

Open Access

Biological Computers - Their Mechanism & Applications

T. Jeevani

Department of Biotechnology, Acharya Nagarjuna University, India

Abstract

Biological computers are special types of microcomputers that are specifically designed to be used for medical applications. The biological computer is an implantable device that is mainly used for tasks like monitoring the body's activities or inducing therapeutic effects, all at the molecular or cellular level. This is made up of RNA, DNA and proteins and can also perform simple mathematical calculations. This could enable the researcher to build an array or a system of biosensors that has the ability to detect or target specific types of cells that could be found in the patient's body. This could also be used to carry out or perform target-specific medicinal operations that could deliver medical procedures or remedies according to the doctor's instructions.

Keywords: Biological computers; Biocomputing; DNA computers; Human genome project; Molecular genetics; Biosensor; Nanobiotechnology.

Introduction

Biological computers are a kind of biosensors [1,2] which have emerged as an interdisciplinary field that draws together molecular biology, chemistry [3], computer science and mathematics. The highly predictable hybridization chemistry of DNA is the ability to completely control the length and content of oligonucleotides and the wealth of enzymes [4] available for modification of the DNA and make use of nucleic acids an attractive candidate for all of these nanoscale applications [5]. These are mainly used for monitoring body's activities by inducing therapeutic effects [6] at molecular and cellular level. Biocomputing is one of the new fields in research which deals with computer science and biology but doesn't fit to both [7]. A 'DNA computer' has been used for the first time to find the only correct answer from over a million possible solutions to a computational problem [8]. Before one can turn living organisms into computational systems, Biocomputing researchers need a way to create and connect multiple "circuits" switches, clocks and so forth within a single cell. The researchers believe that the complexity of the structure of biological molecules could allow DNA computers to outperform from their electronic counterparts in future. The idea of DNA computing came true for the first time in 1994, when Adleman solved the Hamiltonian Path Problem using short DNA oligomers and DNA ligase [9]. In early 2000s a series of biocomputer models were presented by Shapiro and his colleagues who discussed molecular [10] 2 state finite automaton, in which the restriction enzyme FokI constituted hardware and short DNA oligomers were software as well as input/output signals. DNA molecules provided also energy for this machine.

Biological computers used to produce input; output and "software" are all composed of DNA, the material of genes [11], while DNA-manipulating enzymes are used as "hardware." The newest version's input apparatus is designed to assess concentrations of specific RNA molecules, [12] which may be overproduced or under produced, depending on the type of cancer. Using pre-programmed medical [13,14] knowledge, [15,16] the computer then makes its diagnosis [17,18] based on the detected RNA levels. In response to a cancer diagnosis, the output unit of the computer can initiate the controlled release of a singlestranded DNA molecule that is known to interfere with the cancer cell's activities, causing it to self-destruct [19]. This can be a type of biosensor [20-22] which has the ability to detect or target specific types of cells [23] in human body.

Biocomputing

Humans use a variety of gadgets without realizing how the gadgets could be working on a pattern which is already patented and perfected by Mother Nature. Living organisms also carry out complex physical processes under the direction of digital information [24]. Computers and software are no exception in this contrast [25]. DNA was recognized as the most important molecule of living nature. The ability to store billions of data is an important feature of the DNA and hence to biological computing. Human genome project [26] is an effort at an international level. It is a research directed at creating a map [27] of human DNA. Molecular genetics [28] is the best way to understand this project. Geneticists have used a technique called linkage analysis to determine how frequently different forms of two variable traits are inherited together i.e. not separated by recombination during meiosis [29]. While DNA can be measured in nano grams, the silicon chip [30] is far behind when it comes to storage capacity. A single gram of DNA can store as much information as 1 trillion audio CDs [31]. While we live in the age of computers, biological computing is slowly gaining prominence. CPU is replaced by DNA. The cell is now considered as a computational system and its program resides in DNA and its state in the distribution of chemical compounds and electrical charges.

The first major step in computation is to determine how state is to be represented physically. There are different ways to represent for example pebbles, by triangular marks pressed into a clay tablet. Polymers [32] are molecules that consist of repeated structural units called monomers. Proteins [33] are linear polymers based on twenty amino acid monomers hence proteins are strings on a twenty letter alphabet, thus a n individual protein molecule can be represented as state of a computation [34].The second step is to develop a computational technology how to transform the state i.e. how the physical representation of one computational state can be used to produce a physical representation of a successive state. To accomplish this for polymer based com-

*Corresponding author: T. Jeevani, Department Of Biotechnology, Acharya Nagarjuna University, Guntur, India, E-mail: jeevanithota@yahoo.co.in

Received September 11, 2011; Accepted September 29, 2011; Published October 06, 2011

Citation: Jeevani T (2011) Biological Computers -Their Mechanism & Applications. J Biotechnol Biomaterial 1:122. doi:10.4172/2155-952X.1000122

Copyright: © 2011 Jeevani T. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

puters one need to devise sufficiently rich set of transformations. This leads to biochemical polymers and biological processes. The final step is to develop process for iterating those state transformations which is very risky process.

Biocomputers

Computer is an electronic device which is used to store, manipulate, and communicate information, perform complex calculations [35], or control or regulate other devices or machines, and is capable of receiving information and of processing it in accordance with variable procedural instruction. The biological computer is an implantable device that is mainly used for tasks like monitoring the body's activities or inducing therapeutic effects [36], all at the molecular or cellular level [37-39]. Biocomputers use systems of biologically derived molecules, such as DNA and proteins, to perform computational calculations involving storing, retrieving, and processing data. This enables the researcher to build an array [40] of data accordingly [41]. The development of biocomputers has been made possible by the expanding new science of nanobiotechnology. The term nanobiotechnology can be defined in multiple ways; in a more general sense, nanobiotechnology can be defined as any type of technology that uses both nano-scale materials, i.e. materials having characteristic dimensions of 1-100 nanometers, as well as biologically based materials. A more restrictive definition views nanobiotechnology [42] more specifically as the design and engineering of proteins that can then be assembled into larger, functional structures [43,44]. The implementation of nanobiotechnology, as defined in this narrower sense, provides scientists with the ability to engineer biomolecular systems specifically so that they interact in a fashion that can ultimately result in the computational functionality of a computer.

DNA is traditionally a favorite building block for molecular computations and biocomputers [45]. DNA is a biological molecule wherein it serves to store more as genetic information [46] and less as an active participant of reaction networks [47]. DNA-based *in vitro* biocomputer systems have been mainly implemented in test tubes where well-designed species have been assembled and their emergent computational behavior was observed.

Creation of a Biocomputer using RNA [48,49] inside a living yeast cell had demonstrated program to respond to conditions within the cell by taking specific actions. Like the most computers, the RNA device operates on a simple system of Boolean logic wherein it can be programmed to respond to the commands AND, OR, NAND and NOR. By combining the RNA [50] components in certain ways it showed different types of logic gates circuit elements common to any computer. For example, an AND gate produces an output only when its inputs detect the presence of both drugs, while a NOR gate produces an output only when neither drug is detected [51].

Protein [52,53] based biocomputer explored in the molecular computation context *in vitro* both as enzymes and as regulatory motifs [54]. The systems showed complex logic integration of molecular inputs as well as cascades of gates. Peptides [55] were proposed as building block for logic gates, serving as catalytic templates for condensation of other peptides [56] from partial-length precursors. On a chemical-network level, the AND gate was implemented by using two different peptide templates catalyzing the same condensation. The NOR gate was implemented by inhibiting an autocatalytic condensation process independently by two other peptide inputs.

Development of *in vivo* [57] computational networks [58] has mirrored the *in vitro* efforts in many aspects [59]. While DNA-based

networks have relied heavily on the primary DNA sequence [60] as information carrier, *in vivo* systems adapted existing mechanisms for biological regulation, in particular transcriptional [61] and post transcriptional regulatory links, and generally adhered to logic circuits as the guiding model of computation. Most biological regulation [62] interactions can be classified as either activating or inhibitory.

Mechanism

Biological computers are made inside a patient's body. The mere information of the patient's body is called a blueprint [63] along which lines the biological computer would be manufactured. Once the computer's genetic blueprint has been provided, the human body will start to build it on its own using the body's natural biological processes [64] and the cells found in the body. Through boolean logic equations, we can easily use the biological computer to identify all types of cellular [65] activity and determine whether a particular activity is harmful or not. The cellular activities that the biological computer could detect can even include those of mutated genes and all other activities of the genes found in cells. As with conventional computers, the biological computer also works with an output and an input signal. The main inputs of the biological computer are the body's proteins, RNA, and other specific chemicals that are found in the human cytoplasm [66]. The output on the other hand could be detected using laboratory equipment.

Applications

The implantable biological computer is a device which could be used in various medical applications [67,68] where intercellular evaluation and treatment [69] are needed or required. It is especially useful in monitoring intercellular activity including mutation [70-72] of genes. The main advantage of this technology over other like technologies is the fact that through it, a doctor can focus on or find and treat only damaged or diseased cells [73]. Selective cell treatment is made possible. Bio-computers made of RNA [74] strands might eventually serve as brains for producing biofuels from cells, for example, or to control "smart drugs" [75,76] that medicate only under certain conditions.

Conclusion

The future for biological computing is bright. Biological computing is a young field which attempts to extract computing power from the collective action of large numbers of biological molecules. CPU being replaced by biological molecules remains in the far future. Biological computer is a massively parallel machine where each processor consists of a single biological macromolecule. A part of the system can be made of biological and the other using current or new hardware that may become available. This would give us the combined benefit of both systems. Actual biological organisms provide some useful insight into statements of the form Biological computers can't do. Biological organisms routinely convert data about the macroscopic world gathered by senses in to a form that influences biology at molecular level. It seems like a good idea to look to real biological systems for solutions to particular problems. A computational microarchitecture based on membrane justifies the name biological as opposed to merely molecular computing.

References

- Ramírez EA, Granero AM, Zón MA, Fernández H (2011) Development of an Amperometric Biosensor Based on Peroxidases from *Brassica napus* for the Determination of Ochratoxin a Content in Peanut Samples. J Biosens Bioelectron S3: 001.
- 2. Asif MH, Elinder F, Willander M (2011) Electrochemical Biosensors Based on

ZnO Nanostructures to Measure Intracellular Metal Ions and Glucose. J Anal Bioanal Techniques S7: 003.

- Shanthi V, Ramanathan K, Sethumadhavan R (2009) Role of the Cation-π Interaction in Therapeutic Proteins: A Comparative Study with Conventional Stabilizing Forces. J Comput Sci Syst Biol 2: 51-68.
- Parveen S, Asad UK (2 008) Proteolytic Enzymes Database. J Proteomics Bioinform 1: 109-111.
- Rosarin FS, Mirunalini S (2011) Nobel Metallic Nanoparticles with Novel Biomedical Properties. J Bioanal Biomed 3: 85-91.
- Kurioka D, Takagi A, Yoneda M, Hirokawa Y, Shiraishi T, et al. (2011) Multicellular Spheroid Culture Models: Applications in prostate Cancer Research and Therapeutics. J Cancer Sci Ther 3: 60-65.
- 7. http://simson.net/clips/2000/2000.TR.05.BiologicalComputing.pdf.
- Blasiak J, Krasinski T, Poplawski T, Sakowski S (2011) DNA computing. Postepy Biochem 57: 13-32.
- Adleman LM (1994) Molecular computation of solutions to combinatorial problems. Science 266: 1021-1024.
- Shimoyama S (2011) BRAF Mutations and their Implications in Molecular Targeting Therapies for Gastrointestinal Cancers. J Pharmacogenom Pharmacoproteomics 2: e102.
- Pradhan MA, Sharp DM, Mora JS, Wittmer M, Berger W, et al. (2011) A Novel NYX Mutation Associated with X-Linked Congenital Stationary Night Blindness in a New Zealand Family. J Clinic Experiment Ophthalmol 2: 147.
- Ekland, Eric H, Szostak, Jack W, Bartel, David P et al. (1995) Structurally complex and highly active RNA ligases derived from random RNA sequences, 269: 364-370.
- Smt Usha A, Ramachandra B, Dharmaprakash MS (2011) Bio Signal Conditioning and Processing For Biological Real Time Applications Using Mixed Signal Processor. J Biosens Bioelectron 2: 105.
- Singh R, Rajni, Meena A, Meena LS (2011) Multidrug resistant and Extensively drug resistant TB: A Nuisance to Medical Science. J Bacteriol Parasitol 2: 105.
- David SK, Upadhayaya N, Siddiqui MK, Usmani AM (2010) Knowledge Discovery Technique for Web-Based Diabetes Educational System. J Health Med Informat 1: 102.
- Merlyn SM, Valentina SS, Singh S, Vennila JJ, Kumar A (2010) Application of Artificial Intelligence in the Diagnosis of Eosinophilia. J Health Med Informat 1: 103.
- Rosen JE, Yoffe S, Meerasa A, Verma M, Gu FX (2011) Nanotechnology and Diagnostic Imaging: New Advances in Contrast Agent Technology. J Nanomedic Nanotechnol 2: 115.
- John I (2011) Nanotechnology-based Diagnostics; Are we Facing the Biotechnology Eevolution of the 21st Century? Mycobact Diseases 1: e102.
- 19. http://www.seminarprojects.com/Thread-biological-computers.
- Achyuthan K (2011) Whither Commercial Nanobiosensors? J Biosens Bioelectron 2: 102e.
- 21. Tateishi A, Cauchi M, Tanoue C, Migita S, Coleman SK, et al. (2011) Discerning Data Analysis Methods to Clarify Agonistic/Antagonistic Actions on the Ion Flux Assay of Ligand-Gated Ionotropic Glutamate Receptor on Engineered Post-Synapse Model Cells. J Biosens Bioelectron 2: 104.
- Verma N, Kumar S, Kaur H (2010) Fiber Optic Biosensor for the Detection of Cd in Milk. J Biosens Bioelectron 1: 102.
- Balashova EE, Lokhov PG (2010) Proteolytically-cleaved Fragments of Cell Surface Proteins Stimulate a Cytotoxic Immune Response Against Tumor-activated Endothelial Cells *In vitro*. J Cancer Sci Ther 2: 126-131.
- 24. http://www.cs.virginia.edu/~robins/Bringing_DNA_Computers_to_Life.pdf.
- 25. http://arxiv.org/ftp/arxiv/papers/0911/0911.1672.pdf.
- 26. Ebomoyi EW (2011) Establishing Genome Sequencing Centers, the Thematic Units in the Developing Nations and the Potential Medical, Public Health and Economic Implications. J Drug Metabol Toxicol 2: 108.
- 27. Henry R, Durai , Net S, Balraj A, Priya WS (2011) Modeling a Micro Tubule as a Diode. J Biosens Bioelectron 2: 106.

- 28. Shi Huang (2008) The Genetic Equidistance Result of Molecular Evolution is Independent of Mutation Rates. J Comput Sci Syst Biol 1: 92-102.
- 29. http://www.bscs.org/pdf/computers.pdf.
- Lien TTN, Viet NX, Chikae M, Ukita Y, Takamura Y (2011) Development of Label-Free Impedimetric hCG-Immunosensor Using Screen- Printed Electrode. J Biosens Bioelectron 2: 107.
- http://courses.umass.edu/physics890b-parsegia/pdf_files/kamenetskii-dna. pdf.
- Anwunobi AP, Emeje MO (2011) Recent Applications of Natural Polymers in Nanodrug Delivery. J Nanomedic Nanotechnol S4: 002.
- Reddy N, Yang Y (2011) Plant Proteins for Medical Applications. J Microbial Biochem Technol 3: i-i.
- 34. http://www.usc.edu/dept/molecular-science/papers/fp-sci94.pdf.
- 35. Arumay P, Rajasri B, Maitrayee D, Saptarshi M, Pinak C (2009) IntGeom: A Server for the Calculation of the Interaction Geometry between Planar Groups in Proteins. J Proteomics Bioinform 2: 60-63.
- 36. Manjili MH (2011) Therapeutic Cancer Vaccines. J Clin Cell Immunol 2: e101.
- Morishita Y, Kusano E (2011) Cellular and Molecular Basis of Epithelial Epithelial-Mesenchymal Transition in Renal Fibrosis. J Nephrol Therapeutic S3: 001.
- 38. Sweet AD (2011) On the Borderline: Some Observations on Internal Pathological Organizations, Patterns of Early Attachment and their Later Emergence in Criminal Offending and the Therapeutic Relationship. J Psychol Psychother 1: 101e.
- Soto-Pantoja DR, Isenberg JS, Roberts DD (2011) Therapeutic Targeting of CD47 to Modulate Tissue Responses to Ischemia and Radiation. J Genet Syndr Gene Ther 2: 105.
- Liu Y, Wang Y, Gang J (2011) Challenges of microarray applications for microbial detection and gene expression profiling in food. J Microbial Biochem Technol S2: 001.
- Pandey RR, Saini KK, Dhayal M (2010) Using Nano-Arrayed Structures in Sol-Gel Derived Mn2+ Doped Tio2 for High Sensitivity Urea Biosensor. J Biosens Bioelectron 1: 101.
- Menaa B (2011) The Importance of Nanotechnology in Biomedical Sciences. J Biotechnol Biomaterial 1: 105e.
- 43. Suh KS, Tanaka T (2011) Nanomedicine in Cancer. Translational Medic 1:103e.
- 44. Razia M, Raja KR, Padmanaban K, Sivaramakrishnan S, Chellapandi P (2010) A Phylogenetic Approach for Assigning Function of Hypothetical Proteins in *Photorhabdus luminescens* Subsp. *laumondii* TT01 Genome. J Comput Sci Syst Biol 3: 21-29.
- 45. http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2714485/pdf/nihms127316.pdf.
- Towfic G, Munshower J, Kettoola S, Towfic F, Graziano F, et al. (2009) Genetic Mutations Affecting the Success and Failure of HIV Regimens. J Proteomics Bioinform 2: 372-379.
- Chen B (2011) Reconstruction of Local Biochemical Reaction Network Based on Human Chromosome 9 Sequence Data. J Proteomics Bioinform 4: 87-90.
- Croce O, Chevenet F, Christen R (2010) A New Web Server for the Rapid Identification of Microorganisms. J Microbial Biochem Technol 2: 84-88.
- Villela AD, Renard G, Palma MS, Chies JM, Dalmora SL (2010) Human Interferon B1ser17: Coding DNA Synthesis, Expression, Purifi cation and Characterization of Bioactive Recombinant Protein. J Microbial Biochem Technol 2: 111-117.
- 50. Uckun FM (2011) Role of Defective RNA Processing in the Pathogenesis of Pediatric Diseases. Pediatr Therapeut 1: e101.
- http://blogs.discovermagazine.com/80beats/2008/10/17/biocomputer-madeof-rna-understands-boolean-logic/.
- Khrustalev VV, Barkovsky E V (2009) Main Pathways of Proteome Simplification in Alphaherpesviruses Under the Influence of the Strong Mutational GCpressure. J Proteomics Bioinform 2: 88-96.
- Pandey S, Negi YK, Marla SS, Arora S (2011) Comparative Insilico Analysis of Ascorbate Peroxidase Protein Sequences from Different Plant Species. J Bioengineer & Biomedical Sci 1: 103.

- 54. Amanchy R, Kandasamy K, Mathivanan S, Periaswamy B, Reddy R, et al. (2011) Identification of Novel Phosphorylation Motifs Through an Integrative Computational and Experimental Analysis of the Human Phosphoproteome. J Proteomics Bioinform 4: 22-35.
- Henneges C, Hinselmann G, Jung S, Madlung J, Schütz W, et al. (2009) Ranking Methods for the Prediction of Frequent Top Scoring Peptides from Proteomics Data. J Proteomics Bioinform 2: 226-235.
- Gomase VS, Kale KV, Shyamkumar K (2008) Prediction of MHC Binding Peptides and Epitopes from Groundnut Bud Necrosis Virus (GBNV). J Proteomics Bioinform 1: 188-205.
- Jamadar LD, Bhat K, Shirode Y, Musmade PB, Hussen SS, et al. (2010) Comparison of US and Japanese Regulations for Invitro Dissolution and Invivo Bioequivalence Studies. J Bioanal Biomed 2: 17-22.
- Hoskeri JH, Krishna V, Amruthavalli C (2010) Functional Annotation of Conserved Hypothetical Proteins in *Rickettsia Massiliae* MTU5. J Comput Sci Syst Biol 3: 50-52.
- 59. http://uqbar.rockefeller.edu/siggia/Publications/2000-9_files/gertzNature2009.
- Butt AM, Ahmed A (2009) MUTATER: Tool for the Introduction of Custom Position Based Mutations in Protein and Nucleotide Sequences. J Proteomics Bioinform 2: 344-348.
- 61. Ling J (2011) Translation of Human Genome. Biochem & Anal Biochem 1: 101e.
- 62. Yun Y, Conforti L, Muganda P, Sankar J (2011) Nanomedicine-based Synthetic Biology. J Nanomedic Biotherapeu Discover 1: 102e.
- 63. Buchko GW (2011) Structural Genomics-A Goldmine of Blueprints for Structure-Based Drug Design. Metabolomics 1: 104e.
- 64. Ewing GW, Ewing EN (2009) Does an Improved Understanding of the Nature and Structure of the Physiological Systems Lead to a Better Understanding of the Therapeutic Scope of Complementary & Conventional Medicine?. J Comput Sci Syst Biol 2: 174-179.
- Sarvestani AS (2011) On the Effect of Substrate Compliance on Cellular Motility. J Biosens Bioelectron 2: 103.

- 66. Shirotake S, Nakamura J, Kaneko A, Anabuki E, Shimizu N (2009) Screening Bactericidal Action of Cytoplasm Extract from Kumazasa Bamboo (Sasa veitchii) Leaf against Antibiotics-Resistant Pathogens such as MRSA and VRE Strains. J Bioequiv Availab 1: 80-85.
- Aljofan M, Lo MK, Rota PA, Michalski WP, Mungall BA (2010) Off Label Antiviral Therapeutics for Henipaviruses: New Light Through Old Windows. J Antivir Antiretrovir 1: 1-10.
- Mzayek F, Resnik D (2010) International Biomedical Research and Research Ethics Training in Developing Countries. J Clinic Res Bioeth 1: 103.
- Sinnathamby G, Zerfass J, Hafner J, Block P, Nickens Z, et al. (2011) EDDR1 is a Potential Immunotherapeutic Antigen in Ovarian, Breast, and Prostate Cancer. J Clin Cell Immunol 2: 106.
- C Li, Luo Q, Li XM, Zhang XB, Han CL, et al. (2010) Filaggrin Mutations are Associated with Ichthyosis Vulgaris in the Southern Chinese Population. J Clin Exp Dermatol Res 1: 102.
- Tamanna A, Asad UK (2008) Identification of a Point Mutation Causing Splitting of Antigenic Domain in M1 Protein of H5n1 Strain from 2006 Outbreak in India. J Proteomics Bioinform 1: 302-306.
- Berdeli A, Nalbantoglu S, Mir S, Ozsan FM, Cam SF, et al. (2010) Novel Nonsense p.C522X Mutation in SLC5A2 Gene of a Turkish Family with Familial Renal Glucosuria: A Molecular Case Report. J Cytol Histol 1: 104.
- Ammer AG, Kelley LC, Hayes KE, Evans JV, Lopez-Skinner LA, et al. (2009) Saracatinib Impairs Head and Neck Squamous Cell Carcinoma Invasion by Disrupting Invadopodia Function. J Cancer Sci Ther 1: 52-61.
- 74. Koparde P, Singh S (2010) Prediction of micro RNAs against H5N1 and H1N1 NS1 Protein: a Window to Sequence Specific Therapeutic Development. J Data Mining in Genom Proteomics 1: 104.
- Zufía L, Aldaz A, Ibáñez N, Giráldez J (2010) Validation of an LC Method for Therapeutic Drug Monitoring of Voriconazole in Patients. J Bioanal Biomed 2: 35-43.
- Farhangi A, Akbarzadeh A, Mehrabi MR, Chiani M, Saffari Z, et al. (2011) Immunotherapy of 436 Morphine Addicts by Therapeutic Morphine Vaccine in Kerman Province (I.R. Iran). J Vaccines Vaccin 2: 117.

Page 4 of 4