

SHUANGBIN XU

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

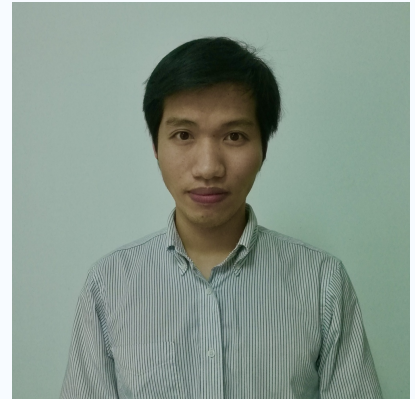
I have leaded and contributed to developing some R packages, including [MicrobiotaProcess](#), [ggtreeExtra](#), [ggstar](#), [ggbreak](#), [ggtree](#), [treeio](#), [tidytree](#) and [ggmsa](#), to help related researchers to explore and understand their data.

EDUCATION

- current
|
2019
- **PhD., Bioinformatics**
Southern Medical University 📍 ChuangZhou, CN
 - Thesis: The development of computational methods for studying microbiome: focus on the data mining and visualization
 - **M.S., Aquatic Biology**
JiMei University 📍 Xiamen, CN
 - Thesis: 大黄鱼环状RNA挖掘与功能分析
 - **B.S., Aquaculture**
Northwest A&F University 📍 XianYang, CN

WORK EXPERIENCE

- 2019
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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
 - **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

🐙 github.com/xiangpin

👤 BT开发者 (公众号)

📞 (86) 13860419424

SELECTED R PACKAGES

Metagenomics
• [MicrobiotaProcess](#)

Phylogeny
• [ggtreeExtra](#)
• [ggtree](#)
• [treeio](#)
• [tidytree](#)

Visualization
• [ggstar](#)
• [ggbreak](#)



PUBLICATIONS



FIRST (AND CO-FIRST) AUTHOR

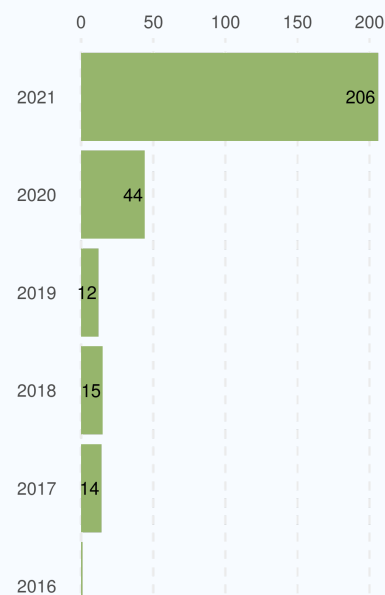
- 2021
- **ggtreeExtra: Compact visualization of richly annotated phylogenetic data**
Molecular Biology and Evolution. 2021, 38(9):4039-4042.
• S Xu, Z Dai, P Guo, X Fu, S Liu, L Zhou, W Tang, T Feng, M Chen, L Zhan, T Wu, E Hu, Y Jiang*, X Bo*, G Yu*
• Impact Factor₂₀₂₀ = 16.24
 - **Use ggbreak to effectively 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 Factor₂₀₂₀ = 4.599
- 2020
- **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
- 2019
- **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
- 2017
- **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

- 2021
- **clusterProfiler 4.0: A universal enrichment tool for interpreting omics data**
The Innovation. 2021, 2(3):100141.
• T Wu#, E Hu#, S Xu, M Chen, P Guo, Z Dai, T Feng, L Zhou, W Tang, L Zhan, X Fu, S Liu, X Bo*, G Yu*

- Citation = 297
- H-index = 8
- IIO-index = 7



data from Google Scholar

- 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*
• Impact Factor = 16.24
 - **Featured Gut Microbiomes Associated With the Progression of Chronic Hepatitis B Disease**
Frontiers in microbiology. 2020, 11:383.
• Z Chen#, Y Xie#, F Zhou, B Zhang, J Wu, L Yang, S Xu, R Stedtfeld, Q Chen, J Liu, X Zhang*, H Xu*, J Ren*
• Impact Factor = 5.64
 - **Preservation of the fecal samples at ambient temperature for microbiota analysis with a cost-effective and reliable stabilizer EfficGut**
Science of The Total Environment. 2020, 741:140423.
• L Yang#, K Hou#, B Zhang#, 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*
• 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#, L Dong#, S Xu, S Xiao, M Fang, Z Wang^*
• 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*
 - **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
- 2015
- **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



2020



**Analysis and visualization of microbiome datasets using
MicrobiotaProcess**

The 10th BiocAsia2020 Conference, 2020

📍 Virtual Conference