Enantiomers for Molecular Computation and Manufacturing Systems (Extended Abstract, will submit to ASPLOS 98 "Wild and Crazy Ideas" session)

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1 Molecular Computing

Molecular computing based on existing biological molecules shows great potential as a computing framework, due to the massive degree of parallelism involved and the ability to use pieces of existing biological systems to perform complex operations. Adelman first demonstrated this by developing a series of steps of DNA processing to solve instances of Hamiltonian Path. His algorithm involved constructing a massive number of potential solutions in parallel and then filtering the resulting strings to find a correct solution. It is a field of ongoing interest, as the theoretical limit is very impressive, since a replicating *E. coli* performs ~2000 bit-copies/second and contains 4 Mb! of storage, all in roughly .0675 μm^3!

The current trend appears to involve using enzymes, DNA, and other structures from existing biological systems for research into computation and molecular scale manufacturing, simply because the biological systems are extremely sophisticated. One could conceivable scale up some proposed biological based molecular computing systems to large computational vats. However, biological contamination is a serious concern, as we are dealing with biologically active materials. A computational vat is not very effective when some bacteria comes along and decides that your computer would make a tasty meal!

2 Enantiomers

All biological systems are based on simple molecules, mostly sugars and amino acids. These molecules are asymmetric, and the mirror inverses, or *enantiomers*[1], are not biologically active. The enantiomers are designated by the prefix **D** or **L** when naming the molecules. For example, although the mirror opposite of sucrose tastes sweet (the receptors on the tongue are not very discriminating), it is undigestable since it won't fit properly in the enzymes which break sucrose apart. It is akin to trying to use screws who's threads are in the opposite direction. All biological systems use **D** sugars and **L** amino acids as primary building blocks.

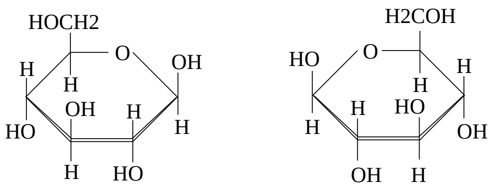

Figure 1: β-**D-Glucose** and β-**L-Glucose**

A hypothesis which needs to be tested is the following: If a protein is built out of **D** amino acids, will the resulting protein be the enantiomer of the original protein? If a portion of a metabolic pathway is built

[1] A molecule composed of the identical atoms in a mirror inverted structure. Another term for this property is *chirality*.

completely out of the mirror opposite building blocks, will it operate on mirror opposite molecules? If the answer is true, this suggests that an infrastructure can be built up by copying bits of biological systems using opposite chirality building blocks. These copied systems can then be used as the basis of our molecular computations and manufacture.

3 Benefits of using enantiomers

Why would using enantiomers be a significant benefit over the current trends in molecular computing? Because they may allow us to build up complex pathways and molecular structures by borrowing and copying designs from existing biological systems while using biologically inert components. The existing biological systems are so much more sophisticated than human designers are capable of inventing in the near future, yet if we simply extract biological material for use in our computations, we have to worry about maintaining sterility. Enantiomer based systems would not have such problems, as they would be unmetabolizeable. Furthermore, since the resulting molecules are structurally different, enantiomeric results can be isolated from biological contaminants.

The requirements for building the infrastructure are initially steep. The basic RNA$\rightarrow$protein transcription system will have to be built "from scratch", using synthetically produced enantiomeric molecules. Once this is complete, synthetically produced building blocks could be used to construct enantiomeric copies of larger metabolic pathways. The eventual goal would be production of photosynthetic pathways and related synthetic processes, allowing all subsequent work to proceed without large inputs of complex, synthetically produced molecules. Such an infrastructure could easily take years to build, but once complete it is a matter of scaling up production and using these pathways as a foundation for future work in molecular computing and manufacturing, while still using most of the techniques currently in development for molecular computing.