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**On the Application of Irreducible Complexity**

Joshua A. Smart\*, 5/31/03

Abstract

The purpose of this paper is to provide a framework and direction for a more rigorous application of irreducible complexity. Critical responses to irreducible complexity have primarily consisted of just-so-stories that substitute vague appeals to chance or other forces for well-thought-out counter-arguments. Intelligent design theorists have noted the lack of substance in critiques of their work, but there has been virtually no attempt to level more specific challenges to evolutionary theory. *Intelligent design will not advance within the scientific community as long as it continues to engage in this exchange of generalities.* Progress lies in application. To that end, this paper describes a process for applying irreducible complexity, with particular attention to determining the irreducible core of a system.

“By *irreducibly complex* I mean a single system composed of several well-matched, interacting parts that contribute to basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning. An irreducibly complex system cannot be produced directly...” - Michael Behe in *Darwin's Black Box*<sup>1</sup>

Introduction

It is doubtful that there will ever be a concept more earth shattering in the intelligent design community than that of irreducible complexity. In many ways its origination and impact can be seen to be analogous to the concept of natural selection in evolutionary biology.

For example, both irreducible complexity and natural selection were first introduced in books, as opposed to journals. Natural selection proposed in Charles Darwin's *The Origin of Species*, and irreducible complexity in Michael Behe's *Darwin's Black Box*. The concepts shared immediate and vigorous denouncement by many. It is also interesting to note that much of the reaction to the idea of natural selection was due to its perceived assault on the theistic underpinnings of both the popular and scientific communities of the day. Many, myself included, believe that much of the reaction to irreducible complexity was also due to its perceived assault on the philosophical underpinnings of the culture in which it was introduced, however this time the philosophy was naturalistic.

While various scientists had promoted a naturalistic origin of life prior to the publication of *The Origin of Species*, it was not until Darwin formulated the concept of natural selection that the idea of evolutionary origins was acknowledged as a theory worthy of scientific consideration. In much the same way, many have claimed that evolution lacks the power to produce complex systems, but it was not until Michael Behe formulated the concept of irreducible complexity that reviews and letters to editors in journals like *Nature* and *Science*, and that debates over irreducible complexity, such as the one hosted by the Smithsonian in 2002, became commonplace.

*The Origin of Species* in no way settled the debate over evolution, nor was it even the final word on natural selection. The arguments Darwin presented were based upon preliminary study of available information and on conjecture. If evolutionary proponents had simply endlessly debated the ideas put forth in *The Origin of Species* and never applied the concepts to nature through rigorous scientific study, evolutionary theory would have fallen flat.

*Darwin's Black Box* too consists chiefly of analysis of information already present. But it remains to be seen if irreducible complexity will ultimately follow natural selection in application and acceptance. While there has been some work with irreducible complexity within the design community, the main thrust of this labor has focused upon restating or refining the theoretical framework. There has been precious little application of the concepts first laid out by Behe. It is eminently important for the field of intelligent design that scientists become more active in the application of irreducible complexity, not merely in philosophical debate about its validity.

The purpose of this paper is to provide a framework and direction for a more rigorous application of irreducible complexity. Critical responses to irreducible complexity have primarily consisted of just-so-stories that substitute vague appeals to chance or other forces for well-thought-out counter-arguments.

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\* Vanderbilt University Intelligent Design and Evolution Awareness Club, VU#352725 Station B, 2301 Vanderbilt Place, Nashville, TN 37235-2725, joshua.a.smart@vanderbilt.edu

Intelligent design theorists have noted the lack of substance in critiques of their work, but there has been virtually no attempt to level more specific challenges to evolutionary theory. *Intelligent design will not advance within the scientific community as long as it continues to engage in this exchange of generalities.* Progress lies in application. To that end, this paper describes a process for applying irreducible complexity, with particular attention to determining the irreducible core of a system.

### Choice of System for Evaluation

The first thing to note in the determining the complexity of a biological system is the immense benefits of working with a system that is biochemical in nature. Indeed, the subtitle of *Darwin's Black Box* is, "The Biochemical Challenge to Evolution." Behe demonstrates how attempts to apply the concept of complexity as a challenge to Darwinism has run into problems in the past, partly because the systems discussed were not biochemical<sup>2</sup>. Behe describes his reasoning in terms of black boxes. A black box is a system, or part of a system, the inner workings of which are not completely clear. For many years scientists only understood biology on a macroscopic level. The underlying causes were a black box. Now that we are able to investigate biochemistry, however, there are no more black boxes. That is, we know that the reason that biomolecules behave the way they do is their chemical composition, not another level of biology.

While Behe is certainly correct to focus on biochemical systems when making the argument for irreducible complexity, it is possible to be more specific. It is desirable that the system in question be understood as the result of a reasonable number of gene products exhibiting as little hierarchy of structure as possible.

Thinking of the system in terms of gene products puts the focus on the actual genetics upon which evolution acts. It also allows for the inclusion of components that are necessary for the production of a system, but are not necessarily seen in the final product (e.g. scaffolding or transcription regulators).

To understand what I mean by hierarchical structure, consider a car. The function of a car is transportation. A major player in the production of this transport is the engine. However, an engine functions in and of itself without necessarily helping a car to transport people. There are also subsystems within the engine that perform functions not necessarily bound to the overall function of the engine. For a car, one can find instructions on putting a particular piece of the engine together, the whole engine together, and putting the final car together with an engine, transmission, etc.

The power of the concept of irreducible complexity is that it invalidates the step-by-step *process* of evolution, not just the *product*. The point mutations, gene duplications, insertions and deletions, and all other mutations that produce the steps in the evolutionary process occur at the genetic level, at the level of instructions. Changing the engine of a car (assuming a change of some importance) involves changing all the levels of instruction listed above. The higher up the hierarchy of structure of the car, the more changes in the instructions must be considered. The farther removed from that genetic level a system is, the more genes must be looked at, and not just more genes, but more complex genetic interactions as well.

Some hierarchy may be unavoidable. For instance, we know the gene products that are responsible for producing the eubacterial flagellum, yet it contains structures such as the motor or the driveshaft that are composed of multiple proteins. Fortunately, in the flagellum and most biochemical systems, this hierarchy is minimal, and it is also relatively easy to determine the number and type of gene products that compose these substructures.

Higher order systems, such as organs or organ systems, are composed many gene products working together in many levels of organization. A protein may be vital for the functioning of some structure within that system, but is that particular structure necessary? Perhaps there is some other combination of gene products that could do the job, though not necessarily with the same structure. Not only would it be necessary to show which gene products and structures are vital to the system (and/or system precursors) but it would also be necessary to investigate the embryonic development of the system to determine if there are any gene products that are required for the development of the system, but are not essential- maybe not even present- in the fully developed organism. In the end, although many higher-level systems could very well be irreducibly complex, there are too many variables involved to make that assessment of their complexity an attractive prospect.

## The Irreducible Core

### *Importance of the Irreducible Core*

Selecting a potentially irreducibly complex system is the easy part. There are thousands of biochemical structures and pathways, many of which give indications of being irreducibly complex. After selecting the system comes the most difficult, the most time consuming, and, I believe, the most important part of the process. That part is determining the irreducible core of the system. What exactly are the gene products that make the system irreducible? No matter how many irreducibly complex systems are found, or how complex those systems are, the notion of irreducible complexity remains vague until irreducible cores are determined. When the concept remains vague, it allows for vague argument.

Take for example Dr. Kenneth Miller. Dr. Miller is a professor at the prestigious Brown University in Rhode Island, and is a notorious opponent of intelligent design. He opposes the notion that the eubacterial flagellum is irreducibly complex, and therefore could not have evolved in a step-by-step Darwinian process. Miller's main argument, for a long time, has been that a part of the flagellum looks like the Type III Secretory System (TTSS) used by some bacteria to introduce toxins to eucaryotic cells (see, for example, [3]). Miller argues that eubacteria borrowed the TTSS for the evolution of the flagellum. This leads him to propose that the flagellum is simply a composite of pieces co-opted from other systems within the cell.

There have been multiple responses to this argument within the intelligent design community (see, for example, [4]), yet about three months ago, Miller posted on his website his contribution to the volume *Debating Design: From Darwin to DNA* due to be released in 2004<sup>5</sup>. The article is entitled, "The Flagellum Unspun: The Collapse of 'Irreducible Complexity.'" In it he rehashes the "co-option of TTSS" argument once again. While I certainly feel that Dr. Miller's intelligent design opponents have gotten the better of their exchanges, I find it troubling that they have not been able to deter him from presenting essentially the same argument over and over again. It has been pointed out (among other arguments) that there is much more to the flagellum than the secretory machinery that Miller discusses<sup>4</sup>. But there has not been anyone (to my knowledge) who has challenged Dr. Miller to account for other specific components of the irreducible core.

The elucidation of irreducible cores is a vital step for proponents of irreducible complexity. Without this, exchanges with antagonists such as Ken Miller will continue to be vague, and not very fruitful.

### *Defining "Irreducible Core"*

The concept of an irreducible core has been around for a while (see, for example, [6]). However, it was William Dembski who formalized the idea in his tome *No Free Lunch*. In chapter five of this book, called, "The Emergence of Irreducibly Complex Systems," Dembski takes Behe's original definition of irreducible complexity and proposes several ways to tighten it up. Behe defined an irreducibly complex system as one: "composed of several well-matched, interacting parts that contribute to the basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning."<sup>1</sup> Dembski points out that, while the concept of irreducible complexity is mostly right when defined in this way, there are some points that can be added, or made more explicit in order to make the definition more rigorous. Dembski's final definition is:

"A system performing a given basic function is *irreducibly complex* if it includes a set of well-matched, mutually interacting, nonarbitrarily individuated parts such that each part in the set is indispensable to maintaining the system's basic, and therefore original, function. The set of these indispensable parts is known as the *irreducible core* of the system."<sup>7</sup>

This definition of irreducible complexity is more explicit and introduces the irreducible core.

As Dembski defined it, the irreducible core of a system is, "The set of these indispensable parts," without which the system could no longer function. So the first question is, naturally, "How do we determine which system components are indispensable?"

### *Knockout Experiments*

The best tool thus far in determining whether a gene product is indispensable has been the knockout experiment. In a knockout experiment, mutagenesis is used to produce a null mutant, a gene that exhibits no phenotype whatsoever.

The use of knockout experiments in determining an irreducible core is obvious. Suppose that a researcher is studying a system that suspected to be irreducibly complex and composed of gene products gpA, gpB, ... gpX. Ideally, a knockout of each one of these genes would be able to be produced. If an organism in which there is a null mutation in the gene that encodes gpA is observed to have a functioning system, even if the system is not functioning as well as when gpA is present, then gpA is not indispensable. If an organism with a null mutation in gpB is observed to have a completely nonfunctioning system (or to not have a system at all) then gpB can be ascribed to the irreducible core.

It seems pretty simple: determine the genes involved, generate knockouts of each of the genes, score the phenotypes and you have an irreducible core. But, of course, nothing in life is ever quite that simple, and there are some complications that are bound to arise.

### *Approaches*

Later, I will discuss three specific problems that can arise when trying to determine an irreducible core, but first, I would like to discuss three different approaches that a researcher can take to solving these problems: Strict, Assumptive, and Concessionary. These are general ways to approach any description (not just the irreducible core). However, no author uses any one of the approaches exclusively. Usually an author will make judgment calls based on the time and expenses involved, and the importance of a particular point.

In the Strict approach nothing is assumed, and nothing is taken for granted. Ideally, this is the way every problem would be approached. If meticulously carried out, a Strict approach leaves no one on the short end of the stick. The disadvantage is that taking the Strict approach often involves going through meticulous, time-consuming detail.

For example, it is possible that the secretory proteins of the eubacterial flagellum have been co-opted from the TTSS. It is also possible, that the TTSS is descended from the flagellum instead of the other way around. A Strict approach to determining the irreducible core of the flagellum would involve gathering the information necessary to determine which system came first. If it was the TTSS, then the excretory proteins could be listed all together as one component of the irreducible core. If it were the flagellum, then all of the indispensable parts would be listed individually.

When the time necessary to fleche out details is not worth the benefit gained, assumptions can be made. These assumptions can take two forms: those that strengthen the argument, and those that weaken the argument.

In the approach I have labeled Assumptive, when the Strict approach becomes unfeasible, or undesirable, assumptions are made that benefit the argument. Taking the Assumptive approach to the TTSS-flagellum problem would mean assuming that the flagellum is not the result of co-option, and that each indispensable gene product can be listed individually as a part of the irreducible core. While this strengthens the results that get put onto paper, it can prove to be detrimental, as self-serving assumptions are easy targets for attack. Because of this, the Assumptive approach is rarely used.

The easiest way to avoid offering up easy targets for counterattack, is to take a Concessionary approach. In this approach simplifying assumptions are made to disfavor one's own argument. In this case the TTSS would be assumed to be the predecessor of the flagellum, and the gene products involved in secretion would all be listed together as one component of the irreducible core. While this may make the end results not appear quite as strong on paper, an argument that is still well backed even with a Concessionary approach is obviously a good one. In the end it may seem even stronger in the mind of the reader.

### *The Substructure Problem*

The first common complication in determining the irreducible core that we will look at is the substructure problem. This problem arises when there is some substructure of the original system that is able to provide a useful function by itself. This could be indicated by knocking out all the other components of the system, or, what is much more likely and feasible, observing that the substructure bears resemblance to part, or all of another structure in the cell.

A good example of the substructure problem is the Type III Secretory System so often called upon by Ken Miller. While I differ with Dr. Miller on the implications of their homology, there is no denying the presence of similarity between the secretory components of the flagellum and the TTSS (for a discussion see [8]). The proteins that are involved in flagellar secretion are indispensable, in that if they are knocked out there will not be a working flagellum. But they can all be packaged together apart from the flagellum, and still benefit the cell. What is to be done in this situation?

One solution, if the substructure actually does appear to have come from the system, or if the author is willing to make a concession, is to simply treat the products of genes that are homologous to TTSS genes as one component. That is, instead of considering the products of FlhB, FliQ, FliR, FliP, FliI, and FlhA all components of the irreducible core, count the export machinery as one component.

To apply this to the generic example, suppose that gene products gpA through gpJ are indispensable for the system, but gpD through gpJ compose a substructure that is homologous to some other system in the cell, SysX. Even though these gene products are each indispensable to the system in question, they would only be counted as one component, and the irreducible core would be scored as gpA, gpB, gpC, and SysX.

### *The Double-Up Problem*

The double-up problem is related to the substructure problem and is exemplified in the claims of the esteemed Dr. Russell Doolittle of the University of California at San Diego. In *Darwin's Black Box*, Michael Behe claimed that the vertebrate blood clotting system was irreducibly complex<sup>9</sup>. He pointed out that if any protein in the blood clotting cascade is eliminated the organism will suffer one of two fates. It may become a "bleeder," (i.e. have difficulty forming blood clots) drastically increasing the likelihood of bleeding to death. The alternative result is that the animal will begin to randomly form clots when they are not necessary. An effect no better than the first, as the animal will likely die at a young age due to a stroke or heart attack.

Dr. Doolittle claimed that Behe had overlooked some contrary evidence<sup>10</sup>. He pointed to a 1996 paper entitled, "Loss of fibrinogen rescues mice from the pleiotropic effects of plasminogen deficiency."<sup>11</sup> He claimed that the paper showed that mice deficient in *two* proteins, fibrinogen and plasminogen, instead of just one or the other were actually as healthy as those with no proteins missing. Now, as it turns out, Doolittle had misread the paper, and those mice that were missing fibrinogen and plasminogen had the same phenotype as mice only missing fibrinogen<sup>12</sup>. Nevertheless, the good doctor brings up an important point. It is conceivable that there would be some system in which a multiple knockout might function to some extent even though either single knockout loses function.

This is somewhat perplexing to the researcher. Is he then to eliminate every single combination of gene products imaginable within the original system? For a system of N components this would mean N! experiments! Chances are, there are going to be very few systems in which this type of approach is even feasible, and it will certainly never be desirable.

### *General Solutions*

The substructure problem, and the double up problem are really two sides of the same coin. In both situations some subset of components are able to perform a function, even though each individual component is indispensable to the original system in question. There are at least two distinct ways of dealing with these problems:

1. Look for homologies.

This is the vital method to use for finding substructures. The TTSS-like subsystem of the bacterial flagellum was discovered by searching for homologs of flagellar components. If a subset of genes or gene products cannot be found to be homologous to some other system, then there is no reason to consider the possibility of labeling that subsystem as one core component.

2. Make reasonable assumptions.

Everyone knows what happens when you assume... and no one enjoys doing it. However, in reality, there are many assumptions that must be made, and oftentimes it is possible to make those assumptions reasonable enough as to not do severe damage to one's argument.

First, for a system that acts as a machine (e.g. the cilium or the flagellum), the main assumption that can be made is that groups of gene products that will be homologous to other systems within the cell will almost always work together on a single task, or small group of related tasks. For example, the

components of the flagellum that are homologous to the TTSS are all involved in excretion. Focusing on gene products that work on the same task may seem obvious, but it is, in fact, an assumption.

For temporally acting systems, i.e. cascades or pathways, a different assumption can be made. It would be a very long and arduous task to knockout every combination of genes possible for the blood clotting cascade. However, the results from the paper that Dr. Doolittle found give hope. The results of the study are just what one would expect. When two components of the cascade were knocked out, the mice had the same phenotype as those who only lost the component that acted *first* in the cascade. As Behe explained in his 2000 response to Doolittle,

“The pathological symptoms of only-plasminogen-deficient mice apparently are caused by uncleared clots. But fibrinogen-deficient mice cannot form clots in the first place. So problems due to uncleared clots don't arise either in fibrinogen-deficient mice or in mice that lack both plasminogen and fibrinogen.”<sup>11</sup>

If it can be shown that this pattern holds with, say, another couple of separate double knockout experiments, I think that there can be a very reasonable assumption made: If genes A, ... X are knocked out in an animal, where the alphabetical sequence is representative of the temporal action of the products of those genes, then the resultant phenotype will be the equivalent of an animal with only gene A knocked out. Of course thought should be given to the specifics of the system beforehand to determine and examine any parts that appear as if they might violate this assumption.

#### *The Compilation Problem*

The final problem that I will deal with will likely be the most ubiquitous. I have called it the compilation problem:

Hardly ever do we find that there is only one species that carries a particular system. Usually many organisms of some higher Linnaean grouping will all contain the machine or pathway. But, of course, if all of these creatures having the exact same version the system it would make things far too easy. The ugly fact is that there are usually multiple, variant editions of a system.

Upon recognizing the compilation problem, the researcher has multiple options from which to choose. He can attempt to sidestep compilation by choosing an exemplar and focusing on that one system, or one or more different techniques to compile data from multiple versions of the system might be attempted. Partly, it depends on how the researcher wishes to report the irreducible core. As seen below, the core can be thought of in terms of components, functions, or mutations. Of course, each approach has its advantages and disadvantages, and different methods will be desirable for different situations or purposes.

#### *Predecessors*

Before describing the different methods of compilation, I would like note two of their predecessors: the concepts of Thematic and UR irreducible complexity. Both of these were developed by the Internet author Julie Thomas (see, for example, [6]).

Thematic irreducible complexity relies on looking at the functions performed by proteins within a system. For example, Thomas gives this table of themes for the eubacterial flagellum (adapted from [6]):

**Table I. Flagellar Components Appear to Demonstrate Thematic IC.**

Theme	Genes/components
Capped filament	fliD, fliC/flaA/flaB*
Hook and adaptors for attachment to filament	flgE, flgK
Drive shaft	flgB, flgC
Motor complex (MS ring complex)	motA,motB, fliF
Switch	fliG
Export machinery	flhA,flhB, fliR, fliQ, fliP,, fliI

Unknown                      fliS - essential, but function unknown  
                                       flhF - GTP-binding protein  
 \*C,A,and B are different variants of flagellin filament proteins and  
 are thus grouped.

Themes are a good concept, and are incorporated into multiple methods that I have listed below. However, I have not included Julie Thomas' original thematic approach in the methods below. Her approach involved listing the proteins that perform essential themes as components of the irreducible core. While this method can give a good idea of proteins likely to be indispensable, the individual proteins may contribute to an indispensable function without being indispensable themselves.

UR irreducible complexity, on the other hand, attempts to piece together what the indispensable components were in the last common ancestor of the various editions of the system. While this is beneficial in that it promotes the development of a possible evolutionary pathway, it too is absent from the list below. The reason that it is not included is that it would be too controversial. There is no way to go about knowing absolutely what the phenotype of a last common ancestor was. While there are often methods of making a good guess, the selection of components to include would quickly become the target of debate, drawing attention away from the goal of determining whether or not a system could have been produced by evolution.

The methods listed below are diverse, but each, in different stages or situations, can serve to help demonstrate the obstacles faced by evolution. To clarify my descriptions of the methods, this general example in which the bold/underlined gene products are indispensable:

Gene Products in Version 1. A B C D E F G  
 Gene Products in Version 2.    **B** **C**    **E** **F** G **H** I  
 Gene Products in Version 3. A B C    E F    H    J

#### *Methods of Compilation*

##### 1. Thomas 1999 (T99)

This first method is another concept originally described by Julie Thomas (see, for example, [6]). T99 (called "minimal complexity" by Thomas) does not actually list the irreducible components, but instead calculates their number. This is a good method for determining level of complexity exhibited by a system, or comparing the complexities of multiple systems.

Thomas began by looking at the indispensable components of systems from diverse organisms. She then weighted the value of each component according to the percentage of system versions that it was indispensable for. In the generic example this would give:

$$3(3/3) + 1(2/3) + 2(1/3) = 4.333 \text{ (4 } 1/3\text{)}.$$

Thomas applied her concept to the eubacterial flagellum by starting out with the eighteen components necessary for the themes in table 1 (from above). She then used the data from these tables (adapted from [6]):

**Table II. Genes found in 3/4 lineages.**

<i>Gene</i>	<i>Species</i>	<i>Function</i>
	<i>missing from</i>	
fliL	H. pylori	flagella assembly
fliH	A. aeolicus	flagella assembly
fliY	A. aeolicus	switch
fliM	A. aeolicus	switch
flgL	H. pylori	hook assembly
fliE	A. aeolicus	hook adaptor prot
flgG	B. subtilis	rod protein

**Table III. Flagellar genes found in 2/4 species**

<i>Gene</i>	<i>Species with Gene</i>
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flgD	T. pallidum/H. pylori
flgH	A. aeolicus/H. pylori
flgI	A. aeolicus/H. pylori
fliN	A. aeolicus/H. pylori

**Table IV. Species-specific flagellar genes**

<i>Species</i>	<i>Genes</i>
T. pallidum	flbD, cpfA
A. aeolicus	flgA
B. subtilis	fliZ, flhD, flhP, fliJ, fliK, fliT
H. pylori	flaG

This information resulted in the final calculation:  
 $18 (1.0) + 7 (0.75) + 4 (0.5) + 2.5 (0.25) = 25.87$

Thomas went on to check the reliability of this figure by evaluating all permutations with one Version removed. This is analogous to taking the number given by calculations using only Versions 1, and 2, then only Versions 2, and 3, then only Versions 1, and 3 in the general example. This calculation gives a benefit similar to that given by the bootstrap calculation used in evolutionary biology. If the range of values given by all permutations is within a reasonable distance of the original number, then it is likely that the original calculation is a good estimate of the level of complexity.

By their nature, methods of determining an irreducible core allow for quantification. T99, however, is the only method listed that consists solely of a calculation. The remaining methods involve a listing of the components of the core.

## 2. Strict Parsimony (SP)

One of the most important but often overlooked tools in the repertoire of a scientist is that of parsimony. Dictionary.com gives this second definition for parsimony (the first definition deals with economics), “Adoption of the simplest assumption in the formulation of a theory or in the interpretation of data, especially in accordance with the rule of Ockham's razor.”

An example of parsimony in science is found in evolutionary biology, where it is often necessary to choose between multiple possible phylogenies (evolutionary histories). One of the first, and most commonly used methods of making this choice is called Maximum Parsimony. Maximum Parsimony dictates that the phylogeny with the fewest steps (changes in the trait of interest) should be chosen (for discussion, see any textbook on molecular evolution).

The Strict Parsimony method of determining the irreducible core dictates that only those gene products that are indispensable in all versions of the system are included in the irreducible core. This results in the fewest gene products possible being listed as components of the irreducible core.

When applied to the generic example above, Strict Parsimony lists the components of the irreducible core as C, E, and F in this case. Even though components B, A, and H all are indispensable in some system, they are not part of the irreducible core because they are not indispensable in all of the versions of the system. Those who are taking a more Concessionary approach will likely favor this method.

While Strict Parsimony gives us a relatively simple approach to determining which components should be considered part of the irreducible core, some may wish to use a more Strict approach (that is, Strict within the context of Strict versus Assumptive or Concessionary). In reality, a system composed of only gene products C, E, and F may not work. It could be that gene products A, B, and H are performing vital functions, but in slightly different manners. In this case, the Strict Parsimony method does not give us a completely accurate picture of just how complex the system is. The rest of the methods attempt to rectify this situation in some fashion.

## 3. Strict Thematic (ST)

This method is essentially an attenuated version of Julie Thomas' original thematic approach. The difference between the two is that the Strict Thematic approach is not concerned with the actual gene

products performing the functions. Suppose that for the system in the general example, gene products A, B, and I are involved in function 1. C performs function 2. E and F perform function 3. And finally D, G, H, and J all play parts in function 4. Instead ST would list functions 1, 2, 3, and 4 as irreducible components (assuming that each function is indispensable).

There are several advantages to using ST to determine the irreducible core. First, the Strict Thematic approach is good for preliminary analyses. It sometimes takes many scientists working for years to determine the exact number and role of every gene product involved in a system. ST allows for a general understanding of the core without necessitating detailed knowledge of knockout experiments or protein interactions.

Second, ST does not run into the problems encountered with Strict Parsimony where some components of a system are necessary, but not included in the irreducible core. Also, by changing the focus from components to functions, ST may allow more freedom in developing a possible evolutionary pathway for evaluation, which is ultimately the challenge being issued.

A final advantage to using the Strict Thematic method is that usually the vast majority of the different versions of a system all have the same indispensable functions even if they have different indispensable parts. This makes the final assessment of the irreducible core less open to debate.

#### 4. Adjusted Parsimony (AP)

Often, it may be desirable to describe the irreducible core primarily in terms of components, without leaving out the vital functions that are not performed by the same gene products in all versions of the system. From our generic example above, this would yield an irreducible core of gene products C, E, and F, and functions 1, and 4. This is the AP method. It is good for the analyses of a system that is generally well understood, but still has aspects under investigation.

#### 5. Simplest System (SS)

Simplest System is the first of two methods that attempts to get around the compilation problem by using one exemplar instead of compiling data from multiple versions. Its major advantage is that it can provide a very clear target for developing a possible evolutionary pathway.

SS is essentially the application of parsimony to the use of an exemplar for determining a system's irreducible core. In this method, the version of the system that contains the fewest indispensable components is chosen as the exemplar, and the irreducible core is limited to those components indispensable in that version. It is one of the easiest solutions to the compilation problem.

From the general example, both Version 1 and Version 3 are candidates to be used in SS. Each has four indispensable components, and three dispensable components. Let us say, for argument's sake, that some external factor yields Version 3 a bit simpler than Version 1. In this case Version 3 would be the exemplar, and the irreducible core would contain C, E, F, and H.

#### 6. Evolutionary Method (EV)

I think that many intelligent design proponents could benefit from taking a more evolutionary perspective. This may not seem to make much sense at first blush, but I feel that it would aid relations between design theorists and evolutionary biologists if both spoke as similar a language as possible. Also, ID is in some sense an evolutionary theory. It is a theory about when evolution is inadequate. In this light, thinking from an evolutionary perspective I think will aid IDers in streamlining some of their ideas, and in anticipating possible objections from the evolutionary community as well.

The application of evolutionary thinking to the concept of an irreducible core yields two major ideas: the Evolutionary Method of determining an irreducible core, and irreducibly complex pathways. EV determines the irreducible core by using the earliest known version of the system in question as the exemplar. It deems the indispensable parts in this version to be the irreducible core.

Let us say that, in our generic example, it appears that the organisms that have Version 1 of the system arose 400 MYA, and those with Versions 2 and 3 arose approximately 300 MYA. In this case EV would dictate that the irreducible core consist of A, C, E, and F as they are the indispensable components of the oldest version of the system. Under the best circumstances (and under the circumstances generally predicted by Darwinian evolution), the EV core and the SS core will be the same.

The appeal of EV is that, when developing a possible evolutionary pathway, the natural endpoint is the earliest version that is known. Thus EV leads almost seamlessly into developing a possible pathway.

### Irreducibly Complex Evolutionary Pathways

In Michael Behe's paper responding to Russell Doolittle mentioned earlier, he also responded to Keith Robison. Keith, who was a Harvard graduate student at the time, attempted to show that the blood clotting system was not irreducibly complex by devising a possible evolutionary pathway for its genesis<sup>13</sup>. The problem with this, Behe concluded, was that Robison's pathway went through multiple unselected steps. The proposed pathway made Behe think, however, and I think it is worth quoting his final thoughts in the paper at some length.

“While thinking of Keith Robison's scenario, I was struck that irreducible complexity could be better formulated in evolutionary terms by focusing on a proposed *pathway*, and on whether each step that would be necessary to build a certain system using that pathway was selected or unselected. If a system has to pass through one unselected step on the way to a particular improvement, then in a real evolutionary sense it is encountering irreducibility... *An irreducibly complex evolutionary pathway is one that contains one or more unselected steps (that is, one or more necessary-but-unselected mutations). The degree of irreducible complexity is the number of unselected steps in the pathway.*”<sup>12</sup> (emphasis mine)

I mentioned earlier that generalities often mar current debates about irreducible complexity. This is one situation, however, in which that did not occur. Keith Robison is to be commended for actually developing a possible evolutionary pathway, even if it proved flawed in the end.

The value of the methods for determining the irreducible core listed above lies in the fact that any proposed evolutionary pathway to achieve them is an irreducibly complex pathway. The only counter to irreducible complexity that will severely damage it is a plausible evolutionary pathway for an irreducibly complex system. Once the irreducible core of a system has been determined it is necessary that claims against the systems irreducible complexity include an explanation for each component of that core. Until that explanation is given the system should be considered out of the reach of evolution.

It is not true, as has been claimed, that intelligent design theorists hold any system that has not been given a detailed evolutionary explanation as something that cannot be produced by evolution (see, for example, [5]). It is true, though, that there has been no detailed evolutionary explanation given for any irreducibly complex structure. A detailed evolutionary explanation does not mean that every base pair and selective pressure involved in the production of the system be accounted for, and every mutation explicitly stated on a timeline. On the other hand it does mean accounting for changes in phenotypes, and the advantages that those changes give.

Finally, intelligent design proponents are encouraged here to actively seek out evolutionary explanations for irreducibly complex systems. Propose pathways. If there is a plausible pathway, put it out in the open. Let it be evaluated. If intelligent design is true, then the proposed pathway will be irreducibly complex and go through some unselectable step. In this case, propose the best possible pathway, and then point out the flaws. Determine the degree of irreducible complexity of the pathway. Challenge others to find a better version. This active exploration of possibilities will, I believe, have more impact than anything else.

### Conclusion

In this paper I have laid out several steps that are key in actively applying the concept of irreducible complexity. Choosing a system not far removed from the genes that produce it, determining the irreducible core, and demanding evolutionary pathways explaining the entire core so that pathway may then be evaluated for *its* irreducible complexity.

*The Origin of Species* did not close the book on natural selection. *Darwin's Black Box* did not close the book on irreducible complexity. And I know that this paper has not closed the book on applying irreducible complexity. Never the less, I hope that it has inspired thought, and, more importantly, I hope it has inspired action.

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