Exploring DNA Sequencing Algorithms as SeSAm Applications.

Nirmal Tej Kumar

Senior Researcher Informatics/Photonics/Nanotechnology/HPC/AI R&D.
R&D Collaborator USA/UK/Israel/BRICS Group of Nations.
Current Member ante Inst,UTD,Dallas,TX,USA.
Contact_info hmfg2014@gmail.com

Abstract :

Understanding Complex Systems via [SeSAm (Shell for Simulated Agent Systems)/Eclipse IDE/PDT Prolog Development Tool/SWI-Prolog/JikesRVM-Research Virtual Machine] for Related Heterogeneous Environments in the Context of Next Generation Bio-informatics R&D.

index words/keywords – just choose from the above mentioned Abstract.

[I] Inspiration + Introduction :

"**Organic computing** is computing that behaves and interacts with humans in an organic manner. The term "organic" is used to describe the system's behavior, and does not imply that they are constructed from organic materials. It is based on the insight that we will soon be surrounded by large collections of autonomous systems, which are equipped with sensors and actuators, aware of their environment, communicate freely, and organize themselves in order to perform the actions and services that seem to be required. " [Source - https://en.wikipedia.org/wiki/Organic_computing]

"**Bio computers** use systems of biologically derived molecules—such as DNA and proteins—to perform computational calculations involving storing, retrieving, and processing data. 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) and biologically based materials.[1]

A more restrictive definition views nanobiotechnology more specifically as the design and engineering of proteins that can then be assembled into larger, functional structures[2][3] 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. "
[Source - https://en.wikipedia.org/wiki/Biological_computing]

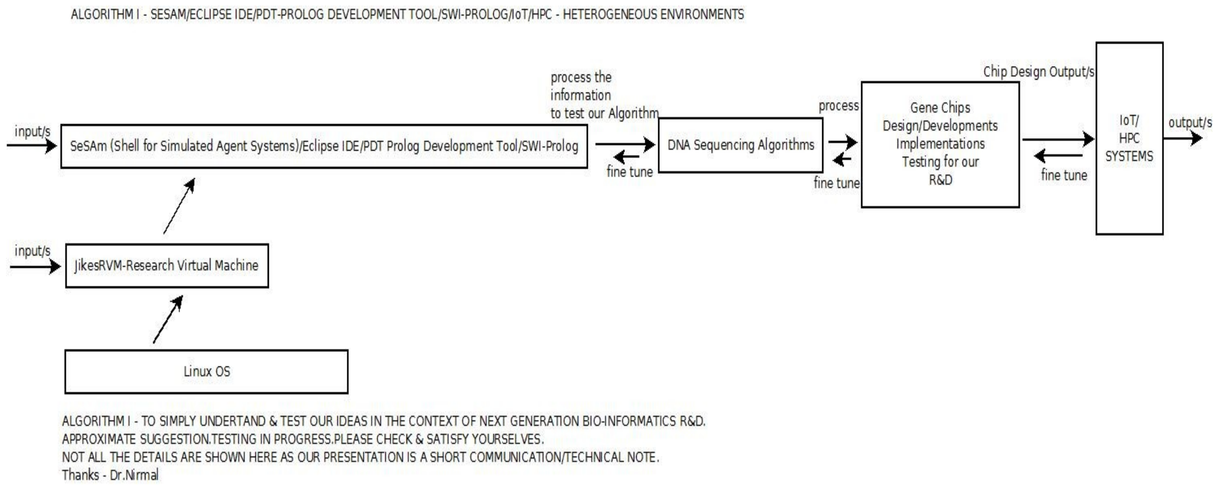
https://www.researchgate.net/publication/274840903_DNA_for_Nano-bio_Scale_Computation..

https://www.researchgate.net/publication/277563749_An_Informatics_Technical_Note_on

"**HOL**) to compute the **sequences** of **Nucleic acids**, DNA and RNA and illustrate the usefulness of higher order logic in computing the **sequences** for bio-sensor, probes, tags and gene-chip applications. What ever the application in question,**sequences** always form the heart and soul of bio-information processing in such demanding and promising tools ... " [Source - *www.scienpress.com/Upload/JAMB/Vol 2_2_6.pdf*· PDF file]

"DNA Sequencing Using Higher Order Logic[HOL] & Stochastic Processes as Mathematical Toolstowards Next Generation/Hi-End Bio-Informatics R&D Frameworks in the Context of [OPAL/Byte Code Engineering/Scala/Java/JikesRVM(RVM-Research Virtual Machine) /JavaVirtual Machine/ Metascala-Scala JVM/IoT/HPC Heterogeneous Computing Environments] –
[Scala/Java/JVM based Languages – The Next BIG Thing in IoT/HPC/Bio-informatics/BIG DATA Revolution – Advanced Software Architecture R&D]". [Source - http://vixra.org/pdf/1907.0375v1.pdf]

[II] Informatics Framework for Implementing R&D Algorithms :


ALGORITHM I - SESAM/ECLIPSE IDE/PDT-PROLOG DEVELOPMENT TOOL/SWI-PROLOG/IoT/HPC - HETEROGENEOUS ENVIRONMENTS

ALGORITHM I - TO SIMPLY UNDERTAND & TEST OUR IDEAS IN THE CONTEXT OF NEXT GENERATION BIO-INFORMATICS R&D.
APPROXIMATE SUGGESTION.TESTING IN PROGRESS.PLEASE CHECK & SATISFY YOURSELVES.
NOT ALL THE DETAILS ARE SHOWN HERE AS OUR PRESENTATION IS A SHORT COMMUNICATION/TECHNICAL NOTE.
Thanks - Dr.Nirmal

[Figure I – Algorithm I – SeSAm based Informatics Framework for our R&D Algorithm]

[III] Information on Mathematics+Software Used/that could be Useful :

Müller-Schloer, Christian; v.d. Malsburg, Christoph and Würtz, Rolf P. *Organic Computing.* Aktuelles Schlagwort in Informatik Spektrum (2004) pp.332–336.

> **[a]** Müller-Schloer, Christian. *Organic Computing – On the Feasibility of Controlled Emergence.* CODES + ISSS 2004 Proceedings (2004) pp 2–5, ACM Press, ISBN1-58113-937-3.**/[b]** Rochner, Fabian and Müller-Schloer, Christian. *Emergence in Technical Systems.* it Special Issue on Organic Computing (2005) pp.188–200, Oldenbourg Verlag, Jahrgang 47, ISSN 1611-2776.**/[c]** Schmeck, Hartmut. *Organic Computing – A New Vision for Distributed Embedded Systems.* Proceedings of the Eighth IEEE International Symposium on Object-Oriented Real-Time Distributed Computing (ISORC'05) (2005) pp.201–203, IEEE, IEEE Computer Society 2005.**/[d]** Würtz, Rolf P. (Editor): *Organic Computing (Understanding Complex Systems).* Springer, 2008. ISBN 978-3642096426.

"SeSAm is short for Shell for Simulated Agent Systems. It is a generic environment for the development and simulation of Multi-Agent models. The main focus is to enable scientists to construct models by visual programming. The main advantage of multi-agent simulation is that the agent paradigm is very intuitive, especially when modeling societies. Moreover it has some valuable properties, like the possibility for formulating flexible interaction between agents, multi-level interaction, adaptivity, etc. SeSAm was developed at the University of Wurzburg and applied in several projects in different application domains. SeSAm is open source (LGPL) and available to download for free. "
[Source – http://130.243.124.21/mediawiki/index.php/SeSAm]

"The **PDT** is a **Prolog** IDE provided as a plug-in for the Eclipse Platform. All **PDT** features are implemented for SWI-**Prolog**, most also for Logtalk 1). All native SWI-**Prolog** development tools (graphical tracer / debugger, profiler, ...) can be used within the **PDT**. If you want to use the **PDT** with other **Prolog** implementations, read this. "
[Source – *https://sewiki.iai.**uni-bonn**.de/research/**pdt**/docs*]
[Source – *https://sewiki.iai.**uni-bonn**.de/research/**pdt**/docs/download*]
[Source – *https://sewiki.iai.**uni-bonn**.de/research/**pdt**/connector*]

"Jikes RVM (Research Virtual Machine) provides a flexible open testbed to prototype virtual machine technologies and experiment with a large variety of design alternatives. The system is licensed under an OSI approved license. Jikes RVM runs on many platforms and advances the state-of-the-art of virtual machine technologies for dynamic compilation, adaptive optimization, garbage collection, thread scheduling, and synchronization."

“A distinguishing characteristic of Jikes RVM is that it is implemented in the Java™ programming language and is self-hosted i.e., its Java code runs on itself without requiring a second virtual machine. Most other virtual machines for the Java platform are written in native code (typically, C or C++). A Java implementation provides ease of portability, and a seamless integration of virtual machine and application resources such as objects, threads, and operating-system interfaces. “ [Source - https://www.jikesrvm.org/]

https://www.genengnews.com/resources/best-of-the-web/bioinformatics-university-of-wurzburg/

http://www.ai.soc.i.kyoto-u.ac.jp/field_en/chapter9.html
https://link.springer.com/chapter/10.1007/978-3-540-71986-1_10
https://academic.oup.com/bib/article/8/1/45/264398

[IV] Acknowledgment/s :

Special Thanks to all my Mentors/Collaborators/Friends. Non-Profit R&D.

[V] Our Important References (((via))) Vixra.org :

[a] http://www.vixra.org/author/nirmal_tej_kumar
[b] http://www.vixra.org/author/d_n_t_kumar
[c] http://www.vixra.org/author/n_t_kumar
[d] http://www.vixra.org/author/nirmal
[e] https://www.semanticscholar.org/author/Nirmal-Kumar/12354503/suggest

[THE END]