

Estimating Active Information in Adaptive Mutagenesis

Jonathan Bartlett

The First Step in Understanding God's Design is Developing Tools to Measure It!

Measuring Specialized Knowledge in Searches

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

I_+ = Active Information

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

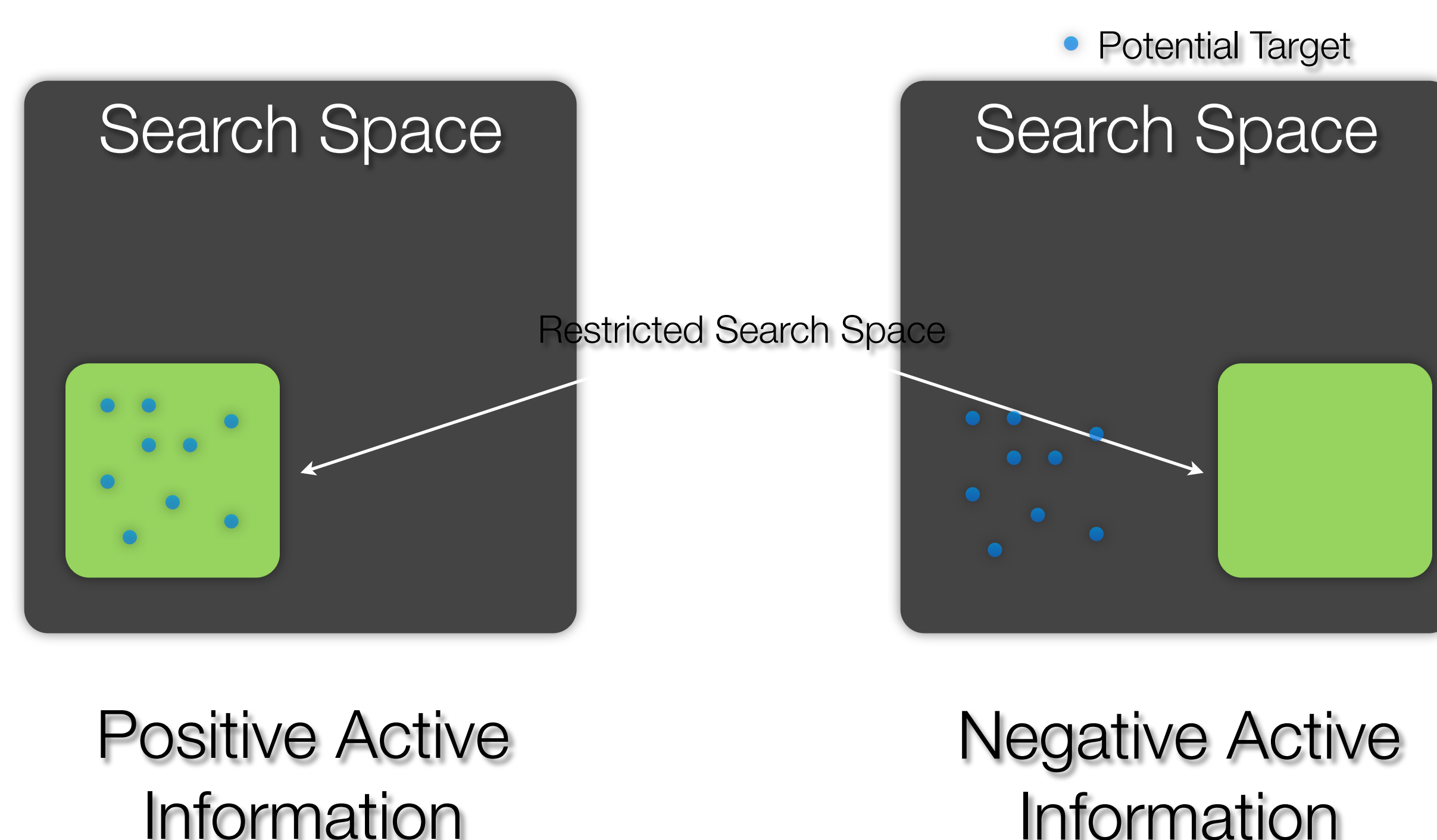
I_S = Probability (in bits) of Success for a Given Search Algorithm

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

Interpreting Active Information

- $I_+ = 0$ → 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

A Visual Look at Active Information



Adaptive mutagenesis refers to processes within cells that produce mutations in response to stresses. In bacteria, this process is mainly regulated by the SOS mechanism. In higher organisms, one of the more well-studied mechanisms is the somatic hypermutation (SMH) process for refining antibody affinity.

Active Information allows us to calculate the amount of information that the cell is contributing to its own evolution. It is calculated by comparing the probability of success of a blind search to the probability of success using a specific search algorithm.

In Somatic Hypermutation, the estimation is simplified because SMH primarily works by physically limiting the mutation space, and we can be relatively certain that this space restriction holds the target mutations we are looking for, while the rest of the space probably does not.

References

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

Bartlett, J. L. 2008. Statistical and Philosophical Notions of Randomness in Creation Biology. *CRSQ* 45(2):91-99.

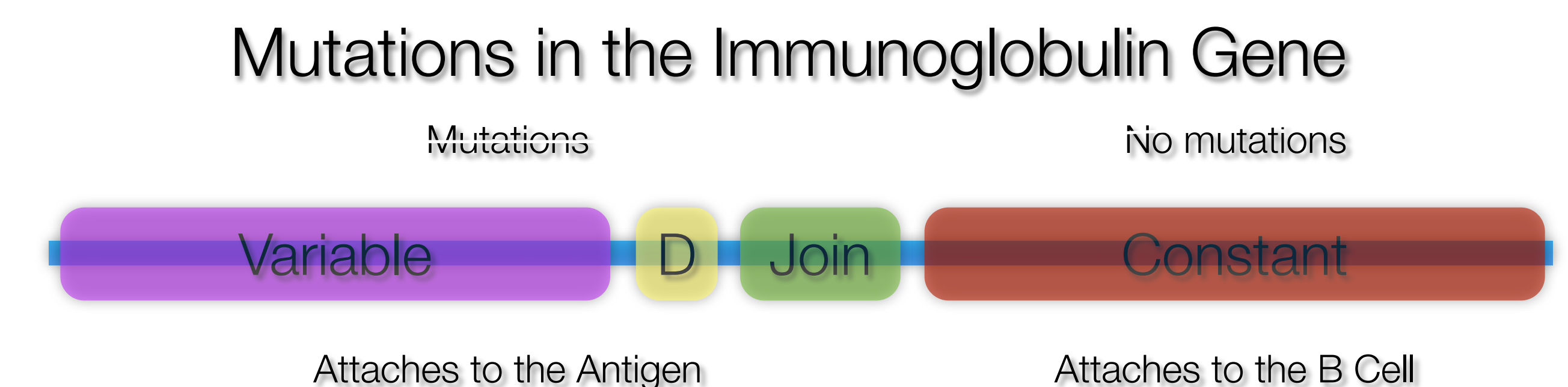
Dembski, W.A. and R. J. Marks II. 2009. Conservation of Information in Search: Measuring the Cost of Success. *IEEE Transactions on Systems, Man, and Cybernetics – Part A: Systems and Humans* 39(5):1051-1061.

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.

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

Visualizing Active Information in SMH

Whole Genome 4,000,000,000 base pairs
Immunoglobulin 1,200 base pairs

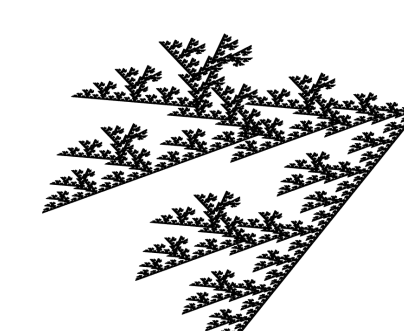


Active Information Calculation (Single Mutation)

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

Active Information Calculation (Multiple Mutations)

- 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: $\log_2(g * (g-1)) - \log_2(z * (z-1))$



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