BSOFT-Ruby/Ruby based Machine Learning(ML)-LLVM-Tcl/Tk Based Analysis of Cryo-EM Images Using Mathematical Software in Probing the Nano-Bio Systems – An Interesting Insight into Ruby/Ruby-ML and Tcl/Tk interfacing in the Context of Electron Microscopy Image Processing Applications.

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[I] Introduction & Inspiration/Abstract :

In this communication the importance of BSOFT-Ruby-LLVM-Tcl/Tk systems based imaging framework to probe Cryo-EM images is presented from a practical implementation point of view. Cryo-EM Technique holds an excellent future.Ruby-LLVM based imaging algorithms could form a powerful informatics framework for researching the challenges arising in the domains of nanotechnology. It is very much useful and important to study the behavior of cross-platform interfacing of existing software tools,fine tuning and adapting them to the domains where the models make bold predictions which could form the basis for the discovery of new nanoscale phenomena. All the methods presented here are also applicable to TEM/SEM/other EM Image Processing tasks as well. Aimed at writing better image processing software directly in Ruby in the near future as Ruby is already a promising tool in medical imaging areas like DICOM and other applications.Ruby also easily interacts with software already developed using C/C++/Java/Tcl/Tk/LLVM with its own extension capabilities.BSOFT, a well established Electron Microscopy Image Processing Software is chosen to experiment with,hence this presentation.

keywords: Cryo-EM/TEM/SEM Imaging, Mathematical Software, BSOFT/Ruby/LLVM/Tcl/Tk

[II] Informatics Framework Design & Implementation :



Approximate BSoft-Ruby-Tcl/tk-RubyML based cryo-EM Imaging & Informatics Platform - in Testing Stage. Actual Implementation Will Vary to Some Extent - Kindly Check & Satisfy Yourselves. Thanks - Nirmal

Figure I – Our Total Overview of the cryogenic-electron-microscopy Informatics Platform -Testing in Progress.

Please check these links for more information & introduction :

- [a] http://vixra.org/author/nirmal_tej_kumar
- [b] http://vixra.org/author/nirmal
- [c] http://vixra.org/author/n_t_kumar
- [d] http://vixra.org/author/d_n_t_kumar

[III] Additional Information on Mathematics & Software Used :

- [a]. https://www.ma.utexas.edu/users/hadani/
- [b]. http://cryoem.berkeley.edu/cryoem
- [c]. https://lsbr.niams.nih.gov/bsoft/#
- [d] https://www.semanticscholar.org/author/Nirmal-Tej-Kumar/12354503/suggest

[IV] Acknowledgment/s :

Special thanks to all those who have made this possible. The author declares no conflict of interest and no competing financial interest/s. This short note or technical communication is for non-profit academic research work.

[V] References :

[1]. Merk et al Breaking Cryo-EM Resolution Barriers to Facilitate Drug Discovery. http://www.sciencedirect.com/science/article/pii/S0092867416305918 https://doi.org/10.1016/j.cell.2016.05.040

[2]. Kumar D.N.T & Shmavonyan G,Understanding JikesRVM in the Context of Cryo-EM/TEM/SEM Imaging Algorithms and Applications – A General Informatics Introduction from a Software Architecture View Point. DOI : 10.5958/0975-8089.2016.00001.4

[3].Nirmal Tej Kumar, An Insight into Cryo-EM Imaging Process Architecture Using GENTLE Compiler Construction System with an Informatics Design Paradigm. DOI:10.5958/0975-8089.2016.00008.7

[4]. https://yunhokim.wordpress.com/research/cryogenic-electron-microscopy/

[5].Heymann JB (2001) Bsoft: Image and molecular processing in electron microscopy. J. Struct. Biol. 133(2/3), 156 - 169.

[6].Heymann JB and Belnap DM (2007) Bsoft: Image processing and molecular modeling for electron microscopy. J. Struct. Biol. 157(1), 3 - 18.

[7]. Heymann JB, Cardone G, Winkler DC and Steven AC (2008) Computational resources for cryoelectron tomography in Bsoft. J. Struct. Biol. 161(3), 232 – 242.