

JUI-HUNG HUNG

03-5712121 ext. 56991

jhhung@nctu.edu.tw

EDUCATION

Boston UNIVERSITY, Program of Bioinformatics, Boston, MA
Doctor of Philosophy in Bioinformatics, May 2011

NATIONAL CHIAO TUNG UNIVERSITY, Institute of Bioinformatics, HsinChu, Taiwan
Master of Bioinformatics, 2007

NATIONAL CENTRAL UNIVERSITY, Department of Computer Science, Jhongli City, Taiwan
Bachelor of Engineering in Computer Science, 2005

TAINAN FIRST SENIOR HIGH SCHOOL, Tainan, Taiwan
Diploma, 2001

Areas of Interest

- Next generation sequencing (NGS) analysis
- Small silencing RNA (miRNA, endo-siRNA, and piRNA) biogenesis
- Epigenetics (histone modification and DNA methylation) in stem cells and cancers
- Bioinformatics algorithms design and cloud/GPU computing
- Pathway enrichment analysis

RESEARCH EXPERIENCE

National Chiao Tung University, HsinChu, Taiwan 2015~present
Associate professor, Institute of Bioinformatics and Systems Biology & Department of biological Science and Technology

- Conducted research on human Argonaute-small RNA sorting and tailing mechanisms, resulting in publication in **Molecular Cell**
- Proposed a hardware acceleration friendly FM-index algorithm for high speed short read mapping, published in **Bioinformatics**

National Chiao Tung University, HsinChu, Taiwan 2012~2015
Assistant professor, Institute of Bioinformatics and Systems Biology & Department of biological Science and Technology

- Conducted bioinformatics analysis to study mouse and human epigenetics. Results published in **Developmental Cell**, **Cell Report** and **PLoS Genetics**
- Developed algorithms and cloud applications for NGS analysis, published in **Nuclear Acids Research**

University of Massachusetts Medical School, Worcester, MA 2011~2012
Post doctoral researcher, Zhiping Weng's Lab, Program in Bioinformatics and Integrative Biology, UMass Med

- Designed algorithms to reconstruct hepatitis C virus quasi-species from NGS data
- Conducted projects pertaining small RNA tailing mechanisms, resulting in publication in **Cell** and **Nature Methods**
- Involved in research of mouse stem cell epigenetics, resulting in publication in **Cell**
- Published a review of enrichment analysis approaches on **Briefings in Bioinformatics**

University of Massachusetts Medical School, Worcester, MA 2009~2011
Research Assistant, Zhiping Weng's Lab, Program in Bioinformatics and Integrative Biology, UMass Med

- Devised novel suffix tree based algorithms to search for trimming and tailing in target RNA directed small RNA silencing effect.
- Designed analysis pipeline for NGS data.
- Discovered the putative model of trimming and tailing, resulting in publication in **Science**, **Genome Research** and **RNA**

Boston University, Boston, MA

2007~2011

Research Assistant, Charles DeLisi's Lab, Bioinformatics program, BU

- Developed network based pathway enrichment analysis algorithms and JAVA based tools. Results published on **Genome Biology** and **Nuclear Acids Research**

PUBLICATIONS

SCI journal:

Chang CH, Chou MT, Wu YC, Hong TW, Li YL, Yang CH, **Hung J.-H.**, *sBWT: memory efficient implementation of the hardware-acceleration-friendly Schindler transform for the fast biological sequence mapping*. **Bioinformatics**. 2016 Jul.

Reimão-Pinto M. M., Ignatova V., Burkard T. R., **Hung J.-H.**, Manzenreither R. A., Sowemimo I., Herzog V. A., Reichholf B., Fariña-Lopez S., Ameres S. L.. *Uridylation of RNA Hairpins by Tailor Confines the Emergence of MicroRNAs in Drosophila*. **Molecular Cell**. Volume 59, Issue 2, Pages 203–216, 2015.

Chou M.-T., Han B. W., Hsiao C.-P., Zamore P. D., Weng Z. and **Hung J.-H.** *Tailor: A Computational Framework for Detecting Non-Templated Tailing of Small Silencing RNAs*. **Nucleic Acids Research**. Volume: 10. 1093. 2015.

Tung Y.-T., Lu Y.-L., Peng K.-C., Yen Y.-P., Chang M., Li J., H. Jung, Thams S., Y.-P. Huang, **Hung J.-H.**, and Chen J.-A. *Mir-17~92 Governs Motor Neuron Subtype Survival by Mediating Nuclear PTEN*. **Cell Reports**. Volume: 11 Pages:1–14. 2015

Li, Y.-L., Weng J.-C., Hsiao C.-C., Chou M.-T., Tseng C.-W. and **Hung J.-H.** *PEAT: an intelligent and efficient paired-end sequencing adapter trimming algorithm*. **BMC Bioinformatics**, 16:S2, 2015

Carone RB., **Hung J.-H.**, Sarah J. Hainer, Min-Te Chou, Dawn M. Carone, Zhiping Weng, Thomas G. Fazio, Oliver J. Rando. *High-Resolution Mapping of Chromatin Packaging in Mouse Embryonic Stem Cells and Sperm*. **Developmental Cell** Vol: 30(1), 2014

Yildirim O., **Hung J.-H.**, Ryan J. Cedeno, Zhiping Weng, Christopher J. Lengner, Oliver J. Rando. *A System for Genome-Wide Histone Variant Dynamics In ES Cells Reveals Dynamic MacroH2A2 Replacement at Promoters*. **PLoS Genetics**, 10.1371, Aug. 2014

Chen PB, **Hung J.-H.**, Hickman TL, Coles AH, Carey JF, Weng Z, Chu F, Fazio TG. *Hdac6 regulates Tip60-p400 function in stem cells*. **eLIFE**, December 3, 2013

Chih-Hung Chou, Feng-Mao Lin, Min-Te Chou, Sheng-Da Hsu, Tzu-Hao Chang, Shun-Long Weng, Sirjana Shrestha, Chiung-Chih Hsiao, **Hung J.-H.** and Hsien-Da Huang. *A computational approach for identifying microRNA-target interactions using high-throughput CLIP and PAR-CLIP sequencing*. **BMC Genomics**, 14:S2, 2013

Jie Wang, Jiali Zhuang, Sowmya Iyer, Xin-Ying Lin, Melissa C. Greven, Bong-Hyun Kim, Jill Moor, Brian G. Pierce, Xianjun Dong, Daniel Virgil, Ewan Birney, **Hung J.-H.** and Zhiping

- Weng. *Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium*. **Nucleic Acids Research**. 41(D1):D171-D176, 2013
- Ryuya Fukunaga, Bo W. Han, **Hung J-H**, Jia Xu, Zhiping Weng, Phillip D. Zamore. *Dicer Partner Proteins Tune the Length of Mature miRNAs in Flies and Mammals*. **Cell**. 2012 Oct 26;151(3):533-46
- Xie J, Ameres SL, Friedline R, **Hung J-H**, Zhang Y, Xie Q, Zhong L, Su Q, He R, Li M, Li H, Mu X, Zhang H, Broderick JA, Kim JK, Weng Z, Flotte TR, Zamore PD, Gao G. *Long-term, efficient inhibition of microRNA function in mice using rAAV vectors*. **Nature Methods**, 2012 Mar 4;9(4):403-9
- Shigemizu D , Hu Z , **Hung J-H** , Huang C-L , Wang Y , et al. *Using Functional Signatures to Identify Repositioned Drugs for Breast, Myelogenous Leukemia and Prostate Cancer*. **PLoS Comput Biol** 8(2): e1002347. doi:10.1371/journal.pcbi.1002347
- Yildirim O, Li R, **Hung J-H**, Chen PB, Dong X, Ee L-Y, Weng Z, Rando OJ and Fazio TG. *Mbd3/NURD complex regulates expression of 5-hydroxymethylcytosine marked genes in embryonic stem cells*. **Cell**. Volume 147, Issue 7, 1498-1510, 23 December 2011
- Han B, **Hung J-H**, Weng Z, Zamore PD, Ameres SL. *The 3'-to-5' Exoribonuclease Nibbler Shapes the 3' Ends of MicroRNAs Bound to Drosophila Argonaute1*. **Current Biology**, November 2011.
- Hung J-H**, Yang TH, Hu Z, Weng Z, Delisi C. *Gene set enrichment analysis: performance evaluation and usage guidelines*. **Brief Bioinform**. 2011 Sep 7.
- Yang T-H, Kon M, **Hung J-H**, DeLisi C. *Combinations of newly confirmed Glioma-Associated loci link regions on chromosomes 1 and 9 to increased disease risk*. **BMC Medical Genomics** 2011, 4:63
- Berezikov E, Robine N, Samsonova A, Westholm JO, Naqvi A, **Hung J-H**, Okamura K, Dai Q, Bortolamiol-Becet D, Martin R, Zhao Y, Zamore PD, Hannon GJ, Marra MA, Weng Z, Perrimon N, Lai EC. *Deep annotation of Drosophila melanogaster micro RNAs yields insights into their processing, modification, and emergence*. **Genome Res.**, 2011; Feb; 21(2):203-15
- Ameres SL, **Hung J-H**, Xu J, Weng Z, Zamore PD. *Target RNA-directed Tailing and Trimming purifies the sorting of endo-siRNA between the two Drosophila argonaute proteins*. **RNA**. 2011; 17(1):54-63.
- Xie J, Xie Q, Zhang H, Ameres SL, **Hung J-H**, Su Q, He R, Mu X, Seher Ahmed S, Park S, Kato H, Li C, Mueller C, Mello CC, Weng Z, Flotte TR, Zamore PD, Gao G. *MicroRNA-regulated, Systemically Delivered rAAV9: A Step Closer to CNS-restricted Transgene Expression*. **Mol Ther** (PMID: 21179009)
- Ameres SL, Horwich MD, **Hung J-H**, Xu J, Ghildiyal M, Weng Z, Zamore PD. *Target RNA-directed trimming and tailing of small silencing RNAs*. **Science**. 320:1534-1539, 2010
- Hung J-H**, Whitfield TW, Yang TH, Hu Z, Weng Z, DeLisi C. *Identification of functional modules that correlate with phenotypic difference: the influence of network topology*. **Genome Biology**. 11:R23, 2010
- Hwang H, Vreven T, Pierce B, **Hung J-H**, Weng Z. *Performance of ZDOCK and ZRANK in CAPRI round 13-19*. **Protein**. 78(15):3104-10
- Hu Z., **Hung J-H**, Chang Y-C, Huang C-L, Huyck M. and DeLisi C. *VisANT 3.5: multi-scale network visualization, analysis and inference based on the gene ontology*. **Nucleic Acids Research**. 37: W115-W121, 2009

Hung J-H, **Hung J-H**, and Chen S-G. *A systematic Optimized Comparison Algorithm for Fast LDPC Decoding*. **ICACT 10th**. Vol. 3, pp. 1513-1526. 2008.

Hung J-H, Huang H-D, and Lee T-Y. *ProKware: integrated software for presenting protein structural properties in protein tertiary structures*. **Nucleic Acids Research**. 34: W89-W94, 2006.

Lee T-Y, Huang H-D, **Hung J-H**, Yang Y-S, and Wang T-H. *dbPTM: An Information Repository of Protein Post-Translational Modification*. **Nucleic Acids Research**. 34: D622-D627. 2006.

Book Chapter:

Hung J-H, and Weng Z. *Bioinformatics Essentials*. Molecular Cloning: A Laboratory Manual, 4th ed. Cold Spring Harbor Laboratory, 2012, ISBN-10: 1936113422.

Hung J-H. *Enrichment Analysis*. Data Mining for Systems Biology. Methods in Molecular Biology series. Springer, 2013, ISBN 978-1-62703-107-3.

International Conference:

Hung J-H, Hung J-H, and Chen S-G. *A General Comparator Structure for LDPC Decoder by Novel Systematic Optimization Algorithms*. ICASSP2007

Hung J-H, Wang W-G, and Huang H-D. *Systematic Identification of RNA Editing Site in Human Genome*. ICS2006

International Patent:

Hung J-H, **Hung J-H**, and Chen S-G. *An Efficient Set-Cyclic Comparison IP for Low Density Parity Check Code*. USA. (Patent No.: US 7945839B2)

Hung J-H, Hung J-H, and Chen S-G. *An Efficient Cyclic Comparison IP for Low Density Parity Check Codes*. USA. (Patent No.: US 7966543B2)

Revisiting mammalian Argonaute-miRNA sorting with in silica analysis

Jui-hung Hung (洪瑞鴻)

Department of Biological Science and Technology, National Chiao Tung University, Hsin-Chu, Taiwan

Argonaute-miRNA sorting is an essential process to direct the specific regulatory cascades in plants, insects, and worms. Although mammals have four AGO clade proteins, preferential loading into specific Argonaute proteins can be seen in only a handful of miRNAs, and the four AGO clade proteins are believed to have largely overlapping functions. In this talk, I will present our work that revisited several Argonaute RIP-seq data and unearthed novel characteristics associated to preferential loading, namely sorting signals, that have been previously omitted. These sorting signals can be found in many miRNAs and linked to other processes such as isomiRs, non-templated tailing, and cellular localization. We hereby suggest that mammalian Argonaute-miRNA sorting could be a valid and powerful gene regulation mechanism and worth more attention.