

Guangchuang Yu

Post-doctoral Fellow

L514, Laboratory Block, Faculty of Medicine Building, 22 Sassoon Road, Pokfulam, Hong Kong

✉ guangchuangyu@gmail.com ☎ +852 6226 9693 🌐 [GuangchuangYu](https://GuangchuangYu.github.io) 📄 guangchuangyu.github.io

🎓 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

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

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 (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

2011 (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

🏠 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

⚙️ SOFTWARE DEVELOPMENT

R ranking: ranked 49/72213 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

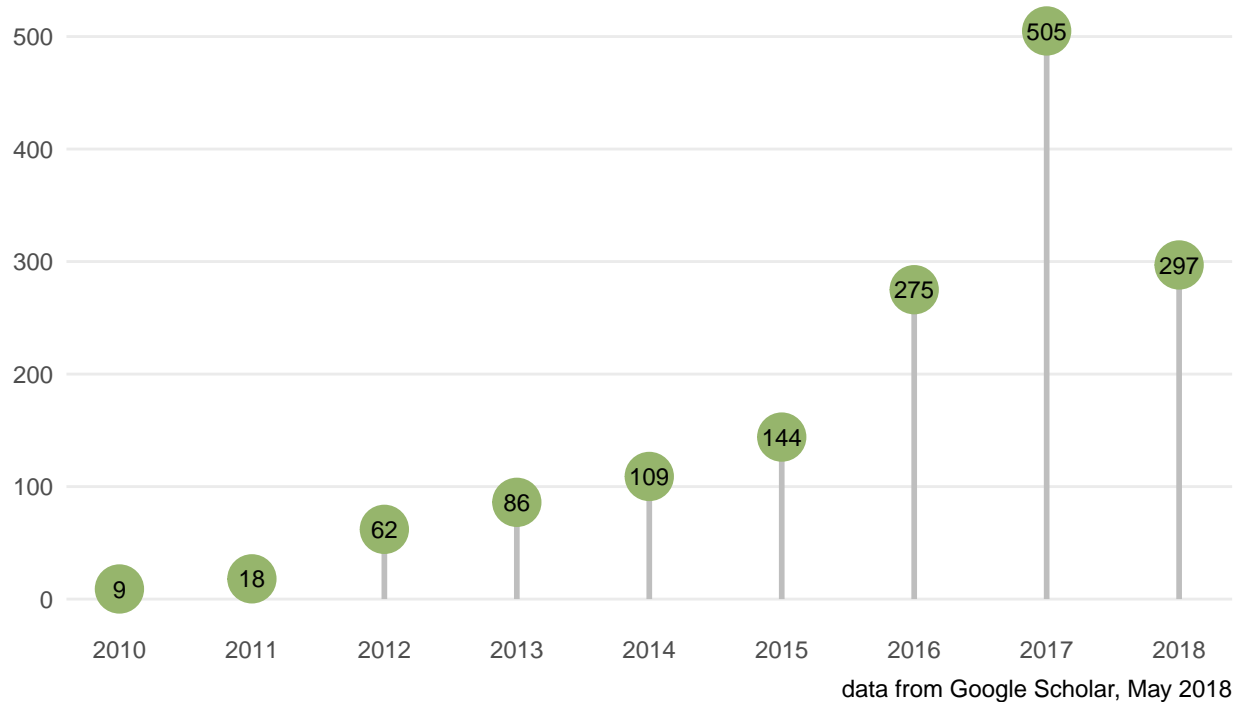
Contributions to open source libraries

- [basicTrendline](#): Add Trendline 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

📄 PUBLICATIONS

Journal Articles

Citation = 1537, H-index = 14, I10-index = 18



🔥 ESI Hot Paper (X1)

🏆 ESI Highly Cited Paper (X4)

第一作者/通讯作者 SCI 文章 9 篇: 1 区 (X4), 2 区 (X1)

期刊排名与分位数来源: InCites Journal Citation Reports

分区来源: 中国科学院文献情报中心 JCR 期刊分区表中小类分区

† 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: 7.307, JCR Mathematical & Computational Biology 2/57 (Q1, 1 区)
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: 107, Impact Factor: 5.708, JCR Ecology 13/153 (Q1, 1 区)
4. **G Yu**, QY He*. ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization. *Molecular BioSystems*. 2016, 12(2):477-479. 🏆 Citation: 70, Impact Factor: 2.781, JCR Biochemistry & Molecular Biology 145/290 (Q2, 3 区)
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: 125, Impact Factor: 7.307, JCR Mathematical & Computational Biology 2/57 (Q1, 1 区)
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: 75, Impact Factor: 7.307, JCR Mathematical & Computational Biology 2/57 (Q1, 1 区)

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 pneumoniae*. *Metallomics*. 2013, 5(7):928-935. Citation: 18, Impact Factor: 3.975, JCR Biochemistry & Molecular Biology 80/290 (Q2, 3 )
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: 22, Impact Factor: 4.041, JCR Biochemistry & Research Methods 15/78 (Q1, 2 )
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: 496, Impact Factor: 2.723, JCR Biotechnology & Applied Microbiology 29/160 (Q2, 3 )
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^{*}. Phosphoproteome profile of human lung cancer cell line A549. *Molecular BioSystems*. 2011, 7(2):472-479. Citation: 12, Impact Factor: 2.781, JCR Biochemistry & Molecular Biology 145/290 (Q2, 3 )
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: 336, Impact Factor: 7.307, JCR Mathematical & Computational Biology 2/57 (Q1, 1 )
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: 8, Impact Factor: 4.076, JCR Microbiology 26/125 (Q1, 2 )
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: 2.885, JCR Infectious Diseases 36/84 (Q2, 3 )
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. *The Journal of Pathology*. 2015, 236(2):175-185. Citation: 24, Impact Factor: 6.894, JCR Pathology 3/79 (Q1, 1 )
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 pneumoniae*. *Metallomics*. 2015, 7(3):448-454. Citation: 10, Impact Factor: 3.975, JCR Biochemistry & Molecular Biology 80/290 (Q2, 3 )
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 pneumoniae*. *Journal of Proteomics*. 2015, 115:107-116. Citation: 7, Impact Factor: 3.914, JCR Biochemistry & Research Methods 17/78 (Q1, 2 )
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: 3.975, JCR Biochemistry & Molecular Biology 80/290 (Q2, 3 )
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: 2.806, JCR Multidisciplinary Sciences 15/64 (Q1, 3 )
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: 4.041, JCR Biochemistry & Research Methods 15/78 (Q1, 2 )
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 Medici-*

- nal Chemistry*. 2013, 20(9):1183-1194. Citation: 1, Impact Factor: 3.249, JCR Pharmacology & Pharmacy 71/257 (Q2, 2 ☒)
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: 3.914, JCR Biochemistry & Research Methods 17/78 (Q1, 2 ☒)
 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: 49, Impact Factor: 4.499, JCR Medicine, Research & Experimental 20/128 (Q1, 2 ☒)
 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: 43, Impact Factor: 4.041, JCR Biochemistry & Research Methods 15/78 (Q1, 2 ☒)
 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: 14, Impact Factor: 2.723, JCR Biotechnology & Applied Microbiology 29/160 (Q2, 3 ☒)

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)

🌿 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

■ PUBLIC MEDIA

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