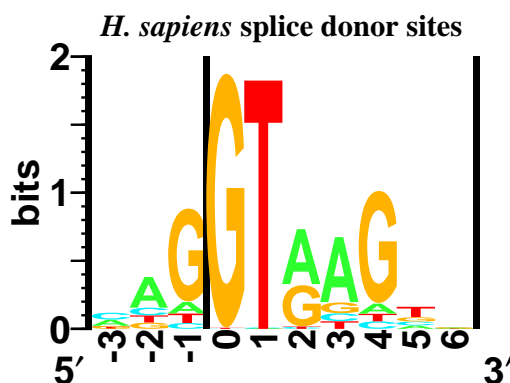


Molecular Information Theory, Energy Efficiency and Molecular Computing

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I am interested in understanding the fundamental mathematics underlying how living things function. It turns out that information theory provides a powerful tool for this purpose. My starting point is to investigate the DNA or RNA sequences that proteins and other molecules bind to to control genes. Using molecular biological techniques, we can determine these binding sequences and they can be aligned. The amount of conservation in the sequences can be determined in bits and the patterns can then be displayed as a sequence logo, shown to the right. The total information in binding sites can be computed and I have shown that it evolves to be the amount of information needed to locate the sites in the genome (<http://alum.mit.edu/www/toms/papers/ev>).



An important question is how the information is related to the binding energetics. A coin can stably hold only two states, heads or tails, but the energy dissipated to get the coin into one or the other state can vary. So there is an inequality relationship between energy and information and the minimum energy that must be dissipated to gain one bit of information is $K_b T \ln 2$ (J/bit) (<http://alum.mit.edu/www/toms/papers/edmm>).

How well do biological systems do relative to this bound, which comes from the second law of thermodynamics? The EcoRI protein binds to 5' GAATTC 3' and so gains $6 \times 2 = 12$ bits per binding. However, it dissipates 17.3 bits worth of energy, so it is only $12/17.3 = 70\%$ efficient. I have discovered that a large variety of molecular systems are 70% efficient and have determined the reason for this efficiency is that the molecules have evolved optimal coding systems (<http://alum.mit.edu/www/toms/papers/emmgeo>). 70% is the highest possible efficiency for a molecular device that makes selections and this therefore provides us with an engineering upper bound or a goal to shoot for in synthetic biology and when designing nanotechnologies.

I am also interested in molecular computing and have invented and patented a method based on a precise molecular flipflop that we discovered:
<http://alum.mit.edu/www/toms/patent/molecularcomputing/>

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