

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
延安干部培训学院	南方医科大学高层次人才“不忘初心 牢记使命”学习教育	2018
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
- Postgraduate Studentships, awarded by The University of Hong Kong 2013–2017
- 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
- 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

TEACHING

Southern Medical University

基因组学 2019

基础医学新进展讲座 2019

University of Southern Denmark

BMB209: Workshops in Applied Bioinformatics 2019

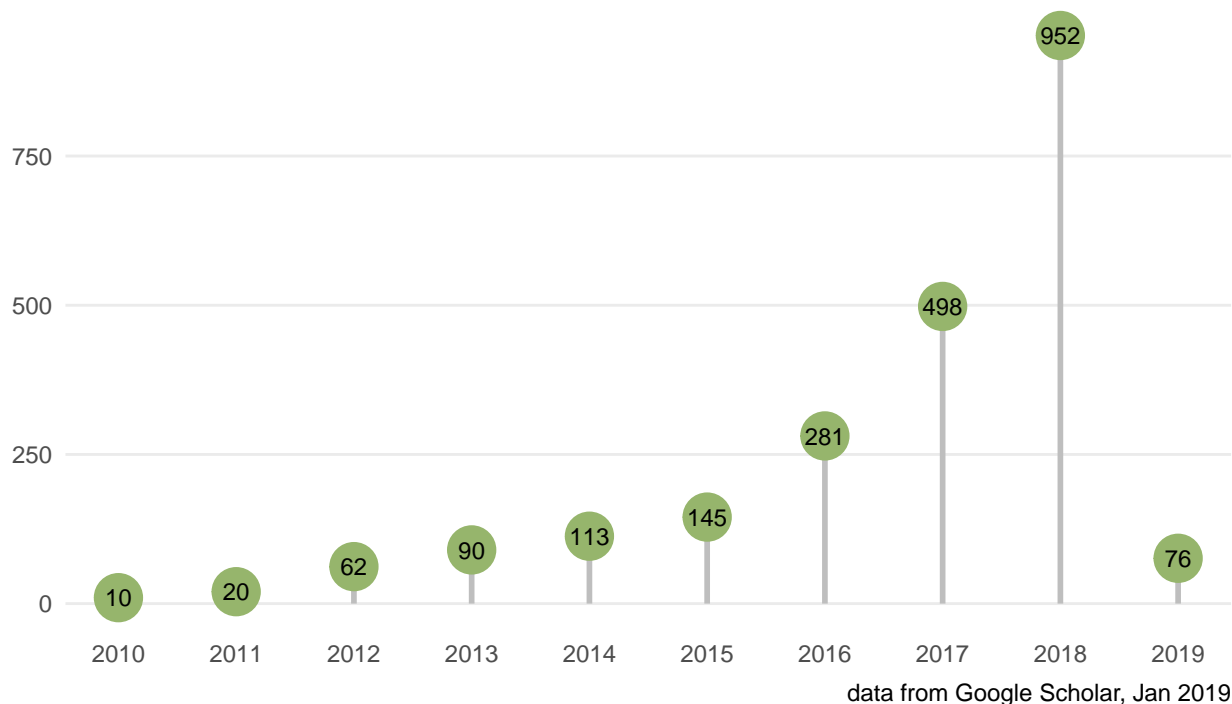
Jinan University

功能蛋白质研究 2011–2012

PUBLICATIONS

Journal Articles

Citation = 2280, H-index = 15, I10-index = 20



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***, TTY Lam, H Zhu, Y Guan*. Two methods for mapping and visualizing associated data on phylogeny using ggtree. *Molecular Biology and Evolution*. 2018, 35(12):3041-3043. Impact Factor: 10.217
3. **G Yu**. Using meshes for MeSH term enrichment and semantic analyses. *Bioinformatics*. 2018, 34(21):3766-3767. Impact Factor: 5.481
4. **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. ESI Hot Paper (X1) ESI Highly Cited Paper (X4) Citation: 213, Impact Factor: 6.363

5. G Yu, QY He*. ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization. *Molecular BioSystems*. 2016, 12(2):477-479. 🏆 Citation: 124, Impact Factor: 2.759
6. 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: 190, Impact Factor: 5.481
7. 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: 105, Impact Factor: 5.481
8. 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
9. 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
10. 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
11. 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: 862, Impact Factor: 2.370
12. G Yu, QY He*. Functional similarity analysis of human virus-encoded miRNAs. *Journal of Clinical Bioinformatics*. 2011, 1(1):15. Citation: 16
13. 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
14. 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
15. 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: 411, Impact Factor: 5.481
16. 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: 14, Impact Factor: 4.019
17. 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
18. 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
19. 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
20. 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: 10, Impact Factor: 3.722
21. 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
22. 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
23. 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
24. 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: 2, Impact Factor: 3.469
25. 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: 8, Impact Factor: 3.722
 26. 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: 61, Impact Factor: 4.302
 27. 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: 52, Impact Factor: 3.532
 28. 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: 16, Impact Factor: 2.370
 29. 余光创, 王超, 许尹, 伯晓晨, 王升启*, 秦宜德*. 结合基因组分析预测炎症相关 miRNA 及其靶标. *军事医学科学院院刊*. 2009, 33(3):245-247.
 30. 余光创, 秦宜德, 伯晓晨, 王升启*. 依赖于 5' 端非编码区高级结构的真核生物 mRNA 翻译调控. *中国生物化学与分子生物学报*. 2007, 23(11):881-887.

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 30/72299 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
- [enrichplot](#): Visualization of Functional Enrichment Result
- [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
- [RIdeogram](#): Visualize and Map Genome Wide Data in Ideograms
- [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. *Two methods for mapping and visualizing associated data on phylogeny using ggtree*, 第一届南方医科大学基础医学学术年会, 南方医科大学, 广州, 2019 年 1 月
2. *Data integration and visualization of phylogenetic trees*, The 3rd South Lake Innovation Forum for International Young Talents, Huazhong Agricultural University, Wuhan, May, 2018
3. *ggtree for tree visualization & annotation* (invited), Phylogenetic tree visualization workshop/hackathon, The Field Museum of Natural History, Chicago, May. 2017
4. *Computational Methods in Ecology and Evolution*, The Second International Workshop on Environmental Microbiomes, Sun Yat-sen University, Guangzhou, April. 2017
5. *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