# Guangchuang Yu

## Post-doctoral Fellow

## **EDUCATION**

The University of Hong Kong,	Ph.D. Evolution Study of Influenza A virus	2017
Anhui Medical University,	M.S. Biochemistry and Molecular Biology	2009
South China Agricultural University,	B.S. Biotechnology	2005
Institut Pasteur, Paris,	Train the Trainers	2015

## **CERTIFICATE**

Certificate of Teaching and Learning in Higher Education, Centre for Enhancement of Teaching and Learning, The University of Hong Kong

## **EMPLOYMENT**

State Key Laboratory of Infectious Diseases, School of Public Health, The University of Hong Kong:

Post-doctoral Fellow 2017

College of Life Science and Technology, Jinan University:

Bioinformatician 2009–2013

## **TEACHING**

Student Helper, The University of Hong Kong

2013-2014

BIOL6001 Presentation Skills and Research Seminars in Biological Sciences

210 20001 Tresentation state the search seminars in 21010 great sciences

Lecturer, Jinan University 2011–2012

**Functional Proteomics** 

## **AWARDS**

2013–2017 Postgraduate Studentships. The University of Hong Kong.

2012 Best paper of the year 2010. Journal of Integrated OMICS.

# **GRANTS**

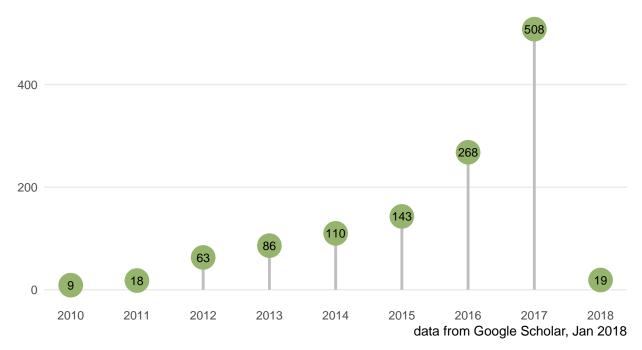
**2013** (*completed*) *PI*, Investigate functions of hnRNPK in regulating cytokinesis of human lung cancer cell. Fundamental Research Funds for the Central Universities (21613414), CNY 100,000

**2011** (completed) PI, Dynamic proteomic analysis of HeLA cell cycle, Fundamental Research Funds for the Central Universities (21611303), CNY 20,000

## **PUBLICATIONS**

## **Journal Articles**

Citation = 1255, H-index = 14, I10-index = 18



▼: ESI Highly Cited Paper (X5)

*Methods in Ecology and Evolution* (X1, rank 11 in *Environment Ecology*, IF = 5.708)

*Bioinformatics* (X<sub>3</sub>, rank 4 in *Computer Science*, IF = 7.307)

(† indicates equal contribution, \* indicates corresponding)

- 2. **G Yu**, QY He\*. ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization. *Molecular BioSystems*. 2016, 12(2):477-479. \*\* cited by 50
- 4. **G Yu**\*, LG Wang, GR Yan, QY He\*. DOSE: an R/Bioconductor package for Disease Ontology Semantic and Enrichment analysis. *Bioinformatics*. 2015, 31(4):608-609. cited by 55
- 5. **G** Yu<sup>†</sup>, LG Wang<sup>†</sup>, XH Meng, QY He<sup>\*</sup>. LXtoo: an integrated live Linux distribution for the bioinformatics community. *BMC Research Notes*. 2012, 5(1):360.
- 6. **G Yu**, LG Wang, Y Han, QY He\*. clusterProfiler: an R package for comparing biological themes among gene clusters. *OMICS: A Journal of Integrative Biology*. 2012, 16(5):284-287. **№** cited by 366
- 7. **G Yu**, QY He\*. Functional similarity analysis of human virus-encoded miRNAs. *Journal of Clinical Bioinformatics*. 2011, 1(1):15.
- 8. **G Yu**<sup>†</sup>, CL Xiao<sup>†</sup>, X Bo, CH Lu, Y Qin, S Zhan, QY He<sup>\*</sup>. A new method for measuring functional similarity of microRNAs. *Journal of Integrated OMICS*. 2011, 1(1):49-54.
- 9. **G** Yu<sup>†</sup>, CL Xiao<sup>†</sup>, CH Lu<sup>†</sup>, HT Jia, F Ge, W Wang, XF Yin, HL Jia, JX He<sup>\*</sup>, QY He<sup>\*</sup>. Phosphoproteome profile of human lung cancer cell line A549. *Molecular BioSystems*. 2011, 7(2):472-479.

- 10. **G** Yu<sup>†</sup>, F Li<sup>†</sup>, Y Qin, X Bo<sup>\*</sup>, Y Wu, S Wang<sup>\*</sup>. GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. *Bioinformatics*. 2010, 26(7):976-978. ♥ cited by 313
- 11. X Sun<sup>†</sup>, **G Yu**<sup>†</sup>, Q Xu, N Li, C Xiao, X Yin, K Cao, J Han, QY He<sup>\*</sup>. Putative cobalt- and nickel-binding proteins and motifs in *Streptococcus pneumonia*. *Metallomics*. 2013, 5(7):928-935.
- 12. YY Zhu<sup>†</sup>, **G** Yu<sup>†</sup>, Y Zhang, Z Xu, YQ Huang, GR Yan<sup>\*</sup>, QY He<sup>\*</sup>. A novel andrographolide derivative AL-1 exerts its cytotoxicity on K562 cells through a ROS-dependent mechanism. *Proteomics*, 2013, 13(1):169-178.
- 13. XY Yang, K He, G Du, X Wu, G Yu, Y Pan, G Zhang\*, X Sun\*, QY He\*. Integrated Translatomics with Proteomics to Identify Novel Iron–Transporting Proteins in *Streptococcus pneumoniae*. *Frontiers in Microbiology*. 2016, 7:78.
- 14. PY Huang, CCD Lee, CH Yip, CL Cheung, **G Yu**, TTY Lam, DK Smith, H Zhu\*, Y Guan\*. Genetic characterization of highly pathogenic H<sub>5</sub> influenza viruses from poultry in Taiwan, 2015. *Infection, Genetics and Evolution*. 2016, 38:96-100.
- 15. SH Xu, JZ Huang, ML Xu, G Yu, XF Yin, D Chen\*, GR Yan\*. ACK1 Promotes Gastric Cancer Epithelial-Mesenchymal Transition and Metastasis through AKT-POU<sub>2</sub>F<sub>1</sub>-ECD Signaling. *The Journal of Pathology*. 2015, 236(2):175-185.
- 16. Z Guo, J Han, XY Yang, K Cao, K He, G Du, G Zeng, L Zhang, **G Yu**, Z Sun, QY He\*, X Sun\*. Proteomic analysis on the copper resistance of *Streptococcus pneumonia*. *Metallomics*. 2015, 7(3):448-454.
- 17. XY Yang, L Zhang, J Liu, N Li, **G Yu**, K Cao, J Han, G Zeng, Y Pan, X Sun\*, QY He\*. Proteomic analysis on the antibacterial activity of a Ru(II) complex against *Strepococcus pneumonia*. *Journal of Proteomics*. 2015, 115:107-116.
- 18. N Wang<sup>†</sup>, J Zhang<sup>†</sup>, L Zhang, XY Yang, N Li, **G Yu**, J Han, K Cao, Z Guo, X Sun<sup>\*</sup>, QY He<sup>\*</sup>. Proteomic analysis of putative heme-binding proteins in *Streptococcus pyogenes*. *Metallomics*. 2014, 6(8):1451-1459.
- 19. H Sun\*, J Weng, **G Yu**, RH Massawe. A DNA-Based Semantic Fusion Model for Remote Sensing Data. *PLoS One*. 2013, 8(10):e77090.
- 20. GR Yan<sup>†</sup>, Z Tan<sup>†</sup>, Y Wang, ML Xu, **G Yu**, Y Li<sup>\*</sup>, QY He<sup>\*</sup>. Quantitative Proteomics Characterization on the Anti-tumor Effects of Isodexyelephantopin against Nasopharyngeal Carcinoma. *Proteomics*. 2013, 13(21):3222-3232.
- 21. J Li, X Lu, Q Wu, **G Yu**, Z Xu, L Qiu, Z Pei, Y Lin, J Pang\*. Design, SAR, angiogenic activities evaluation and pro-angiogenic mechanism of new marine cyclopeptide analogs. *Current Medicinal Chemistry*. 2013, 20(9):1183-1194.
- 22. Y Han, **G Yu**, H Sarioglu, A Caballero-Martinez, F Schlott, M Ueffing, H Haase, C Peschel, AM Krackhardt\*. Proteomic investigation of the interactome of FMNL1 in hematopoietic cells unveils a role in calcium-dependent membrane plasticity. *Journal of Proteomics*. 2013, 78:72-82.
- 23. Y Ma<sup>†</sup>, J Yang<sup>†</sup>, X Fan<sup>†</sup>, H Zhao, W Hu, Z Li, **G Yu**, X Ding, J Wang, X Bo, X Zheng, Z Zhou<sup>\*</sup>, S Wang<sup>\*</sup>. Cellular MicroRNA let-7c Inhibits M1 Protein Expression of the H1N1 Influenza A Virus in Infected Human Lung Epithelial Cells. *Journal of Cellular and Molecular Medicine*. 2012, 16(10):2539-2546.
- 24. GR Yan<sup>†</sup>, FY Zhou<sup>†</sup>, BL Dang, Y Zhang, **G Yu**, X Liu, QY He<sup>\*</sup>. Genistein-induced mitotic arrest of gastric cancer cells by downregulating KIF20A, a proteomics study. *Proteomics*. 2012, 12(14):2391-2399.
- 25. X Sun<sup>†</sup>, XY Yang<sup>†</sup>, XF Yin, **G Yu**, CL Xiao, X He, QY He<sup>\*</sup>. Proteomic Analysis of Membrane Proteins from *Streptococcus pneumoniae* with Multiple Separation Methods plus High Accuracy Mass Spectrometry. *OMICS: A Journal of Integrative Biology*. 2011, 15(10):683-694.

## **Books**

**G Yu**, "Bioinformatics II", in "Functional Protein Research", 385-425, Qing-Yu He (*Eds*), *Science Press*, 2012. (China's Twelfth Five-Year National Important Books Project, in Chinese)

## **CONFERENCE PROCEEDINGS**

#### Presentations

- 1. **ggtree for tree visualization & annotation** (invited), Phylogenetic tree visualization workshop/hackathon, The Field Museum of Natural History, Chicago, May. 2017
- 2. **Computational Methods in Ecology and Evolution**, The Second International Workshop on Environmental Microbiomes, Sun Yat-sen University, Guangzhou, April. 2017
- 3. **ggtree for visualization and annotation of phylogenetic trees** (invited), The 9<sup>th</sup> China-R Conference, Renmin University of China, Beijing, May. 2016

## Posters

- ggtree: a programming package for complex data integration and analysis in phylogeny to identify potential genetic markers of influenza a virus that determine interspecies transmission, Scientific Advisory Board (SAB) Meeting for the Theme-based Research Scheme on Viral, Host and Environmental Determinants of Influenza Virus Transmission and Pathogenesis, The University of Hong Kong, Hong Kong, Jun. 2017
- 2. Phylogeny-guided genome assembly method for short read nucleotide sequences from coinfecting influenza A viruses, Options IX for the control of influenza, International Society for Influenza and other Respiratory Virus Disease, Chicago, Aug. 2016
- 3. **ggtree:** an *R* package for visualization and annotation of phylogenetic tree with different types of meta-data, The 20<sup>th</sup> Research Postgraduate Symposium, The University of Hong Kong, Hong Kong, Dec. 2015

## **PUBLIC MEDIA**

"Plotting trees + data" lecture by Guangchuang Yu. https://youtu.be/tqspAXMoUQE

## PROFESSIONAL AFFILIATIONS

- Member, International Society for influenza and other Respiratory Virus Disease
- Steering Committee, International Network for Data Analysis, Institut Pasteur

Steeling Committee, International Network for Data Analysis, Institut I asteu

• Visiting student, Beijing Institute of Radiation Medicine

2015 2005-2009

2016

## PROFESSIONAL SERVICES

#### Associate Editor

• Journal of Integrated OMICS, 2011-present

#### Reviewer

- Bioinformatics
- BMC Bioinformatics
- Computational Biology and Chemistry
- Current Bioinformatics
- Gastroenterology Research and Practice
- Molecular BioSystems
- R Journal

## **SOFTWARE DEVELOPMENT**

R ranking: ranked 51/68825 worldwide by Git Awards

- badger: Badge for R Package
- dlstats: Download Stats of R Packages
- emojifont: Emoji and Font Awesome in Graphics
- ggimage: Use Image in 'ggplot2'
- meme: Create Meme
- rvcheck: R/Package Version Check
- scatterpie: Scatter Pie Plot
- shadowtext: Shadow Text Grob and Layer
- ChIPseeker: ChIPseeker for ChIP peak Annotation, Comparison, and Visualization
- clusterProfiler: statistical analysis and visualization of functional profiles for genes and gene clusters
- DOSE: Disease Ontology Semantic and Enrichment analysis
- ggtree: an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data
- GOSemSim: GO-terms Semantic Similarity Measures
- meshes: MeSH Enrichment and Semantic analyses
- ReactomePA: Reactome Pathway Analysis
- segcombo: Visualization Tool for Sequence Recombination and Reassortment
- tidytree: A Tidy Tool for Phylogenetic Tree Data Manipulation
- TIPars: Taxa Insertion by Parsimony
- treeio: Base Classes and Functions for Phylogenetic Tree Input and Output

# Contributions to open source libraries

- cowsay: Messages, Warnings, Strings with Ascii Animals
- fitting: Fit Different Regression Lines and Show Equation Parameters
- kableExtra: Construct Complex Table with 'kable' and Pipe Syntax
- MSnbase: Base Functions and Classes for Mass Spectrometry and Proteomics
- scholar: Analyse Citation Data from Google Scholar