Hsuan-Chun Lin

Permanent Resident
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SUMMARY

Biomedical data science professional with 8+ years academic experience in design, analysis and publication of high-impact biomedical research using real world data. Expert in communication of scientific research findings to demonstrate drug discovery, biomolecule interactions, and development of novel high throughput methods. Passionate about integrating data science and 10+ years lab experience to improve quality, efficiency and value of drug discovery and medicinal industry.

SKILLS

- Languages: R, MATLAB, Python, Perl, SQL, C++
- Technical Skills: Data mining and processing, statistical analysis, feature engineering, scikit-learn, Pandas, seaborn, Matplotlib, TensorFlow, Linux, Git.
- Soft Skills: Business acumen, oral and written communication, data driven-strategic planning.

EXPERIENCE

Postdoctoral Associate,
University of Florida, Gainesville FL, USA 2017 2020

- Managed 4 projects and presented in national ACS meeting.
- Accelerated data analysis pipeline 10-fold faster by using Unix/Linux shell commands, Perl, Python, R, Pandas, scikit-learn, MATLAB, data mining and machine learning algorithms.
- Optimized the accuracy and efficiency of enzyme kinetic isotope effect measurements for drug discovery 10-fold by introducing HPLC, LC-MS, and mass spectrometry.
- Optimized the throughput of kinetic assays by FRET, stopped-flow, CD spectroscopy, and microplate assay.

Graduate Research Assistant

Case Western Reserve University, Cleveland OH, USA 2011 2017

- Integrated biological knowledge and numerical methods to explore and convert unstructured data (e.g. Next generation sequencing results and RNA structures) into numerical features and developed feature selection and pattern recognition pipeline by Python, scikit-learn, R and MATLAB.
- Applied Machine learning algorithms (e.g. k-mean, random forest, neural network, novel linear regression models) to predict the rules of biomolecule interactions and accelerate the data driven experimental design 30 folds faster than current methods.
- Led 3 projects, presented in 7 national/regional conferences and published 5 papers on top peer reviewed journals.
- Developed and implemented High Throughput Sequencing KINetics and EQuilibrium (HTS-KIN/EQ) to increase the pace of enzyme research by more than 4000 times.

EDUCATION

Ph.D. in Biochemistry 2011 - 2017

Case Western Reserve University, Cleveland OH, USA

Dissertation: Development and Application of High Throughput Methods for Interrogating RNA Binding Specificity

M.S. in Biochemistry and Molecular Biology 2005 - 2007

National Cheng Kung University, Tainan Taiwan.

Thesis: Study the Function of Kringle Proteins in Atherosclerosis

B.S. in Chemistry 2001 - 2005

National Taiwan University, Taipei Taiwan.

PUBLICATIONS

1. Jain, N.*; Lin, H. C.*; Morgan, C. E.; Harris, M. E.; Tolbert, B. S., Rules of RNA specificity of hnRNP A1 revealed by global and quantitative analysis of its affinity distribution. Proc Natl Acad Sci USA 2017.

*N.J. and H.-C.L. contributed equally to this work.

2. Lin, H. C.; Zhao, J.; Niland, C. N.; Tran, B.; Jankowsky, E.; Harris, M. E., Analysis of the RNA Binding Specificity Landscape of C5 Protein Reveals Structure and Sequence Preferences that Direct RNase P Specificity. Cell Chem Biol 2016, 23 (10), 1271-1281.

3. Lin, H. C., Yandek, L.E., Gjermeni, I. & Harris, M.E. Determination of relative rate constants for in vitro RNA processing reactions by internal competition. Anal. Biochem. 467, 54-61 (2014).

4. Niland, C. N.; Zhao, J.; Lin, H. C.; Anderson, D. R.; Jankowsky, E.; Harris, M. E., Determination of the Specificity Landscape for Ribonuclease P Processing of Precursor tRNA 5' Leader Sequences. ACS chemical biology 2016, 11 (8), 2285-92.

5. Yandek, L.E., Lin, H.C. & Harris, M.E. Alternative substrate kinetics of Escherichia coli ribonuclease P: determination of relative rate constants by internal competition. J. Biol. Chem. 288, 8342-8354 (2013).

6. Chang, P.C., Wu, H.L., Lin, H.C., Wang, K.C. & Shi, G.Y. Human plasminogen kringle 1-5 reduces atherosclerosis and neointima formation in mice by suppressing the inflammatory signaling pathway. J Thromb Haemost 8, 194-201 (2010).