

# Guangchuang Yu

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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** 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 58/64317 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,  $L^A T^E X$  Bash, C/C++ and Java
- Basic knowledge of Perl, Python and Matlab

## Software Development

### R

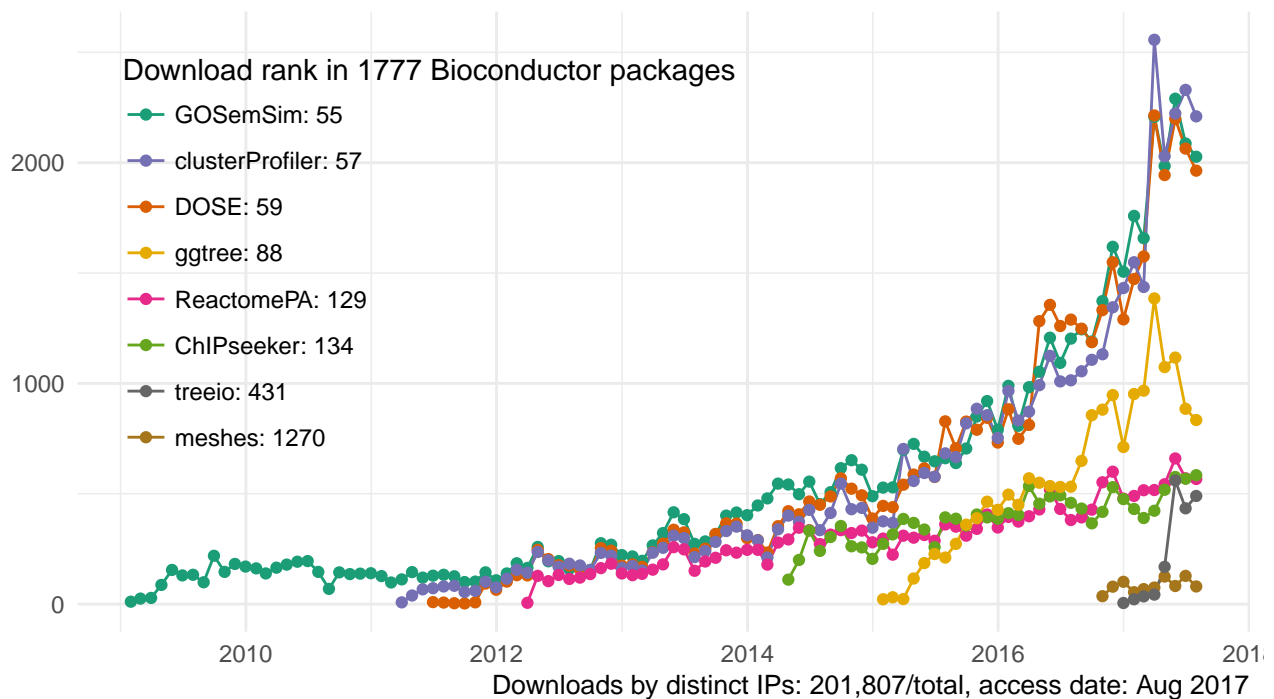
**badger** Badge for R Package

<b>dlstats</b>	Monthly download stats of 'CRAN' and 'Bioconductor' packages
<b>emojifont</b>	Using emoji font in both 'base' and 'ggplot2' graphics
<b>ggimage</b>	Use images in 'ggplot2' graphic system
<b>rvcheck</b>	Check latest release version of R and R package
<b>scatterpie</b>	Creates scatterpie plots, especially useful for plotting pies on a map

## Bioconductor

<b>ChIPseeker</b>	ChIP peak Annotation, Comparison and Visualization
<b>clusterProfiler</b>	Statistical analysis and visualization of functional profiles for genes and gene clusters
<b>DOSE</b>	Disease Ontology Semantic and Enrichment analysis
<b>ggtree</b>	Visualization and annotation of phylogenetic trees with associated data
<b>GOSemSim</b>	GO and gene semantic similarity measurement
<b>meshes</b>	MeSH enrichment and semantic analyses
<b>ReactomePA</b>	Reactome pathway analysis
<b>treeio</b>	Base Classes and Functions for Phylogenetic Tree Input and Output

## Monthly download stats



## Java

<b>TIPars</b>	Taxa Insertion by Parsimony
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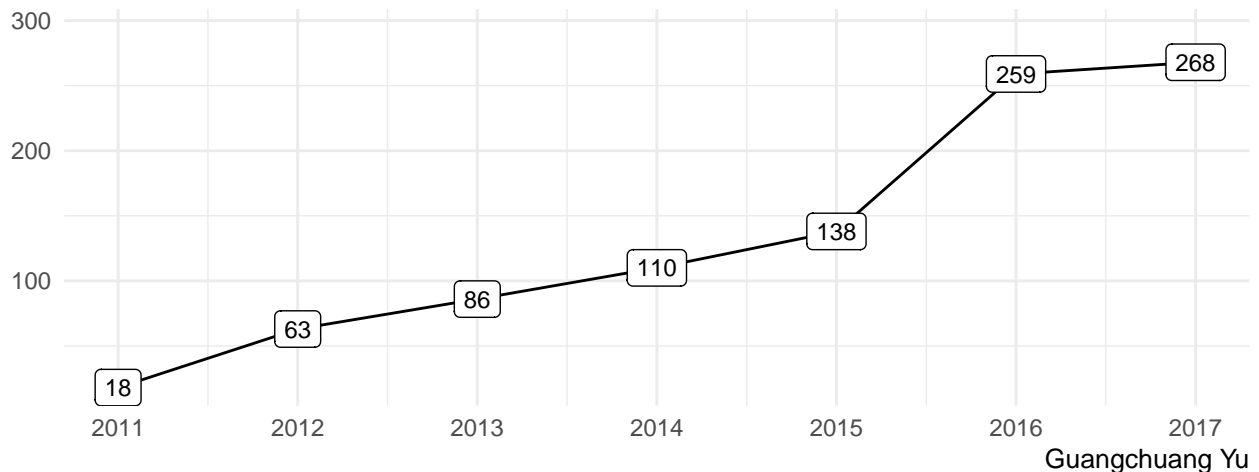
## Contributions to open source libraries

**cowsay** Messages, Warnings, Strings with Ascii Animals

**MSnbase** Base Functions and Classes for MS-based Proteomics

## Research Highlights

Citation = 979, H-index = 13, I10-index = 16  
data from Google Scholar, Aug 2017



- 25 peer-reviewed publications (IF5 = 5-year Impact Factor)
  - *Methods in Ecology of Evolution* (X1, rank 11 in *Environment Ecology*, IF5 = 8.121)
  - *Bioinformatics* (X3, rank 4 in *Computer Science*, IF5 = 7.685)
  - *Frontiers in Microbiology* (X1, rank 21 in *Microbiology*, IF5 = 4.36)
  - *Proteomics* (X3)
  - *Journal of Proteomics* (X2)
  - *Metallomics* (X3)
  - *Molecular BioSystems* (X2)
- 12 peer-reviewed publications of first author
- 4 papers of first author with IF5  $\geq 5$
- 2 papers of first author with citations  $\geq 200$
- 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<sup>\*</sup>. **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<sup>\*</sup>. **ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization.** *Molecular BioSystems*. 2016, 12(2):477-479.
3. **G Yu<sup>\*</sup>**, LG Wang, QY He<sup>\*</sup>. **ChIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization.** *Bioinformatics*. 2015, 31(14):2382-2383.
4. **G Yu<sup>\*</sup>**, LG Wang, GR Yan, QY He<sup>\*</sup>. **DOSE: an R/Bioconductor package for Disease Ontology Semantic and Enrichment analysis.** *Bioinformatics*. 2015, 31(4):608-609.
5. **G Yu<sup>†</sup>**, LG Wang<sup>†</sup>, XH Meng, QY He<sup>\*</sup>. **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<sup>\*</sup>. **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<sup>\*</sup>. **Functional similarity analysis of human virus-encoded miRNAs.** *Journal of Clinical Bioinformatics*. 2011, 1(1):15.
8. **G Yu<sup>†</sup>**, CL Xiao<sup>†</sup>, X Bo, CH Lu, Y Qin, S Zhan, QY He<sup>\*</sup>. **A new method for measuring functional similarity of microRNAs.** *Journal of Integrated OMICS*. 2011, 1(1):49-54.
9. **G Yu<sup>†</sup>**, CL Xiao<sup>†</sup>, CH Lu<sup>†</sup>, HT Jia, F Ge, W Wang, XF Yin, HL Jia, JX He<sup>\*</sup>, QY He<sup>\*</sup>. **Phosphoproteome profile of human lung cancer cell line A549.** *Molecular BioSystems*. 2011, 7(2):472-479.
10. **G Yu<sup>†</sup>**, F Li<sup>†</sup>, Y Qin, X Bo<sup>\*</sup>, Y Wu, S Wang<sup>\*</sup>. **GOSemSim: an R package for measuring semantic similarity among GO terms and gene products.** *Bioinformatics*. 2010, 26(7):976-978.
11. X Sun<sup>†</sup>, **G Yu<sup>†</sup>**, Q Xu, N Li, C Xiao, X Yin, K Cao, J Han, QY He<sup>\*</sup>. **Putative cobalt- and nickel-binding proteins and motifs in *Streptococcus pneumonia*.** *Metallomics*. 2013, 5(7):928-935.

12. YY Zhu<sup>†</sup>, **G Yu<sup>†</sup>**, Y Zhang, Z Xu, YQ Huang, GR Yan<sup>\*</sup>, QY He<sup>\*</sup>. **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<sup>\*</sup>, X Sun<sup>\*</sup>, QY He<sup>\*</sup>. **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<sup>\*</sup>, Y Guan<sup>\*</sup>. **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<sup>\*</sup>, GR Yan<sup>\*</sup>. **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<sup>\*</sup>, X Sun<sup>\*</sup>. **Proteomic analysis on the copper resistance of *Streptococcus pneumoniae*.** *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<sup>\*</sup>, QY He<sup>\*</sup>. **Proteomic analysis on the antibacterial activity of a Ru(II) complex against *Streptococcus pneumoniae*.** *Journal of Proteomics*. 2015, 115:107-116.
18. N Wang<sup>†</sup>, J Zhang<sup>†</sup>, L Zhang, XY Yang, N Li, **G Yu**, J Han, K Cao, Z Guo, X Sun<sup>\*</sup>, QY He<sup>\*</sup>. **Proteomic analysis of putative heme-binding proteins in *Streptococcus pyogenes*.** *Metalloids*. 2014, 6(8):1451-1459.
19. H Sun<sup>\*</sup>, 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<sup>†</sup>, Z Tan<sup>†</sup>, Y Wang, ML Xu, **G Yu**, Y Li<sup>\*</sup>, QY He<sup>\*</sup>. **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<sup>\*</sup>. **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<sup>\*</sup>. **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<sup>†</sup>, J Yang<sup>†</sup>, X Fan<sup>†</sup>, H Zhao, W Hu, Z Li, **G Yu**, X Ding, J Wang, X Bo, X Zheng, Z Zhou<sup>\*</sup>, S Wang<sup>\*</sup>. **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<sup>†</sup>, FY Zhou<sup>†</sup>, BL Dang, Y Zhang, **G Yu**, X Liu, QY He<sup>\*</sup>. **Genistein-induced mitotic arrest of gastric cancer cells by downregulating KIF20A, a proteomics study.** *Proteomics*. 2012, 12(14):2391-2399.
25. X Sun<sup>†</sup>, XY Yang<sup>†</sup>, XF Yin, **G Yu**, CL Xiao, X He, QY He<sup>\*</sup>. **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 9<sup>th</sup> 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 20<sup>th</sup> Research Postgraduate Symposium, The University of Hong Kong, Hong Kong, Dec. 2015