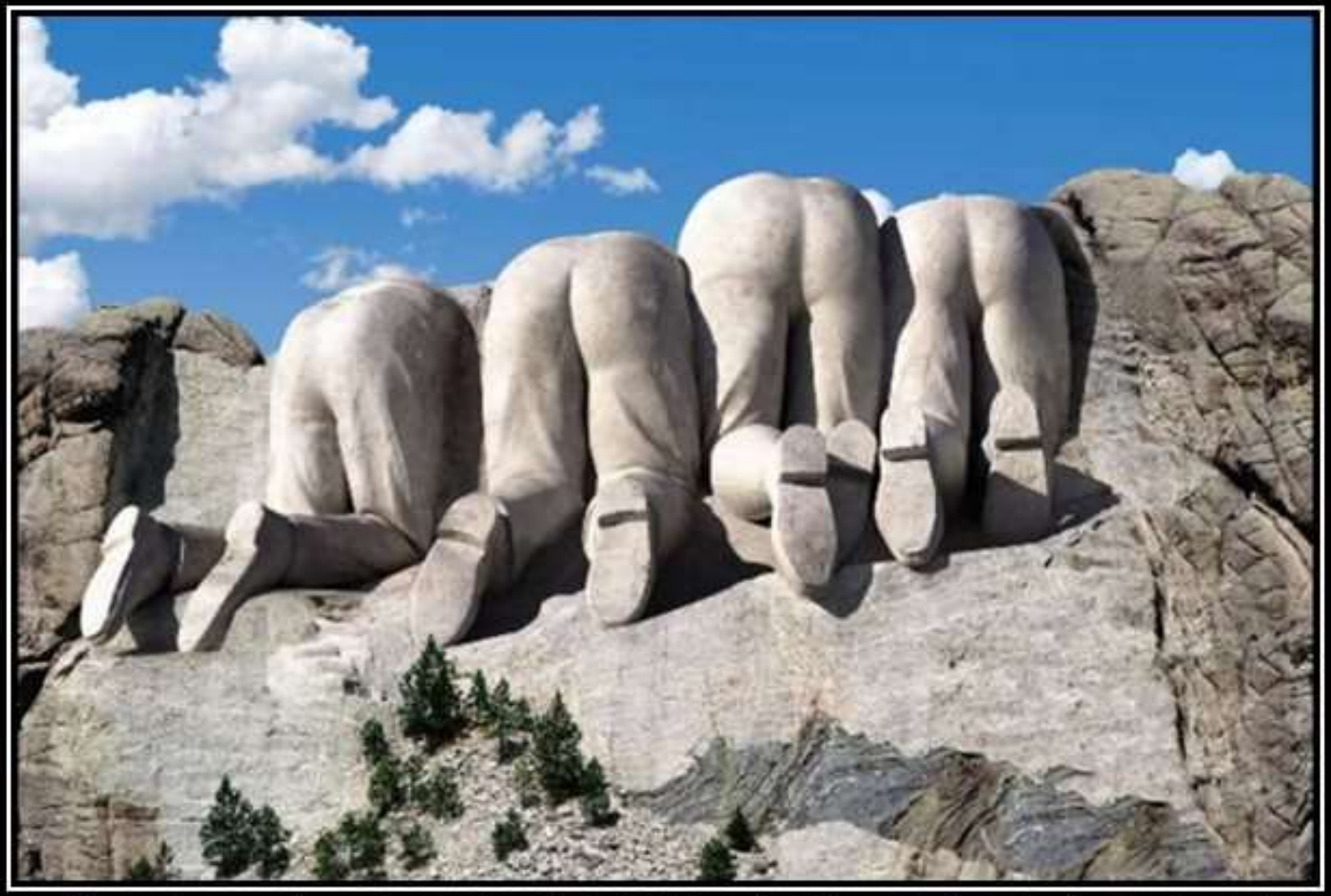
Method(s) of Design Detection

William A. Dembski

www.discovery.org

www.evoinfo.org

www.swbts.edu



MT. RUSHMORE

The backside

TWO TYPES OF CAUSES

Natural

Intelligent

Sand Dune

Sand Castle

TWO TYPES OF CAUSES

Unintelligent ← → **Intelligent**

Sand Dune

Sand Castle

TWO TYPES OF EFFECTS

Unintelligent ← → **Intelligent**

Sand Dune ***Sand Castle***

TWO TYPES OF EFFECTS

Intelligence Undetectable

Intelligence Detectable

Sand Dune

Sand Castle

Definition of Intelligent Design

The study of patterns in nature that are best explained as the result of intelligence.

Definition of Intelligence

Any causal power capable of matching means to ends.

How Do We Detect Design?

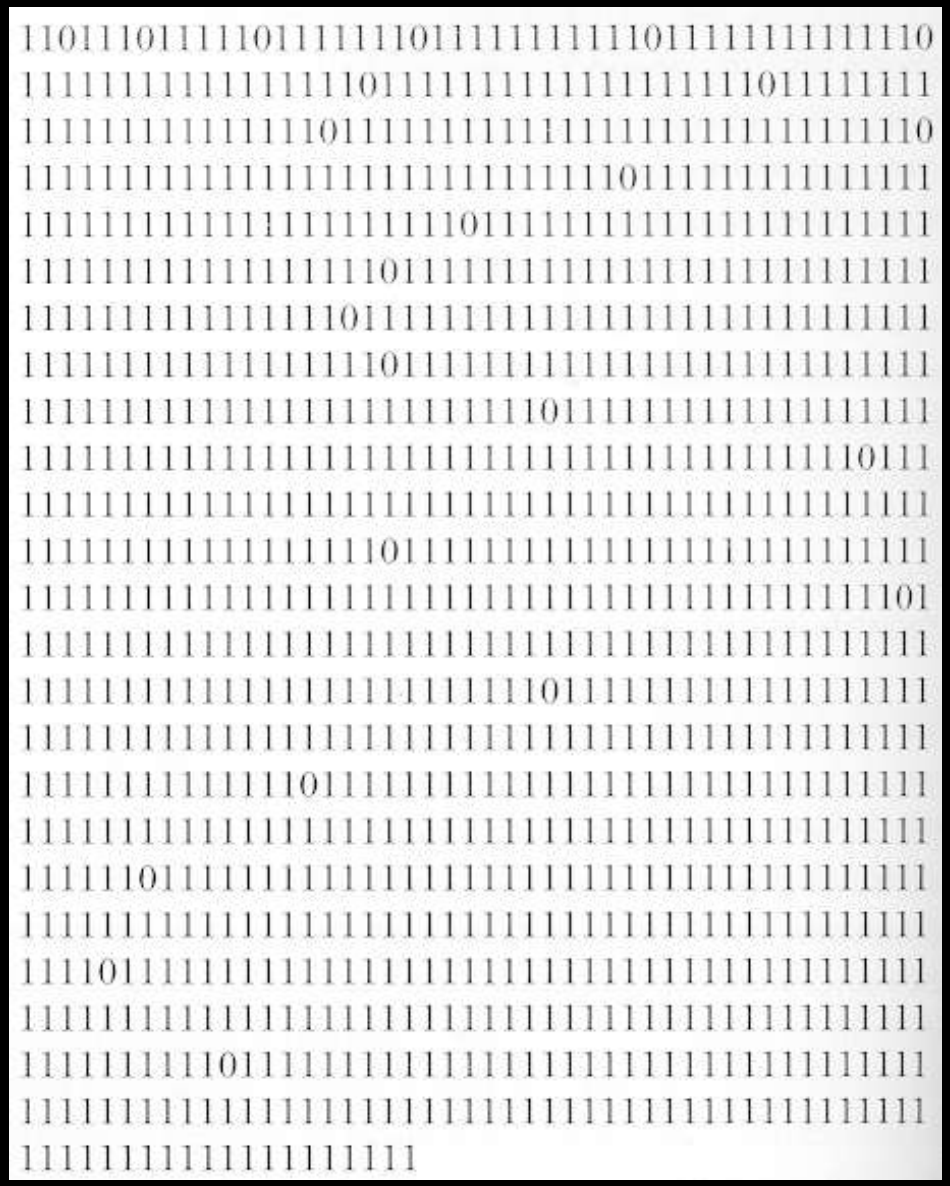
SETI: The Search for Extraterrestrial Intelligence

Discerning Design: Jodie Foster as a SETI researcher in *Contact*.

What persuaded the scientists that they had found an extra-terrestrial intelligence?

The detection of a highly improbable or complex specified event!

2 3 5 7 11 13



A Criterion for Detecting Design

What should we be looking for?

- Complexity (improbability)
- Specification (independent pattern)

Connection between Complexity and Probability

Why Probability?

Unless we discipline how we attribute chance, we can explain anything.

This is Spinal Tap

Dumb and Dumber

"We can accept a certain amount of luck in our [scientific] explanations, but not too much."

–Richard Dawkins (TBW, 1987, p. 139)

Why a Pattern?

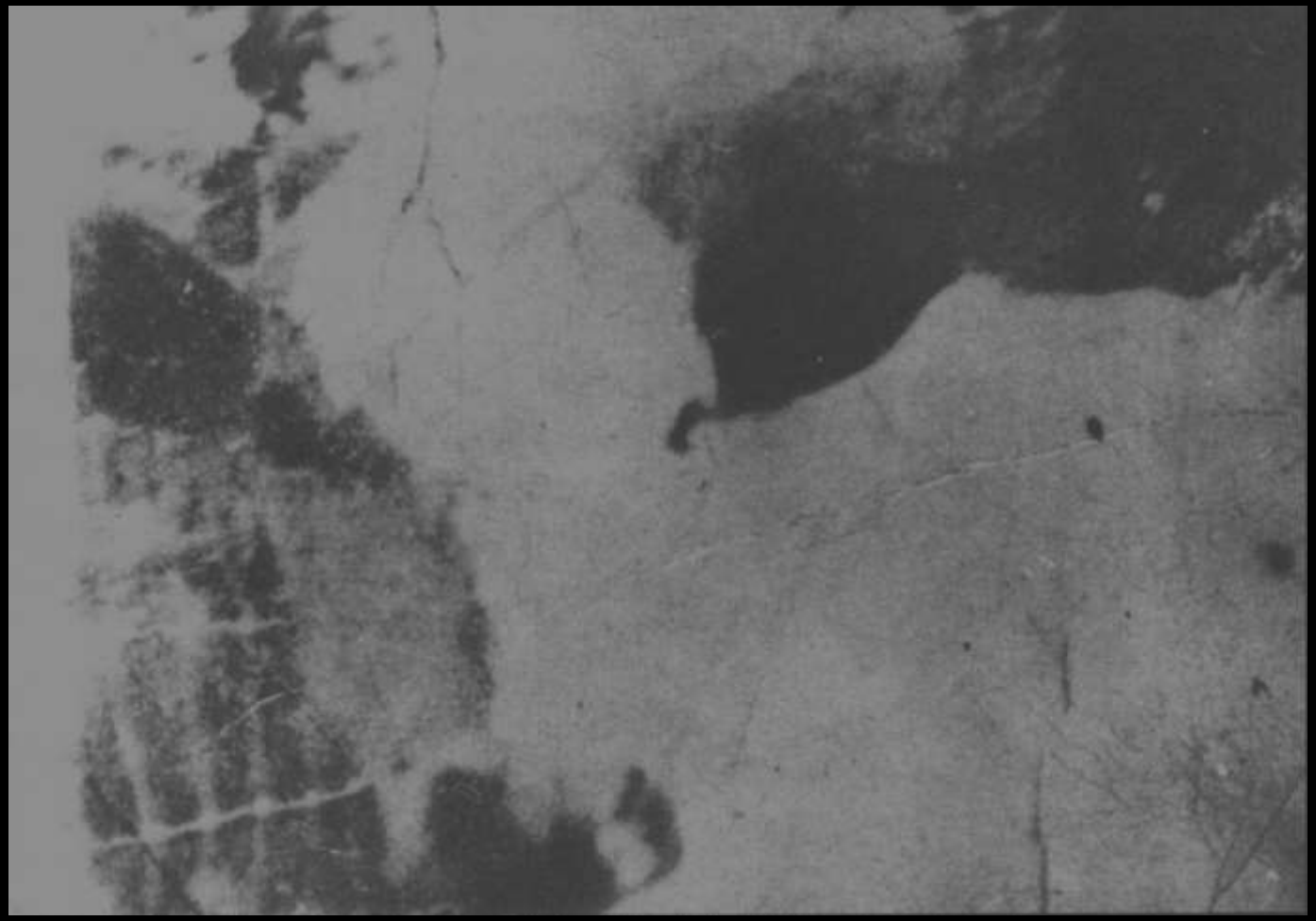
Just about anything that happens is highly improbable/complex. Thus to ensure that something didn't just happen by chance, it must conform to a pattern.

Seeing What We Want to See?

"Perceiving the world as well designed and thus the product of a designer ... may be the product of a brain adapted to finding patterns in nature. We are pattern-seeking as well as pattern-finding animals. ... Finding patterns in nature may have an evolutionary explanation: There is a survival payoff for finding order instead of chaos in the world…."

— Michael Shermer
WDM, 2006

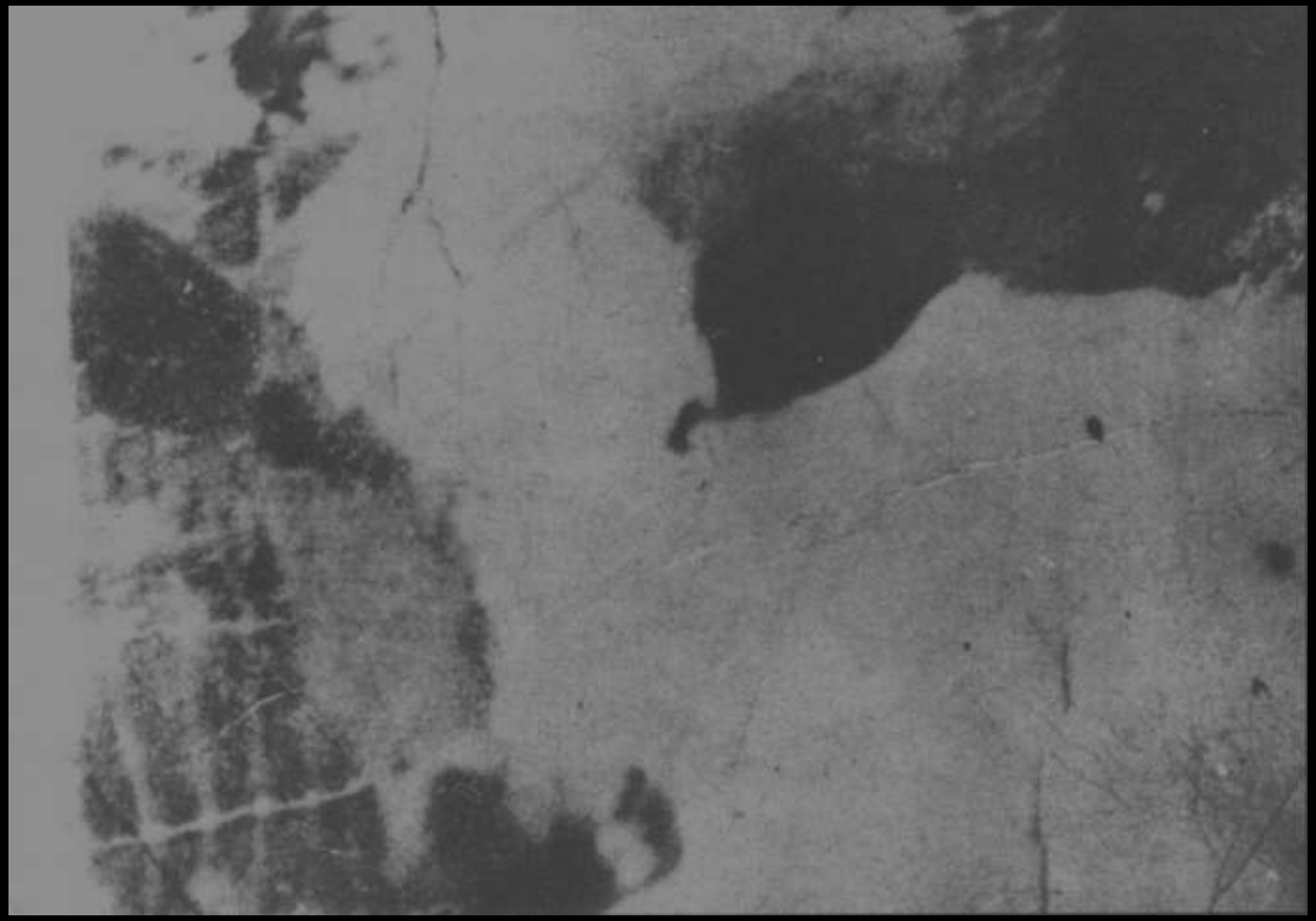
What Do You See?



Why a Specification?

Although we need a pattern to identify design, we also need to make sure that that we're not just reading the pattern into what we're seeing.

What Do You See?



The Case of Archery

The Case of Cryptography

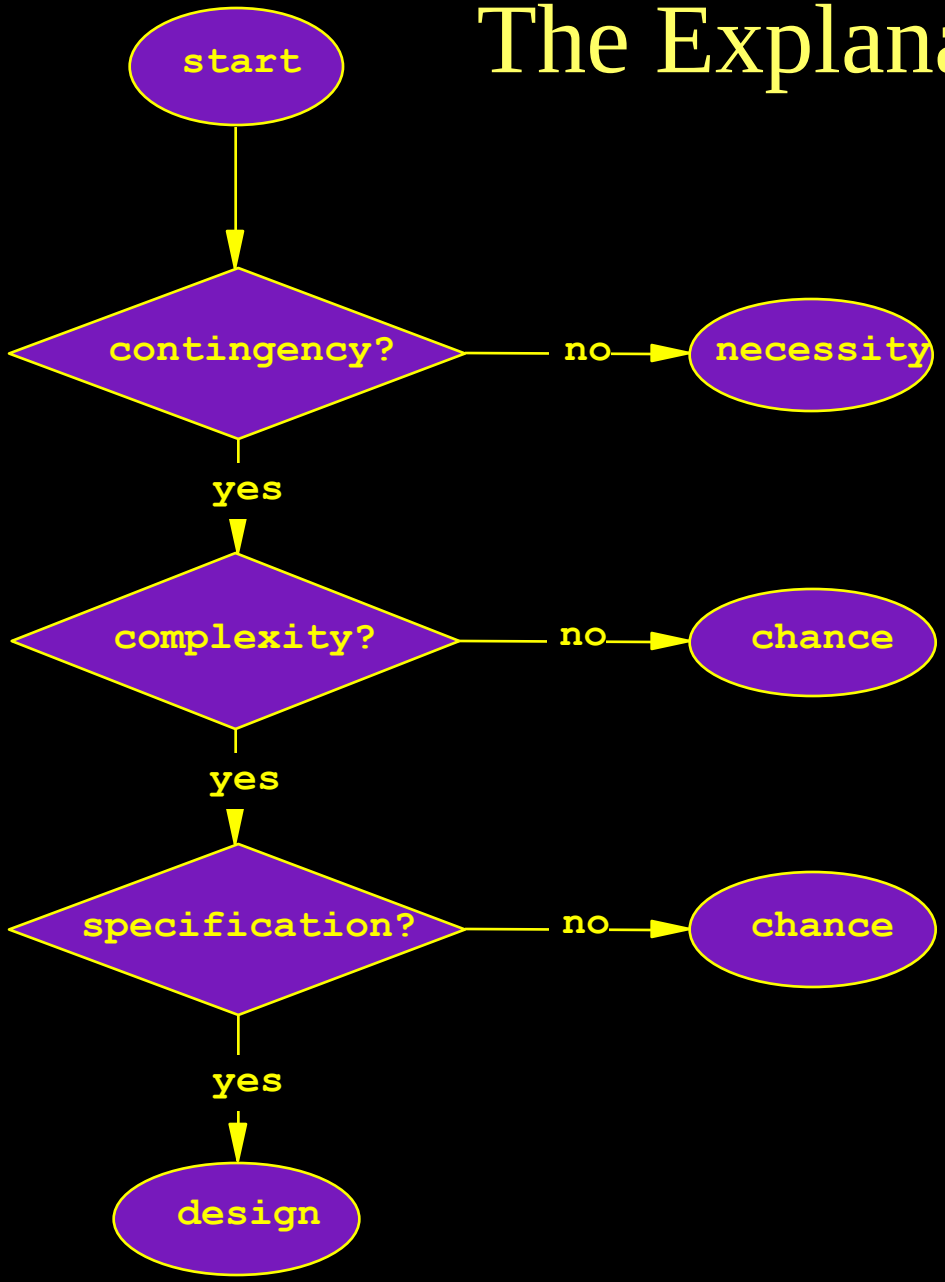
Encrypted Text

`nfuijolt ju jt mjlf b xfbtfm`

Decrypted Text

`methinks it is like a weasel`

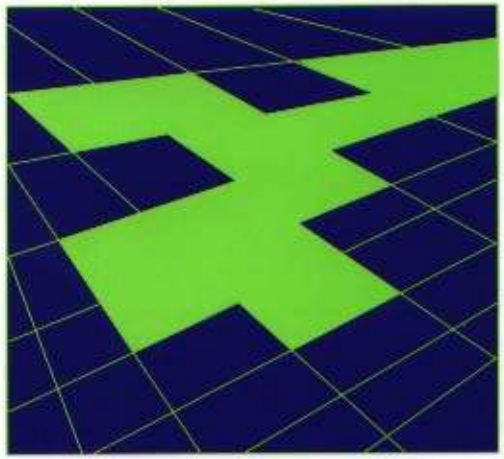
The Explanatory Filter



Cambridge Studies in Probability, Induction, and Decision Theory

THE DESIGN INFERENCE

ELIMINATING CHANCE THROUGH SMALL PROBABILITIES



WILLIAM A. DEMBSKI

What does the filter identify?

Specified Complexity

From Specified Complexity to Biological Complexity:

$$\mathbf{p}_{origin} \leq \mathbf{p}_{avail} \times \mathbf{p}_{synch} \times \mathbf{p}_{local} \times \mathbf{p}_{i\text{-}c\text{-}r} \times \mathbf{p}_{i\text{-}f\text{-}c} \times \mathbf{p}_{o\text{-}o\text{-}a} \times \mathbf{p}_{config}$$

Seven Hurdles Facing Biological Complexity

- Availability
- Synchronization
- Localization
- Interfering Cross-Reactions
- Interface Compability
- Order of Assembly
- Configuration

Availability

Are the parts needed to evolve an irreducibly complex biochemical system like the bacterial flagellum even available?

Synchronization

Are these parts available at the right time so that they can be incorporated when needed into the evolving structure?

Localization

Even with parts that are available at the right time for inclusion in an evolving system, can the parts break free of the systems in which they are currently integrated and be made available at the "construction site" of the evolving system?

Interfering Cross-Reactions

Given that the right parts can be brought together at the right time in the right place, how can the wrong parts that would otherwise gum up the works be excluded from the “construction site” of the evolving system?

Interface Compatibility

Are the parts that are being recruited for inclusion in an evolving system mutually compatible in the sense of meshing or interfacing tightly so that, once suitably positioned, the parts work together to form a functioning system?

Order of Assembly

Even with all and only the right parts reaching the right place at the right time, and even with full interface compatibility, will they be assembled in the right order to form a functioning system?

Configuration

Even with all the right parts slated to be assembled in the right order, will they be arranged in the right way to form a functioning system?

The Origination Inequality

$$\mathbf{p}_{origin} \leq \mathbf{p}_{avail} \times \mathbf{p}_{synch} \times \mathbf{p}_{local} \times \mathbf{p}_{i\text{-}c\text{-}r} \times \mathbf{p}_{i\text{-}f\text{-}c} \times \mathbf{p}_{o\text{-}o\text{-}a} \times \mathbf{p}_{config}$$

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Report

Continuous Molecular Evolution of Protein-Domain Structures by Single Amino Acid Changes

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sequences leads us to believe that the mutations we introduced to stabilize each structure reflect the birth of new protein folds in evolution.

Results

Evidence for the conformational diversity of proteins and the biological relevance of this diversity has gathered over the last years. Biological processes are driven by confined structural fluctuations [9–11] and local secondary-structure interconversions [7, 12], as well as tertiary- and quaternary-structural rearrangements, most prominently those involved in folding disorders such as prion diseases [13, 14]. Although there is not yet direct proof for the role of conformational diversity in protein evolution, an RNA sequence has been shown to assume two unrelated ribozyme folds with different activities in solution [4]. Such "bridge states" that form two different folds from a single sequence could evolve two different functions upon gene duplication and muta-

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Estimating the Prevalence of Protein Sequences Adopting Functional Enzyme Folds

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Proteins employ a wide variety of folds to perform their biological functions. How are these folds first acquired? An important step toward answering this is to obtain an estimate of the overall prevalence of sequences adopting functional folds. Since tertiary structure is needed for a typical enzyme active site to form, one way to obtain this estimate is to measure the prevalence of sequences supporting a working active site. Although the immense number of sequence combinations makes wholly random sampling unfeasible, two key simplifications may provide a solution. First, given the importance of hydrophobic interactions to protein folding, it seems likely that the sample space can be restricted to sequences carrying the hydropathic signature of a known fold. Second, because folds are stabilized by the cooperative action of many local interactions distributed throughout the structure, the overall problem of fold stabilization may be viewed reasonably as a collection of coupled local problems. This enables the difficulty of the whole problem to be assessed by assessing the difficulty of several smaller problems. Using these simplifications, the difficulty of specifying a working β-lactamase domain is assessed here. An alignment of homologous domain sequences is used to deduce the pattern of hydropathic constraints along chains that form the domain fold. Starting with a weakly functional sequence carrying this signature, clusters of ten side-chains within the fold are replaced randomly, within the boundaries of the signature, and tested for function. The prevalence of low-level function in four such experiments indicates that roughly one in 10^{64} signature-consistent sequences forms a working domain. Combined with the estimated prevalence of plausible hydropathic patterns (for any fold) and of relevant folds for particular functions, this implies the overall prevalence of sequences performing a specific function by any domain-sized fold may be as low as 1 in 10^{77}, adding to the body of evidence that functional folds require highly extraordinary sequences.

Is there a scientific debate?

The evolution of complex qualities like for example new protein structures through evolution is largely unsolved. While advocates of intelligent design-theory, like the US-american scientist Michael J. Behe, exclude the invention of new complex protein structures through few mutational steps, evolutionary biologists have found hints that new proteins can originate out of transistional forms that unite primitive and new properties. However, until now this has only shown by the accumulation of artificial mutations, that merely simulate evolutionary processes.

http://idw-online.de/pages/en/news?id=193184

From the press release

CONCLUSIONS:

1. Specified complexity is a reliable empirical marker of actual design.
2. Our best evidence suggests that many instances of biological complexity exhibit specified complexity.
3. Conventional evolutionary mechanisms give no indication of providing a general solution to the problem of biological complexity (and thus dissolving the specified complexity that appears to be there).