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Erratum: *Ksak*: a high-throughput tool for alignment-free phylogenetics

Frontiers Production Office*

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KEYWORDS

k-mer, phylogentic tree, alignment free, open source, microbiome

An Erratum on

Ksak: a high-throughput tool for alignment-free phylogenetics

by Liu, X., Cheng, Z., Xu, G., Xie, J., Liu, X., Ren, B., Ai, D., Chen, Y., and Xia, L. C. (2023). Front. *Microbiol.* 14:1050130. doi: 10.3389/fmicb.2023.1050130

Due to a production error, there were errors in affiliations 1 and 2. Instead of "¹Department of Cardiology, Sun Yat-sen Memorial Hospital of Sun Yat-sen University, Guangzhou, Guangdong, China, ²Guangzhou Key Laboratory of Molecular Mechanism and Translation in Major Cardiovascular Disease, SunYat-Sen Memorial Hospital, Sun Yat-Sen University, Guangzhou, Guangdong, China," these should be "¹School of Physics and Optoelectronics, South China University of Technology, Guangzhou, Guangdong, China, ²Guangzhou Boguan Telecommunication Technology Limited, Guangzhou, Guangdong, China."

Further, there was an error in the affiliations for author "Yangxin Chen." Instead of having affiliations 2 and 5, the author should have affiliation 5 and "⁶Guangzhou Key Laboratory of Molecular Mechanism and Translation in Major Cardiovascular Disease, Sun Yat-sen Memorial Hospital, Sun Yat-sen University, Guangzhou, China."

The publisher apologizes for this mistake. The original article has been updated.