

# SHUANGBIN XU (徐双斌)

A Ph.D. student of Bioinformatics, I am broadly interested in metagenomics, bioinformatics, machine learning, data mining and visualization.

I have leaded or contributed to developing some R packages, including [MicrobiotaProcess](#), [ggtreeExtra](#), [ggstar](#), [ggbreak](#), [ggtree](#), [treeio](#), [tidytree](#) and [ggmsa](#), to help related researchers to explore and understand their data.



## 🎓 EDUCATION

current  
|  
2019

- **Ph.D., Bioinformatics**  
Southern Medical University 📍 ChuangZhou, CN
  - Thesis: The development and application of R packages for the analysis and visualization of microbiome downstream data

2017  
|  
2014

- **M.S., Aquatic Biology**  
JiMei University 📍 Xiamen, CN
  - Thesis: The identification and functional classification of circular RNA in the teleost large yellow croaker (*Larimichthys crocea*)

2014  
|  
2010

- **B.S., Aquaculture**  
Northwest A&F University 📍 XianYang, CN

## 💼 WORK EXPERIENCE

2019  
|  
2017

- **Senior Bioinformatics Engineer**  
Xiamen TreatGut Company 📍 XiaMen, CN
  - Helping build the workflow of microbiome data analysis
  - Helping the mining of related microbiome data
  - Helping develop the related testing products

2016

- **Bioinformatics Engineer Intern**  
FraserGen Genetic Information Company 📍 Wuhan, CN
  - Helping the deployment and using with slurm and pbs scheduling systems of the software (PacBio diploid assembler: Falcon, canu, etc) of the TianHe and company's Supercomputer platform

## CONTACT

- ✉ [xshuangbin@163.com](mailto:xshuangbin@163.com)
- ⌚ [github.com/xiangpin](https://github.com/xiangpin)
- 👤 BT开发者 (公众号)
- 📞 (86) 13860419424

## SELECTED R PACKAGES

- Microbiome
  - MicrobiotaProcess

- Phylogeny
  - ggtreeExtra
  - ggtree
  - treeio
  - tidytree
  - ggmsa

- Visualization
  - ggstar
  - ggbreak

## PUBLICATIONS

### FIRST (AND CO-FIRST) AUTHOR

2022

- **MicrobiotaProcess: A comprehensive R package for managing and analyzing microbiome and other ecological data within the tidy framework**

*Nature Portfolio.* 2022, PREPRINT.

- S Xu, L Zhan, W Tang, Z Dai, L Zhou, T Feng, M Chen, S Liu, X Fu, T Wu, E Hu, G Yu\*
- Under Review

- Citation = 720
- H-index = 9
- I10-index = 9

2021

- **ggtreeExtra: Compact visualization of richly annotated phylogenetic data**

*Molecular Biology and Evolution.* 2021, 38(9):4039-4042.

- S Xu, Z Dai, P Guo, X Fu, S Liu, L Zhou, W Tang, T Feng, M Chen, L Zhan, T Wu, E Hu, Y Jiang\*, X Bo\*, G Yu\*
- Impact Factor = 16.24

2020

- **Use ggbreak to effectively utilize plotting space to deal with large datasets and outliers**

*Frontiers in Genetics.* 2021, 12:774846.

- S Xu#, M Chen#, T Feng, L Zhan, L Zhou, G Yu\*
- Impact Factor = 4.599

2019

- **Gut microbiota and metabolite alterations associated with reduced bone mineral density or bone metabolic indexes in postmenopausal osteoporosis**

*Aging (Albany NY).* 2020, 12(9):8583-8604.

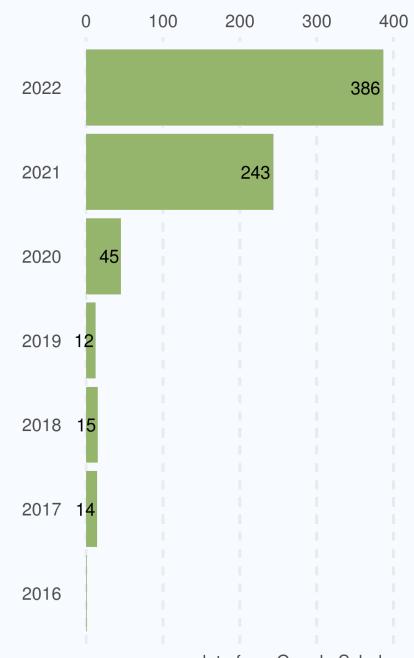
- J He#, S Xu#, B Zhang#, C Xiao, Z Chen, F Si, J Fu, X Lin, G Zheng\*, G Yu\*, J Chen\*
- Impact Factor = 5.682

2017

- **Leveraging Fecal Bacterial Survey Data to Predict Colorectal Tumors**

*Frontiers in Genetics.* 2019, 10:447.

- B Zhang#, S Xu#, W Xu#, Q Chen, Z Chen, C Yan, Y Fan, H Zhang, Q Liu, J Yang, J Yang, C Xiao, H Xu\*, J Ren\*
- Impact Factor = 3.258



data from Google Scholar

- **Transcriptome-wide identification and functional investigation of circular RNA in the teleost large yellow croaker (*Larimichthys crocea*)**

*Marine genomics.* 2017, 32:71-78

- S Xu, S Xiao, C Qiu, Z Wang\*
- Impact Factor = 1.937

### CONTRIBUTING AUTHOR

- 2022
- **ggmsa: a visual exploration tool for multiple sequence alignment and associated data**  
*Briefings in Bioinformatics.* 2022.
    - L Zhou<sup>#</sup>, T Feng<sup>#</sup>, S Xu, F Gao, TT Lam, Q Wang, T Wu, H Huang, L Zhan, L Li, Y Guan, Z Dai<sup>\*</sup>, G Yu<sup>\*</sup>
    - Impact Factor = 11.622
- 2021
- **clusterProfiler 4.0: A universal enrichment tool for interpreting omics data**  
*The Innovation.* 2021, 2(3):100141.
    - T Wu<sup>#</sup>, E Hu<sup>#</sup>, S Xu, M Chen, P Guo, Z Dai, T Feng, L Zhou, W Tang, L Zhan, X Fu, S Liu, X Bo<sup>\*</sup>, G Yu<sup>\*</sup>
- 2020
- **treeio: an R package for phylogenetic tree input and output with richly annotated and associated data**  
*Molecular Biology and Evolution.* 2020, 37(2):599-603.
    - LG Wang, TTY Lam, S Xu, Z Dai, L Zhou, T Feng, P Guo, CW Dunn, BR Jones, T Bradley, H Zhu, Y Guan, Y Jiang, G Yu<sup>\*</sup>
    - Impact Factor = 16.24
  - **Featured Gut Microbiomes Associated With the Progression of Chronic Hepatitis B Disease**  
*Frontiers in microbiology.* 2020, 11:383.
    - Z Chen<sup>#</sup>, Y Xie<sup>#</sup>, F Zhou, B Zhang, J Wu, L Yang, S Xu, R Stedtfeld, Q Chen, J Liu, X Zhang<sup>\*</sup>, H Xu<sup>\*</sup>, J Ren<sup>\*</sup>
    - Impact Factor = 5.64
  - **Preservation of the fecal samples at ambient temperature for microbiota analysis with a cost-effective and reliable stabilizer EffcGut**  
*Science of The Total Environment.* 2020, 741:140423.
    - L Yang<sup>#</sup>, K Hou<sup>#</sup>, B Zhang<sup>#</sup>, C Ouyang, A Lin, S Xu, D Ke, L Fang, Q Chen, J Wu, C Yan, Y Lian, T Jiang, J He, H Wang, Y Fu, C Xiao, Z Chen<sup>\*</sup>
    - Impact Factor = 7.963
- 2018
- **Genome-wide association study using single marker analysis and Bayesian methods for the gonadosomatic index in the large yellow croaker**  
*Aquaculture.* 2018, 486:26-30.
    - Y Gao<sup>#</sup>, L Dong<sup>#</sup>, S Xu, S Xiao, M Fang, Z Wang<sup>\*</sup>
    - Impact Factor = 3.022
- 2017
- **Cloning and expression profiling of gsdf and amh genes in large yellow croaker (*Larimichthys crocea*)**  
*South China Fisheries Science.* 2017, 13(6):1-13.
    - A Lin, Y Xie, S Xu, K Ye, S Gong, Z Wang<sup>\*</sup>

- 2015
- Identification of a male-specific DNA marker in the large yellow croaker (*Larimichthys crocea*)  
*Aquaculture*. 2017, 480:116-122.
    - A Lin, S Xiao, S Xu, K Ye, X Lin, S Sun, Z Wang\*
    - Impact Factor = 2.71
  - Rapid construction of genome map for large yellow croaker (*Larimichthys crocea*) by the whole-genome mapping in BioNano Genomics Irys system  
*BMC Genomics*. 2015, 16(1):1-10
    - S Xiao, J Li, F Ma, L Fang, S Xu, W Chen, Y Wang\*
    - Impact Factor = 3.867

## AWARDS

- 2021
- 国家奖学金
    - Southern Medical University,ChuangZhou, CN

## CONFERENCE PROCEEDINGS

- 2020
- Analysis and visualization of microbiome datasets using MicrobiotaProcess
    - The 10<sup>th</sup> BiocAsia2020 Conference, 2020
    - Virtual Conference