I don’t want to write a math paper like some that I am citing. Einstein wasn’t writing math. Adelmann doesn’t dwell on the math symbolictry neither do Hug and schuler.

Note that they are not attempting to form a biologically ‘realistic’ model of computing, but that their approach is an extreme simplification meaning that the actual capacity of an immune system is probably much greater

The need for infinite molecules of a certain type of interaction is a common short coming of biological computation paradigms like DNA and immune computing.

Biology will do most of its computation with the most efficient system. While many human systems are capable of computation, over time mechianical systems are replaced with silicon systems and most of human computing is done by the same chips and the remaining computational problem becomes building a network and algorithms to xlate these computations into reality at different scales

Turing studied factorial patterns in biology towards the end of his life. I might guess that he chose these systems, because exploring this simple calculation would expose a more general computation method in biology (I should read the paper to find out). Note that I plan to continue turing’s work.

Mattick proposed that RNA acts as software for DNA’s hardware. I plan to continue this line of inquiry.

order of operations is a huge difference between biological and silicon systems and understanding a turing machine that can process parrellelly is very important… though certainly many biological process proceed in sequence, like polyII behavior

turing\_biology\_aside.docx - To frame the study of turing biology

Biology and computation have an intertwined history. Computers have been used to model complex biological processes like gene regulation and interpret massive biological datasets as demanded, for instance, by sequencing efforts. Biology, in turn, has inspired computing from its early theoretical inception, as in the theory of cellular automata, to its modern application as seen in genetic learning algorithms and artificial neural networks (Kari and Rozenberg 2008).

More recently, efforts have been made to compute using biological tools. Adleman and a stream of researchers following him have proven that biological elements, mainly DNA and proteins, can be employed to perform complex computations (Adleman 1994). Currently, these biologically derived computers cannot compete with their silicon counterparts, though they offer some interesting advantages reviewed elsewhere (Shapiro and Gil 2007).

Still another current of research, smaller than the rest and the subject of this paper, has attempted to explore computation in natural biological systems. While work on this subject has been scattered, its synthesis overwhelmingly supports the concept that biology is ripe with computation across multiple systems and scales.

Approaching biology as a computational process has more than just theoretical implications. It supports the idea that complex biological processes, including diseases like cancer and alzheimers, depend on information processing. Mechanistic changes that produce phenotype may often be preceeded by procedural changes that are the product of biology’s codes. The interventions necessary to treat complex diseases may prove to be more informational than mechanistic.

Like medicine, computing stands to benefit from an exploration of biological information processing. While silicon, radio, and fiber optics have produced fastest and most reliable computational and communication systems known, biological computing may well represent the most ubiquitous and cost effective computation system in existence. A future for computing might be imagined that represents the synthesis of powerful cheap biological computing interwoven with high speed, ultra-reliable human inventions.

This paper will seek to lay a groundwork for future work on computation in biology by reviewing well established computation models in biology and proposing additional ones (which ones?). It will begin with a brief discussion of what is meant by a model of computation.

Note: Wolfram proposes molecular computers using 2, 3 Turing systems for molecular level computations (provided we can manufacture more efficient compilation algorithms)

http://blog.wolfram.com/index.php?year=2007&monthnum=10&name=the-prize-is-won-the-simplest-universal-turing-machine-is-proved

Note:include the concept of pancomputationalism, though do not give it too much weight

Note that RNA computing is attractive over other forms because of its scale an within lifetime modifications.

I should include DNA computing and other in vitro work as a small section

[Kari's Natural Computing notes](http://localhost/Archives/Kari_Natural_Computing.txt)

Adleman, L. M. (1994). "Molecular computation of solutions to combinatorial problems." Science **266**(5187): 1021-1024.

Kari, L. and G. Rozenberg (2008). "The many facets of natural computing."

Shapiro, E. and B. Gil (2007). "Biotechnology: Logic goes in vitro." Nature **2**(2): 84-85.