no such thing. And he cannot, since we do not know just how much of the wall is covered with targets, nor how many arrows the archer has launched to get just one hit, nor how many archers there are in the universe.

It is peculiar that Dembski makes this mistake, because when it suits him he recognizes that you have to consider an ensemble of possibilities. Thus, in *No Free Lunch* (p. 221), he describes a calculation for designing a radio antenna that radiates uniformly in all directions. According to Dembski, such an antenna can be designed by using a genetic algorithm. A genetic algorithm is a mathematical formalism that gradually modifies the antenna, one step at a time, until the antenna radiates uniformly or nearly so. Oddly, the resulting antenna is not a regular geometric shape such as a pyramid but rather is a tangled mass of wires.

Such an antenna, says Dembski, is highly improbable, since it is one of an infinity of possible antennas. High improbability or low probability is by Dembski's definition complex. A genetic algorithm mimics biological evolution. If the genetic algorithm can generate complexity, then so can descent with modification.

Figure of merit. Dembski does not deny that the formula for describing the antenna exhibits specified complexity, but claims instead that the specified complexity has been sneaked in. How?

The function that describes the radiation by the antenna in any direction is called the antenna pattern. The desired antenna pattern is uniform, that is, it can be described by a single constant value that represents the strength of the radiation in any direction. On a three-dimensional graph, such an antenna pattern is a sphere.

A real antenna pattern will differ measurably from a sphere. To quantify the difference between the real antenna pattern and the sphere, we define a *fitness function*. (Kauffman, 1995) Dembski claims that the engineers sneaked complexity into their calculation when they defined the fitness function.

My job is to make hard subjects easy, rather than the other way around. Let us therefore consider a simple case: a system of three numbers, each of which can be either 0 or 1. Let us say that the system is most fit when all three numbers are 1. Initially, however, the three numbers are chosen randomly and are not all equal to 1. We want to use a mathematical algorithm (it does not matter which one) that repeatedly changes one or more of the three numbers in some random fashion until they converge on the fittest configuration (111).

For the purpose, we define an *ad hoc* fitness function. For this example, the fitness function may be the sum of the three numbers. The fitness function thus equals 0 if all three numbers are equal to 0; 1 if one of the numbers is 1; 2 if any two of the numbers are 1; and 3 if all three of the numbers are 1. We apply our algorithm time after time until all the numbers are equal to 1, that is, until the value of the fitness function equals 3.

Thus, we begin with a random configuration of the three numbers, say (010). The value of the fitness function is 1. We roll some dice or toss a coin to tell us how to rearrange the numbers according to some rule. If the fitness function becomes 2, we keep the new configuration, say (110); otherwise, we keep the old configuration and roll the dice again. We keep rolling until we attain the configuration (111).

The fitness function, then, is not some information that we sneaked in from the outside. It is not an array of numbers that we have imported in a look-up table. It is, rather, a series of numbers that we calculate as we go along. These numbers are based on the values of the three numbers in our three-number configuration *and on nothing else*. Indeed, we need not ever plot the entire fitness function, and we do not need to retain any but the previous value.

Suppose that we wanted to manufacture a bow that could launch an arrow as far as possible but yet cost as little as possible. How would we decide when the cost was too high for a given range? We might define a *figure of merit* that is equal to the range divided by the cost. Then, if one design had a lower cost or a higher range, the figure of merit would increase. Our job is to design a bow with the highest figure of merit. The figure of merit is by no stretch imported information about the design; it is rather a number that we calculate as an aid to evaluating our success. The fitness function is all possible values of the figure of merit, plotted as a function of cost and range.

Far from importing the fitness function and thereby sneaking complexity into the problem, the electrical engineers repetitively calculated a figure of merit and kept recalculating it until it converged to the desired value. The term fitness function can be misleading: Dembski would never have been fooled into thinking that the fitness function provides external information if it had been called a sequence of figures of merit.

Of spheres and flakes. Dembski thus agrees that the antenna is complex, but he argues that the genetic algorithm did not generate that complexity; rather, the engineers sneaked in complexity by choosing their fitness function judiciously and simply rearranged the information, that is, transferred it from the fitness function to the antenna. As we have seen, however, the fitness function is just a series of calculated values of a figure of merit and does not represent external or imported information.

On page 12 of *No Free Lunch*, by contrast, Dembski tells us that a regular geometric pattern such as a snowflake is not complex, because it has been formed “simply in virtue of the properties of water.” As Perakh (2002) points out, the formation of a snowflake is by no means assured when a droplet of water crystallizes in the air. Under certain conditions, triangular or hexagonal crystals may form instead. The formation of such crystals depends on the chance occurrence of unusual weather conditions. Thus, the formation of a snowflake, though likely, depends on both chance and law, not just law. Further, each snowflake is slightly different from all others, and that difference depends on the continuously changing conditions of temperature and humidity that the snowflake experienced as it fell through the atmosphere. The formation of a particular snowflake is far from determined in the way that, say, the formation of a single crystal of salt is determined.

Thus, a snowflake is only one of an infinity of possible patterns, so by Dembski’s definition, any given snowflake ought to be every bit as complex as an antenna. But when it suits Dembski, a spherical pattern is complex, whereas a snowflake remains simple because it forms by necessity. The inconsistency is transparent.

A Tangled Web

Behe and Dembski have an agenda: to *prove that* an intelligence guides evolution, rather than to *find out whether*. They have thus constructed a tangled web of analogies to convince impressionable readers that evolution must necessarily have been directed. I leave it to others to show that their chemistry and their mathematics are faulty. Here I point out only that their analogies themselves are faulty: The mousetrap is not irreducibly complex and did not evolve gradually, whereas irreducibly complex structures need not have been created out of whole cloth but rather could have evolved, like the mammalian ear, from borrowed components. Dembski's archer, meantime, is shooting at a wall that may for all we know be so thickly covered with targets that he will certainly hit several after a large number of shots.

Endnote

* Dembski makes another interesting conceptual error: On page 292 of *No Free Lunch*, he calculates the probability that all the proteins in the bacterial flagellum will come together "in one spot." Besides the assumptions of equal and independent probabilities, that is simply the wrong calculation. Dembski should have calculated the probability of the genes that code for the flagellum, not of the flagellum itself. He treats the protein URF13 similarly on pages 218-219.

Matt Young is the author of *No Sense of Obligation, Science and Religion in an Impersonal Universe*, 1stBooks Library, Bloomington, Indiana (2001); www.1stBooks.com/bookview/5559.

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