The

Biomolecules

Continued from age 2

are scientifically significant. They bring together scientists with deep knowledge of many different fields and it is certain that their contributions will elev

Biomolecules

Continued from age 3

ferent then a brute force search but the use of the "massive parallelism" of DNA made it very novel. A very large number of molecules, 10^{15} or more, can be used in a single reaction and the WC-complementarity assures that in the first step of the algorithm, the sequences representing paths are formed. A very large number of them are formed, such that, if a solution to the problem exists, with a high probability it will be represented within one of the formed sequences. So the immense labor required to solve the problem was taken care of with the massive parallelism — the fact that many molecules were "working" on the problem at once — and the WC-complementarity. In his article, Adleman asserted that if we consider each DNA molecule as a computational devise, DNA based computers can bring potential savings in energy and increase in speed and storage of 10^8 fold. This was certainly one of the reasons for excitement.

Several theoretical models based on the lab protocols used in the Adleman's experiment can be found in the literature. They all use more or less the same set of operations: *merge, separate, detect, amplify*, etc., and it is feasible that they all can be executed by a robotic system. These operations can be even used to break the Data Encryption Standard (DES) code. Approximately one gram of DNA is needed and using robotic arms (assuming each operation to last one minute) breaking DES is estimated to take five days. The most significant advantage in the analysis for breaking DES is that the success is quite likely even with the (at this point unavoidable) large number of errors within the lab protocols.

The big drawback in the Adleman's approach is the need to have a very large pool of initial molecules that have to be generated in order to assure correct solution to the problem. In Figure 1, the graph has only 7 vertices. The first step of the algorithm requires approximately 2^7 distinct molecules to be generated in order to be sure that the solution (if exists) will be present in the mix. Working with over 10^{15} DNA molecules, generating 2^7 distinct molecules does not seem difficult. But for a larger graph, say a modest size of 200 vertices, one needs (as Hartmanis noted) "DNA more than the weight of the Earth". The subsequent studies have concentrated on developing algorithms such that not necessarily all of the potential solutions are constructed at once.

The field of DNA computing has already branched so that other biomolecules such as RNA and liposomes and even cells are considered as potential computational tools. Recently, the chemists at New York University constructed a molecular mechanical device attributed to the properties of B-Z (right-handed and left-handed double helix) transition of DNA. This opens a horizon for design of computational three dimensional DNA objects that can participate in biochemical processes, and at the same time perform controlled mechanical movements.

Much work remains to be done on both experimental and theoretical level. We are at the beginning of a very exiting era. Biomolecular computers are in the stage equivalent to the one that the electronic computers were in mid 30's when Turing introduced the idea of a universal computer, of which the Turing machine is the primeval example. It is impossible to say which one, or whether any of the numerous theoretical models and experimental investigations will emerge as a successful new way of computing, but the knowledge that we acquire along the way will certainly be enormous. This field has become a common platform for exchanging ideas between computer science, mathematics, molecular biology, chemistry ... . Its development is bound to change our ideas and understanding of both, computing and the biological processes in vivo.

Events alendar

More information about upcoming events will appear at our website,

`http://www.math.usf.edu`,

as the event approaches. So mark the event on your calendar, and plan on taking part.

Professor *F. Alberto Grunbaum* of UC Berkeley will talk about **Mathematics in medical imaging: the present and the future** on Nov. 1, at 7:30 pm, in the University Lecture Hall (ULH).

see Events *on age 5*

Events

Continued from age 4

The talk will be on the mathematics, physics, and engineering that went into the development of Computerized Tomography (CAT) and other techniques like Magnetic Resonance Imaging (MRI). For more information, consult the Departmental website.

Nagle Lecture Series

Last Fall, Professor A. K. Dewdney of the University of Waterloo gave the Nagle Lecture on "Do Aliens Do Math?" The question is whether extraterrestrials might do mathematics (and science) as we understand it. This question leads to the philosophical question of whether mathematics is about "real" objects (like stars, planets, and automobiles) or about social conventions (like words, customs, and clothing fashions).

A. K. Dewdney is a Professor of Computer Science, and a longtime

Faculty

Continued from age 5

journals, and Director of the USF Institute for Constructive