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DNA COMPUTING BASED ON INSERTIONS AND DELETIONS

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Abstract. The author argues that biological computing has in potential the advantage of extraordinary speed, storage capacity and energy efficiency. She outlines the principles and points to the practical possibilities.

1. DNA solutions to mathematical problems

History of computation is almost as old as the history of *Homo sapiens* and the means used for computing have evolved in parallel with the evolution of humankind. Starting with the *manual computing* in base 10 using the fingers, and continuing with various devices for *mechanical computing* (abacus, slide rule), computation reached a new level of complexity in the beginning of this century with the discovery of *electronic computing*. The last years of the 20th century bring yet another means for computation that promises to yield tremendous advantages in speed, information storage and energy efficiency: *biological computing* using DNA.

Despite the complexity of the technology involved, the idea behind DNA computing is the simple observation that the following two processes, one biological and one mathematical, are analogous:

> (a) the very complex structure of a living being is the result of applying simple operations (copying, splicing, etc.) to initial information encoded in a DNA sequence,
>
> (b) the result $f(w)$ of applying a computable function to an argument w can be obtained by applying a combination of basic simple functions to w (see Yasuhara 1971 for details).

If noticing this analogy were the only ingredient necessary to cook a computing DNA soup, we would have been playing computer games on our DNA laptops a long time ago! It took in fact the ripening of several factors and a renaissance mind like Adleman's, a mathematician knowledgeable in biology, to bring together these apparently independent phenomena. Adleman realized that not only are the two processes similar but, thanks to the advances in molecular biology technology, one can use the biological to simulate the mathematical. More precisely, DNA strings can be used to encode information while enzymes can be employed to simulate simple computations, in a way described below.

DNA (deoxyribonucleic acid) is found in every living creature as the storage medium for genetic information. It is composed of units called nucleotides, distinguished by the chemical group, or base, attached to them. The four bases are *adenine*, *guanine*, *cytosine* and *thymine*, abbreviated as A, G, C, and T. Single nucleotides are linked together end-to-end to form DNA strands. The DNA sequence has a *polarity:* a sequence of DNA is distinct from its reverse. Taken as pairs, the nucleotides A and T and the nucleotides C and G are said to be *complementary*. Two complementary single-stranded DNA sequences with opposite polarity will join together to form a double helix in a process called *annealing*. The reverse process – a double helix coming apart to yield its two constituent single strands – is called *melting*.

A single strand of DNA can be likened to a string consisting of a combination of four different symbols, A, G, C, T. Mathematically, this means we have at our disposal a 4 letter alphabet $X = \{A, G, C, T\}$ to encode information, which is more than enough, considering that an electronic computer needs only two digits, 0 and 1, for the same purpose.

The simple operations that can be performed on DNA sequences are accomplished by a number of commercially available enzymes that execute some basic tasks. One class of enzymes, called *restriction endonucleases*, will recognize a specific short sequence in a strand and then "cut" the strand at that location. Another enzyme, called the *DNA ligase*, will hook together, or "ligate", the sticky end of a freshly cut DNA strand to another strand. There are many other enzymes that could potentially be useful, but for our models of computation these are sufficient.

The practical possibilities of encoding information in a DNA sequence and of performing simple biooperations were used in Adleman (1994) to solve a 7 node instance of the Directed Hamiltonian Path Problem. A directed graph G with designated vertices v_{in} and v_{out} is said to have a Hamiltonian path if and only if there exists a sequence of compatible "one-way" edges $e_1, e_2, \ldots, e_z$ (that is, a path) that begins at v_{in}, ends at v_{out} and enters every other vertex exactly once.

The following (nondeterministic) algorithm solves the problem:

> Step 1. Generate random paths through the graph.
>
> Step 2. Keep only those paths that begin with v_{in} and end with v_{out}.

Step 3. If the graph has n vertices, then keep only those paths that enter exactly n vertices.

Step 4. Keep only those paths that enter all of the vertices of the graph at least once.

Step 5. If any paths remain, say "YES"; otherwise say "NO".

To implement Step 1, each vertex of the graph was encoded into a random 20-nucleotide strand (20-letter sequence) of DNA. Then, for each (oriented) edge of the graph, a DNA sequence was created consisting of the second half of the sequence encoding the source vertex and the first half of the sequence encoding the target vertex. By using complements of the vertices as splints, DNA sequences corresponding to compatible edges were ligated, that is, linked together. Hence, the ligation reaction resulted in the formation of DNA molecules encoding random paths through the graph.

To implement Step 2, the product of Step 1 was amplified by polymerase chain reaction (PCR). Thus, only those molecules encoding paths that begin with v_{in} and end with v_{out} were amplified.

For implementing Step 3, a technique called gelelectrophoresis was used, that makes possible the separation of DNA strands by length. (The molecules are placed at the top of a wet gel, to which an electric field is applied, drawing them to the bottom. Larger molecules travel more slowly through the gel. After a period, the molecules spread out into distinct bands according to size.)

Step 4 was accomplished by iteratively using a process called affinity purification. This process permits single strands containing a given subsequence v (encoding a vertex of the graph) to be filtered out from a heterogeneous pool of other strands. (After synthesizing strands complementary to v and attaching them to magnetic beads, the heterogeneous solution is passed over the beads. Those strands containing v anneal to the complementary sequence and are retained. Strands not containing v pass through without being retained.)

To implement Step 5, the presence of a molecule encoding a Hamiltonian path was checked. (This was done by amplifying the result of Step 4 by polymerase chain reaction and then determining the DNA sequence of the amplified molecules).

A remarkable fact about Adleman's result is that not only does it give a solution to a mathematical problem, but that this is a hard computational problem in the sense explained below (see Gifford 1994, Garey & Johnson 1979).

Problems can be ranked in difficulty according to how long the best algorithm to solve the problem will take to execute on a single computer. Algorithms whose running time is bounded by a polynomial (respectively exponential) function, in terms of the size of the input describing the problem, are in the "polynomial time" class P (respectively the "exponential time" class EXP). A problem is called *intractable* if it is so hard that no polynomial time algorithm can possibly solve it.

A special class of problems, apparently intractable, including P and included in EXP is the "nondeterministic polynomial time" class, or NP. The following inclusions between classes of problems hold:

$P \subseteq NP \subseteq EXP \subseteq$ Universal.

NP contains the problems for which no polynomial time algorithm solving them is known, but that can be solved in polynomial time by using a nondeterministic computer (a computer that has the ability to pursue an unbounded number of independent computational searches in parallel). The directed Hamiltonian path problem is a special kind of problem in NP known as "NP-complete". An NP-complete problem has the property that every other problem in NP can be reduced to it in polynomial time. Thus, in a sense, NP-complete problems are the "hardest" problems in NP.

The question of whether or not the NP-complete problems are intractable, mathematically formulated as "Does P equal NP?", is now considered to be one of the foremost open problems of contemporary mathematics and computer science. Because the directed Hamiltonian path problem has been shown to be NP-complete, it seems likely that no efficient (that is, polynomial time) algorithm exists for solving it with an electronic computer.

Following Adleman (1994), in Lipton (1995) a potential DNA experiment was described for finding a solution to another NP-complete problem, the Satisfiability Problem. The Satisfiability Problem consists of a Boolean expression, the question being whether or not there is an assignment of truth values – true or false – to its variables, that makes the value of the whole expression true. The method from Lipton (1995) is used by Lipton (manuscript) to show how other NP-complete problems can be solved.

In Boneh et al. (1995a), a "molecular program" was given for breaking the U.S. government's Data Encryption Standard (DES). DES encrypts 64 bit messages and uses a 56-bit key. Breaking DES means that given one (plain-text, cipher-text) pair, we can find a key which maps the plain-text to the cipher-text. A conventional attack on DES would need to perform an exhaustive search through all of the 2^{56} DES keys, which, at a rate of 100,000 operations per second, would take 10,000 years. In contrast, it was estimated that DES could be broken by using molecular computation in about 4 months of laboratory work.

The problems mentioned above show that molecular computation has the potential to outperform existing computers. One of the reasons is that the operations molecular biology currently provides can be used to organize massively parallel searches. It is estimated that DNA computing could yield tremendous advantages from the point of view of *speed, energy efficiency* and *economic information storing*. For example, in Adleman's model (1995), the number of operations per second could be up to approximately 1.2×10^{18}. This is approximately 1,200,000 times faster than the fastest supercomputer. While existing supercomputers execute 10^9 operations per Joule, the energy efficiency of a DNA computer could be 2×10^{19} operations per Joule, that

is, a DNA computer could be about 10^{10} times more energy efficient (see Adleman 1994). Finally, according to Adleman (1994), storing information in molecules of DNA could allow for an information density of approximately 1 bit per cubic nanometer, while existing storage media store information at a density of approximately 1 bit per 10^{12} nm^3. As estimated in Baum (1995), a single DNA memory could hold more words than all the computer memories ever made.

2. Can DNA compute everything?

The potential advantages of DNA computing versus electronic computing are clear in the case of problems like the Directed Hamiltonian Path Problem, the Satisfiability Problem, and breaking DES. On the other hand, these are only particular problems solved by means of molecular biology. They are one-time experiments to derive a combinatorial solution to a particular sort of problem.

This immediately leads to two fundamental questions, posed in Adleman's article and in Gifford (1994) and Lipton (1994):

> (1) What kind of problems can be solved by DNA computing?
>
> (2) Is it possible, at least in principle, to design a programmable DNA computer?

More precisely, one can reformulate the problems above as:

> (1) Is the DNA model of computation computationally complete in the sense that the action of any computable function (or, equivalently, the computation of any Turing machine) can be carried out by DNA manipulation?
>
> (2) Does there exist a universal DNA system, i.e., a system that, given the encoding of a computable function as an input, can simulate the action of that function for any argument? (Here, the notion of function corresponds to the notion of a program in which an argument w is the input of the program and the value $f(w)$ is the output of the program. The existence of a universal DNA system amounts thus to the existence of a DNA computer capable of running programs.)

Opinions differ as to whether the answer to these questions has practical relevance. One can argue as in Boneh et al. (1995b) that from a practical point of view it may not be that important to simulate a Turing machine by a DNA computing device. Indeed, one should not aim to fit the DNA model into the Procrustean bed of classical models of computation, but try to completely rethink the notion of computation. On the other hand, finding out whether the class of DNA algorithms is computationally complete has many important implications. If the answer to it were unknown, then the practical efforts for solving a particular problem might be proven futile at any time: a Gödel minded person could suddenly announce that it belongs to a class of problems that are impossible to solve by DNA manipulation. The same holds for the theoretical proof of the existence of a DNA computer. As long as it is not proved that such a thing theoretically exists, the danger that the practical efforts will be in vane is always lurking in the shadow.

One more indication of the relevance of the questions concerning computational completeness and universality of DNA-based devices is that they have been addressed for most models of DNA computation that have so far been proposed.

The existing models of DNA computation are based on various combinations of a few primitive *biological operations:*

- *Synthesis* of a desired polynomial-length strand (Adleman 1994, 1995, Beaver 1995b, 1995c)
- *Separation* of the strands by length (Adleman 1994, 1995, Boneh at al. 1995b, Beaver 1995b, 1995c);
- *Merging*: pour two test tubes into one to do union (Adleman 1994, 1995, Lipton 1994);
- *Extraction:* extract those strands containing a given pattern as a substring (Adleman 1994, 1995, Lipton 1994, Boneh et al. 1995b, Beaver 1995c);
- *Melting/Annealing*: break apart/bond together two single DNA strands with complementary sequences (Boneh et al. 1995b, Smith & Schweitzer 1995, Winfree 1995);
- *Amplifying*: make copies of DNA strands by using the Polymerase Chain Reaction (Adleman 1994, 1995, Lipton 1994, Boneh et al. 1995b, Beaver 1995b, 1995c, Smith & Schweitzer 1995);
- *Cutting*: cut DNA strands by using restriction enzymes (Boneh et al. 1995b, Beaver 1995b, 1995c, Head 1987, Rothemund 1995, Smith & Schweitzer 1995);
- *Ligation*: paste DNA strands with complementary sticky ends by using ligases (Beaver 1995b, 1995c, Winfree 1995, Head 1987, Rothemund 1995, Smith & Schweitzer 1995);
- *Detection*: given a tube, say "yes" if it contains at least one DNA strand, and "no" otherwise (Adleman 1994, 1995, Lipton 1994, Boneh et al. 1995b).

These operations are then used to write "programs" which receive a tube containing DNA strands as input and return as output either "yes" or "no" or a set of tubes. A computation consists of a sequence of tubes containing DNA strands.

There are pro's and con's for each model (combination of operations). Overall, the existence of different models with complementing features shows the versatility of DNA computing and increases the likelihood of practically constructing a DNA-computing-based device.

It the sequel we will restrict our attention to the *insertion/deletion system* model of DNA computation that has been introduced in Kari & Thierrin (1997) and further studied in Kari et al. (1997). A formal definition of *contextual insertions and deletions,* that can be used as the sole primitives for carrying out a computation, is given in Section 3. We will then prove that for the DNA model based on in-

sertions/deletions we can affirmatively answer both questions posed at the beginning of this section.

3. A mathematical model: insertion/deletion systems

As described in Section 1, a DNA strand call be likened to a string over a four letter alphabet. Consequently, a natural way to model DNA computation is within the framework of formal language theory, which deals with letters and strings of letters. We specify here only the notions and notations necessary for our exposition. For further formal language notions the reader is referred to Salomaa (1973).

An alphabet is a finite nonempty set X; its elements are called *letters* or *symbols*. $|X|$ denotes the cardinality of X, i.e. the number of elements in X, and X^* denotes the free monoid generated by the alphabet X under the operation of catenation (juxtaposition). The elements of X^* are called *words* or *strings*. The empty string (the null element of X^*) is denoted by λ. A *language* over the alphabet X is a subset of X^*. For instance, if $X = \{a,b\}$ then $aaba$, $aabbb = a^2b^3$ are words over X, and the following sets are languages over X: $L_1 = \{\lambda\}$, $L_2 = \{a,ba,aba,abbaa\}$, $L_3 = \{a^p \mid p \text{ prime}\}$.

Since languages are sets, we may define the set-theoretic operations of union, intersection, difference, and complement in the usual fashion. The catenation of languages L_1 and L_2, denoted L_1L_2, is defined by $L_1L_2 = \{uv \mid u \in L_1, v \in L_2\}$.

A finite language can always be defined by listing all of its words. Such a procedure is not possible for infinite languages and therefore other devices for the representation of infinite languages have been developed. One of them is to introduce an *accepting device* and define the language as consisting of all the words accepted by the device. One of the basic accepting devices used for specifying languages are *Turing machines*

Recall that (Salomaa 1973) a triple $(S, X \cup \{\#\}, F)$ is called a *Turing machine* iff the following conditions are satisfied:

(i) S and $X \cup \{\#\}$, (with $\# \notin X$ and $X \neq \emptyset$) are two disjoint alphabets referred to as the *state* and *tape* alphabet.

(ii) Elements $s_0 \in S$, $b \in X$, and a subset $S_f \subseteq S$ are specified, namely, the *initial state*, the *blank symbol*, and the *final state set*. A subset $V_f \subseteq X$ is specified as the *final alphabet*.

(iii) The productions in F are of the forms

(1) $s_ia \Rightarrow s_jb$ overprint

(2) $s_iac \Rightarrow as_jc$ move right

(3) $s_ia\# \Rightarrow as_jb\#$ move right and extend workspace

(4) $cs_ia \Rightarrow s_jca$ move left

(5) $\#s_ia \Rightarrow \#s_jba$ move left and extend the workspace

where $s_i, s_j \in S$ and $a, b, c \in X$. Furthermore, for each $s_i, s_j \in S$ and $a \in X$, F either contains no productions (2) and (3) (resp. (4) and (5)) or else contains both (2) and (3) (respectively (4), (5)) for every $c \in X$. For no $s_i \in S$ and $a \in X$, the word s_ia is a subword of the left side in two productions of the forms (1), (3) and (5).

We say that a word sw, where $s \in S$ and $w \in (X \cup \{\#\})^*$ is *final* iff w does not begin with a letter a such that sa is a subword of the left side of some production in F. The language *accepted* by a Turing machine TM is defined by

$$L(TM) = \{w \in V^*_f \mid \#s_0w\# \Rightarrow^* \#w_1s_fw_2\# \text{ for some } s_f \in S_f,$$

$w_1, w_2 \in X^*$ such that $s_fw_2\#$ is final$\}$

where $\Rightarrow$ denotes derivation according to the rewriting rules (1) - (5) of the Turing machine. A language is acceptable by a Turing machine iff $L = L(TM)$ for some TM. It is to be noted that TM is *deterministic:* at each step of the rewriting process, at most one production is applicable.

Using these formal language theory prerequisites, we can proceed now to define *contextual insertions and deletions.*

The insertion operation has been introduced in Kari (1991) as a generalization of catenation. Given words u and v, the insertion of v into u consists of all words that can be obtained by inserting v in an arbitrary position of u:

$$u \leftarrow v = \{u_1vu_2 \mid u_1u_2 = u, u_1, u_2 \in X^*\}.$$

This type of insertion is too nondeterministic for modeling the insertion and deletion action of the enzymes that could be used for molecular computing. The enzymes actually perform insertions only between certain specified sites (Smith & Schweitzer 1995). Consequently, an attempt to better model their action is to modify our definition of insertion so that insertion of a word takes place only if a certain context is present. This can be formalized by the notion of contextual insertion, detailed below.

Let $(x, y) \subseteq X^* \times X^*$ be a pair of words called a *context.* The (x, y)-*contextual insertion* of $v \in X^*$ into $u \in X^*$ is defined as:

$$u \leftarrow_{(x,y)} v = \{u_1xvyu_2 \mid u_1, u_2 \in X^*, u = u_1xyu_2\}.$$

If the word u does not contain xy as a subword, the result of the (x, y)-contextual insertion is the empty set.

If $C \subseteq X^* \times X^*$ is a set of contexts, the *C-contextual insertion* of u into v is defined as:

$$u \leftarrow_C v = \{u_1xvyu_2 \mid (x, y) \in C, u = u_1xyu_2\}.$$

If the context set C is understood, the C-contextual insertion will be called shortly *contextual insertion.*

Informally, given a set C of pairs of words called contexts and words u and v, the contextual insertion of v into u is performed as follows. If for a pair (x, y) of words in C, u contains xy as a subword, the result of the contextual insertion consists of the words obtained by inserting v into u, between x and y. If $C = \{1\} \times \{1\}$, then the C-contextual insertion amounts to the usual insertion (see Kari 1991, 1994).

The C-contextual insertion of a language $L_2 \subseteq X^*$ into a language $L_1 \subseteq X^*$ can be defined in the natural way as

$$L_1 \leftarrow_C L_2 = \bigcup_{u \in L_1, v \in L_2} (u \leftarrow_C v).$$

In a manner similar to the contextual insertion, we can define the contextual deletion: deletion of a word takes place only if certain contexts are present. More precisely, let $(x, y) \in X^* \times X^*$ be a context.

The (x, y)-*contextual deletion* of $v \in X^*$ from $u \in X^*$ is defined as:

$$u \rightarrow_{(x,y)} v = \{u_1 x y u_2 \mid u_1, u_2 \in X^*, u = u_1 x v y u_2\}.$$

If $C \subseteq X^* \times X^*$ is a set of contexts, then the C-contextual deletion of v from u is

$$u \rightarrow_C v = \{u_1 x y u_2 \mid (x, y) \in C, u = u_1 x v y u_2\}.$$

The C-contextual deletion of a language $L_2 \subseteq X^*$ from a language $L_1 \subseteq X^*$ can then be defined as

$$L_1 \rightarrow_C L_2 = \bigcup_{u \in L_1, v \in L_2} (u \rightarrow_C v).$$

If $C = \{1\} \times \{1\}$, then the contextual deletion amounts to the usual deletion operation (see Kari 1991, 1994).

An *insertion scheme INS* is a pair $INS = (X, I)$ where X is a finite alphabet with $|X| \geq 2$ and $I \subseteq X^* \times X^* \times X^*$, $I \neq \emptyset$. The elements of I are denoted by $(x, z, y)_I$ with $x, y, z \in X^*$ and are called the *contextual insertion rules* of the scheme. For every word $u \in X^*$, let

$$cins_I(u) = \{v \in X^* \mid v \in u \leftarrow_{(x,y)} z, (x, z, y)_I \in I\}$$

(Informally, in a contextual insertion rule (x, z, y), the pair (x, y) represents the context of insertion while z is the word to be inserted.) To simplify, we can use the notation $cins(u)$ instead of $cins_I(u)$ when there is no possible ambiguity. If $L \subseteq X^*$ and I is fixed, then

$$cins(L) = \{cins(u) \mid u \in L\}.$$

A *deletion scheme DEL* is a pair $DEL = (X, D)$ where X is a finite alphabet with $|X| \geq 2$ and $D \subseteq X^* \times X^* \times X^*$, $D \neq \emptyset$. The elements of D are denoted by $(x, z, y)_D$ and are called the *contextual deletion rules* of the scheme. For every word $u \in X^*$, let

$$cdel_D(u) = \{v \in X^* \mid v \in u \rightarrow_{(x,y)} z, (x, z, y)_D \in D\}$$

(In a contextual deletion rule (x, z, y), the pair (x, y) represents the context of deletion while z is the word to be deleted.) To simplify, we can use the notation $cdel(u)$ instead of $cdel_D(u)$ when there is no possible ambiguity. If $L \subseteq X^*$ and D is fixed, then

$$cdel(L) = \{cdel(u) \mid u \in L\}.$$

An *insdel scheme* is a triple $ID = (X, I, D)$ where X is a finite alphabet with $|X| \geq 2$, I is a set of insertion rules and D is a set of deletion rules.

Definition 3.1 *An insdel system ID is a quintuple:*

$$ID = (X, T, I, D, w)$$

where X is a finite alphabet with $|X| \geq 2$, (X, I) is an insertion scheme, (X, D) is a deletion scheme, I, D are finite, $T \subseteq X$ is the terminal alphabet, and $w \in X^+$ is a fixed word called the axiom of the insdel system.

If $u \in X^*$ and $v \in cins(u) \cup cdel(u)$, then v is said to be directly ID-derived from u and this derivation is denoted by $u \rightarrow v$. The sequence of direct derivations:

$$u_1 \rightarrow u_2 \rightarrow \ldots \rightarrow u_k, \quad k \geq 0,$$

is denoted by $u_1 \rightarrow {}^* u_k$ and u_k is said to be derived from u.

The *language* $L_g(ID)$ *generated* by the insdel system ID is the set:

$$L_g(ID) = \{v \in T^* \mid \omega \rightarrow {}^* v \text{ where } \omega \text{ is the axiom}\}$$

and analogously we can define the *language* $L_a(ID)$ *accepted* by the insdel system as

$$L_a(ID) = \{v \in T^* \mid v \rightarrow {}^* \omega \text{ where } \omega \text{ is the axiom}\}$$

Having defined an insertion/deletion based mathematical model of DNA computation, we now proceed to answer – for this model – the questions raised in Section 2. We start by showing that the insdel systems are computationally complete. By computational completeness of insdel systems we mean that every algorithm (effective procedure) can be carried out by using only contextual insertions and deletions. It is obvious that this is not a mathematical definition of computational completeness. For an adequate definition, the intuitive notion of an algorithm (effective procedure) must be replaced by a formalized notion.

Since 1936, the standard accepted model of universal computation has been the Turing machine introduced in Turing (1936). The Church-Turing thesis, the prevailing paradigm in computer science, states that no realizable computing device can be more powerful than a Turing machine One of the main reasons that Church -Turing's thesis is widely accepted is that very diverse alternate formalizations of the class of effective procedures have all turned out to be equivalent to the Turing machine formalization.

Showing that the insdel systems are computationally complete amounts thus, for example, to showing that the action of a Turing machine can be realized by an insdel system.

Theorem *3.1 If a language is acceptable by a Turing machine TM, then there exists an insdel system ID accepting the same language.*

Informally, Theorem 3.1 tells us that everything that is Turing-computable can be computed also by this DNA model of computation. This answers the question as regards to what kinds of algorithms (effective procedures, computable functions) can be simulated by DNA computing devices based on contextual insertions and deletions, and the answer is: all of them. (Stronger results have been obtained in Kari et al. 1997: one can obtain full computational power of a Turing machine even when restricting the length of the contexts to 2, and the operations involved to insertions of a single letter.)

Theorem 3.1 shows that every program (computable function, Turing machine) can be simulated by an insdel system, but this does not say anything about the existence of a *programmable DNA computer* based on contextual insertions and deletions. However, based on the existence of universal Turing machines (programmable electronic com-

puters) and Theorem 3.1 we can conclude the existence of universal insdel systems. The interpretation of this result from the point of view of DNA computing is that, theoretically, there exist *universal programmable DNA computers* based on contextual insertions and deletions.

The only bio-operations used in these computers are contextual insertions and deletion. In the case of insdel systems, we can conclude we found an affirmative answer to the second question posed in Section 2 with regards to the existence of programmable DNA computers.

Constructions showing how to simulate the work of a Turing machine by a DNA model of computation have also been proposed in Paun (in press), Freund et al. (1995), Csuhaj-Varju et al. (1996), Yokomori & Kobayashi (1995), Smith & Schweitzer (1995), Rothemund (1995), Adleman (1995), Boneh et al. (1995b), Beaver (1995c), Winfree (1995) and Reif (1995). In an optimistic way, one may think of an analogy between these results and the work on finding models of computation carried out in the 30's, which has laid the foundation for the design of the electronic computers. In a similar fashion, the results obtained about the models of DNA computation show that programmable DNA computers are not science fiction material, but the reality of the near future.

4. Meta-thoughts on biomathematics

We have seen in Section 2 that the bio-operations are quite different from the usual arithmetical operations. Indeed, even more striking than the quantitative differences between a virtual DNA computer and an electronic computer (the DNA computer winning the comparison on most fronts) are the qualitative differences between the two.

DNA computing is a new way of thinking about computation altogether. Maybe this is how nature does mathematics: not by adding and subtracting, but by cutting and pasting, by insertions and deletions. Perhaps the primitive functions we currently use for computation are just as dependent on the history of humankind, as the fact that we use base 10 for counting is dependent on our having ten fingers. In the same way humans moved on to counting in other bases, maybe it is time we realized that there are other ways to compute besides the ones we are familiar with.

The fact that phenomena happening inside living organisms (copying, cutting and pasting of DNA strands) could be computations in disguise suggests that life itself may consist of a series of complex computations. As life is one of the most complex natural phenomena, we could generalize by conjecturing the whole cosmos to consist of computations. The differences between the diverse forms of matter would then only reflect various degrees of computational complexity, with the qualitative differences pointing to huge computational speedups. From chaos to inorganic matter, from inorganic to organic, and from that to consciousness and mind, perhaps the entire evolution of the universe is a history of the ever-increasing complexity of computations.

Just imagine. Perhaps all there was in the beginning was a universal cocktail of particles. They combined randomly for millions of years, until, by chance, some patterns of beautiful mathematical symmetry started to emerge: the inorganic matter. They continued to mix and intermingle until some formations started to self-replicate (see fractals and iterated functions) and then to do computations: life appeared. The more complex the computations grew, the more complex the life forms became, until there was again a sudden leap and consciousness and mind appeared, apparently out of thin air, but in reality an inevitable corollary to complexity. Who knows what the next step could be in this infinite spiral of mathematical evolution?...

Of course, the above is only a hypothesis, and the enigma whether modern man is "*homo sapiens*" or "*homo computans*" still awaits solving. But this is what makes DNA computing so captivating. Not only may it help compute faster and more efficiently, but it stirs the imagination and opens deeper philosophical issues. What can be more mesmerizing than something that makes you dream?

To a mathematician, DNA computing tells that perhaps mathematics is the foundation of all there is. Indeed, mathematics has already proven to be an intrinsic part of sciences like physics and chemistry, of music, visual arts (see Hofstadter 1979) and linguistics, to name just a few. The discovery of DNA computing, indicating that mathematics also lies at the root of biology, makes one wonder whether mathematics isn't in fact the core of all known and (with non-Euclidean geometry in mind) possible reality.

Why not? Sometimes a graceful move of a dancer seems to hide the truth of a remarkable theorem, to be the fluid graph of a function with properties of amazing depth. The more profound the mathematics behind is, the more striking the beauty. I may discover a (little and insignificant) theorem once in a while, but she is able to create them by the dozen, theorem after theorem, function after function with breathtaking properties, just by moving an arm or hand, just by smiling. The beauty seems ephemeral, but is reproducible and therefore as eternal as the underlying mathematical truth.

Maybe indeed, Plato was right: Truth, Beauty and Good are one and the same. Maybe indeed, the material things are mere instances of "ideas" that are everlasting, never being born nor perishing. By intimating that – besides everything else – mathematics lies at the very heart of life. DNA computing suggests we take Plato's philosophy one step further: the eternal "ideas" reflected in the ephemeral material world could be mathematical ones.

If this were the case, and the quintessence of reality is the objective world of mathematics, then we should feel privileged to be able to contemplate it.

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