

- Ph.D. in Bioinformatics and biochemistry with 3 years postdoc experience.
- 6 high-impact publications and 10 conference presentations of research results.
- Accelerated NGS and gene therapy data analysis and visualization pipeline 10-fold faster by using Python, pandas, matplotlib, R, C++, scikit-learn, statistical modeling, data visualization, and machine learning.
- Developed novel next-generation sequencing (NGS) methods to increase over 4,000-time efficiency in improvement of efficacy and safety in gene editing therapeutics.
- 7 cross-functional biochemical projects, resulting in 4 scientific collaborations with \$2,540,000 funding.

SKILLS

Programming Languages	Python, R, Perl, Matlab, SQL, C++, L ^A T _E X, Markdown
Experienced with	Next-generation sequencing (NGS) methods development, RNA-Seq, classification, regression, clustering algorithms, DNA, Apache Airflow, Tensorflow, PyTorch, pandas, matplotlib, scikit-learn, Data visualization, Natural language processing, Origin, High throughput assays, HPLC, Mass Spectroscopy, Biochemistry, Molecular Biology, RNA, Protein Purification, time-management, communication skills
Miscellaneous	SQL, git

EXPERIENCE

Postdoctoral Associate

Department of Chemistry, University of Florida

Feb 2017 — Dec 2019

Gainesville FL, USA

- Managed 4 projects and presented in 2018 national ACS meeting.
- Accelerated NGS data analysis pipeline 10-fold faster by using Unix/Linux shell commands, Perl, Python, R, C++, Pandas, scikit-learn, MATLAB, statistical modeling, data visualization, 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, mass spectrometry, FRET, stopped-flow, CD spectroscopy, and micro-plate assay.

Technologies: Python, R, Tensorflow, Pytorch, Scikit-learn, Data visualization, Perl, LC-MS, Next Generation Sequencing (NGS), RNA-Seq, Enzyme assays, Origin, FPLC, HPLC, Mass Spectroscopy

Graduate Research Assistant

Case Western Reserve University,

Aug 2011 — Jan 2017

Cleveland OH, USA

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

Technologies: R, Python, Matlab, Scikit-learn, Data visualization, Tensorflow, Pytorch, t-SNE, PCA, NGS, Origin, FPLC

Research Assistant

Kaohsiung Medical University,

Jun 2009 — July 2011

Kaohsiung Taiwan

- Developed and optimized BMP-2 gene therapy for osteonecrosis by applying micro-CT, immunohistochemistry, Western blot, ELISA, and real-time PCR.

HANDS-ON EXPERIENCE

- Built CycleGAN voice converter and miRNA generator from scratch by Tensorflow 2.0 and Keras.
- Applied Natural language processing, Embedding, LSTM, and Transformer models to generate texts, categorize articles, and visualize the rules of RNA-Protein interactions.

EDUCATION

Ph.D. in Biochemistry , <i>Case Western Reserve University, Cleveland OH, USA</i>	2011 — 2017
M.S. in Biochemistry and Molecular Biology , <i>National Cheng Kung University, Tainan Taiwan</i>	2005 — 2007
B.S. in Chemistry , <i>National Taiwan University, Taipei Taiwan</i>	2001 — 2005

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. U.S.A** 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 Chem. Biol** 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).

CONFERENCE TALKS

1. Hsuan-Chun Lin, Benjamin Weissman, Syed Shahbaz Gardezi, Vernon Anderson, Darrin York, Joseph Piccirilli, Michael Harris 2018 ACS National meeting New Orleans, March 22-26
Kinetic isotope effects on catalysis by the HDV ribozyme-precise determination of isotope ratios using electrospray ionization time-of-flight mass spectrometry
2. Hsuan-Chun Lin, 2014 Rustbelt RNA meeting Pittsburgh, October 17-18
Next-generation tools for RNA enzymology: Determination of rate and equilibrium constants for large populations of RNA substrate variants using high throughput sequencing.