SHUANGBIN XU

A Ph.D. 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

Ph.D., Bioinformaitcs
Southern Medical University   📍 ChuangZhou, CN

· Thesis: The development of computational methods for studying microbiome: focus on the data mining and visualization

2017 | 2014

M.S.,Aquatic Biology
JiMei University   📍 Xiamen, CN

· Thesis: 大黄鱼环状RNA挖掘与功能分析

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
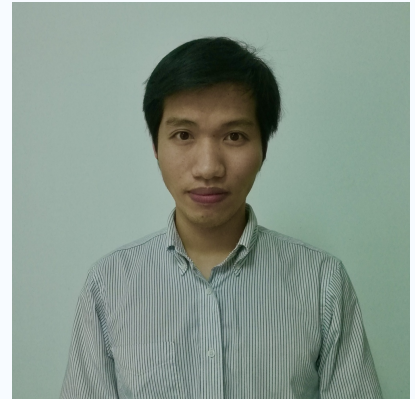
CONTACT

✉ xshuangbin@163.com
🐙 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

Last updated on 2021-12-23.

📖 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 Factor$_{2020}$ = 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 Factor$_{2020}$ = 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$_{2020}$ = 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$_{2019}$ = 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$_{2017}$ = 1.937
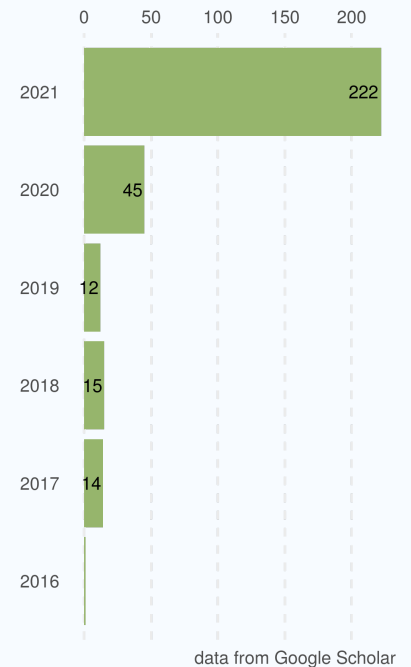
🔖 CONTRIBUTING AUTHOR

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 = 317
· H-index = 8
· I10-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$_{2020}$ = 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$_{2020}$ = 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[#], 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$_{2020}$ = 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$_{2018}$ = 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$_{2017}$ = 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$_{2015}$ = 3.867

CONFERENCE PROCEEDINGS

2020

Analysis and visualization of microbiome datasets using MicrobiotaProcess

The 10th BiocAsia2020 Conference, 2020

 Virtual Conference