Exploring [C/C++/Bio-C++] based Bio-informatics R&D Framework Using [XNA-Xeno Nucleic Acids/Machine Learning/Minsky Machines/Group Theory/Grobner Bases.]

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[I] Abstract –

[BioCPP Computational Libraries/dlibC++(Machine Learning-Library)/Group Theory/Grobner Bases] interaction With C++ based Template Turing Machine w.r.t Minsky Machines in the Context of XNA Sequencing Mechanisms – A Simple Idea to Test Minsky Machines.We intend to explore Synthetic Biology Theoretically.Hence,this Short Communication on Synthetic Biology R&D.To understand XNA related mechanisms like Sequencing we are also using/considering Minksy Machines for better Bio-informatics Applications.

index words/key words – observe from the above mentioned Abstract.

[II] Inspiration + Introduction :

"Probing XNA/Machine Learning/Minsky Machines based Algorithm Research for Next Generation Novel Drug Design/Applications Using Bio-informatics Concepts."

[a] BioCPP-Computational Libraries in C++ – "The BioC++ project provides an accessible and comprehensive framework of C/C++ tools and libraries for computational biology.Our goal is to create object libraries for a wide range of biological information and to create a simplified framework for the incorporation of those objects into bio-informatics projects.

BioC++ is a new bio-informatics library that de-emphasizes obscure parsers and instead focuses on internal data structures and analysis, communicating directly with biological analysis programs and limiting persistence to robust data file formats including SQL,XML,FASTA, and PDB.BioC++ is available under the BSD license. We utilize several libraries whose licenses are either consistent with or have been granted permission to use with BioC++."

[Source – http://biocpp.sourceforge.net/]

[b] C++ Template Turing Machine – "It's well-known that the C++ template language is Turing-complete, but I realised I'd never actually seen anybody implement a Turing Machine using it. I decided to take that as a challenge, and here you see the results."

" demo-minsky is a 7-state 4-colour Universal Turing Machine (discovered by Marvin Minsky in 1962)."

[Source – https://github.com/tinyplasticgreyknight/template-turing]

[c] dlibC++ Machine Learning Library/Software – "Dlib is a modern C++ toolkit containing machine learning algorithms and tools for creating complex software in C++ to solve real world problems. It is used in both industry and academia in a wide range of domains including robotics, embedded devices, mobile phones, and large high performance computing environments. Dlib's open source licensing allows you to use it in any application, free of charge. "

[Source – http://dlib.net/]

[d] XNA Information/Synthetic Biology R&D – "**Xeno nucleic acids (XNA)** are synthetic nucleic acid analogues that have a different sugar backbone than the natural nucleic acids DNA and RNA.[1] As of 2011, at least six types of synthetic sugars have been shown to form nucleic acid backbones that can store and retrieve genetic information. Research is now being done to create synthetic polymerases to transform XNA. The study of its production and application has created a field known as xenobiology. "

[Source – https://en.wikipedia.org/wiki/Xeno_nucleic_acid]

[e] Xenobiology (XB) – "**Xenobiology** (XB) is a subfield of synthetic biology, the study of synthesizing and manipulating biological devices and systems. The name "xenobiology" derives from the Greek word *xenos*, which means "stranger, alien". Xenobiology is a form of biology that is not (yet) familiar to science and is not found in nature.[1] In practice it describes novel biological systems and biochemistries that differ from the canonical DNA–RNA–20 amino acid system (see central dogma of molecular biology)."

"For example, instead of DNA or RNA, XB explores nucleic acid analogues, termed Xeno Nucleic Acid (XNA) as information carriers.[2] It also focuses on an expanded genetic code[3] and the incorporation of non–proteinogenic amino acids into proteins.[4] "

[Source – https://en.wikipedia.org/wiki/Xenobiology]

[f] Schur Group Theory Software – "Schur is a stand alone C program for interactively calculating properties of Lie groups and symmetric functions. Schur has been designed to answer questions of relevance to a wide range of problems of special interest to chemists, mathematicians and physicists – particularly for persons who need specific knowledge relating to some aspect of Lie groups or symmetric functions and yet do not wish to be encumbered with complex algorithms."

"The objective of Schur is to supply results with the complexity of the algorithms hidden from view so that the user can effectively use Schur as a scratch pad, obtaining a result and then using that result to derive new results in a fully interactive manner. Schur can be used as a tool for calculating branching rules, Kronecker products, Casimir invariants, dimensions, plethysms, S–function operations, Young diagrams and their hook lengths etc. "

[Source – http://schur.sourceforge.net/]

[g] Minsky Machines & Algorithmic Problems – "This is a survey of using Minsky machines to study algorithmic problems in **semigroups**, **groups** and other **algebraic systems**. "

[Source – DOI: 10.1007/978-3-319-23534-9_17 · Source: arXiv]

*** Also Please see – Refs [a] [b] [c] mentioned in our present Short Communication .

[h] Symmetries, Groups Theory and Lie Algebras in Physics – "Symmetries have been the cornerstone of modern physics in the last century. Symmetries are used to classify solutions to physical theories, as well as a guiding principle informulating new physical theories."

"From the mathematical viewpoint, symmetries naturally fall into the subject of group theory, Lie algebras and their representations. In the select lectures,we intend to very briefly discuss these issues ".

[Source – http://physics.ipm.ac.ir/conferences/symmetries/notes/Symmetry-Lectures.pdf]

[i] Grobner Bases as Signal Processing Tool – "Gröbner Bases : A Short Introduction for Systems Theorists –Bruno Buchberger Research Institute for Symbolic Computation University of Linz,A4232 Schloss,Hagenberg,Austria ".

https://link.springer.com/chapter/10.1007/978-3-642-15582-6_15
https://www.researchgate.net/publication/221333735_CoCoALib_A_C_Library_for.
https://en.wikipedia.org/wiki/Commutative_algebra
https://www.jmilne.org/math/xnotes/CA.pdf
https://github.com/BrentBaccala/CoCoA

A Simple Example : "An Insight into Commutative Algebra Based Informatics & Computational Architecture for Cryo–EM Image Processing involving Gröbner Bases Using C++/Java/HOL/Scala/Scalalab/ImageJ Software Environments – A Short Communication on Gröbner Bases With Applications in Signals and Systems Using JikesRVM/JVM."

[Source – http://www.vixra.org/pdf/1709.0389v1.pdf]

[III] Informatics R&D Framework Using C++ based Software Tools :

Try to derive your own R&D Algorithms based on our Technical Notes – Our Guess is
"One" can easily come up with interesting option/s.

General Approach to our Future Algorithms :

input/s → **{** C/C++/Bio–C++ based Bio–informatics R&D Framework Using [XNA–Xeno Nucleic Acids/Machine Learning/Minsky Machines/Group Theory/Grobner Bases.] **}** → **output/s**

[Figure I – Approximate Algorithm I – Novel Drug Design Informatics Platform]
Testing in progress at the time of submission. Not Straight Forward.

** We have already demonstrated a number of Algorithms (((via))) Vixra.org using Block Diagrams.
   Please read & satisfy yourselves –Keep going – Keep Testing. Thanks – Dr.Nirmal.

[IV] Acknowledgment/s :

Special Thanks to all my FRIENDS+MENTORS+COLLEAGUES. Non-Profit R&D.

[V] Conclusions With Future Perspective/s :

We conclude that C++ Computational Libraries for Bio-informatics/C++ based Minsky Machines are very much useful in the context of DNA Sequencing/XNA Sequencing for developing " Next Generation " Bio-informatics Platforms to probe Novel Drugs.

[VI] Reference/s :

[a] vixra.org/pdf/1901.0445v1.pdf – Minsky Machines R&D Technical Notes via Vixra.org

[b] vixra.org/pdf/1909.0490v1.pdf - Minsky Machines R&D Technical Notes via Vixra.org

[c] http://vixra.org/abs/1910.0257 - Minsky Machines R&D Technical Notes via Vixra.org

[d] https://link.springer.com/chapter/10.1007/978-3-319-21088-9_2

[e] https://www.researchgate.net/publication/275669934_Minsky_Machines

[f] https://core.ac.uk/display/28127268

[g] https://www.liebertpub.com/doi/abs/10.1089/106652703321825973

[h] Diagnostics based on nucleic acid sequence variant profiling: PCR,hybridization, and NGS approaches –
D. Khodakov et al. / Advanced Drug Delivery Reviews 105 (2016) 3─19.

[i] https://www.sciencedirect.com/science/article/pii/S0169409X16301041

[j] Nucleic Acids Data Sequencing using Higher Order Logic-A ...
www.scienpress.com/Upload/JAMB/Vol 2_2_6.pdf

[k] Functional nucleic acids tailoring and its application – ScienceDirect –
https://www.sciencedirect.com/science/article/pii/S0165993619302055

Thank you for your kind attention & sincere encouragement.

[THE END]