

Guangchuang Yu

Professor

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🎓 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 2015

🏢 EMPLOYMENT

Institute of Bioinformatics, School of Basic Medical Sciences, Southern Medical University:

Professor 2018–

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

Post-doctoral Fellow 2017–2018

Key Laboratory of Functional Protein Research of Guangdong Higher Education Institutes, College of Life Science and Technology, Jinan University:

Bioinformatician 2009–2013

♥ SCHOLARSHIPS & AWARDS

- 南方医科大学高层次人才引进（第三层次） 2018
- Travel Grant for the 3rd South Lake Innovation Forum for International Young Talents, awarded by Huazhong Agricultural University 2018
- Travel Grant for Phylogenetic tree visualization workshop/hackathon, awarded by The Field Museum of Natural History, USA 2017
- Travel Grant for the 2nd International Workshop on Environmental Microbiomes, awarded by Sun Yat-sen University 2017
- Travel Grant for Options IX for the control of influenza, awarded by Areas of Excellence Scheme (AoE) and Theme-based Research Scheme (TRS), Hong Kong 2016
- Travel Grant for the 9th China-R conference, awarded by Capital of Statistics 2016
- Postgraduate Studentships, awarded by The University of Hong Kong 2013–2017
- Best paper of the year 2010, awarded by Journal of Integrated OMICS 2012

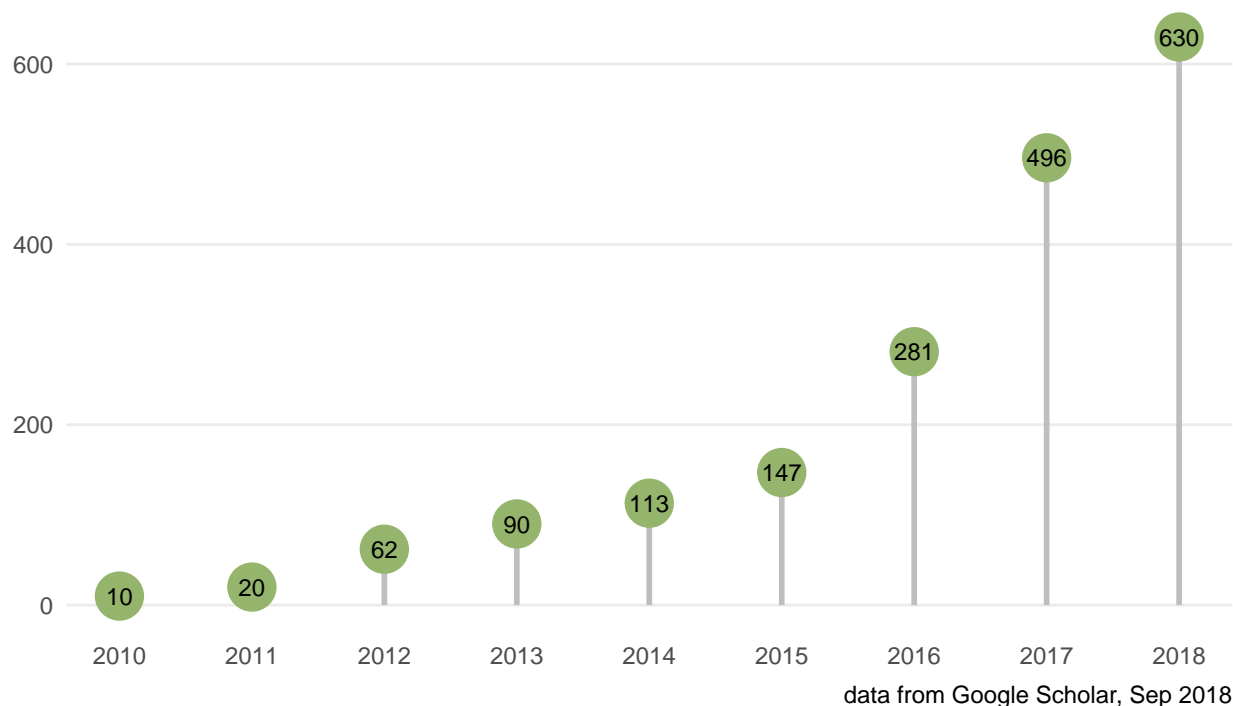
GRANTS

- (在研) **PI**, 南方医科大学第三层次人才引进科研项目, 南方医科大学 (c1051022), CNY ¥1,500,000 2018–2019
- (完成) **PI**, *hnRNPK* 蛋白在调控人肺癌细胞周期胞质分裂中的作用研究, 中央高校基本科研业务费专项资金 (21613414), CNY ¥100,000 2013
- (完成) **PI**, *Hela* 细胞周期动态蛋白质组学分析, 中央高校基本科研业务费专项资金 (21611303), CNY ¥20,000 2011

PUBLICATIONS

Journal Articles

Citation = 1880, H-index = 14, I10-index = 19



🔥 ESI Hot Paper (X1)

🏆 ESI Highly Cited Paper (X4)

indicates equal contribution, * indicates corresponding

1. **G Yu**. clusterProfiler: universal enrichment tool for functional and comparative study. *bioRxiv*. 2018, <https://doi.org/10.1101/256784>
2. **G Yu**. Using meshes for MeSH term enrichment and semantic analyses. *Bioinformatics*. accepted. Impact Factor: 5.481
3. **G Yu**, DK Smith, H Zhu, Y Guan, TTY Lam*. ggtree: an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data. *Methods in Ecology and Evolution*. 2017, 8(1):28-36. 🔥 🏆 Citation: 156, Impact Factor: 6.363
4. **G Yu**, QY He*. ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization. *Molecular BioSystems*. 2016, 12(2):477-479. 🏆 Citation: 98, Impact Factor: 2.759
5. **G Yu***, LG Wang, QY He*. ChIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization. *Bioinformatics*. 2015, 31(14):2382-2383. 🏆 Citation: 148, Impact Factor: 5.481

6. 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. Citation: 90, Impact Factor: 5.481
7. X Sun[#], G Yu[#], Q Xu, N Li, C Xiao, X Yin, K Cao, J Han, QY He^{*}. Putative cobalt- and nickel-binding proteins and motifs in *Streptococcus pneumonia*. *Metallomics*. 2013, 5(7):928-935. Citation: 19, Impact Factor: 4.069
8. YY Zhu[#], G Yu[#], Y Zhang, Z Xu, YQ Huang, GR Yan^{*}, QY He^{*}. A novel andrographolide derivative AL-1 exerts its cytotoxicity on K562 cells through a ROS-dependent mechanism. *Proteomics*, 2013, 13(1):169-178. Citation: 23, Impact Factor: 3.532
9. G Yu[#], LG Wang[#], XH Meng, QY He^{*}. LXtoo: an integrated live Linux distribution for the bioinformatics community. *BMC Research Notes*. 2012, 5(1):360. Citation: 6
10. 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. 🏆
Citation: 656, Impact Factor: 2.370
11. G Yu, QY He^{*}. Functional similarity analysis of human virus-encoded miRNAs. *Journal of Clinical Bioinformatics*. 2011, 1(1):15. Citation: 14
12. G Yu[#], CL Xiao[#], X Bo, CH Lu, Y Qin, S Zhan, QY He^{*}. A new method for measuring functional similarity of microRNAs. *Journal of Integrated OMICS*. 2011, 1(1):49-54. Citation: 20
13. G Yu[#], CL Xiao[#], CH Lu[#], HT Jia, F Ge, W Wang, XF Yin, HL Jia, JX He^{*}, QY He^{*}. Phospho-proteome profile of human lung cancer cell line A549. *Molecular BioSystems*. 2011, 7(2):472-479. Citation: 14, Impact Factor: 2.759
14. G Yu[#], F Li[#], Y Qin, X Bo^{*}, Y Wu, S Wang^{*}. GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. *Bioinformatics*. 2010, 26(7):976-978. Citation: 378, Impact Factor: 5.481
15. 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. Citation: 12, Impact Factor: 4.019
16. PY Huang, CCD Lee, CH Yip, CL Cheung, G Yu, TTY Lam, DK Smith, H Zhu^{*}, Y Guan^{*}. Genetic characterization of highly pathogenic H5 influenza viruses from poultry in Taiwan, 2015. *Infection, Genetics and Evolution*. 2016, 38:96-100. Citation: 7, Impact Factor: 2.545
17. 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-POU2F1-ECD Signaling. *Journal of Pathology*. 2015, 236(2):175-185. Citation: 28, Impact Factor: 6.253
18. 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. Citation: 11, Impact Factor: 4.069
19. 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 *Streptococcus pneumonia*. *Journal of Proteomics*. 2015, 115:107-116. Citation: 9, Impact Factor: 3.722
20. N Wang[#], J Zhang[#], L Zhang, XY Yang, N Li, G Yu, J Han, K Cao, Z Guo, X Sun^{*}, QY He^{*}. Proteomic analysis of putative heme-binding proteins in *Streptococcus pyogenes*. *Metallomics*. 2014, 6(8):1451-1459. Citation: 0, Impact Factor: 4.069
21. H Sun^{*}, J Weng, G Yu, RH Massawe. A DNA-Based Semantic Fusion Model for Remote Sensing Data. *PLoS One*. 2013, 8(10):e77090. Citation: 6, Impact Factor: 2.766
22. GR Yan[#], Z Tan[#], Y Wang, ML Xu, G Yu, Y Li^{*}, QY He^{*}. Quantitative Proteomics Characterization on the Anti-tumor Effects of Isodexyephantopin against Nasopharyngeal Carcinoma. *Proteomics*. 2013, 13(21):3222-3232. Citation: 14, Impact Factor: 3.532
23. 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. Citation: 1, Impact Factor: 3.469
24. 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. Citation: 7, Impact Factor: 3.722

25. Y Ma[#], J Yang[#], X Fan[#], H Zhao, W Hu, Z Li, **G Yu**, X Ding, J Wang, X Bo, X Zheng, Z Zhou^{*}, S Wang^{*}. [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. Citation: 55, Impact Factor: 4.302
26. GR Yan[#], FY Zhou[#], BL Dang, Y Zhang, **G Yu**, X Liu, QY He^{*}. [Genistein-induced mitotic arrest of gastric cancer cells by downregulating KIF20A, a proteomics study](#). *Proteomics*. 2012, 12(14):2391-2399. Citation: 48, Impact Factor: 3.532
27. X Sun[#], XY Yang[#], XF Yin, **G Yu**, CL Xiao, X He, QY He^{*}. [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. Citation: 15, Impact Factor: 2.370

E-Letters

1. Y Wan[#], **G Yu**[#], J Zou[#], W Liu[#], Q Liu^{*}, Why animals have escaped the Indian Ocean tsunami? *Science*. 2017, <http://science.sciencemag.org/content/356/6340/841/tab-e-letters>
2. M Tang, S Weng, **G Yu**, K Yang, M Pan, S He, Q Liu^{*}, RE: Sequence features of the virulence protein VP24 of Ebola virus. *Science*. 2017, <http://science.sciencemag.org/content/351/6279/1339/tab-e-letters>

Books

- 余光创, “生物信息学 II”, 《功能蛋白质研究》, 385-425, 何庆瑜 (主编), 科学出版社, 2012. (“十二五”国家重点图书出版规划项目)

⚙️ SOFTWARE DEVELOPMENT

R ranking: ranked 49/72258 worldwide by [Git Awards](#)

- [badger](#): Badge for R Package
- [dlstats](#): Download Stats of R Packages
- [emojifont](#): Emoji and Font Awesome in Graphics
- [ggplotify](#): Convert Plot to ‘grob’ or ‘ggplot’ Object
- [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
- [seqcombo](#): Visualization Tool for Sequence Recombination and Reassortment
- [tidytrees](#): 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

- [basicTrendline](#): Add Trendline and Confidence Interval of Basic Regression Models to Plot
- [cowsay](#): Messages, Warnings, Strings with Ascii Animals
- [kableExtra](#): Construct Complex Table with 'kable' and Pipe Syntax
- [microbiomeViz](#): Visualizing Microbiome Data
- [MSnbase](#): Base Functions and Classes for Mass Spectrometry and Proteomics
- [pheatmap](#): Pretty Heatmaps
- [scholar](#): Analyse Citation Data from Google Scholar

PROFESSIONAL AFFILIATIONS

- Member, International Society for Influenza and other Respiratory Virus Disease 2016
- Steering Committee, International Network for Data Analysis, Institut Pasteur 2015
- Visiting student, Beijing Institute of Radiation Medicine 2005-2009

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, Nucleic Acids Research, R Journal

PUBLIC MEDIA

- “Plotting trees + data” lecture by Guangchuang Yu. <https://youtu.be/tqspAXM0UQE>

CONFERENCE PROCEEDINGS

Presentations

1. *Data integration and visualization of phylogenetic trees*, The 3rd South Lake Innovation Forum for International Young Talents, Huazhong Agricultural University, Wuhan, May, 2018
2. *ggtree for tree visualization & annotation* (invited), Phylogenetic tree visualization workshop/hackathon, The Field Museum of Natural History, Chicago, May. 2017
3. *Computational Methods in Ecology and Evolution*, The Second International Workshop on Environmental Microbiomes, Sun Yat-sen University, Guangzhou, April. 2017
4. *ggtree for visualization and annotation of phylogenetic trees* (invited), The 9th China-R Conference, Renmin University of China, Beijing, May. 2016

Posters

1. *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 co-infecting 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 20th Research Postgraduate Symposium, The University of Hong Kong, Hong Kong, Dec. 2015

TEACHING

The University of Hong Kong

Student Helper, Presentation Skills and Research Seminars in Biological Sciences 2013–2014

Jinan University

Lecturer, Functional Proteomics 2011–2012