

Exploring & Examining Cryo-EM Images in the Context of Helical Protein Polymers/Bio-Polymers for Helical Reconstructions Using Ruby Language/Machine Learning/Image Processing/ruby-LLVM Informatics Framework.

[An Insight into Fourier-Bessel Synthesis]

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[I] Introduction & Inspiration :

Helical Protein Polymers are often dynamic and complex assemblies, with many conformations and flexible domains possible within the helical assembly. We could easily investigate and demonstrate that our approach is able to distinguish helical polymers that differ in conformation, composition, and helical symmetry.

[Source : Clustering Cryo-EM Images of Helical Protein Polymers for Helical Reconstructions Ultramicroscopy, 2018; <https://doi.org/10.1016/j.ultramic.2018.12.009>]

<https://structure.m.u-tokyo.ac.jp/English/software/Ruby-Helix-Page/ruby-helix.html>

<https://structure.m.u-tokyo.ac.jp/resources/guide.pdf>

<https://structure.m.u-tokyo.ac.jp/English/software/Installation/Installation.html>

In this short technical note, the authors consider and intend to use Ruby Helix Software in the context of cryo-EM Image Processing, there could be other option/s also.

Viral Molecular Machines - edited by Michael G. Rossmann, Venigalla B. Rao - Springer Science & Business Media, 02-Feb-2012- [Medical](#) - 687 pages.

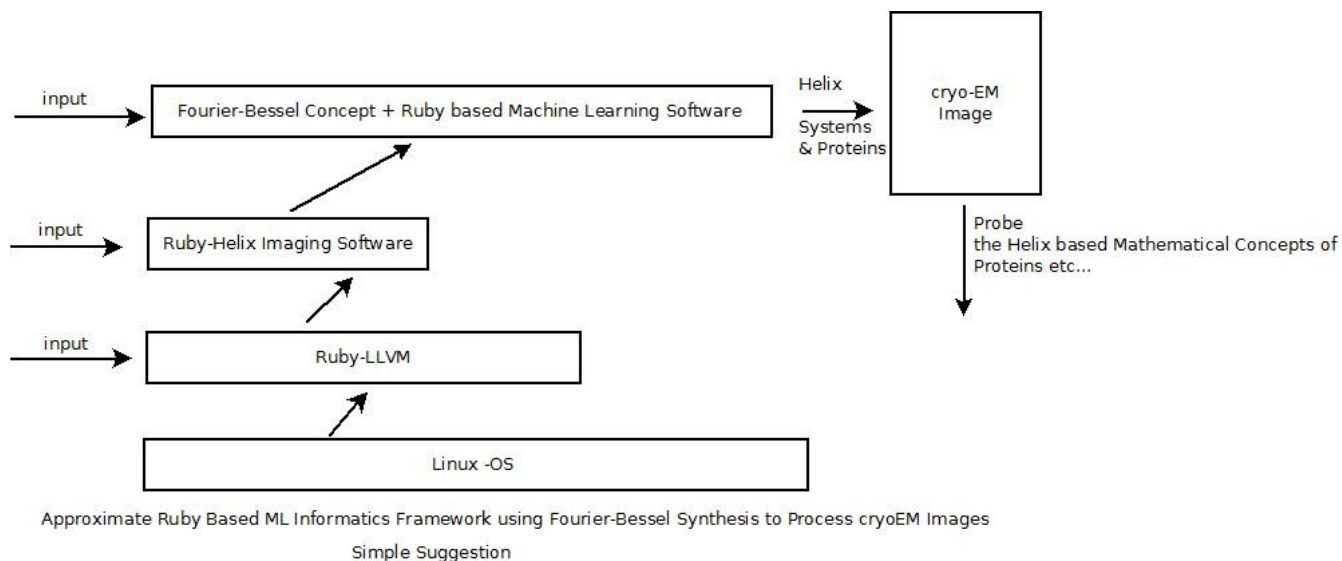
http://calla.rnet.missouri.edu/cheng/ieee_review.pdf – Machine Learning & Protein Structure Prediction.

https://en.wikipedia.org/wiki/Fourier%E2%80%93Bessel_series

J. Schroeder, Signal processing via Fourier–Bessel series expansion, Digital Signal Process. 3 (1993), 112–124.

A. Vergaraa, E. Martinelli, R. Huerta, A. D'Amico and C. Di Natale, Orthogonal decomposition of chemo-sensory signals: Discriminating odorants in a turbulent ambient, Procedia Engineering 25 (2011), 491–494.

[II] Ruby & ML Image Processing Framework :



**Figure I – Our Ruby Informatics Framework to Probe cryo-EM Images.
[Helical Protein Polymers]
[Actual Implementation will vary – Please Check/Fine Tuning is required]**

[III] Information on Mathematics & Ruby based Software Used/Useful :

[a] [Metlagel, Z., Y. S. Kikkawa, and M. Kikkawa](#) -Ruby-Helix : An implementation of helical image processing based on object-oriented scripting language,*J. Struc. Biol.*157:95-105, 2007.

[b] [Kikkawa, M.](#) - A new theory and algorithm for reconstructing helical structures with a seam. *Journal of Molecular Biology*, 343:943-955, 2004.

[c] <https://github.com/ruby-llvm/ruby-llvm> - “Ruby-LLVM is a Ruby language binding to the LLVM compiler infrastructure library. LLVM allows users to create just-in-time (JIT) compilers, ahead-of-time (AOT) compilers for multiple architectures, code analyzers and more.”

[d] <http://llvm.org/>

[e] http://vixra.org/author/nirmal_tej_kumar

[f] <http://vixra.org/author/nirmal>

[g] http://vixra.org/author/n_t_kumar

[h] http://vixra.org/author/d_n_t_kumar

[i] <http://www.ocaml.org/> && <https://coq.inria.fr/> && <http://biocaml.org/>

[j] <https://www.math.upenn.edu/~rimmer/math241/ch12sc6frbess.pdf>

[k] <https://doi.org/10.1093/qmath/os-19.1.164>

[l] <http://vixra.org/pdf/1802.0050v1.pdf>

Ruby based Software :

<https://github.com/arbox/machine-learning-with-ruby>

<https://medium.com/@ryanflach/basic-machine-learning-in-ruby-9cce4a67b40b>

<https://www.crondose.com/2016/12/practical-machine-learning-ruby/>

<http://www.rubyflow.com/p/ru1xjq-machine-learning-with-ruby>

<https://developers.google.com/api-client-library/ruby/apis/ml/v1>

<https://cloud.google.com/ruby/>

<https://www.sitepoint.com/machine-learning-ruby-naive-bayes-theorem/>

[IV] Acknowledgment/s :

Special thanks to all and this is Non-Profit Academic R&D.

[V] References :

- [1] [Oda T. and M. Kikkawa](#) -Novel Structural Labeling Method using Cryo-electron Tomography and Biotin-Streptavidin System *Journal of Structural Biology*, 183:305-11, 2013
- [2] [Oda T., T. Yagi, H. Yanagisawa, and M. Kikkawa](#) - Identification of the Outer-Inner Dynein Linker as a Hub Controller for Axonemal Dynein Activities *Current Biology*,23:656-64, 2013
- [3] [Kikkawa M, Hirokawa N.](#) - High-resolution cryo-EM maps show the nucleotide binding pocket of KIF1A in open and closed conformations. *EMBO J.*2006 Sep 20;25(18):4187-94.
- [4] [Mizuno N, Narita A, Kon T, Sutoh K, Kikkawa M.](#) - Three-dimensional structure of cytoplasmic dynein bound to microtubules.*Proc Natl Acad Sci U S A.*2007 Dec 26;104(52):20832-7. Epub 2007 Dec 19.
- [5] [Oda T, Hirokawa N, Kikkawa M.](#)- Three-dimensional structures of the flagellar dynein-microtubule complex by cryoelectron microscopy.*J Cell Biol.*2007 Apr 23;177(2):243-52. Epub 2007 Apr 16.
- [6] [Bodey AJ, Kikkawa M, Moores CA.](#) - 9-Angström structure of a microtubule-bound mitotic motor.*J Mol Biol.* 2009 May 1;388(2):218-24.
- [7] <https://structure.m.u-tokyo.ac.jp/English/publications/publications.html> [some recent publications]

THE END.