

BIO-COMPUTERS: MECHANISM AND APPLICATIONS

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Abstract: Bio-computers are unique class of microcomputers that are particularly intended to be used for medical applications. The biological computer is generally used for functions such as inspecting the body's activities, bring on therapeutic effects. This implantable device accomplishes these functions at the molecular or cellular level. This is comprised of RNA, DNA and proteins and can likewise execute simple mathematical calculations. The biological computer empowers the scientist to develop a range or an arrangement of biosensors that has the capability to find or aim particular types of cells that could be found in the patient's body. This is also used in performing target-specific medicinal operations that could deliver medical measures or cures as per the doctor's directives.

Index Terms- Bio-computers, DNA computers, Molecular genetics, Nano-biotechnology

I. INTRODUCTION

Biological computers are a sort of biosensors (Asif et. al., 2011). These have come out as an interdisciplinary field that exemplifies together molecular biology, chemistry, computer science and mathematics (Shanthi et. al., 2009). The well predictable hybridization chemistry of DNA is the capability to fully control the length and content of oligo-nucleotides and the abundance of enzymes (Parveen et. al., 2008) available for alteration of the DNA and make use of nucleic acids an appealing possibility for all of these nano-scale applications (Rosarin and Mirunalini, 2011).

Biological computers are mostly used for monitoring activities of body at molecular and cellular level by inducing therapeutic effects (Kurioka et. al., 2011). As a new field bio-computing deals with both with computer science and biology however does not fit to both. A 'DNA computer' has been applied for the first time to get the single correct answer from over a numerous possible solutions to a computational problem (Blasiak et. al., 2022). Before transforming living organisms into computational systems, Bio-computing scientists require an approach not only to create multiple 'circuits' switches, clocks etc within a single cell but also to connect them. The scientists suppose that the complexity of the structure of biological molecules could allow DNA computers to do better than their electronic counterparts in future. In 1994, the idea of DNA computing materialized for the first time, when Adleman solved the Hamiltonian Path Problem through short DNA oligomers and DNA ligase (Adleman, 1994). Shapiro and his colleagues were presented a series of bio-computer models in first decade of 21st century. They talked about molecular state finite automaton. In this the restriction enzyme FokI constituted hardware and short DNA oligomers were software as well as input/out-put signals (Shimoyama, 2011).

Bio-computers used to induce input. Output and *software* are altogether made out of DNA (Pradhan et. al., 2011), while DNA-manipulating enzymes are used as *hardware*. Modern Bio-computer is designed to determine concentrations of particular RNA molecules, (Ekland et. al., 1995) which might be overproduced or under produced, depending on the nature of cancer. By Use of pre-programmed medical data, (Usha et. al., 2011) the computer subsequently makes its analysis (Rosen et. al., 2011) in light of the identified RNA levels. In respond to a cancer diagnosis, the out-put unit of the computer can start the controlled ejection of a single-stranded DNA molecule, which interferes with the functions of cancer cell, making it to self-destruct. This can be a sort of biosensor with ability to find or target particular types of cells in human body (Verma et. al., 2010).

II. BIO-COMPUTERS AND BIO-COMPUTING

We use various types of gadgets without knowledge of working pattern of the gadgets which is before now already adopted and executed by nature. As gadgets, living organisms also perform complex physical processes as per the direction of digital information. Computer software is no exception in this differentiation. DNA was perceived as the most essential molecule of living nature. The capability to keep numerous data is an imperative feature of the DNA and thus to biological computing. Linkage analysis is the technique used by geneticists to determine how frequently different forms of two variable attributes are acquired together during meiosis. As DNA can be quantified in nano grams, the silicon chip is a long ways behind with regards to storage capacity (Lien et. al., 2011). A single gram of DNA can store as much data as one trillion compact discs. In the era of computers, biological computing is gradually picking up importance. Now, the cell is considered as a computer and its program exists in DNA. As we know, proteins are linear polymers made up of twenty amino acid monomers. Consequently proteins are strings on a twenty letter alphabet, in this way an individual protein molecule can be symbolized as state of a computation (Reddy and Yang, 2011). At this stage a question arises that how the physical representation of one computational state can be used to produce a physical representation of a successive state. To determine this for polymer based computers, a devise with sufficiently set of transformations is required. This prompts biochemical polymers and biological processes. The last pace is to elaborate process for repeating those state transformations which is a process with high risk.

The bio-computer is a device that is used for monitoring the body's activities or inducing therapeutic effects (Manjili 2011), all at the molecular or cellular level (Morishita and Kusano 2011). Biologically derived molecules, such as DNA and proteins, are used by bio-computers to execute computational calculations including storing, retrieving, and processing data. Expansion of new stream of science i.e. nanobiotechnology made a path of the development of bio-computers. Nanobiotechnology can be defined as a technology that uses both nano-scale materials (materials having characteristic measurements of 1-100 nanometers) and biologically based materials. According to Razia et. al. (2010) nanobiotechnology is design and engineering of proteins that can then be assembled into larger, functional structures. The execution of nanobiotechnology provides scientists with the facility to engineer bio-molecular systems particularly so that they connect in a manner that can finally outcome in the computational functionality of a computer.

DNA is a building block for molecular computations and bio-computers. DNA serves more as to store genetic data and less as an active participant of reaction networks (Chen, 2011). DNA-based in vitro bio-computer systems have been mostly executed in test tubes where well-designed species have been accumulated and their evolving computational behavior was observed. Fabrication of a Bio-computer by RNA (Croce et. al., 2010) inside a living yeast cell had shown program to respond to conditions inside the cell by taking particular activities. Similar to the most computers, the RNA device works on a simple system of Boolean logic wherein it tends to be customized to respond to the commands AND, OR, NAND and NOR. Combination of the RNA components in certain ways shows different types of logic gates circuit common to any computer (Uckun, 2011). For instance, when inputs of an AND gate detect the presence of drugs only then AND gate produces an output, while a NOR gate produces an output only when neither drug is detected.

Protein based bio-computers are explored in the molecular computation context (Pandey et. al., 2011). The systems demonstrated complex logic integration of molecular inputs and in addition cascades of gates. Peptides (Henneges et. al., 2009) were considered as building block for logic gates, act as catalytic model for condensation of other peptides (Gomase et. al., 2008). At chemical-network level, the AND gate was executed by utilizing two different peptide layouts catalyzing a similar condensation. The NOR gate was actualized by inhibiting an autocatalytic condensation process in parallel by two other peptide inputs. Advancement of in vivo computational systems has reflected the in vitro endeavors in several aspects (Hoskeri et. al., 2010). While DNA-based systems have relied vigorously on the primary DNA sequence (Butt et. al., 2009) as information bearer, in vivo systems tailored existing mechanisms for biological regulation, and generally attached to logic circuits as the guiding model of computation (Ling, 2011). Most biological regulation interactions can be classified as either activating or inhibitory (Yun et. al., 2011).

III. MECHANISM AND APPLICATIONS

Bio-computers are made inside a patient's body. The complete information of the patient's body is known as a blueprint along which lines the bio-computer would be fabricated (Buchko, 2011). Once the computer's genetic blueprint has been given, the human body will begin to build it on its own using the cells found in the body and body's natural biological processes (Ewing and Ewing, 2009). Bio-computer can easily be used to identify all types of cellular (Sarvestani, 2011) activity through Boolean logic equations and useful in determining whether a specific action is damaging or not. Bio-computer could identify the cellular activities that even incorporate those of transformed genes and all other activities of the genes found in cells. Like traditional computers, the bio-computer also works with an output and an input signal. Body's proteins, RNA, and other specific chemicals that are found in the human cytoplasm are the main inputs of the bio-computer (Shirotake et. al., 2009). The output on the other hand could be recognized with help of laboratory equipment.

The implantable bio-computer is a device which could be utilized in different therapeutic purposes (Mzayek and Resnik, 2010) where intercellular evaluation and treatment is required (Sinnathamby et. al., 2011). It is particularly helpful in observing intercellular activity including mutation of genes (Tamanna and Asad, 2008). Through this technology a doctor can focus on and treat only damaged or diseased cells, this is the main advantage of bio-computer (Ammer et. al., 2009). Specific cell treatment is possible with this technology. Bio-computers made of RNA (Koparde and Singh, 2010) strands may in due course serve as brains for producing bio-fuels from cells.

IV. CONCLUSION

The future for bio-computing is splendid. Bio-computing is a new field which makes an effort to extract computing power from the communal action of a big number of biological molecules. Bio-computer is a parallel machine, in which each processor consists of a single biological macromolecule. The system can be made of a biological part and the other available advanced hardware. This would give the combined advantage of both the systems. Real biological organisms provide some valuable understanding. Biological organisms characteristically switch information about the macroscopic world congregated by senses into a form that affects biology at molecular level. For solutions to specific problems, a real biological system appears like a smart thought. Based on membrane, a computational micro-architecture validates the name biological instead of molecular computing.

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