Tensor Flow + QRNG + Ruby +Z3 Theorem Prover [ZTP] - > Developing Advanced Bio-Imaging Algorithms -> To Probe COVID-19/Nano-Bio Material Systems & Informatics.

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Abstract :

A Novel R&D Bio-Informatics Framework Using Tensor Flow/ruby-Helix/lib-qrng-ruby/Bio-ruby/mruby/Bio-linux/Smart Devices/IoT/HPC Systems. Exploring + Understanding → AI FOR CRYOEM DATA SELECTION AND CLASSIFICATION.

index words/keywords : easy to guess.

[I] Introduction + Inspiration → Develop Novel Ruby based Bio-informatics Framework :

"Single particle cryo-electron microscopy (cryo-EM) is an imaging technology that allows direct observation of proteins in native and near-native states in atomic detail. However, determining the structure of a protein from projections captured by the EM requires collecting millions of examples.
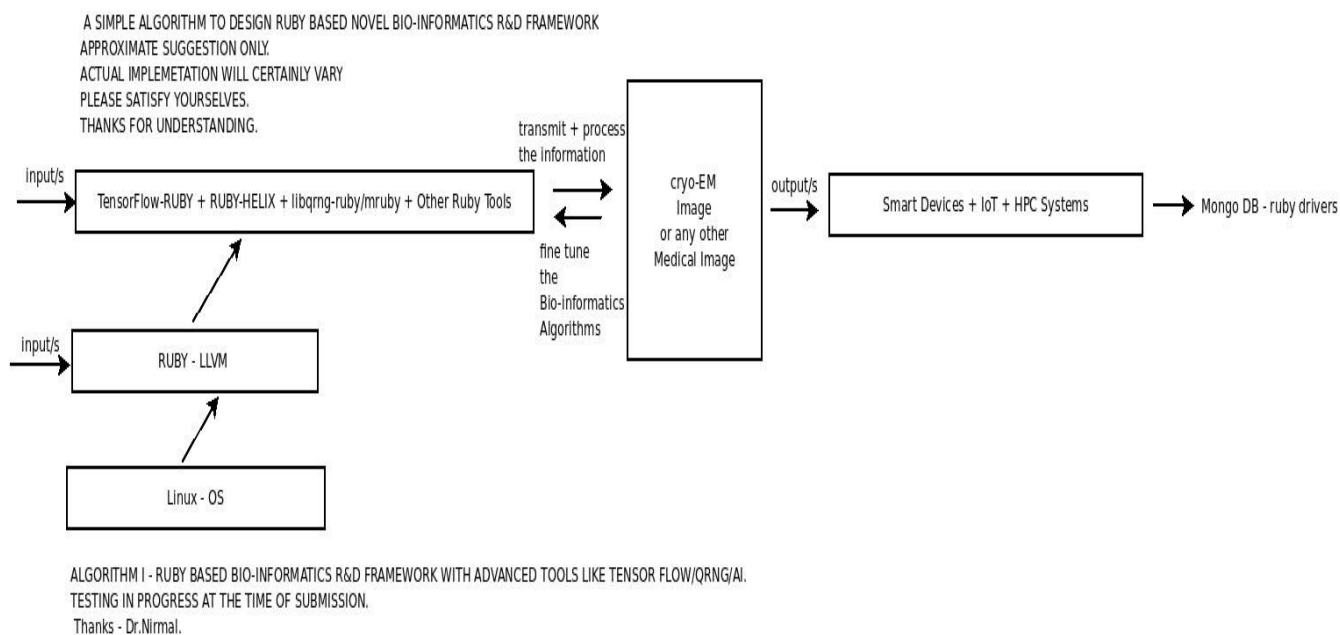
By leveraging positive-unlabeled learning, we can use a small number of example protein projections, provided by the user, to train a neural network to detect proteins of any size or shape. Topaz, the implementation of this framework, can detect significantly more proteins than all other software tested while also minimizing manual labeling required by the user. Furthermore, the positive-unlabeled approach to object detection is broadly applicable to other microscopy domains. "
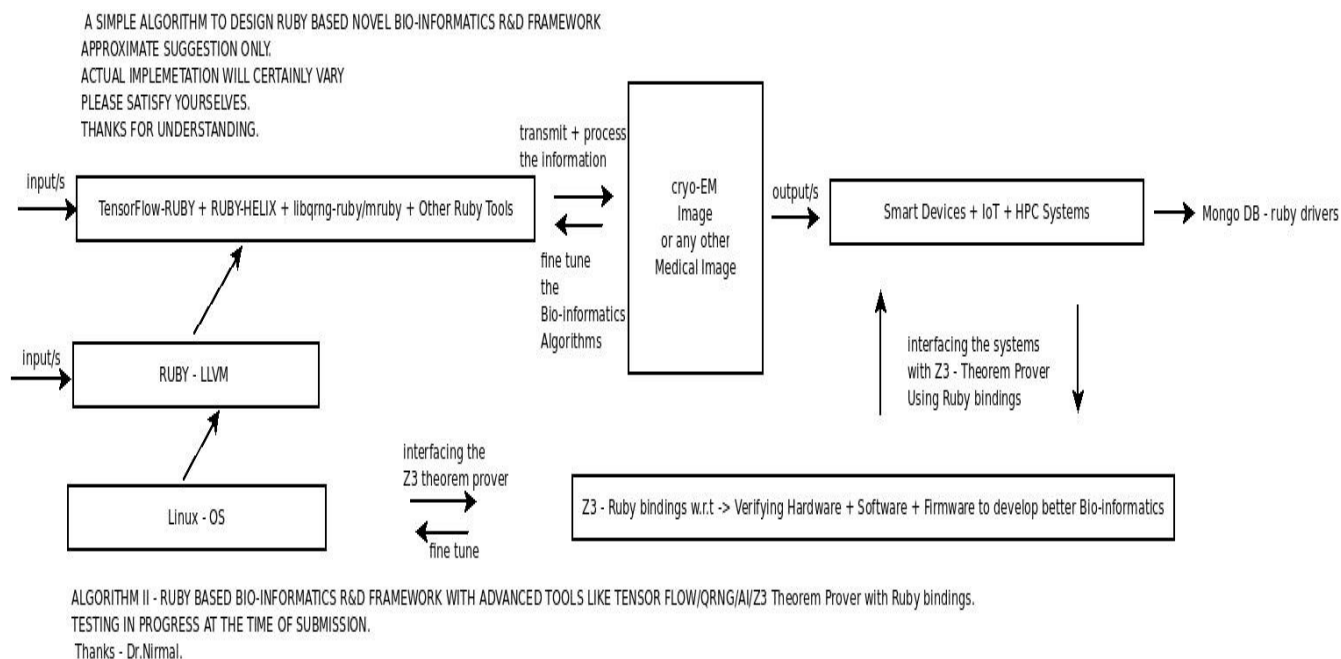
[Source - https://info.nvidia.com/ai-cryoem-data-selection-reg-page?ncid=em-ded-n3-83180]

"Earlier this summer, there was a startling report of a structure of the HIV surface proteins gp120 and gp41 obtained through cryogenic electron microscopy. This is a very important and very challenging field to work in. What you've got there is a membrane-bound protein-protein interaction, which is just the sort of thing that the other major structure-determination techniques can't handle well. At the same time, though, the number of important proteins involved in this sort of thing is almost beyond listing ".

[Source - https://blogs.sciencemag.org/pipeline/archives/2013/08/16/an_hiv_structure_breakthrough_or_complete_rubbish]

[II] R&D Image Processing + Informatics Framework Using Tensor Flow + Ruby :

A SIMPLE ALGORITHM TO DESIGN RUBY BASED NOVEL BIO-INFORMATICS R&D FRAMEWORK
APPROXIMATE SUGGESTION ONLY.
ACTUAL IMPLEMETATION WILL CERTAINLY VARY
PLEASE SATISFY YOURSELVES.
THANKS FOR UNDERSTANDING.

transmit + process the information

input/s

TensorFlow-RUBY + RUBY-HELIX + libqrng-ruby/mruby + Other Ruby Tools

fine tune the Bio-informatics Algorithms

cryo-EM Image or any other Medical Image

output/s

Smart Devices + IoT + HPC Systems

Mongo DB - ruby drivers

input/s

RUBY - LLVM

Linux - OS

ALGORITHM I - RUBY BASED BIO-INFORMATICS R&D FRAMEWORK WITH ADVANCED TOOLS LIKE TENSOR FLOW/QRNG/AI.
TESTING IN PROGRESS AT THE TIME OF SUBMISSION.
Thanks - Dr.Nirmal.

[Figure I - Simple Algorithm Using Ruby + Tensor Flow]

A SIMPLE ALGORITHM TO DESIGN RUBY BASED NOVEL BIO-INFORMATICS R&D FRAMEWORK
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input/s → TensorFlow-RUBY + RUBY-HELIX + libqrng-ruby/mruby + Other Ruby Tools

transmit + process the information

fine tune the Bio-informatics Algorithms

cryo-EM Image or any other Medical Image

output/s → Smart Devices + IoT + HPC Systems → Mongo DB - ruby drivers

input/s → RUBY - LLVM

Linux - OS

interfacing the Z3 theorem prover
fine tune

interfacing the systems with Z3 - Theorem Prover Using Ruby bindings

Z3 - Ruby bindings w.r.t -> Verifying Hardware + Software + Firmware to develop better Bio-informatics

ALGORITHM II - RUBY BASED BIO-INFORMATICS R&D FRAMEWORK WITH ADVANCED TOOLS LIKE TENSOR FLOW/QRNG/AI/Z3 Theorem Prover with Ruby bindings.
TESTING IN PROGRESS AT THE TIME OF SUBMISSION.
Thanks - Dr.Nirmal.

[Figure II - Simple Algorithm Using Ruby + Tensor Flow + Z3 Theorem Prover]

[III] Important References w.r.t → Ruby + Tensor Flow + Related Mathematics :

[a] https://www.tensorflow.org/

[b] https://www.tensorflow.org/tutorials/keras/classification

[c] https://www.tensorflow.org/tutorials/generative/dcgan

[d] https://medium.com/@Arafat./image-recognition-in-ruby-tensorflow-df5d5c05389b#.ty1vygtrg

******* Image Recognition in Ruby Tensorflow | by Arafat Khan | Medium →
Simply Superb Work.**

[e] https://blogs.sciencemag.org/pipeline/archives/2013/08/16/an_hiv_structure_breakthrough_or_complete_rubbish
[to avoid future Image Recognition Problems]

[IV] Conclusion/s With Future Perspectives :

Image Recognition in Ruby TensorFlow Using Above Mentioned Tools.One of the pioneering efforts to probe COVID-19 R&D Bio-informatics Framework w.r.t cryo-EM Image Processing Techniques.

{   Ruby + Tensor Flow + Other Tools → is a Very Powerful Combination }

[V] Acknowledgment/s :

Sincere Thanks to all WHO made this happen in my LIFE. Non-Profit R&D.
Inspiring Others is always GOOD.

[VI] References :

[a] https://info.nvidia.com/ai-cryoem-data-selection-reg-page?ncid=em-ded-n3-83180

[b] https://github.com/tejdnk-2019-ShortNotes

[c] https://vixra.org/pdf/1903.0105v1.pdf

[d] https://www.vixra.org/author/nirmal_tej_kumar

[THE END]