Introduction - "First we're going to cover the broad scope of problems in Creation Biology and gradually narrow it down to one manageable problem."

Estimating Active Information in Adaptive Mutagenesis

A First Step towards Measuring God's Design in Functional Adaptation

Additional Things to Cover:
- Bernoulli's principle of insufficient reason - i.e. it is good to be random where you don't know the answer, and we can thus use randomness to detect where the answer is known or unknown
- The origins of the idea of "random mutations" (i.e. Muller and mutagens + pre-existing mutations in Luria-Delbruck and Lederberg)
- The phrase "mutations are random in the sense that how often a mutation occurs is not related to its usefulness" can be used as a yardstick to measure functional adaptive design within mutations. In addition, it can be modeled with a random search through search space because of the properties of a random search - Active Information is the measure of how wrong this is
- No Free Lunch theorem

The Blyth Institute
http://www.blythinstitute.org/

Elements of a Theory of Design

Elements of a Theory of Design

- Biological Similarity
- Functional Adaptation
- Biological Imperfection
- Non-Survival Features
- Macrobiogeography

Wood, T. C. and M. J. Murray. 2003. *Understanding the Pattern of Life*. Broadman and Holman.

Elements of a Theory of Design

Functional Adaptation

Elements of a Theory of Design

Functional Adaptation

Biological Imperfection

Extending Mutation Theory for Creationary Use

- Traditional Viewpoint:
  - Beneficial / Neutral / Detrimental

Focuses on near-term effects of each individual mutation

- Creationary Viewpoint:
  - Design-consistent / Design-inconsistent

Focuses on the relationship between the mutation and the holistic design of life

Deciphering Design-Consistent Mutations

- Metabolic Consistency
- Mutational Mechanism
- Mutation Rate
- Reversibility
- Preservation of Genomic Semantics

Bartlett, J. L. 2009. Towards a Creationary Classification of Mutations. *ARJ* 2:169-174.

Deciphering Design-Consistent Mutations

Mutational Mechanism

"A mutation which is in response to a specific stress or group of stresses, or is timed to occur with a particular stage of life for an organism, or for which there is an enzyme whose core function is to produce such a mutation"

Segue - an interesting concept, but how do you measure it?

Bartlett, J. L. 2009. Towards a Creationary Classification of Mutations. *ARJ* 2:169-174.

Measuring God’s Design in Mutational Mechanisms

Types of Mutations

- Spontaneous Mutations
  - Covered in Bartlett, J. L. 2008. Statistical and Philosophical Notions of Randomness in Creation Biology. *CRSQ* 45(2):91-99.
- Adaptive Mutations
  - Evolution as a search for a solution to a biological problem

Types of Mutations

- Adaptive Mutations
  - Evolution as a search for a solution to a biological problem

Adaptive Mutation

- Organisms under stress can increase mutation rates
- These mutations often lead to new, adaptive genotypes
- When the stress is over, mutation usually returns to its normal rate
- In other words, in adaptive mutagenesis, there is an evolutionary search for a solution to the biological problem

Adaptive Mutation: Examples

- SOS Mechanism in Bacteria
- Somatic Hypermutation Mechanism in Adaptive Immune System

What Makes a Good Search?

What Makes a Good Search?

- There is **no searching technique** that is universally good *in the absence of knowledge about the solution space*
- Search techniques always make use of **specialized knowledge** about the solution space in order to increase likelihood of results
- In the absence of specialized knowledge, a **randomized search** will yield the best g

Why? Randomized search doesn't privilege any location, and it is guaranteed to hit all of them eventually

What Makes a Good Search?

- Use specialized knowledge about the search space
- Search the most likely areas for the solution first
- Search the least likely areas for the solution last
- If two areas are equally likely to have the solution, pick the one to search first at random (Bernoulli's *Principle of Insufficient Reason*)

Measuring Specialized Knowledge in Searches

Measuring Specialized Knowledge in Searches

- Active Information is a measurement of the **specialized knowledge** that a search algorithm brings to the search
- Active Information is measured by the **average increase in probability** that a search algorithm gives to a search from a random search, **measured in bits**

Dembski, W. A. and R. J. Marks II. 2009. Conservation of Information in Search: Measuring the Cost of Success. *IEEE Transactions on Systems, Man, and Cybernetics -- Part A: Systems and Humans* 39(5): 1051-1061.

Measuring Specialized Knowledge in Searches

$$I_+ = I_\Omega - I_S$$

I_+ = Active Information

I_Ω = Probability (in bits) of Success for Random Search

I_S = Probability (in bits) of Success for a Given Search Algorithm

$-\log_2(p)$ = Conversion from Probability to Bits

Dembski, W. A. and R. J. Marks II. 2009. Conservation of Information in Search: Measuring the Cost of Success. *IEEE Transactions on Systems, Man, and Cybernetics -- Part A: Systems and Humans* 39(5): 1051-1061.

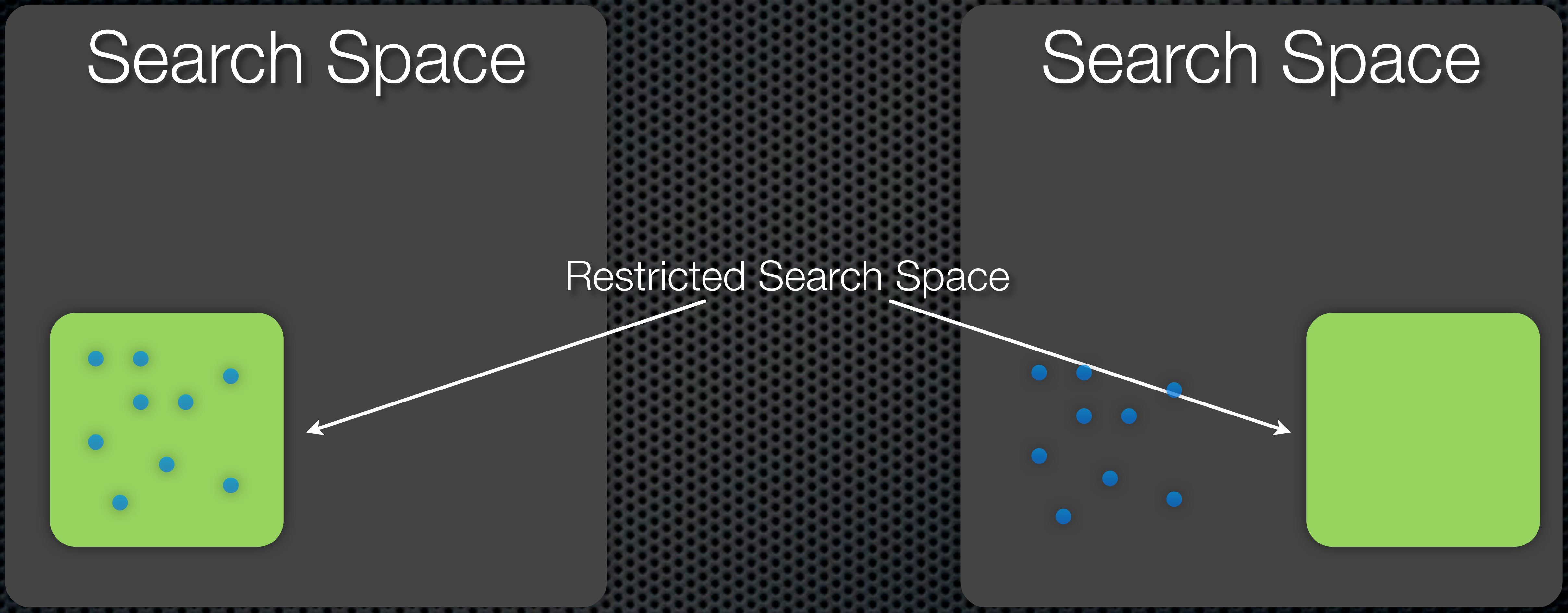
Interpreting Active Information

- $I_+ \approx 0$ → the search algorithm does not affect the likelihood of success much
- $I_+ < 0$ → the search algorithm tends to lead *away* from successful results
- $I_+ > 0$ → the search algorithm tends to lead *toward* successful results

Dembski, W. A. and R. J. Marks II. 2009. Conservation of Information in Search: Measuring the Cost of Success. *IEEE Transactions on Systems, Man, and Cybernetics -- Part A: Systems and Humans* 39(5): 1051-1061.

A Visual Look at Active Information

● Potential Target



Positive Active Information

Negative Active Information

Measuring Specialized Knowledge in Evolution

Measuring Specialized Knowledge in Evolution

- Active Information allows us to quantitatively estimate specialized information in some evolutionary searches
- The rate of success for mutations in certain circumstances can be compared to estimated rate of success for random searches
- The **difference** is the amount of specialized knowledge (Active Information) in the evolutionary search

Mention evolutionary definition of randomness

Example Application: Somatic Hypermutation

- Somatic Hypermutation (SMH) is the process that the immune system uses to fine-tune immunoglobulins to match new antigens
- It operates by mutating existing immunoglobulin genes repeatedly until it gets a good match
- It has many features that enable us to estimate active information simply

Simplifying Features of SMH

$$I_+ = I_\Omega - I_S$$

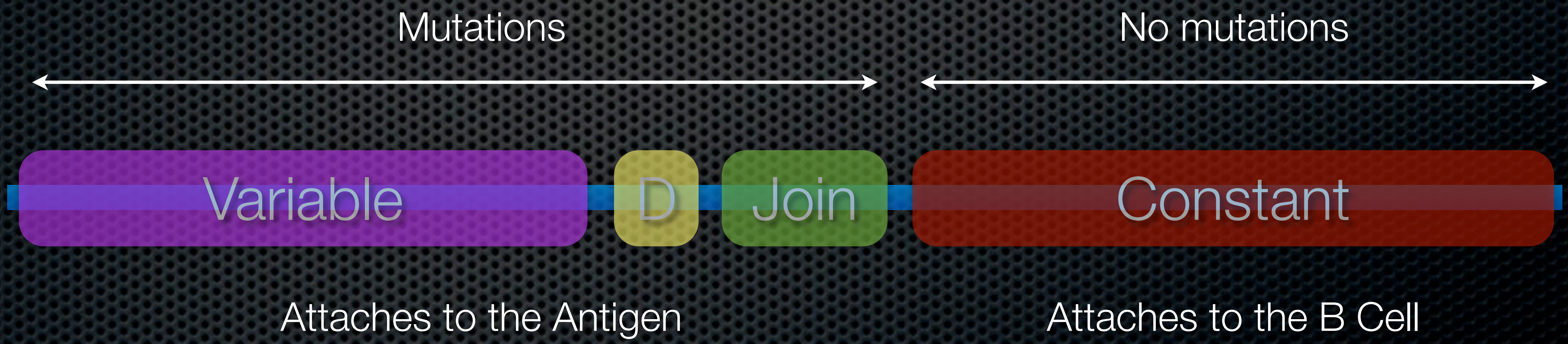
- I_Ω can be estimated because we know where the likely real successful targets are
- I_S can be estimated because
  - the cell does a physical localization of mutation
  - this localization fits with where we know the likely targets are

Visualizing Active Information in SMH

Whole Genome 4,000,000,000 base pairs

Immunoglobulin 1,200 base pairs

Mutations in the Immunoglobulin Gene



Mutations

No mutations

Variable

D

Join

Constant

Attaches to the Antigen

Attaches to the B Cell

Papavasiliou, F. N. and D. G. Schatz. 2002. Somatic Hypermutation of Immunoglobulin Genes: Merging Mechanisms for Genetic Diversity. *Cell* 109(2, Supplement 1) 1:S35-S44.

Active Information Calculation (Single Mut.)

- Assumed # of Mutations Required = 1
- Size of entire genome ≈ 4,000,000,000 base pairs
- Size of mutation region ≈ 600 base pairs
- $I_+ = I_\Omega - I_S$
- $I_\Omega = \log_2(4{,}000{,}000{,}000)$; $I_S = \log_2(600)$
- $I_+ \approx 31.9 - 9.2 = 22.7$ bits

Active Information Calculation (Multiple Mut.)

- g = genome size; m = maximum number of mutations; z = reduced search space size
- $I_\Omega = \log_2(g!/(g-m)!)$
- $I_S = \log_2(z!/(z-m)!)$
- $I_+ = \log_2(g!/(g-m)!) - \log_2(z!/(z-m)!)$
- Example for 2 mutations: $\log_2(g * (g-1)) - \log_2(z * (z-1))$

Active Information Calculation (Simplified)

- $I_\Omega = \log_2(g!/(g-m)!) - \log_2(z!/(z-m)!)$
- For simplified estimation (for large g and small m):
  - $I_+ = \log_2(g^m) - \log_2(z^m)$
  - $I_+ = m(\log_2(g) - \log_2(z))$

Additional Issues

- Are there other ways for the evolutionary problem to be dealt with (with mutations outside of I_S)?
- Is the assumption that a result is within the SMH search space correct?
- This did not deal with the specificity of the mutation (the substituted base), only the search space.

Additional Issues

Some measures (temperature, length, etc.) require no modeling. If we were to define those measures operationally, we could do so in terms of physical systems rather than mathematical abstractions.

I think that active information is not such a measure. Given a search space, a subset of that space designated as the target, and a method for selecting points in the space, active info is unambiguous. But if we need to impose the space/target/method model on a given system, our choice of how to do so may depend on what question we're trying to answer. For example, the question of how far somatic hypermutation deviates from the "mutation is random with respect to fitness" generalization yields a different model than the question of whether mutations are uniformly random across the 600-base variable region. -- Robert Stenger (personal communication)

Applications to Baraminology

Applications to Baraminology

- Cataloging which evolutionary searches have more or less active information can help us understand God’s intended design
  - What sort of biological problems do organisms solve well? Poorly?
  - How does this vary between baramins?
  - What does this tell us about God’s plan/purpose for each baramin and for life as a whole?

Questions?