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Education

2013.10-2017.09 **PhD**; The University of Hong Kong; *Evolution Study of Influenza A Virus*

2006.09-2009.07 **MSc**; Anhui Medical University; *Biochemistry and Molecular Biology*

2001.09-2005.07 **BSc**; South China Agricultural University; *Biotechnology*

2015.10 Institut Pasteur, Paris; *Train the Trainers 2015*

Professional Experience

2017.09-2017.10 **Research Assistant I**; State Key Laboratory of Emerging Infectious Diseases, The University of Hong Kong

2016.01-2016.12 **Member**; International Society for Influenza and other Respiratory Virus Diseases

2015.10 **INDA Steering Committee**; International Network for Data Analysis, Institut Pasteur

2009.12-2013.09 **Bioinformatician**; College of Life Science and Technology, Jinan University

2007.03-2009.05 **Visiting Student**; Beijing Institute of Radiation Medicine

Teaching Experience

2013.10-2014.03 **Student Helper**; BIOL6001 Presentation Skills and Research Seminars in Biological Sciences (postgraduate course), The University of Hong Kong

2011.09-2012.07 **Lecturer**; Functional Proteomics (postgraduate course), Jinan University

Awards

2013.10-2017.09 Postgraduate Studentships (for PhD students at The University of Hong Kong)

2012.09 Best paper of the year 2010, Journal of Integrated OMICS.

Grants

- 2013.01-2013.12** (completed) PI, Investigate functions of hnRNPK in regulating cytokinesis of human lung cancer cell, Fundamental Research Funds for the Central Universities (21613414), 100,000
- 2011.01-2011.12** (completed) PI, Dynamic proteomic analysis of HeLa cell cycle, Fundamental Research Funds for the Central Universities (21611303), 20,000

Professional Services

Associate Editor	Journal of Integrated OMICS, 2011-
Reviewer	Bioinformatics
	BMC Bioinformatics
	Computational Biology and Chemistry
	Current Bioinformatics
	Gastroenterology Research and Practice
	Molecular BioSystems
	R Journal

Languages

Teochew	Native language
Chinese Mandarin	Very fluent
Cantonese	Very fluent
English	fluent

Programming Skills

R

- More than 8 years of experience
- Developed 14 packages (6 on CRAN and 8 on Bioconductor)
- Ranked 58/66119 worldwide by **Git Awards**

Unix

- More than 14 years of experience (Linux & BSD)
- Experience of server setup, management and application deployment

Other

- Good knowledge of Git, $\text{L}^{\text{A}}\text{T}_{\text{E}}\text{X}$ Bash, C/C++ and Java
- Basic knowledge of Perl, Python and Matlab

Software Development

R

badger	Badge for R Package
dlstats	Download Stats of R Packages
emojifont	Emoji and Font Awesome in Graphics
ggimage	Use Image in 'ggplot2'
rvcheck	R/Package Version Check
scatterpie	<code>r packageTitle('scatterpie', 'CRAN')</code>

Bioconductor

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
treeio	Base Classes and Functions for Phylogenetic Tree Input and Output

Java

TIPars	Taxa Insertion by Parsimony
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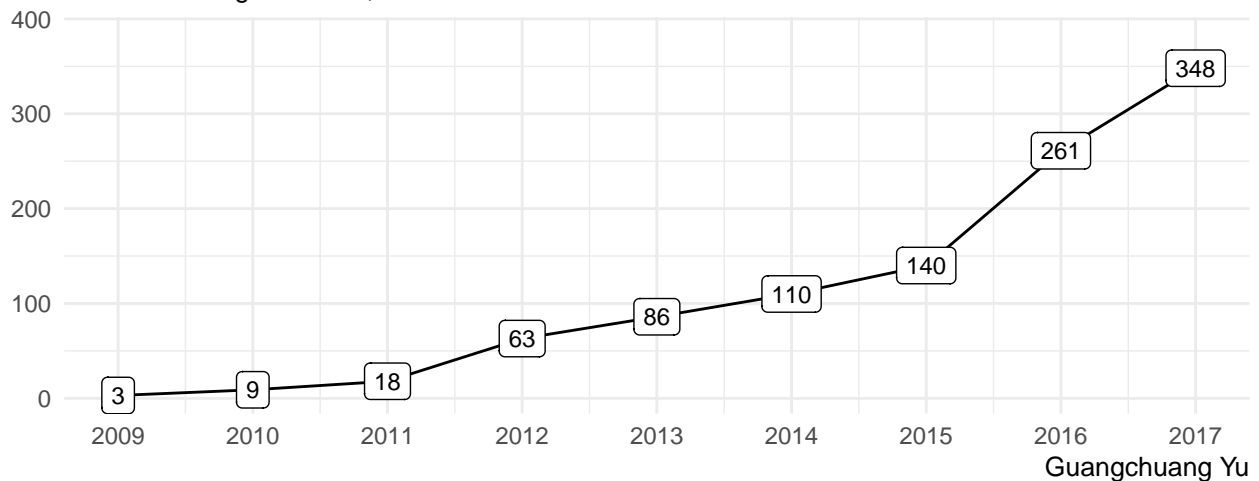
Contributions to open source libraries

cowsay	Messages, Warnings, Strings with Ascii Animals
MSnbase	Base Functions and Classes for Mass Spectrometry and Proteomics

Research Highlights

Citation = 1063, H-index = 14, I10-index = 17

data from Google Scholar, Oct 2017



- 25 peer-reviewed publications
 - *Methods in Ecology of Evolution* (X1, rank 11 in *Environment Ecology*, IF = 5.708)
 - *Bioinformatics* (X3, rank 4 in *Computer Science*, IF = 7.307)
 - *Frontiers in Microbiology* (X1, rank 21 in *Microbiology*, IF = 4.076)
 - *Proteomics* (X3)
 - *Journal of Proteomics* (X2)
 - *Metallomics* (X3)
 - *Molecular BioSystems* (X2)
- 12 peer-reviewed publications of first author
- 3 papers of first author with IF ≥ 5
- 2 papers of first author with citations ≥ 200
- view my publication impact on [Impactstory](#)

Ontology Semantic Similarity Analysis

- developed 3 packages: *GOSemSim*, *DOSE* and *meshes*
- propose a method for measuring functional similarity of microRNAs and applied it to analyze human virus-encoded miRNAs
- published 4 papers, including 2 in *Bioinformatics*

Pathway Analysis

- developed 2 packages: *clusterProfiler* and *ReactomePA*
- published 2 papers in *OMICS: A Journal of Integrative Biology* and *Molecular BioSystems*

Genomic Analysis

- developed *ChIPseeker* for ChIP-seq data annotation, visualization and data mining (by integrated GEO database)
- published 1 paper in *Bioinformatics*

Proteomic Analysis

- contributed to open source library, *MSnbase*, developed by Laurent Gatto (University of Cambridge)

- published 9 papers in *Molecular BioSystems*, *Metallomics*, *Proteomics* and *Journal of Proteomics*

Evolutionary Analysis

- developed *treeio* for parsing tree files
- developed *ggtree* for supporting tree visualization and annotation by grammar of graphics
- developing phylogeny-guided genome assembly method for short read nucleotide sequences from co-infecting influenza viruses
- published 1 paper in *Methods in Ecology and Evolution*

Publications

1. **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.
2. **G Yu**, QY He^{*}. **ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization.** *Molecular BioSystems*. 2016, 12(2):477-479.
3. **G Yu^{*}**, LG Wang, QY He^{*}. **ChIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization.** *Bioinformatics*. 2015, 31(14):2382-2383.
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.
5. **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.
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.
7. **G Yu**, QY He^{*}. **Functional similarity analysis of human virus-encoded miRNAs.** *Journal of Clinical Bioinformatics*. 2011, 1(1):15.
8. **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.
9. **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.
10. **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.
11. 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.
12. 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.
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 H5 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-POU2F1-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***. *Metalomics*. 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 *Streptococcus pneumonia***. *Journal of Proteomics*. 2015, 115:107-116.
18. 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***. *Metalomics*. 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[†], 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.
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[†], 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.
24. 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.
25. 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.

Book Chapters

1. **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 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 9th China-R Conference, Renmin University of China, Beijing, May. 2016

Conference 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