Yonghao Jin

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Education

UNIVERSITY OF SCIENCE AND TECHNOLOGY OF CHINA (USTC), HEFEI, CHINA

Bachelor of Science (Biophysics, Department of Physics)

Sept. 2013 - June 2017

Overall GPA: 3.49/4.3 or 85.23/100

Research Experience

STRUCTURE AND SEQUENCE MOTIF OF RBP BINDING SITES – 2016-PRESENT
Advisor: Prof. Kun Qu, School of Life Sciences, USTC

- Redesign and rewrite an iCLIP-seq (individual-nucleotide resolution Cross-Linking and ImmunoPrecipitation) data analysing pipeline with python

- Fine-tune an iCLIP peak-calling algorithm, greatly reducing the evaluation time in P-Value estimation

- Analyse PARS (parallel analysis of RNA structure) data and reconstruct transcript secondary structures from PARS probing data with ViennaRNA Package

- Integrate PARS and iCLIP data to detect RBP sequence and structure binding motif to better predict RBP binding sites

VARIATION OF WATER MOLECULES VIBRATION WITH TEMPERATURE – 2015
Advisor: Dr. Wei Zhao, School of Physics, USTC

- Peak detection and analysis on Raman spectrum of water molecules

- Design algorithm to remove Rayleigh backgrounds of Raman spectrum

- Analyse the change of molecules vibration from the peak shift in Raman spectrum and interpret the observation with variation in hydrogen bond strength with temperature

Open Source Projects

MMACLONE
Github Repository: https://github.com/jyh1/mmaclone

A cross-platform term rewriting system (TRS) with syntax similar to Wolfram Mathematica. This interpreter is turing complete, with sophisticate pattern matching facilities and featured with symbolic computation, lambda calculus, etc. It consists of 41 source files and thousands of lines of Haskell codes, including sufficient amounts of unit tests to ensure robustness.

SEQUENCE

Github Repository: https://github.com/jyh1/sequence

A windows GUI program developed with the GTK library. This program is mainly calibrated to help sequence validation in molecular cloning experiments. It has a user-friendly interface to generate fasta format file from related sequencing files to be used for down-stream alignment validation.

Fields of Interest

Bioinformatics; Genomics; Big data analysis; Biomedical informatics, Protein-RNA Interaction; Computational Biology; RNA secondary structure;

Skills

Adept in: Python, C/C++, Mathematica(Graphing, Programming), Haskell, Pascal, Scheme, Git, Atom

Familiar with: Bash, Matlab, C#, Java, JavaScript, HTML, Office, Stack, WordPress

Standardised Tests

TOEFL iBT: 29(Reading) + 29(Listening) + 22(Speaking) + 27(Writing) = 107

GRE General: 170(QR) + 155(VR) + 3.5(AW)

Awards and Honours

- Bronze Merit Scholarship – 2014

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- First Prize, the 17th National Olympiad in Informatics in Provinces (NOIP) – 2011