

## *Curriculum Vitae*

**NAME:** HUI YU  
**Office Address:** University of New Mexico  
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### EDUCATION

<b>Ph.D. in Bioinformatics</b>	<b>2012</b>
University of Chinese Academy of Sciences, Shanghai, China	
<b>M.Sc. In Bioinformatics</b>	<b>2004</b>
Harbin Medical University, Harbin, China	
<b>B.Sc. in Biology</b>	<b>2001</b>
East China Normal University, Shanghai, China	

### PROFESSIONAL EXPERIENCE

**Bioinformatics Research Fellow (Nov. 2017 – present)**, Bioinformatics Shared Resources, University of New Mexico Comprehensive Cancer Center

**Research Assistant Professor** (2016 – Oct. 2017), Center for Quantitative Sciences, Vanderbilt University Medical School, Nashville, TN

**Bioinformatics Research Fellow** (2012 – 2016), Department of Biomedical Informatics, Vanderbilt University Medical School, Nashville, TN

**Bioinformatics Research Fellow** (2005 – 2012), Systems Biology Group, Shanghai Center for Bioinformation Technology, Shanghai, China

**Assistant Bioinformatics Engineer** (2004 – 2005), Key Laboratory of Brain Functional Genomics, Ministry of Education, Shanghai, China

### PROFESSIONAL ACTIVITIES

#### Honors/Awards

2021 Travel Award, International Conference on Intelligent Biology & Medicine (ICIBM 2021, @Virtual\_Meeting, U.S.A.)

2019 Outstanding Poster Presentation, Research Day 2019, UNM Comprehensive Cancer Center

2019 Travel Award, International Conference on Intelligent Biology & Medicine (ICIBM 2019, @Columbus, U.S.A.)

2010 Young Investigator fellowship funded by Chinese National Natural Science Foundation

2007, 2009, 2010 Annual Outstanding Employee, Shanghai Center for Bioinformation Technology, Shanghai, China

2004 Outstanding master dissertation of Harbin Medical University, Harbin, China

2001 Shanghai Outstanding Graduate, Shanghai, China

### Editorial Activities

#### Conference Reviewer:

International Conference on Intelligent Biology and Medicine (ICIBM 2019)

International Conference on Intelligent Biology and Medicine (ICIBM 2018)

International Conference on Bioinformatics (InCoB) 2013

Genome Informatics Workshop 2010

#### Journal Reviewer:

<https://publons.com/researcher/1370278/hui-yu/>

American Journal of Cardiology

Bioinformatics

BioMed Research International

BMC Medical Genomics

Briefing in Bioinformatics

Experimental and Molecular Pathology

Genomics

Genome Biology and Evolution

ISRN Bioinformathematics

Nucleic Acids Research

PLoS ONE

Scientific Reports

## TEACHING ACTIVITIES

**2015, Teaching Assistant** to Prof. Yu Shyr, in course *Biostatistics I* to Master of Public Health students, Vanderbilt University Medical School. Nashville, TN.

**November 11th, 2011, 3-hour Lecturer:** *Basic statistical tests and R solutions for bioinformatics research.* In: Workshop of Deep Sequencing Analysis in Bioinformatics (hosted by Shanghai Center for Bioinformation Technology). Shanghai, China.

**September, 2009, 3-hour Lecturer:** *Fundamentals of gene expression analysis and implementation via Bioconductor.* In: the 4th Bioinformatics workshop (hosted by Shanghai Center for Bioinformation Technology). Shanghai, China.

**Sep 15th, 2005, 3-hour Lecture:** *Introduction of Kyoto Encyclopedia of Genes and Genomes.* In: Free science/research tutorial series to interested audience (hosted by Shanghai Center for Bioinformation Technology). Venue: Ruijin Hospital, Science & Education Building 411, Shanghai, China.

**2002, Teaching Assistant** to Prof. Xia Li. Taught *Calculus* to medical undergraduates in Harbin Medical University, Harbin, China.

## GRANTS

NSFC/31000380 (PI: Hui Yu)

1/1/2011-12/31/2013

¥ 200,000

### National Natural Science Foundation of China

*Identifying type-II diabetes relevant genes through quantitative differential co-expression methods*

## PUBLICATIONS

(# equal-contribution)

### Submitted Journal Articles

- Wang J, Ness S, Brown R, **Yu H**, et al. EditPredict: prediction of RNA editable site with convolutional neural network. Submitted to *Genomics*.

### Peer Reviewed Journal Articles as first/co-first author:

1. Guo Y #, **Yu H #**, et al. (2021) MetaGSCA: A tool for meta-analysis of gene set differential coexpression. *PLOS Computational Biology* 17 (5), e1008976
2. **Yu H**, Guo Y, Chen J, Chen X, Jia P, Zhao Z. (2021). Rewired Pathways and Disrupted Pathway Crosstalk in Schizophrenia Transcriptomes by Multiple Differential Coexpression Methods. *Genes* 12 (5), 665.
3. Sheng QH #, **Yu H #**, et al. (2021). A streamlined solution for processing, elucidating and quality control of cyclobutane pyrimidine dimer sequencing data. *Nature Protocol* 16: 2190-2212.
4. **Yu H.\***, et al. (2021). Conditional transcriptional relationships may serve as cancer prognostic markers. *BMC Med Genomics* 13(Suppl 9): 134
5. **Yu, H.**, D. Chen, O. Oyebamiji, Y. Y. Zhao and Y. Guo (2020). Expression correlation attenuates within and between key signaling pathways in chronic kidney disease. *BMC Med Genomics* 13(Suppl 9): 134. [ICIBM 2019 special issue]
6. **Yu, H.\***, S. Zhao, S. Ness, H. Kang, Q. Sheng, D. C. Samuels, O. Oyebamiji, Y. Y. Zhao and Y. Guo \* (2020). "Non-canonical RNA-DNA differences and other human genomic features are enriched within very short tandem repeats." *PLoS Comput Biol* 16(6): e1007968.
7. Sheng, Q. #, **H. Yu #**, O. Oyebamiji, J. Wang, D. Chen, S. Ness, Y. Y. Zhao and Y. Guo (2020). AnnoGen: Annotating Genomewide Pragmatic Features. *Bioinformatics*. doi: 10.1093/bioinformatics/btaa027
8. **Yu H**, Samuels DC, Zhao YY, Guo Y. (2019) Architectures and accuracy of artificial neural network for disease classification from omics data. *BMC Genomics*. 2019 Mar 4;20(1):167. doi: 10.1186/s12864-019-5546-z.
9. **Yu H #**, Wang J #, Sheng QH, Liu Q, Shyr Yu. (2019) beRBP: Binding Estimation for human RNA-Binding Proteins. *Nucleic Acids Res* 47(5): e26.
10. Masuzaki R #, **Yu H #**, Kingsley P, Marnett L, Zhao Z, Karp S. (2015) Functional Implications of Biochemical and Molecular Characteristics of Donation After Circulatory Death Livers. *Transplantation DIRECT* 1: e18 doi: 10.1097/TXD.0000000000000527
11. **Yu H**, Mitra R, Yang J, Li Y, Zhao Z (2014). Algorithms for network-based identification of differential regulators from transcriptome data: a systematic evaluation. *Sci China Life Sci* 57: 1090-1102.
12. Yang J #, **Yu H #**, Liu BH, Zhao Z, Liu L, Ma LX, Li YX, Li YY. (2013) DCGL v2.0: An R Package for Unveiling Differential Regulation from Differential Co-expression. *PLoS One* 8:e79729.
13. **Yu H**, Lin CC, Li YY, Zhao Z (2013) Dynamic protein interaction modules in human hepatocellular carcinoma progression. *BMC Syst Biol*, 7(Suppl 5): S2. [ICIBM 2013]
14. Hu SN #, **Yu H #**, Zhang YB, Wu ZL, Yan YC, Li YX, Li YY, Li YP. (2012) Splice blocking of zygotic sox31 leads to developmental arrest shortly after Mid-Blastula Transition and induces apoptosis in zebrafish. *FEBS Lett* 586(3): p. 222-8.

15. **Yu H #**, Tu K #, Wang YJ, Mao JZ, Xie L, Li YY, Li YX. (2012) Combinatorial Network of Transcriptional Regulation and microRNA Regulation in Human Cancer. *BMC Systems Biology* 6:61 [labeled **Highly accessed** by BMC]
16. **Yu H #**, Liu BH #, Ye ZQ, Li C, Li YX, Li YY. (2011) Link-based quantitative methods to identify differentially coexpressed genes and gene pairs. *BMC Bioinformatics* 12: p. 315. [labeled **Highly accessed** by BMC]
17. Liu BH #, **Yu H #**, Tu K, Li C, Li YX, Li YY. (2010) DCGL: an R package for identifying differentially coexpressed genes and links from gene expression microarray data. *Bioinformatics* 26(20): p. 2637-8.
18. **Yu H**, Tu K, Xie L, Li YY. (2010) DigOut: viewing differential expression genes as outliers. *J Bioinform Comput Biol* 8 Suppl 1:p.161-75. [GIW 2010]
19. Tu, K #, **Yu, H #**, Hua, YJ, Li, YY, Liu, L, Xie, L. and Li, Y.X. (2009) Combinatorial network of primary and secondary microRNA-driven regulatory mechanisms, *Nucleic Acids Res* 37: 5969-5980.
20. **Yu, H.**, Yu, F.-D., Zhang, G.-Q., Shen, X., Chen, Y.-Q., Li, Y.-Y. and Li, Y.-X. (2009) DBH2H: vertebrate head-to-head gene pairs annotated at genomic and post-genomic levels, Database: The Journal of Biological Databases and Curation, bap006.
21. **Yu H**, Li YY. (2009) Recovering context-specific gene network modules from expression data: a brief review. *Frontiers of Biology in China* 4: 414-418.
22. **Yu H**, Wang F, Tu K, Xie L, Li YY, Li YX. (2007) Transcript-level annotation of Affymetrix probesets improves the interpretation of gene expression data. *BMC Bioinformatics* 8: p. 194. [labeled **Highly accessed** by BMC]
23. Li YY #, **Yu H #**, Guo ZM, Guo TQ, Tu K, Li YX. (2006) Systematic analysis of head-to-head gene organization: evolutionary conservation and potential biological relevance. *PLoS Comput Biol* 2(7): p. e74.
24. **Yu H**, Gao L, Tu K, Guo Z (2005) Broadly predicting specific gene functions with expression similarity and taxonomy similarity. *Gene* 352: p. 75-81.

#### **Peer Reviewed Journal Articles as co-author:**

25. Wu YM, Guo Y, **Yu H**, Guo T. (2021) RNA editing affects cis-regulatory elements and predicts adverse cancer survival. *Cancer Medicine* DOI: 10.1002/cam4.4146.
26. Jiang, L., M. Duan, F. Guo, J. Tang, O. Oyebamiji, **H. Yu**, S. Ness, Y. Zhao, P. Mao and Y. Guo (2020). "SMDB: Pivotal Somatic Sequence Alterations Reprogramming Regulatory Cascades." *NAR Cancer* 2(4): zcaa030.
27. Samuels, D. C., J. E. Below, S. Ness, **H. Yu**, S. Leng and Y. Guo (2020). "Alternative Applications of Genotyping Array Data Using Multivariant Methods." *Trends Genet* 36(11): 857-867.
28. Ye, B., J. Shi, H. Kang, O. Oyebamiji, D. Hill, **H. Yu**, S. Ness, F. Ye, J. Ping, J. He, J. Edwards, Y. Y. Zhao and Y. Guo (2019). "Advancing Pan-cancer Gene Expression Survival Analysis by Inclusion of Non-coding RNA." *RNA Biol*: 1-8.
29. Ping, J., O. Oyebamiji, **H. Yu**, S. Ness, J. Chien, F. Ye, H. Kang, D. Samuels, S. Ivanov, D. Chen, Y. Y. Zhao and Y. Guo (2019). "MutEx: a multifaceted gateway for exploring integrative pan-cancer genomic data." *Brief Bioinform*.
30. Guo, Y., **H. Yu**, D. Chen and Y. Y. Zhao (2019). "Machine learning distilled metabolite biomarkers for early stage renal injury." *Metabolomics* 16(1): 4.
31. Chen, D. Q., G. Cao, H. Chen, C. P. Argyopoulos, **H. Yu**, W. Su, L. Chen, D. C. Samuels, S. Zhuang, G. P. Bayliss, S. Zhao, X. Y. Yu, N. D. Vaziri, M. Wang, D. Liu, J. R. Mao, S. X. Ma, J. Zhao, Y. Zhang, Y. Q. Shang, H. Kang, F. Ye, X. H. Cheng, X. R. Li, L. Zhang, M. X. Meng, Y.

- Guo and Y. Y. Zhao (2019). "Identification of serum metabolites associating with chronic kidney disease progression and anti-fibrotic effect of 5-methoxytryptophan." *Nat Commun* 10(1): 1476.
32. Chigaev M, **Yu H**, Samuels DC, Sheng Q, Oyebamiji O, Ness S, Yue W, Zhao Y-y and Guo Y (2019) Genomic Positional Dissection of RNA Editomes in Tumor and Normal Samples. *Front. Genet.* 10:211. doi: 10.3389/fgene.2019.00211
33. Jimenez L, **Yu H**, McKenzie A, Franklin JL, Patton JG, Liu Q, Weaver AM. (2019) Quantitative proteomic analysis of small and large extracellular vesicles (EVs) reveals enrichment of adhesion proteins in small EVs. *J Proteome Res.* 2019 Jan 4. doi:10.1021/acs.jproteome.8b00647
34. Guo, M., W. Yue, D. C. Samuels, **H. Yu**, J. He, Y. Y. Zhao and Y. Guo (2019). "Quality and concordance of genotyping array data of 12,064 samples from 5840 cancer patients." *Genomics* 111(4): 950-957.
35. Sheng, Q., D. C. Samuels, **H. Yu**, S. Ness, Y. Y. Zhao and Y. Guo (2018). "Cancer-specific expression quantitative loci are affected by expression dysregulation." *Brief Bioinform.*
36. Guo Y, **Yu H**, Samuels DC, Yue W, Ness S, Zhao YY. (2018) Single Nucleotide Variants in Human RNA: RNA editing and Beyond. *Briefings in Functional Genomics*, doi:10.1093/bfpg/ely032
37. Iams W, **Yu H**, Shyr Y, Patil T, Horn L, McCoach C, Kelly K, Doebele RC, Camidge R. (2018) First line chemotherapy responsiveness and patterns of metastatic spread identify clinical syndromes present within advanced KRAS mutant non-small cell lung cancer with different prognostic significance. *Clinical Lung Cancer* 19(6): 531-543.
38. Saxon JA, **Yu H**, et al. (2018) p52 expression enhances lung cancer progression through regulation of cell cycle genes. *Scientific Reports*, accepted.
39. Guo Y, **Yu H**, Wang J, Sheng QH, Zhao SL, Zhao YY, Lehmann B. (2018) The Landscape of small non-coding RNAs in Triple-Negative Breast Cancer. *Genes* 9(1), 29.
40. Guo Y, Dai YL, **Yu H**, Zhao SL, Samuels D, Shyr Y. (2017) Improvements and impacts of GRCh38 human reference on high throughput sequencing data analysis. *Genomics* 109(2): 83-90.
41. Chen J, Silvia-Alin B, **Yu H**, et al., Chen X. (2016) Genetic relationship between schizophrenia and nicotine dependence. *Scientific Reports* 6, accepted.
42. Wang Q, **Yu H**, Zhao Z, Jia P. (2015) EW\_dmGWAS: Edge-Weighted dense module search for genome-wide association studies and gene expression profiles. *Bioinformatics*, doi: 10.1093/bioinformatics/btv150
43. Lin CC, Jiang W, Mitra R, Cheng FX, **Yu H**, and Zhao Z. (2015) Regulation rewiring analysis reveals mutual regulation between STAT1 and miR-155-5p in tumor immunosurveillance in seven major cancers. *Scientific Reports* 5, Article No. 12063, doi: 10.1038/srep12063
44. Zhao Z, Xu J, Chen J, Kim S, Reimers M, Bacanu SA, **Yu H**, Liu C, Sun J, Wang Q, Jia P, Xu F, Zhang Y, Kendler KS, Peng Z, Chen X. (2014) Transcriptome sequencing and genome-wide association analyses reveal lysosomal function and actin cytoskeleton remodeling in schizophrenia and bipolar disorder. *Mol Psychiatry*, doi: 10.1038/mp.2014.82
45. Mitra, R., M. D. Edmonds, J. Sun, M. Zhao, **H. Yu**, C. M. Eischen and Z. Zhao (2014). "Reproducible combinatorial regulatory networks elucidate novel oncogenic microRNAs in non-small cell lung cancer." *RNA* 20(9): 1356-1368.
46. Xu H, **Yu H**, Tu K, Shi Q, Wei C, Li YY, Li YX. (2013) cGRNB: a web server for building combinatorial gene regulatory networks through integrated engineering of seed-matching sequence information and gene expression datasets. *BMC Syst Biol* 7 Suppl 2: S7.
47. Ye Z-Q, Niu S, Yu Y, **Yu H**, Liu B-H, Li RX, Xiao HS, Zeng R, Li YX, Wu JR, Li YY. (2010) Analyses of Copy Number Variation of GK Rat Reveal New Putative Type 2 Diabetes Susceptibility Loci. *PLoS One* 5(11): p. e14077.
48. Chen, YQ, **Yu H**, Li YX, Li YY. (2010) Sorting out inherent features of head-to-head gene pairs by evolutionary conservation. *BMC Bioinformatics* 11 Suppl 11: p. S16.

49. Ye, B.C., Zhang, Y., **Yu, H.**, Yu, W.B., Liu, B.H., Yin, B.C., Yin, C.Y., Li, Y.Y., Chu, J. and Zhang, S.L. (2009) Time-resolved transcriptome analysis of *Bacillus subtilis* responding to valine, glutamate, and glutamine, PLoS One, 4, e7073.
50. Tu, K., **Yu H.**, and Li YX (2006) Combining gene expression profiles and protein-protein interaction data to infer gene functions. J Biotechnol 124(3): p. 475-85.
51. Tu, K., **Yu H.**, and Zhu M (2005) MEGO: gene functional module expression based on gene ontology. Biotechniques 38(2): p. 277-83.
52. Tu K, **Yu H.**, Guo Z, Li X (2004) Learnability-based further prediction of gene functions in Gene Ontology. Genomics 84(6): p. 922-928.

## PRESENTATIONS

### Talks

- Aug 10, 2021 *Rewired Pathways and Disrupted Pathway Crosstalk in Schizophrenia Transcriptomes by Multiple Differential Coexpression Methods*  
International Conference on Intelligent Biology and Medicine (ICIBM) 2021, Virtual Meeting (due to COVID-19)
- Aug 10, 2020 *Conditional transcriptional relationships may serve as cancer prognostic markers*  
International Conference on Intelligent Biology and Medicine (ICIBM) 2020, Virtual Meeting (due to COVID-19)
- Nov 18, 2019 *Contribution and prognosis value of mutational signatures across 33 cancer types*  
UNM Comprehensive Cancer Center Research Day (2019), Albuquerque, U.S.A.
- Jun 10, 2019 *Expression correlation attenuates within and between key signaling pathways in chronic kidney disease*  
International Conference on Intelligent Biology and Medicine (ICIBM 2019), Columbus, U.S.A.
- May 19, 2018 *Deep learning versus classical machine learning for omics-based disease classification*  
UNM Comprehensive Cancer Center Research Day (2018), Albuquerque, U.S.A.
- April 12, 2014 *Evaluating four major algorithms for identifying differential regulators in condition-specific transcriptional responses*  
UT-KBRIN Bioinformatics Summit 2014, Cadiz, U.S.A.
- August 13, 2013 *DCGL v2.0: from differential co-expression analysis to differential regulation analysis*  
International Conference on Intelligent Biology and Medicine (ICIBM 2013), Nashville, U.S.A.
- December 17, 2010 *Digout: Viewing differential expression genes as outliers*

Genome Informatics Workshop 2010, Hangzhou, China

**Conference poster/abstracts**

June 10-12, 2018      *Deep architectures are not necessary for anomaly classification of matrix-formed omics data*

International Conference on Intelligent Biology and Medicine (ICIBM) 2018, Los Angeles, U.S.A.

July 8-12, 2016      *Identifying target genes for RNA-binding proteins*

Intelligent Systems for Molecular Biology (ISMB) 2016, Orlando, U.S.A.