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Education

- 2013-2017** **PhD**; The University of Hong Kong; *Evolution Study of Influenza A Virus*
- 2006-2009** **MSc**; Anhui Medical University; *Biochemistry and Molecular Biology*
- 2001-2005** **BSc**; South China Agricultural University; *Biotechnology*
- 2015** Institut Pasteur, Paris; *Train the Trainers 2015*

Professional Experience

- 2016** **Member**; International Society for Influenza and other Respiratory Virus Diseases
- 2015** **INDA Steering Committee**; International Network for Data Analysis, Institut Pasteur
- 2009-2013** **Bioinformatician**; College of Life Science and Technology, Jinan University
- 2007-2009** **Visiting Student**; Beijing Institute of Radiation Medicine

Teaching Experience

- 2013-2014** **Student Helper**; BIOL6001 Presentation Skills and Research Seminars in Biological Sciences (postgraduate course), The University of Hong Kong
- 2011-2012** **Lecturer**; Functional Proteomics (postgraduate course), Jinan University

Awards

- 2013-2017** Postgraduate Studentships (for PhD students at 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), 100,000

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

Professional Services

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

Languages

Teochew Native language
Chinese Mandarin Very fluent, complete professional competence
Cantonese Very fluent
English fluent

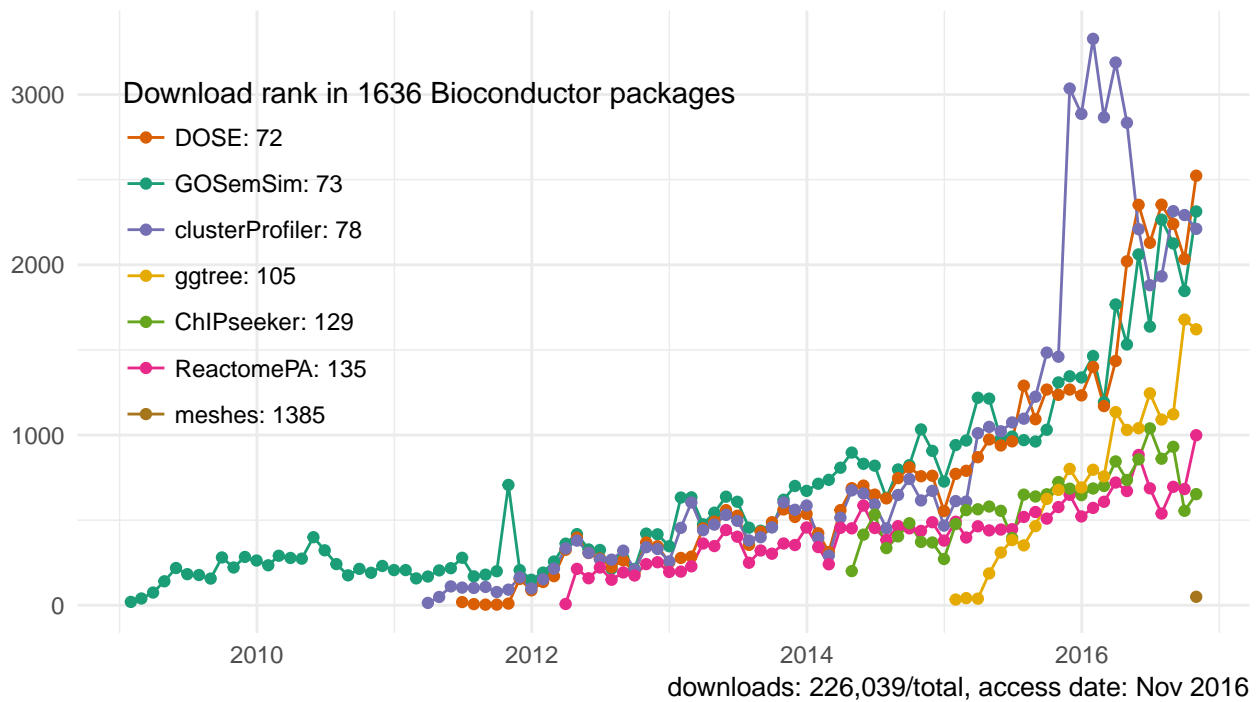
Programming Skills

R More than 8 years of experience. Developed 10 packages (3 in CRAN and 7 in Bioconductor)
Unix More than 14 years of experience (Linux & BSD). Experience of server setup, management and application deployment.
Other Good knowledge of Git, $L^A T^E X$ Bash, C/C++ and Java. Basic knowledge of Perl, Python and Matlab.

Software Development

ChIPseeker 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
emojifont Using emoji font in both 'base' and 'ggplot2' graphics
ggtree Visualization and annotation of phylogenetic trees with associated data
GOSemSim GO and gene semantic similarity measurement
meshes MeSH enrichment and semantic analyses
ReactomePA Reactome pathway analysis

Monthly download stats



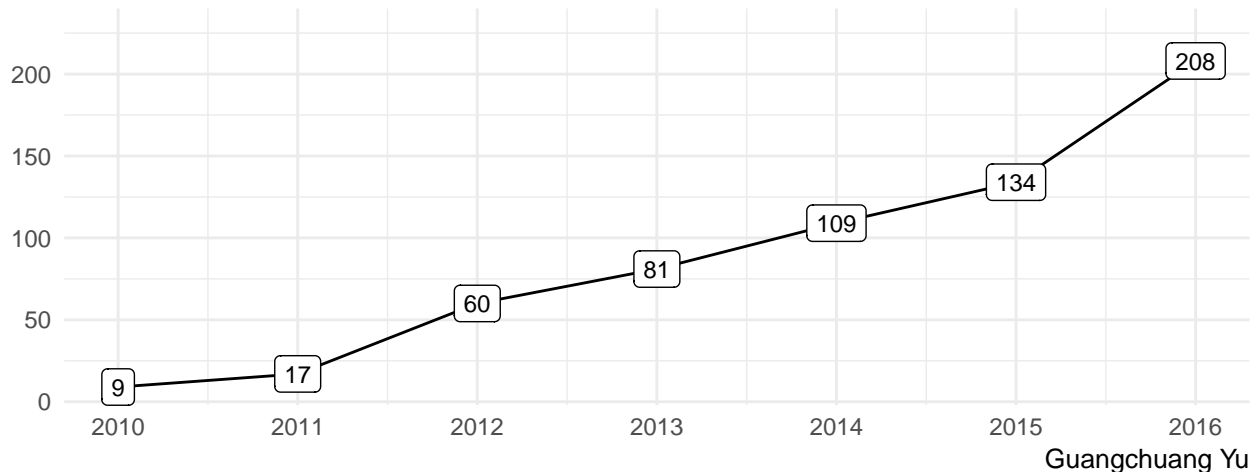
Contributions to open source libraries

MSnbase

Base Functions and Classes for MS-based Proteomics

Research Highlights

Citation = 645, H-index = 12, I10-index = 14
data from Google Scholar, Nov 2016



25 peer-reviewed publications, including *Methods in Ecology of Evolution* (X1, rank 11 in *Environment Ecology*, 5 year IF = 8.121), *Bioinformatics* (X3, rank 4 in *Computer Science*, 5 year IF = 7.685), *Proteomics* (X3), *Metallomics* (X3), *Molecular BioSystems* (X2). 4 papers of first authors with IF \geq 5.

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 3 papers in *Molecular BioSystems*, *Metallomics* and *Proteomics*

Evolutionary Analysis

- developed *ggtree* for parsing tree files and 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*. Accepted
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 pneumonia*.** *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 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*.** *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 *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*.** *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[†], 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

- 2016 **ggtree for visualization and annotation of phylogenetic trees** (invited), The 9th China-R Conference, Renmin University of China, Beijing, May. 2016

Conference Posters

- 2016 **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
- 2015 **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