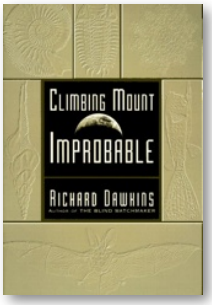
Paul Nelson

"Easily the biggest challenge facing the ID community is to develop a fully-fledged theory of biological design. We don't have such a theory right now, and that's a problem. Without a theory, it's very hard to know where to direct your research focus. Right now, we've got a bag of powerful intuitions, and a handful of notions … but, as yet, no general theory of biological design."

Touchstone Magazine 7/8 (2004), pp. 64

Richard Dawkins



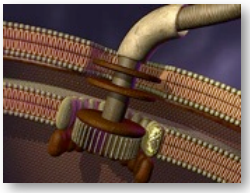
"Biology is the study of complicated things that give the appearance of having been designed for a purpose."

The MacGuyver Principle

- "The simpler the solution to a problem, the more intelligence and ingenuity it requires." (Mark Perakh)
- *Intelligent* design will result in simple, optimal, minimal, solutions to design problems.
- *Unintelligent* design will result in complex, sub-optimal, sprawling, redundant, solutions to design problems.

The Design Argument

Evolution couldn't have produced many of the structures in living cells because …



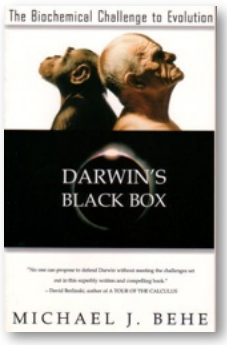
these structures possess "Irreducible Complexity" (Behe)

or

these structures possess "Complex Specified Information" (Dembski)

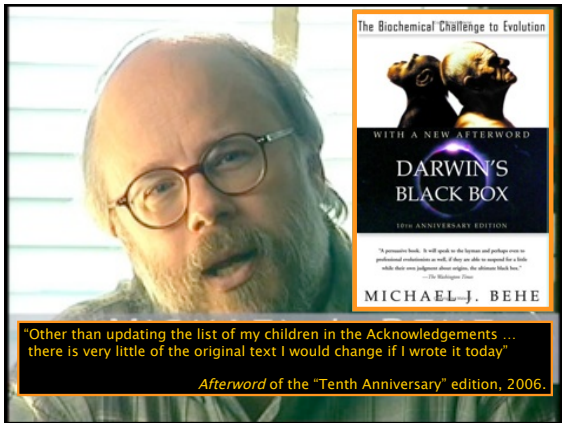
"Irreducible complexity is a special case of specified complexity"

Dembski, *No Free Lunch*, 289

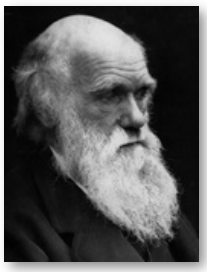


1996

1997



Charles Darwin



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

"But I can find no such case."

Michael Behe

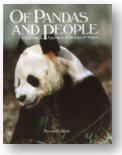
- Claims that Darwinism cannot explain biochemical complexity
- "Irreducibly complex systems … cannot evolve in a Darwinian fashion"
- "Purposeful arrangement of parts" implies Design

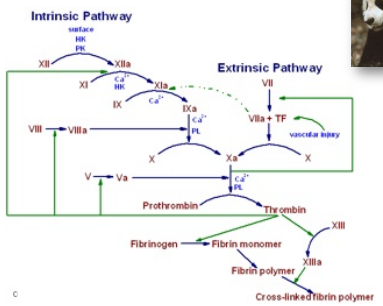
Behe's Neo-Paleyite Argument

- We infer design whenever parts appear arranged to accomplish a function
- The strength of the inference is quantitative and depends on the evidence; the more parts, and the more intricate and sophisticated the function, the stronger is our conclusion of design
- Aspects of life overpower us with the appearance of design
- Since we have no other convincing explanation for that strong appearance of design … then we are rationally justified in concluding that parts of life were indeed purposely designed by an intelligent agent

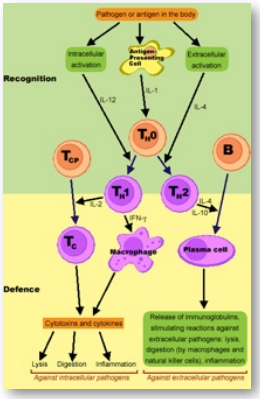
2006, p. 265

Blood Clotting Cascade

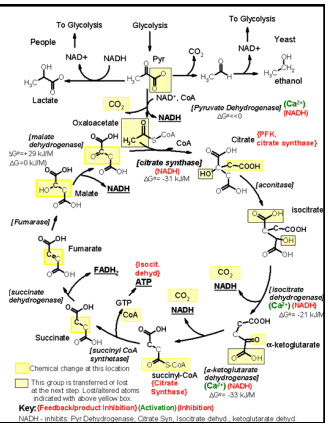




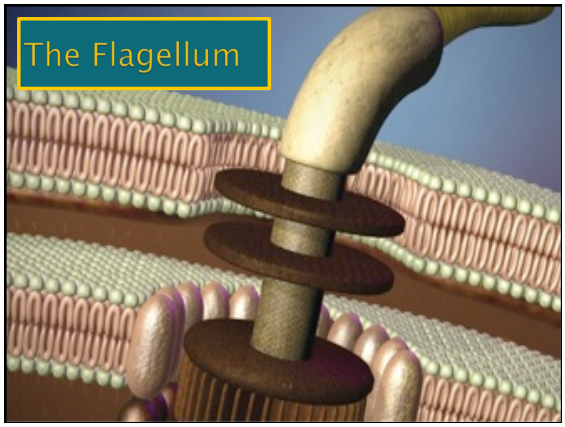
Immune Response



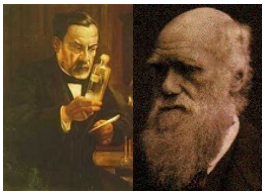
Citric Acid Cycle



The Flagellum



A Momentous Breakthrough



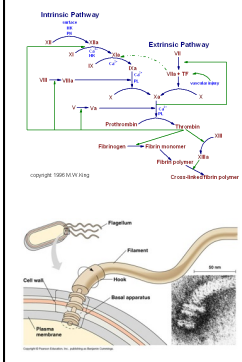
"The result … is a loud, clear, piercing cry of *"design*!" The result is so unambiguous and so significant that it must be ranked as one of the greatest achievements in the history of science. The discovery rivals those of Newton & Einstein, Lavoisier & Schrödinger, Pasteur & Darwin. The observation of the intelligent design of life is as momentous as the observation that the earth goes round the sun or that disease is caused by bacteria or that radiation is emitted in quanta" (233)

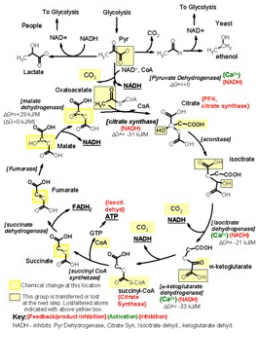
But result is ignored due to implications.

Michael "Call me Ishmael" Behe

"[I]f random evolution is true, there must have been a large number of transitional forms between the Mesonychid and the ancient whale. Where are they?"

1994





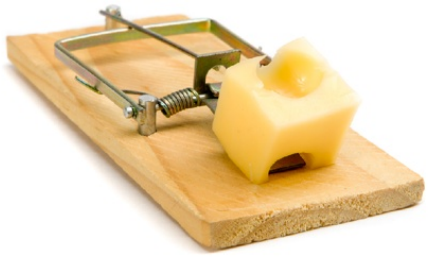
Irreducible Complexity

"By irreducibly complex I mean a single system 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. … An irreducibly complex biological system, if there is such a thing, would be a powerful challenge to Darwinian evolution." (39)

Testing Behe is Difficult

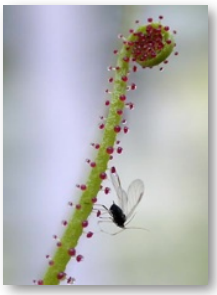
- He acknowledges the driving forces of evolutionary change
  - natural selection, genetic drift, founder effects, gene flow, meiotic drive, gene duplication, transposition …
- "The production of some biological improvements by mutation and natural selection – by evolution – is quite compatible with intelligent design theory."
  - i.e. design exists only when and where evolution cannot explain it

A mouse trap

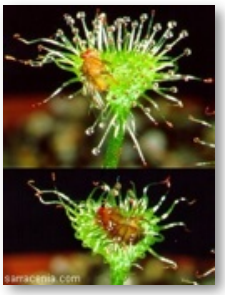


A biological trap

Variation



***Drosophyllum*:**
Passive glue trap, no motion

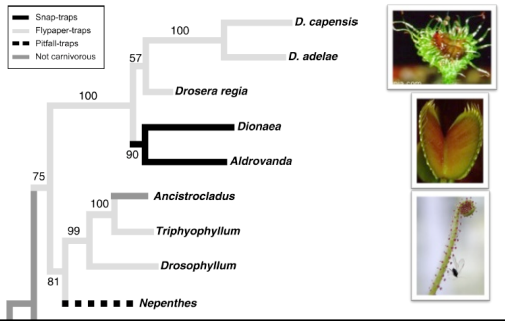


Sundew (*Drosera rotundifolia*):
Active glue trap, slow motion

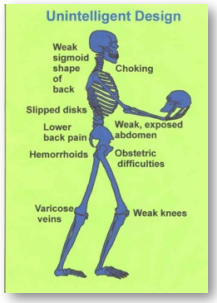
Insectivorous Plants (1875)

"The[se] six known genera…all capture insects. This is effected by *Drosophyllum* … solely by the viscid fluid secreted from their glands; by *Drosera*, through the same means, together with the movements of the tentacles; by *Dionaea* … through the closing of the blades of the leaf. In [this] last genera rapid movement makes up for the loss of viscid secretion. … The parent form of *Dionaea* … seems to have been closely allied to *Drosera*, and to have had rounded leaves, supported on distinct footstalks, and furnished with tentacles all round the circumference, with other tentacles and sessile glands on the upper surface."

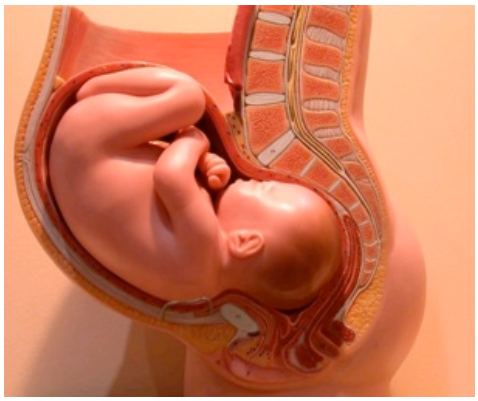
Molecular Evidence Vindicates Darwin



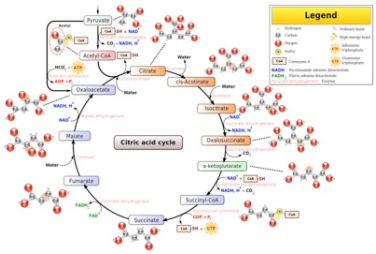
What About "Odd" Design?



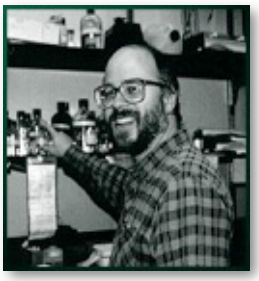
"Features that strike us as odd in a design might have been placed there by the designer for a reason – for artistic reasons, for variety, to show off, for some as-yet-undetected practical purpose, or for some unguessable [sic] reason."



Evolution of Biochemical Systems



Behe claims that …



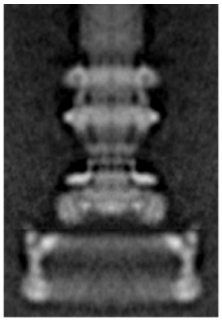
"[T]here is no publication in the scientific literature – in prestigious journals, specialty journals, or books – that describes how the molecular evolution of any real, complex, biochemical system either did occur or even might have occurred." (p. 185)

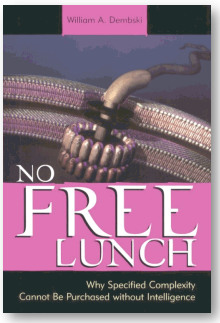
ID's "clear and daring prediction"

"Darwinists will not begin filling in plausible, testable scenarios for any of the irreducibly complex cellular systems."

Thomas Woodward, *Darwin Strikes Back: Defending the Science of Intelligent Design* (2006), p. 78

The Flagellum





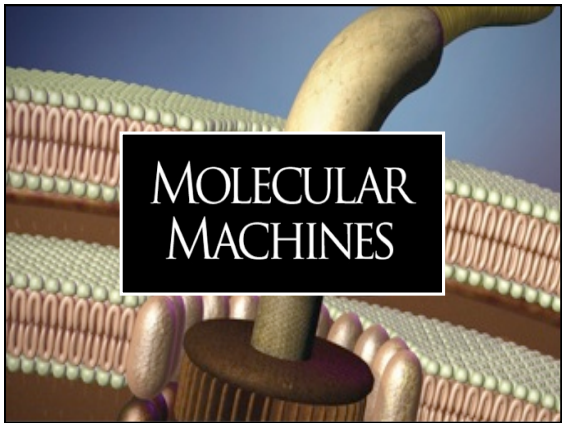
The Flagellum and ID

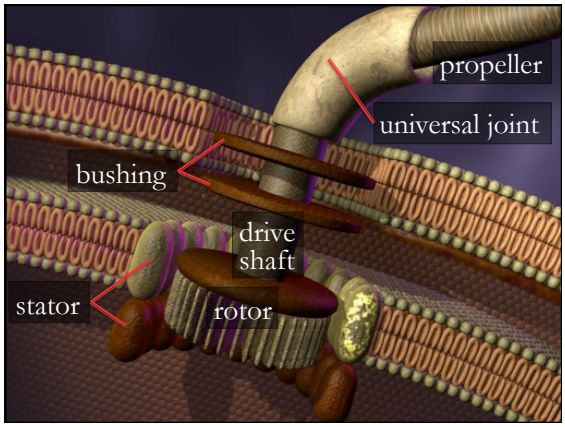
The flagellum "has a machinelike *irreducible complexity,* which is an empirical marker of design because it rules out step-by-step evolution through selection. Take one part away from the flagellum and its rotary system won't work ... Its forty parts, all of them precisely shaped proteins, are *prima facie* evidence for an intelligence behind life, and the flagellum is just the tip of the iceberg. The cell is chock-full of such complex, multipart systems that continue to defy a step-by-step Darwinian explanation."

Woodward, 2006, p. 11

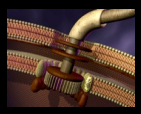
Behe's Logic

1. Observation: The cell contains biochemical machines in which the loss of a single component may abolish function.
2. Assertion: Any of these machines that are missing a part is, by definition, non-functional and leaves natural selection with nothing to select for.
3. Conclusion: These machines could not have been produced by natural selection.





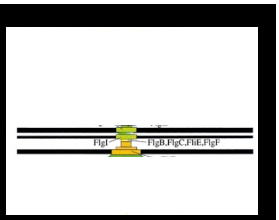
Indispensable Bacterial Motor Parts

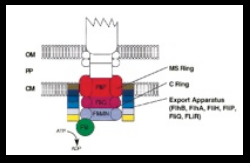


- 30* different protein parts
  ... for the motor's ***structure***
- 10* more protein parts
  ... for sensor and control ***circuitry***
- 10* more protein parts
  ... to ***construct*** the motor

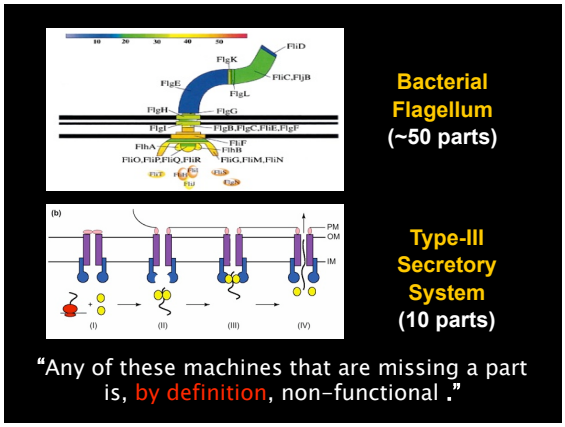
*These numbers may vary in different species of bacteria

Start with the 50-part bacterial flagellum. . . . And let's take away 40 of the parts:





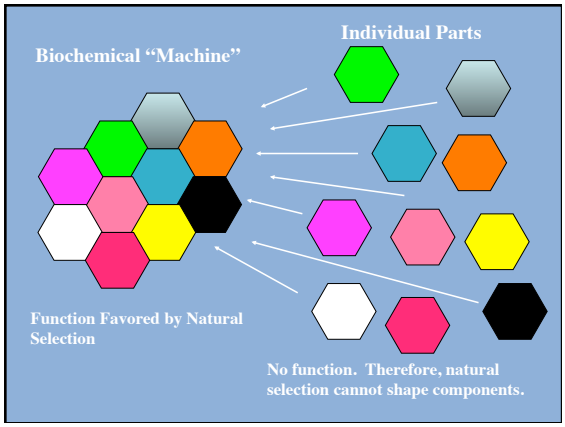
Leaving just 10. What's left should be non-functional according to Behe.

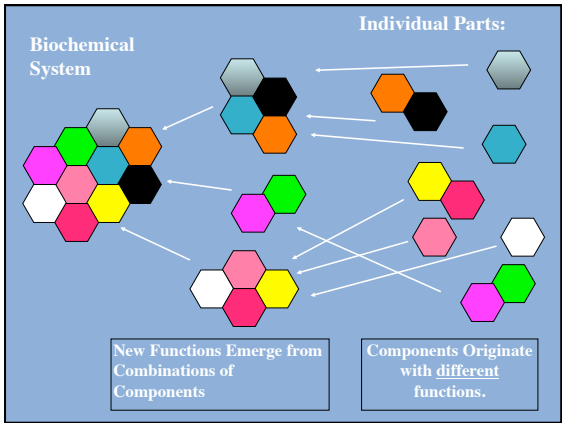


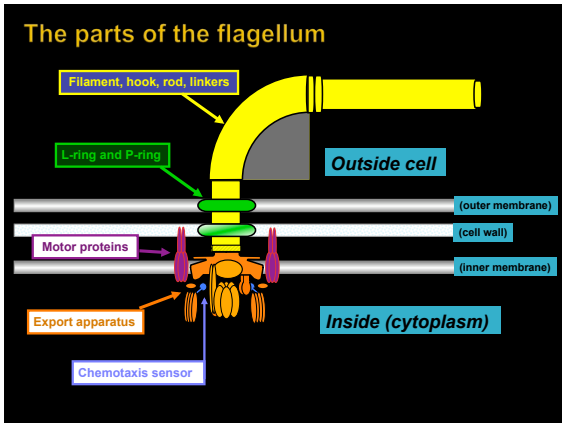
Bacterial Flagellum (~50 parts)

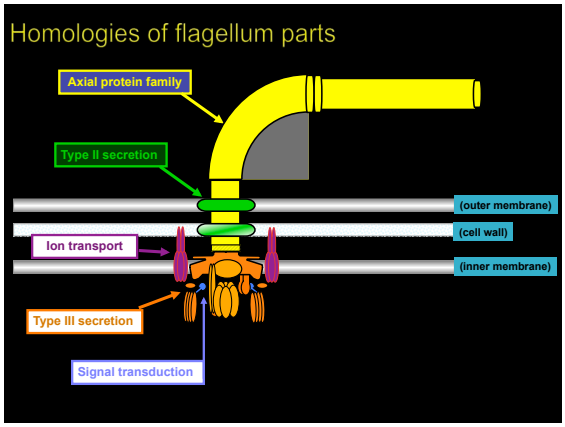
Type-III Secretory System (10 parts)

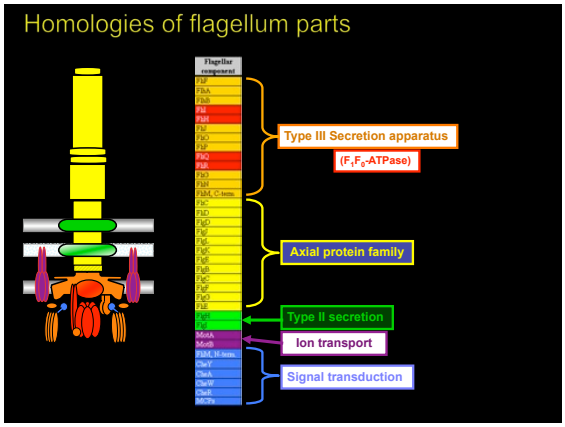
"Any of these machines that are missing a part is, by definition, non-functional."











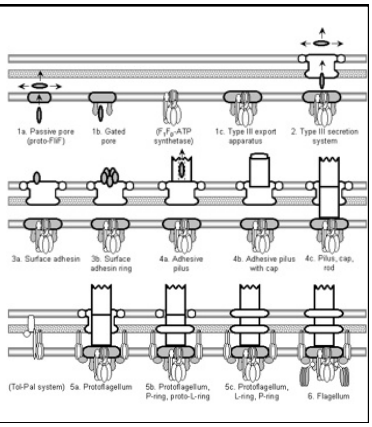
Number of peer-reviewed journal articles:

17

Out of these, the number that Behe has ever written about:

0

Possible pathway to the bacterial flagellum



Stage	Function of core system	Analogs
1. Primitive type III export system and precursors	Export	Passive inner membrane pores Gated pores Export systems (e.g. sec system)
2. Primitive type III secretion system	Secretion	Secretion systems (Table 4, Figure 5)
3. Surface adhesin	Adhesion	Outer membrane adhesins (Table 4)
4. Type III pilus		Pili (Table 4, Figure 5b,c)
5. Protoflagellum	Dispersal	Random dispersal mechanisms (Vogel, 1994) Dispersal by modern flagella (Dusenbery, 1997)
6. Flagellum	Taxis	Motility systems (Table 3, Figure 5d)

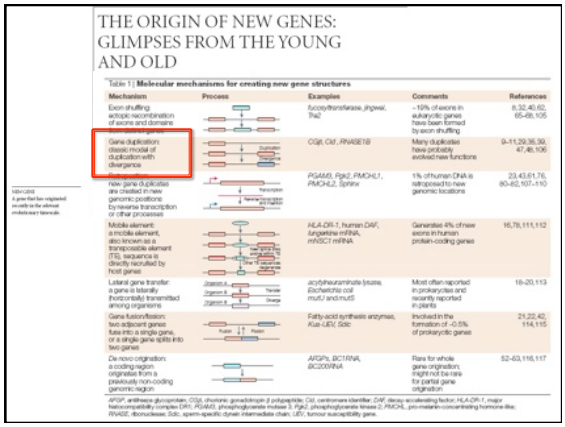
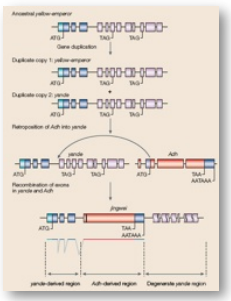

THE ORIGIN OF NEW GENES: GLIMPSES FROM THE YOUNG AND OLD

Table 1 | **Molecular mechanisms for creating new gene structures**

Mechanism	Process	Examples	Comments	References
Exon shuffling: ectopic recombination of exons and domains		Acetyltransferase, jingwei, Rai2	~10% of exons in eukaryotic genes have been formed by exon shuffling	8,32,40,62, 65–69,105
Gene duplication: classic model of duplication with divergence		CG9, Cid, RWABE1B	Many duplicates have probably evolved new functions	9–11,29,35,39, 47,48,106
New gene duplicates are created in new genomic positions by reverse transcription or other processes		PGAM3, Rpk2, PMCHL1, PMCHL2, Sphinx	1% of human DNA is retroposed to new genomic locations	23,43,61,76, 80–82,107–110
Mobile element: a mobile element, also known as a transposable element (TE), sequence is directly recruited by host genes		HLA-DR-1, human DAF, lungetrina mRNA, mNSC1 mRNA	Generates 4% of new exons in human protein-coding genes	16,78,111,112
Lateral gene transfer: a gene is laterally (horizontally) transmitted among organisms		acetyltheuraminate lyase, *Escherichia coli* mutU and mutS	Most often reported in prokaryotes and recently reported in plants	18–20,113
Gene fusion/fission: two adjacent genes fuse into a single gene, or a single gene splits into two genes		Fatty-acid synthesis enzymes, Kua-UEV, Sdc	Involved in the formation of ~0.5% of prokaryotic genes	21,22,42, 114,115
De novo origination: a coding region originates from a previously non-coding genomic region		AFGPs, BC1 RNA, BC200 RNA	Rare for whole gene origination; might not be rare for partial gene origination	52–63,116,117

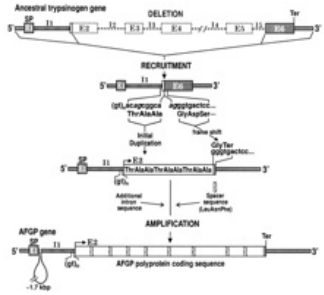
AFGP, antifreeze glycoprotein; CG9, chorionic gonadotropin β polypeptide; Cid, centromere identifier; DAF, decay-accelerating factor; HLA-DR-1, major histocompatibility complex DR1; PGAM3, phosphoglycerate mutase 3; Rpk2, phosphoglycerate kinase 2; PMCHL, pro-melanin-concentrating hormone-like; RWABE, ribonuclease; Sdc, sperm-specific dynein intermediate chain; UEV, tumour susceptibility gene.

Importance of Duplication



Creation of new copy allows evolution of new function while maintaining old function.

Mechanism by which an ancestral trypsinogen gene was transformed into an AntiFreeze GlycoProtein gene



Chen *et al.* (1997) "Evolution of antifreeze glycoprotein gene from a trypsinogen gene in Antarctic notothenioid fish" *PNAS* **94:** 3811.

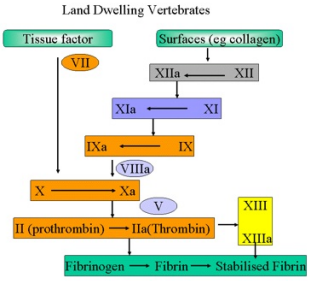
Gene Duplication in the Vertebrate Clotting System

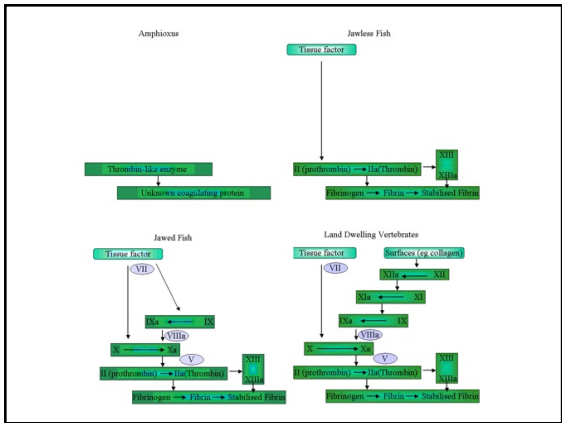
Orange: Duplicates of core serine proteases.

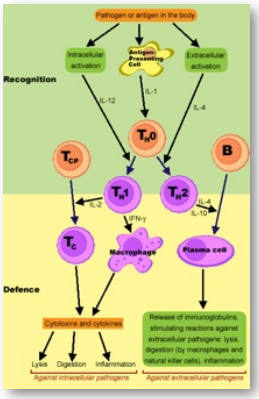
Light Blue: Duplicates of the ceruloplasmin family.

Yellow: Duplicates of the transglutamase family.

Dark blue: Duplicates of prekallikrein.







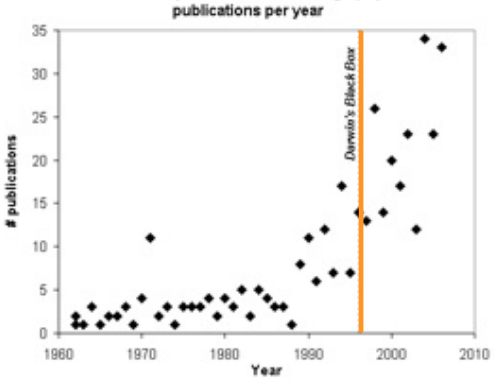
Immune Response

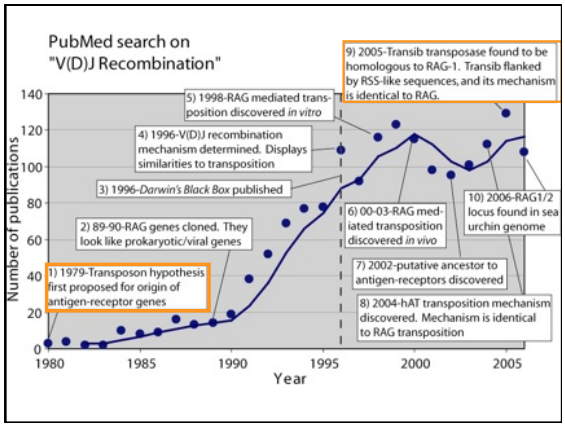
"We can look high or we can look low, in books or in journals, but the result is the same. The scientific literature has no answers to the question of the origin of the immune system."

At *Kitzmiller*, Behe was presented with 58 articles and other books.

His response?

"I am quite skeptical, although I haven't read them, that in fact they present detailed rigorous models for the evolution of the immune system by random mutation and natural selection."





Leave the research to someone else

Q. And I'm correct when I asked you, you would need to see a step-by-step description of how the immune system, vertebrate immune system developed?

A. Not only would I need a step-by-step, mutation by mutation analysis, I would also want to see relevant information such as what is the population size of the organism in which these mutations are occurring, what is the selective value for the mutation, are there any detrimental effects of the mutation, and many other such questions.

Q. And you haven't undertaken to try and figure out those?

A. I am not confident that the immune system arose through Darwinian processes, and so I do not think that such a study would be fruitful.

Q. It would be a waste of time?

A. It would not be fruitful.

William Dembski

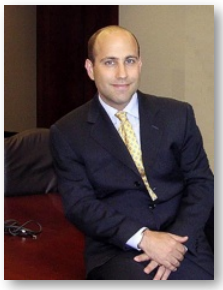
"Behe's challenge was not simply to find a Darwinian explanation for the origin of a biochemical machine, but to find a *detailed* Darwinian explanation for the origin of an *irreducibly complex* biochemical machine."

No Free Lunch, 2002, p. 269.

A Double Standard

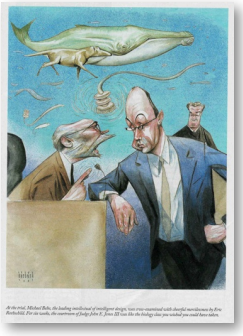
"It's not ID's task to match your pathetic level of detail in telling mechanistic stories."

Eric Rothschild



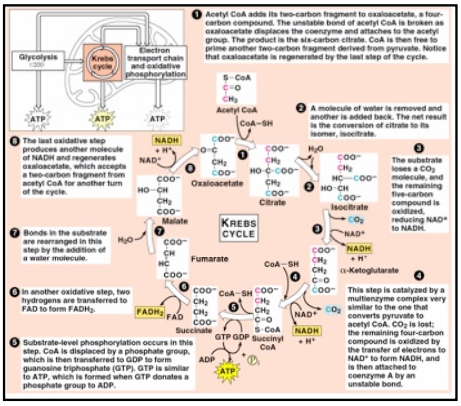
"Thankfully, there are scientists who do search for answers to the question of the origin of the immune system. It's the immune system. It's our defense against debilitating and fatal diseases. The scientists who wrote those books and articles toil in obscurity, without book royalties or speaking engagements. Their efforts help us combat and cure serious medical conditions. By contrast, Professor Behe and the entire intelligent design movement are doing nothing to advance scientific or medical knowledge and are telling future generations of scientists, don't bother."

Judge John Jones, III



"[Behe] was presented with fifty-eight peer-reviewed publications, nine books, and several immunology textbook chapters about the evolution of the immune system; however, he simply insisted that this was still not sufficient evidence of evolution, and that it was not "good enough" …

We find that such evidence demonstrates that the ID argument is dependent upon setting a scientifically unreasonable burden of proof for the theory of evolution."



Do the calculation: Your easy access to cutting-edge Intelligent Design technology

Created: 2002/03/20 Last Updated: 2002/03/20

Enter the lengths of a number of proteins, one per line, in the text box below. Click on the button and the "origination" probability will be computed in accordance with Dr. William Dembski's formula given on p. 301 of "No Free Lunch"

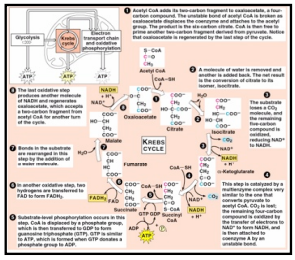
Protein lengths, one per line

271
780
418
206
685
135
470
320

# of proteins = 8, total origination probability = 20^-338.5 or 10^-440.398653532258

If you have a specification for those proteins, you have found an instance of *specified complexity*!!!

10^{-440} = "impossible"



http://www.antievolution.org/people/dembski_wa/origprob.html

Allen Orr

"An irreducibly complex system can be built gradually by adding parts that, while initially just advantageous, become – because of later changes – essential. The logic is very simple. Some part (A) initially does some job (and not very well, perhaps). Another part (B) later gets added because it helps A. This new part isn't essential, it merely improves things. But later on, A (or something else) may change in such a way that B now becomes indispensable. This process continues as further parts get folded into the system. And at the end of the day, many parts may all be required."

Boston Review, Dec 1996

J Mol Evol (1996) 43:[illegible]–305

JOURNAL OF MOLECULAR EVOLUTION

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The Puzzle of the Krebs Citric Acid Cycle: Assembling the Pieces of Chemically Feasible Reactions, and Opportunism in the Design of Metabolic Pathways During Evolution

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Received: 10 May 1995 / Accepted: 3 November 1996

A "paleo-pathway"

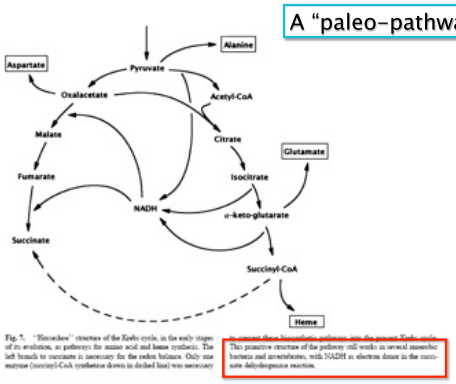
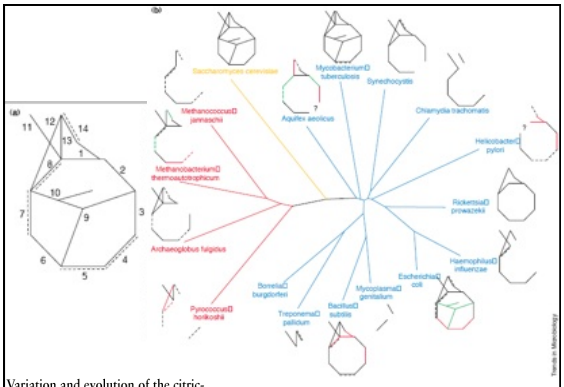


Fig. 7. "Horseshoe" structure of the Krebs cycle, in the early stages of its evolution, as pathways for amino acid and heme synthesis. The left branch to succinate is necessary for the redox balance. Only one enzyme (succinyl-CoA synthetase drawn in dashed line) was necessary

This primitive structure of the pathway still works in several anaerobic bacteria and invertebrates, with NADH as electron donor in the succinate dehydrogenase reaction.



Variation and evolution of the citric-acid cycle: a genomic perspective

Martijn A. Huynen, Thomas Dandekar and Peer Bork

Evolving a Biochemical Pathway

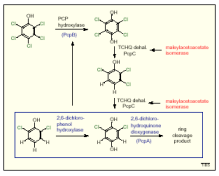
... in 65 years (or less)

TIBS 25 – JUNE 2000

Evolution of a metabolic pathway for degradation of a toxic xenobiotic: the patchwork approach

Shelley D. Copley

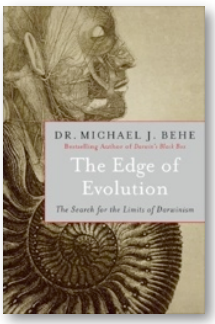
The pathway for degradation of the xenobiotic pesticide pentachlorophenol in *Sphingomonas chlorophenolica* probably evolved in the past few decades by the recruitment of enzymes from two other catabolic pathways. The first and third enzymes in the pathway, pentachlorophenol hydroxylase and 2,6-dichlorohydroquinone dioxygenase, may have originated from enzymes in a pathway for degradation of a naturally occurring chlorinated phenol. The second enzyme, a reductive dehalogenase, may have evolved from a maleylacetoacetate isomerase normally involved in degradation of tyrosine. This apparently recently assembled pathway does not function very well: pentachlorophenol hydroxylase is quite slow, and tetrachlorohydroquinone dehalogenase is subject to severe substrate inhibition.



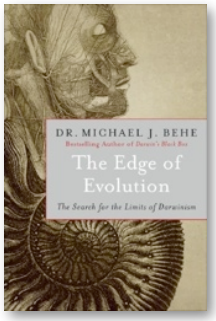
Michael Behe

"There is no publication in the scientific literature – in prestigious journals, specialty journals, or books – that describes how the molecular evolution of any real, complex, biochemical system either did occur or even might have occurred."

(p. 185)



The Edge of Incoherence



"Fine Tuned" Arthropoda

Domain
Kingdom
Phylum
Class
Order
Family
Genus
Species

- Subphylum Chelicerata
  - Class Merostomata (horseshoe crabs, eurypterids)
  - Class Pycnogonida (sea spiders)
  - Class Arachnida (spiders, ticks, mites)
- Subphylum Crustacea
  - Class Remipedia
  - Class Cephalocarida
  - Class Branchiopoda (fairy shrimp, water fleas, etc.)
  - Class Maxillopoda (ostracods, copepods, barnacles)
  - Class Malacostraca (isopods, amphipods, krill, crabs, shrimp, etc.)
- Subphylum Uniramia
  - Class Chilopoda (centipedes)
  - Class Diplopoda (millipedes)
  - Class Insecta

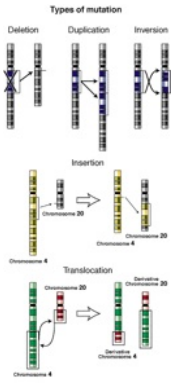
Accepts common ancestry

1. Vitamin C pseudogene: "Both humans and chimps have a broken copy of a gene that in other mammals helps make vitamin C." (71); "It's hard to imagine how there could be stronger evidence for common ancestry of chimps and humans." (72)
2. Hemoglobin pseudogene: "[C]ompelling evidence for the shared ancestry of humans and other primates comes from ... a broken hemoglobin gene." (71)

- At the origin of life: "intelligent design is quite compatible with the view that the universe operates by unbroken natural law, with the design of life perhaps packed into its initial set-up." [166]
- Three billion years later: "Explicit design appears to reach into biology to a certain level, to the level of the vertebrate class, but not necessarily further" [220]

"Front loading" as a Mechanism

"Suppose that nearly four billion years ago the designer made the first cell, already containing all of the irreducibly complex biochemical systems discussed here and many others. (One can postulate that the designs for systems that were to be used later, such as blood clotting, were present but not 'turned on.'…)" (*DBB* 227–8)



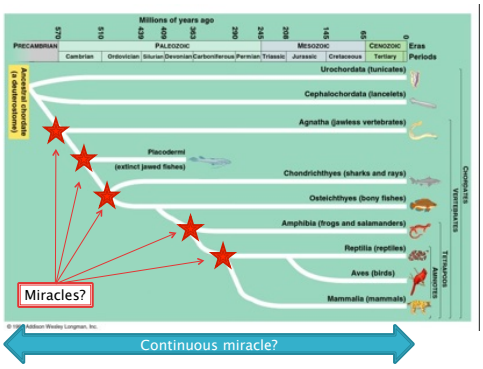
Behe himself admits …

"[G]enes that are useless in the real world are not rewarded; the genes are rapidly lost or degraded by mutation."

Vertebrate Classes

Domain
Kingdom
Phylum
Class
Order
Family
Genus
Species

- Hyperoartia (Lampreys)
- Chondrichthyes (Cartilagenous fish)
- Actinopterygii (Ray-finned fish)
- Sarcopterygii (Lobe-finned fish)
- Amphibia (Amphibians)
- Sauropsida (Reptiles and Birds)
- Mammalia (Mammals)



Non-random mutation

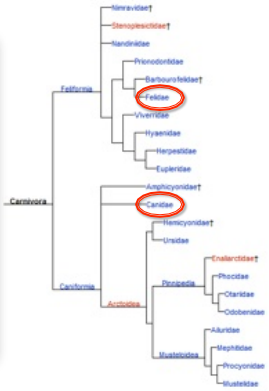
- "Most mutations that built the great structures of life must have been nonrandom." [82]
- "Random mutation does not account for the 'mind-boggling' systems discovered in the cell. So what does? If random mutation is inadequate, then (since common descent with modification strongly appears to be true) of course the answer must be nonrandom mutation." [165]

Cats,Dogs & Elephants

Medved: "What you're talking about really is the leaps, aren't you. I mean the kind of random mutations, or allegedly random mutations, who [*sic*] create a new species."

Behe: "Yeah, well I wouldn't call it species. I'd, I'd go a little higher, maybe genus or something in biology. Biology has a number of levels and you might be able to get, say, from a wolf to a dog using random mutation and natural selection. But I don't think you can get from a dog to a cat or a precursor organism and get from a dog to a cat or certainly to an elephant."

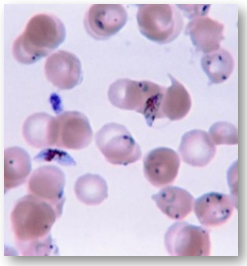
The Michael Medved Show June 5th 2007.



"exquisitely purposeful arrangement of parts"

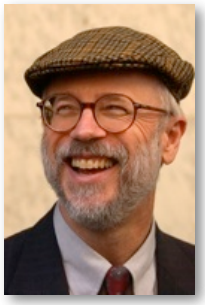
- astonishingly complex, coherent systems
- stupendously complex systems
- enormously complex cellular mechanisms
- startlingly complex pathway of flagellum assembly
- staggering complexity of modern biology
- tremendously complex elegant complexity
- stunning complexity
- enormously complex coherent molecular machinery
- elegant molecular outboard motors
- elegant immune system
- intricate genetic control programs
- stupendously intricate cellular machines
- sophisticated living machinery
- highly sophisticated, automated mechanisms
- ultrasophisticated molecular machinery

Plasmodium falciparum

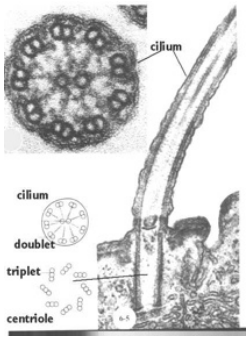


"Here's something to ponder long and hard: Malaria was intentionally designed. The molecular machinery with which the parasite invades red blood cells is an exquisitely purposeful arrangement of parts." (p. 237)

Natural Dys-Theology

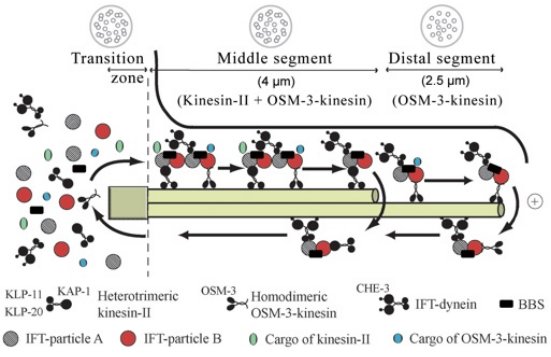


Malaria kills between one and three million people a year, most of them children in Sub-Saharan Africa. It "was intentionally designed".



The Eukaryotic Cillium

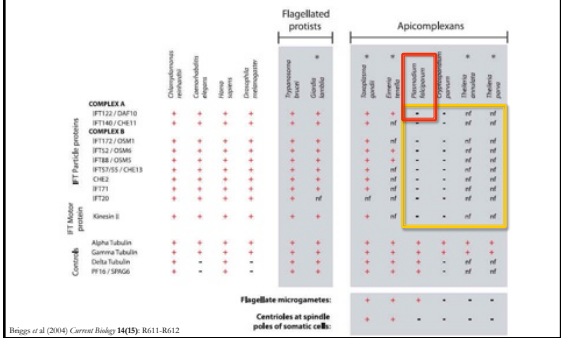
Intra-Flagellar Transport (IFT)



Behe:
"Irreducible Complexity Squared"

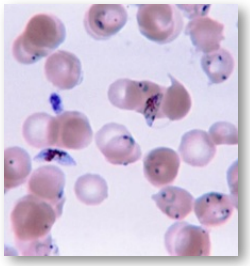
"IFT exponentially increases the difficulty of explaining the irreducibly complex cilium. It is clear from careful experimental work with all ciliated cells that have been examined, from alga to mice, that a functioning cilium requires a working IFT. The problem of the origin of the cilium is now intimately connected to the problem of the origin of IFT. [p. 94]

"More than one way to build a cillium"



Briggs *et al.* (2004) *Current Biology* **14(15)**: R611-R612

Plasmodium falciparum



Jerry Coyne

"If ID were science, we could … ask Behe to produce a complete step-by-step accounting of what God (sorry, the Intelligent Designer) did when He designed the cilia. And of course Behe would not be able to do that – nor does he even try. IDers never produce their own "scientific" explanation of life. They just carp about evolution. And as evolutionists explain one thing after another, IDers simply ignore these successes and move on to the ever-dwindling set of unsolved problems in which they continue to see the hand of God."

"The Great Mutator" *The New Republic* 18th June 2007

Jerry Coyne

"So let us put some empirical questions to Behe, since his theory is supposedly scientific.

[1] Which features of life were designed, as opposed to evolved?

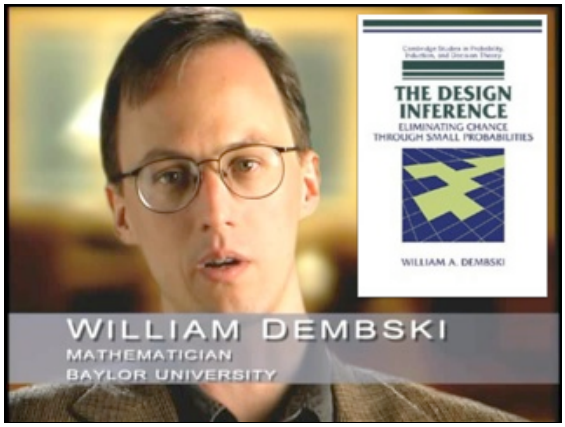
[2] How exactly did the mutations responsible for design come about?

[3] Who was the Designer?

[4] To what end did the Designer work?

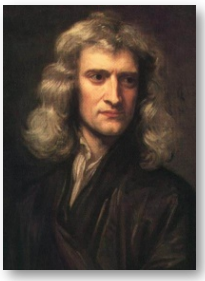
[4] The Designer's Goal?

- "What we sense, as elaborated through modern science's instruments and our reasoning, is that we live in a universe fine-tuned for intelligent life."
- "Parts were moving into place over geological time for the subsequent, purposeful, planned emergence of intelligent life."

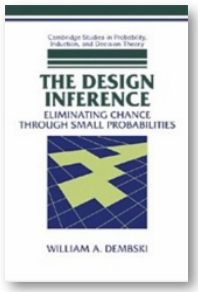


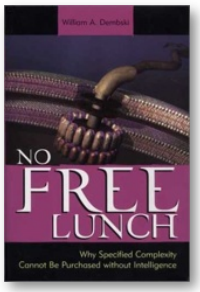
Rob Koons

Philosopher of Religion, UT Austin



"Dembski is the Isaac Newton of information theory, and since this is the Age of Information, that makes Dembski one of the most important thinkers of our time. "

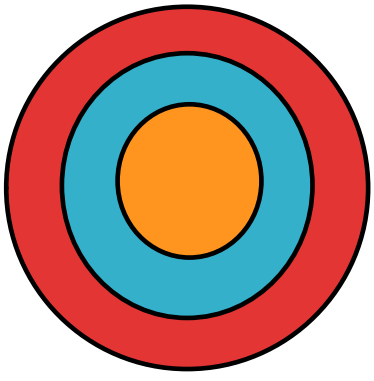




The Design Inference

1. $oc(E)$
2. $(\forall H \in \Re) sp(E, H)$
3. $(\forall H \in \Re) SP(E, H)$
4. $(\forall X)(\forall H \in \Re)[oc(X) \& sp(X, H) \& SP(X, H) \rightarrow \sim ch(X, H)]$
5. $\sim reg(E)$
6. $reg(E) \vee (\exists H \in \Re) ch(E, H) \vee des(E)$

Conclusion : $des(E)$



Complex
Specified
Information

a.k.a

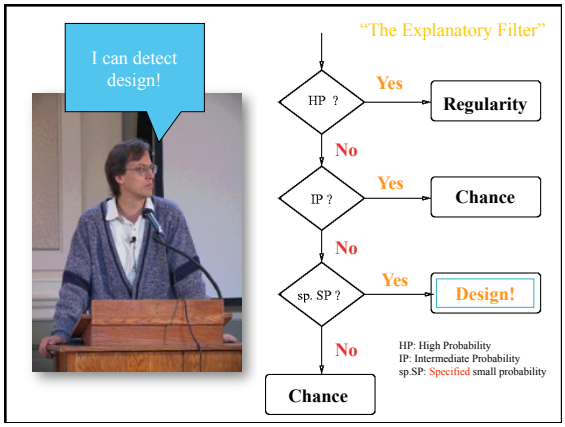
Specified
Complexity

Requirements

- Contingency: There is a choice (vs. necessity)
- Complexity: Not so simple that the object can be explained by chance
- Specification: Object exhibits a pattern characteristic of intelligence

Specification

- "Specification depends on the knowledge of subjects. Is specification therefore subjective? Yes."
- "Everything depends on what [one] knows, believes, determines, and provisionally accepts"
  - Therefore, specification depends on current state of knowledge.
  - Something is specified if an ID supporter says it is!
  - This is ultimately a "God of the Gaps" type argument



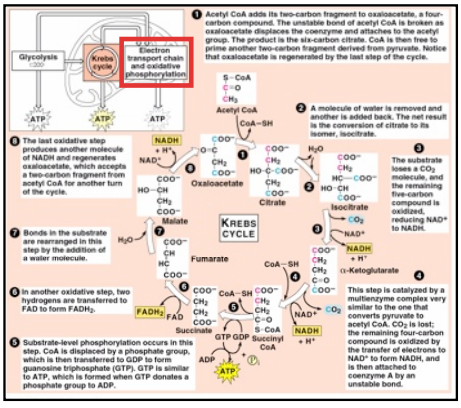
Measuring information

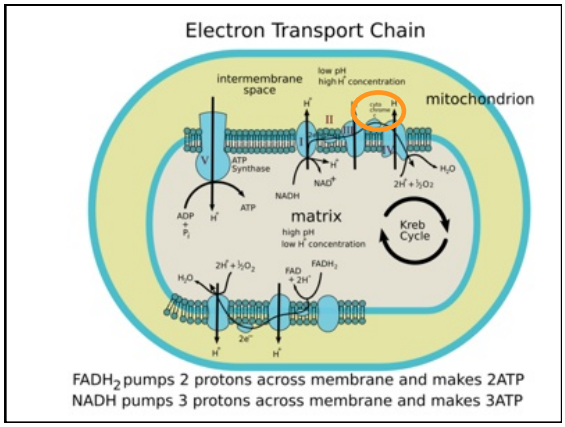
- Information is seen as a removal of possibilities (decrease in uncertainty)
- Information (surprisal, entropy) is given by:

$$I_x = -\log_2 p_x$$

CSI and the information cut-off

- CSI is "any specified information whose complexity exceeds 500 bits of information"
- This is Dembski's *Universal Probability Bound* (UPB) as 500 bits has a probability of 10^{-150}.



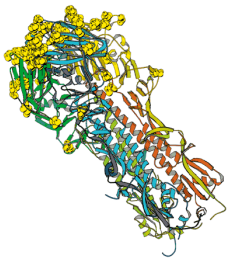


$FADH_2$ pumps 2 protons across membrane and makes 2ATP
NADH pumps 3 protons across membrane and makes 3ATP

Cytochrome C

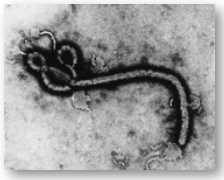
- Part of the electron transport chain (ATP production)
- Highly conserved across groups
- Weighs in at 233 bits, therefore not CSI, according to Dembski's criteria
- *Cyt-c* could have arisen by chance.

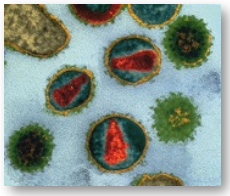
Protein Binding Sites



- Human splice acceptor sites contain on average 9.4 bits of information.
- Below 500 bit limit, but clearly CSI.

What about the bad stuff?

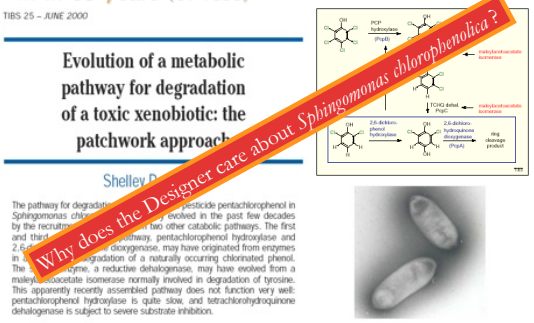


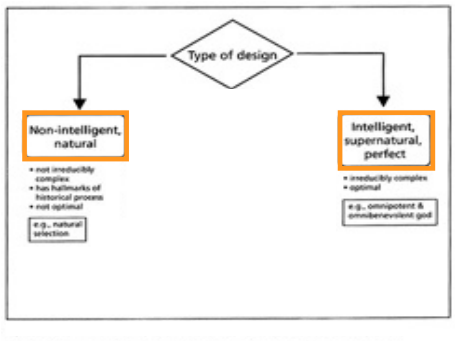


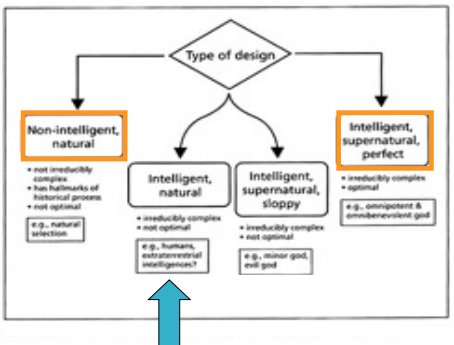
- Viruses, oncogenes, and "jumping genes" cause diseases (e.g. ebola, avian flu, AIDS), cancers and genetic disruption
- All have information content beyond the 500 bit limit of Dembski.
- According to Dembski they must have been designed.

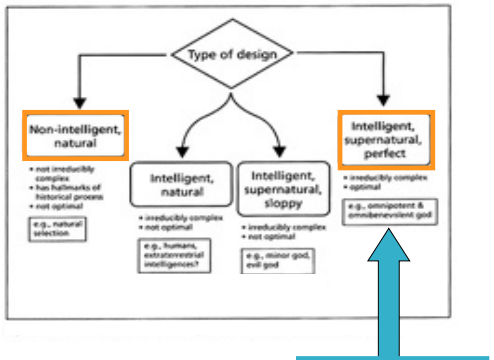
Evolving a Biochemical Pathway

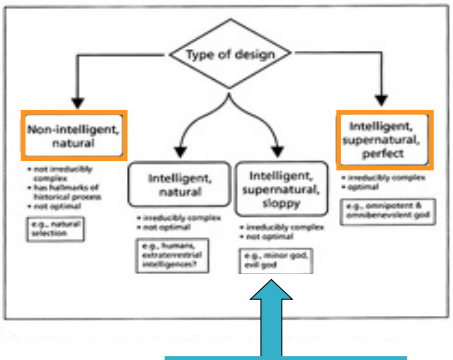
... in 65 years (or less)







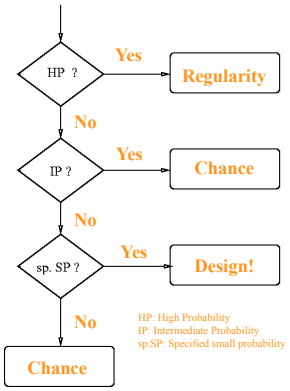


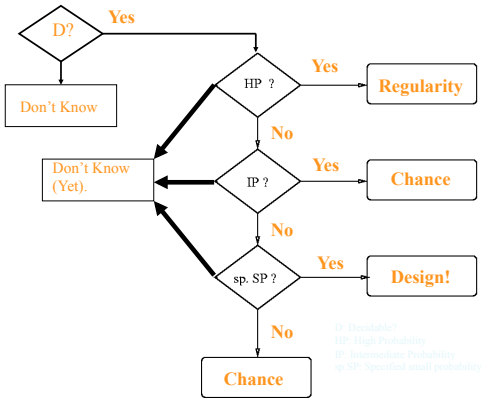


What is the "unit" of examination?

Section of DNA
Gene
Gene family
Functional group of genes
Whole genome
All genomes on Earth
All genomes in Universe?

- Defines "design" in purely negative terms.
- Where is the cut-off between HP, IP & sp/SP?
- How do you define "specified" particularly if it is highly sensitive to changes in current knowledge?

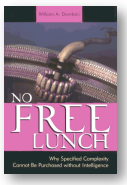




Dembski "Does The Math" (1997)

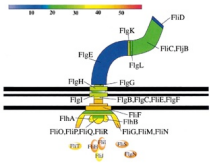
"Do the calculation. Take the numbers seriously. See if the underlying probabilities really are small enough to yield design."

The Design Inference, p. 228.



"I show that undirected natural processes like the Darwinian mechanism are incapable of generating the specified complexity that exists in biological organisms."

How? By a calculation showing that the probability of spontaneous assembly of the proteins in the flagellum lies beyond the range of the "universal probability bound" (1 x 10 $^{-150}$)

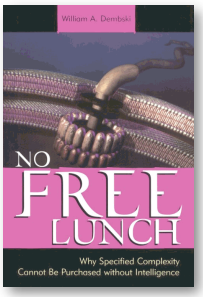


Dembski 2008

"I've pretty much dispensed with the EF. It suggests that chance, necessity, and design are mutually exclusive. They are not. Straight CSI is clearer as a criterion for design detection."

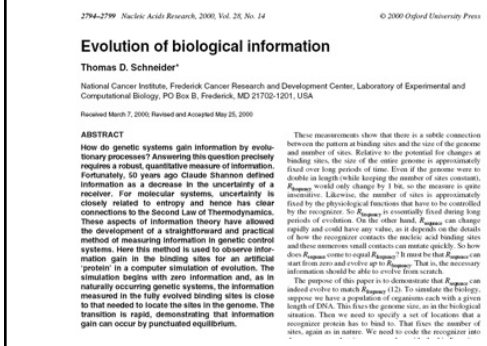
- http://www.uncommondescent.com/intelligent-design/some-thanks-for-professor-olofsson/#comment-299021

Dembski 2008



"The challenge for determining whether a biological structure exhibits CSI is to find one that's simple enough on which the probability calculation can be convincingly performed but complex enough so that it does indeed exhibit CSI. The example in NFL ch. 5 doesn't fit the bill."

http://www.uncommondescent.com/intelligent-design/some-thanks-for-professor-olofsson/#comment-299021



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Evolution of biological information

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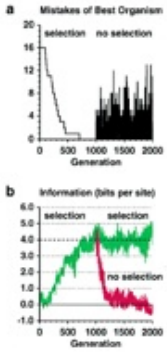
ABSTRACT

How do genetic systems gain information by evolutionary processes? Answering this question precisely requires a robust, quantitative measure of information. Fortunately, 50 years ago Claude Shannon defined information as a decrease in the uncertainty of a receiver. For molecular systems, uncertainty is closely related to entropy and hence has clear connections to the Second Law of Thermodynamics. These aspects of information theory have allowed the development of a straightforward and practical method of measuring information in genetic control systems. Here this method is used to observe information gain in the binding sites for an artificial 'protein' in a computer simulation of evolution. The simulation begins with zero information and, as in naturally occurring genetic systems, the information measured in the fully evolved binding sites is close to that needed to locate the sites in the genome. The transition is rapid, demonstrating that information gain can occur by punctuated equilibrium.



Schneider's *ev* program

Using a starting random base sequence of 256 bases, and a population of 64, *ev* generated (using random mutation and natural selection with *no* human intervention) a "CSI" binding site in 704 generations.

http://www.lecb.ncifcrf.gov/~toms/paper/ev/

Efficiency?

- This gain in information required the "death" of 32 organisms in each of 704 generations, i.e. 22,528 deaths.
- This is very inefficient, yet a site with a probability of 1 in 500,000,000,000,000,000,000 (I=68.76 bits) is generated in ~1000 generations
- The entire human genome (~4,000,000,000 bits) could evolve in a billion years
- This does not consider sexual recombination or realistic population size

Beating the UPB

- UPB = No of particles *x* Planck time *x* Age of Universe
- UPB = 10^{80} *x* 10^{45} *x* 10^{25} = 10^{150}
- "All the probabilistic resources in the known physical universe cannot conspire to render *remotely probable* an event whose probability is less than this universal probability bound." (Dembski, *The Design Revolution*, p. 87)
- Schneider looked for the evolution of 512 bits in a small (n=512) asexual population of creatures. He allowed one mutation per generation.
- He defeated the UPB in 15,000 generations

Living things create information ("specified complexity") via environmental selection and random mutations. Living things and their environment are the "intelligent designer"

Major Criticisms with CSI

- Information theory approach is just probability "dressed-up" as the framework offers nothing new
- How do you assign the probability thresholds? What is the cut-off between CSI and CI, etc.?
- The "Explanatory Filter" is a method for justification of belief rather than detection

Reaction to CSI

- Organismal Biologists … little time for abstractions, especially as no predictions are made
- Mathematicians … little notice
- Philosophers … negative due to problems with Explanatory Filter
- Number of papers using Dembski's method?