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iMeta: Integrated meta-omics for biology and environments

The microbiomes, collective communities of trillions of microorganisms in humans, animals, and environments, play crucial roles in all aspects of our society, including but not limited to human health [1], food industry [2], agriculture [3], sustainable environment [4], and biodiversity [5]. In the past decades, our knowledge of the microbiome has expanded exponentially [6]. Several ground-breaking initiatives, such as the Human Microbiome Project (HMP) [7], Earth Microbiome Project (EMP) [8], *Tara* Oceans [9], Metagenomics of the Human Intestinal Tract (MetaHIT) project [10], the Integrative HMP [11], and China Microbiome Initiative (CMI) [12], have opened up this new horizon by generating experimental pipelines [13,14], sequencing technologies [15,16], reference catalogs [17,18], and bioinformatics tools [19,20]. Big data and bioinformatics advancements have become one of the major driving forces behind flourishing microbiome researches [21,22]. However, scientific journals focusing on this aspect are lacking. In this context, *iMeta* was founded to promote scientific research that combines microbiome research with big data and innovative, current state-of-the-art (bioinformatics) methodologies.

iMeta (ISSN: 2770-5986; eISSN: 2770-596X) is an open-access and Wiley partner journal launched in 2022. The journal aims to publish original research, reproducible methods and protocols, and systemic reviews to promote metagenomics and bioinformatics advancement. The editorial office is based in Beijing, China, and embraces the scientific community worldwide. Accepted publications are expected to have a high impact (top 10%) with a broad readership, and provide peers with novel findings, easy-to-use analysis tools, or systematic knowledge. The first papers were published online in February 2022.

Microbiology, biotechnology, and applied microbiology are also included in the scope of *iMeta*. *iMeta* focuses on wide-scope topics of microbiome research in humans, animals, plants, and environments; meta-omics methods and protocols development and application; bioinformatics tools, pipelines, and databases; systematic

reviews in metagenomics, bioinformatics, and microbiome. Some unique features of *iMeta* include video summaries of the submitted work, video tutorials for methods and tools, figure polishing, and promotion by social media (Twitter, Facebook, and WeChat) with 500,000 followers in metagenomics, bioinformatics, and microbiome [23]. In this fast development era, we believe that online publication is just the beginning. Promotion, translation, and updates (protocols, software, databases, or scripts) to publications are all required and would be scheduled by editors and authors.

The inaugural issue (Figure 1) features 12 papers from 57 authors and 10 countries or regions. We are glad to provide you with a snapshot of the contents first:

- Convenient tools would greatly facilitate scientists' research. Chen et al. [24] designed ImageGP, a popular data visualization web server that has been cited over 300 times (Google Scholar by 2/20/2022). Yu et al. [25] created a platform for microbiome and metabolome integrative analysis. Using a deep neural network, Lv et al. [26] developed a software (include local and online tool) to predict lysine lactylation sites in proteins.
- Some exciting findings are also reported in this issue. Jiao et al. [27] presented a story about soil fungi with bacterial community assembly in Hexi Corridor. Zheng et al. [28] connected the traditional Chinese medicine liquorice with the detoxification of cadmium and explored its potential mechanism at the metagenomic and metabolomic levels. Huang et al. [29] conducted a meta-analysis of gut microbiota in a population with an Altitude diet.
- Innovative methods are the propeller to promote the development of science. To make user analysis and visualization easier, Chen et al. [30] developed an integrative microbiome analysis pipeline. Michel-Mata et al. [31] introduced a deep learning algorithm to predict microbiome composition.
- Reviews are also essential for peers to learn and begin their studies readily. Dufault-Thompson et al. [32] provided a comprehensive and insightful review of






FIGURE 1 The cover of *iMeta*'s inaugural issue. The galaxy represents the complexity and value of bioinformatics and metagenomics. DNA, which represents genetic components that guide biological diversity, is at the center of the galaxy. The spiral arms are the microbiome welcoming scientists from all over the world to make novel discoveries. Let us usher in the metaverse era of the microbiome

de Bruijn graphs' progress and future applications in microbiome studies. Wang et al. [33] reviewed plant genetics-mediated remodeling of microbiota and techniques in response to stress, and Yang et al. [34] reviewed the advantages of the targeted approach in integrating metagenome data for accurate protein structure prediction.

The editorial team at *iMeta* hope that you will support this endeavor by submitting your research and review articles, and furthering our understanding of bioinformatics, metagenomics, and microbiome.

AUTHOR CONTRIBUTIONS

All authors read and approved the final manuscript.

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REFERENCES

- Lloyd-Price, Jason, Cesar Arze, Ashwin N. Ananthakrishnan, Melaine Schirmer, Julian Avila-Pacheco, Tiffany W. Poon, Elizabeth Andrews, et al. 2019. "Multi-omics of the Gut Microbial Ecosystem in Inflammatory Bowel Diseases." *Nature* 569: 655–62. <https://doi.org/10.1038/s41586-019-1237-9>
- Filippis, Francesca De, Eugenio Parente, and Danilo Ercolini. 2018. "Recent Past, Present, and Future of the Food Microbiome." *Annual Review of Food Science and Technology* 9: 589–608. <https://doi.org/10.1146/annurev-food-030117-012312>
- Zhang, Jingying, Yong-Xin Liu, Na Zhang, Bin Hu, Tao Jin, Haoran Xu, Yuan Qin, et al. 2019. "NRT1.1B is Associated with Root Microbiota Composition and Nitrogen Use in Field-Grown Rice." *Nature Biotechnology* 37: 676–84. <https://doi.org/10.1038/s41587-019-0104-4>
- Chen, Qing-Lin, Hang-Wei Hu, Zi-Yang He, Li Cui, Yong-Guan Zhu, and Ji-Zheng He. 2021. "Potential of Indigenous Crop Microbiomes for Sustainable Agriculture." *Nature Food* 2: 233–40. <https://doi.org/10.1038/s43016-021-00253-5>

5. Nayfach, Stephen, Simon Roux, Rekha Seshadri, Daniel Udwarý, Neha Varghese, Frederik Schulz, Dongying Wu, et al. 2021. "A Genomic Catalog of Earth's Microbiomes." *Nature Biotechnology* 39: 499–509. <https://doi.org/10.1038/s41587-020-0718-6>
6. Berg, Gabriele, Daria Rybakova, Doreen Fischer, Tomislav Cernava, Marie-Christine Champomier Vergès, Trevor Charles, Xiaoyulong Chen, et al. 2020. "Microbiome Definition Re-visited: Old Concepts and New Challenges." *Microbiome* 8: 103. <https://doi.org/10.1186/s40168-020-00875-0>
7. Turnbaugh, Peter J., Ruth E. Ley, Micah Hamady, Claire M. Fraser-Liggett, Rob Knight, and Jeffrey I. Gordon. 2007. "The Human Microbiome Project." *Nature* 449: 804–10. <https://doi.org/10.1038/nature06244>
8. Gilbert, Jack A., Folker Meyer, Dion Antonopoulos, Pavan Balaji, C. Titus Brown, Christopher T. Brown, Narayan Desai, et al. 2010. "Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project." *Standards in Genomic Sciences* 3: 243–48. <https://doi.org/10.4056/sigs.1433550>
9. Sunagawa, Shinichi, Luis Pedro Coelho, Samuel Chaffron, Jens Roat Kultima, Karine Labadie, Guillem Salazar, Bardya Djahanschiri, et al. 2015. "Structure and Function of the Global Ocean Microbiome." *Science* 348: 1261359. <https://doi.org/10.1126/science.1261359>
10. Qin, Junjie, Ruiqiang Li, Jeroen Raes, Manimozhiyan Arumugam, Kristoffer Solvsten Burgdorf, Chaysavanh Manichanh, Trine Nielsen, et al. 2010. "A Human Gut Microbial Gene Catalogue Established by Metagenomic Sequencing." *Nature* 464: 59–65. <https://doi.org/10.1038/nature08821>
11. Proctor, Lita M., Heather H. Creasy, Jennifer M. Fettweis, Jason Lloyd-Price, Anup Mahurkar, Wenyu Zhou, Gregory A. Buck, et al. 2019. "The Integrative Human Microbiome Project." *Nature* 569: 641–48. <https://doi.org/10.1038/s41586-019-1238-8>
12. Liu, Shuangjiang, Wenyuan Shi, and Guoping Zhao. 2017. "China Microbiome Initiative: Opportunity and Challenges." *Bulletin of Chinese Academy of Sciences* 32: 241–50. <https://doi.org/10.16418/j.issn.1000-3045.2017.03.004>
13. Costea, Paul I, Georg Zeller, Shinichi Sunagawa, Eric Pelletier, Adriana Alberti, Florence Levenez, Melanie Tramontano, Marja Driessen, et al. 2017. "Towards Standards for Human Fecal Sample Processing in Metagenomic Studies." *Nature Biotechnology* 35: 1069–76. <https://doi.org/10.1038/nbt.3960>
14. Zhang, Jingying, Yong-Xin Liu, Xiaoxuan Guo, Yuan Qin, Ruben Garrido-Oter, Puben Schulze-Lefert, and Yang Bai. 2021. "High-Throughput Cultivation and Identification of Bacteria from the Plant Root Microbiota." *Nature Protocols* 16: 988–1012. <https://doi.org/10.1038/s41596-020-00444-7>
15. Wang, Yunhao, Yue Zhao, Audrey Bollas, Yuru Wang, and Kin Fai Au. 2021. "Nanopore Sequencing Technology, Bioinformatics and Applications." *Nature Biotechnology* 39: 1348–65. <https://doi.org/10.1038/s41587-021-01108-x>
16. Caporaso, J. Gregory, Christian L. Lauber, William A. Walters, Donna Berg-Lyons, James Huntley, Noah Fierer, Sarah M. Owens, et al. 2012. "Ultra-High-Throughput Microbial Community Analysis on the Illumina HiSeq and MiSeq Platforms." *The ISME Journal* 6: 1621–24. <https://doi.org/10.1038/ismej.2012.8>
17. Zhu, Jie, Liu Tian, Peishan Chen, Mo Han, Liju Song, Xin Tong, Zhipeng Lin, et al. 2021. "Over 50,000 Metagenomically Assembled Draft Genomes for the Human Oral Microbiome Reveal New Taxa." *Genomics, Proteomics & Bioinformatics* 352: 565. <https://doi.org/10.1016/j.gpb.2021.05.001>
18. Pasolli, Edoardo, Francesco Asnicar, Serena Manara, Moreno Zolfo, Nicolai Karcher, Federica Armanini, Beghini Francesco, et al. 2019. "Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle." *Cell* 176: 649–62.e620. <https://doi.org/10.1016/j.cell.2019.01.001>
19. Bolyen, Evan, Jai Ram Rideout, Matthew R. Dillon, Nicholas A. Bokulich, Christian C. Abnet, Gabriel A. Al-Ghalith, Harriet Alexander, et al. 2019. "Reproducible, Interactive, Scalable and Extensible Microbiome Data Science Using QIIME 2." *Nature Biotechnology* 37: 852–57. <https://doi.org/10.1038/s41587-019-0209-9>
20. Chen, Tong, Haiyan Zhang, Yu Liu, Yong-Xin Liu, and Luqi Huang. 2021. "EVENN: Easy to Create Repeatable and Editable Venn Diagrams and Venn Networks Online." *Journal of Genetics and Genomics* 48: 863–66. <https://doi.org/10.1016/j.jgg.2021.07.007>
21. Knight, Rob, Alison Vrbanac, Bryn C. Taylor, Alexander Aksenov, Chris Callewaert, Justine Debelius, Antonio Gonzalez, et al. 2018. "Best Practices for Analysing Microbiomes." *Nature Reviews Microbiology* 16: 410–22. <https://doi.org/10.1038/s41579-018-0029-9>
22. Liu, Yong-Xin, Yuan Qin, Tong Chen, Meiping Lu, Xubo Qian, Xiaoxuan Guo, and Yang Bai. 2021. "A Practical Guide to Amplicon and Metagenomic Analysis of Microbiome Data." *Protein & Cell* 12: 315–30. <https://doi.org/10.1007/s13238-020-00724-8>
23. 2020. "Science on WeChat." *Nature Methods* 17: 863–63. <https://doi.org/10.1038/s41592-020-0954-1>
24. Chen, Tong, Yong-Xin Liu, and Luqi Huang. 2022. "ImageGP: An Easy-to-Use Data Visualization Web Server for Scientific Researchers." *iMeta* 1: e5. <https://doi.org/10.1002/imt2.5>
25. Yu, Gang, Cuifang Xu, Danni Zhang, Feng Ju, and Yan Ni. 2022. "MetOrigin: Discriminating the Origins of Microbial Metabolites for Integrative Analysis of the Gut Microbiome and Metabolome." *iMeta* 1: e10. <https://doi.org/10.1002/imt2.10>
26. Lv, Hao, Fu-Ying Dao, and Hao Lin. 2022. "DeepKla: An Attention Mechanism-Based Deep Neural Network for Protein Lysine Lactylation Site Prediction." *iMeta* 1: e11. <https://doi.org/10.1002/imt2.11>
27. Jiao, Shuo, Haiyan Chu, Baogang Zhang, Xiaorong Wei, Weimin Chen, and Gehong Wei. 2022. "Linking Soil Fungi to Bacterial Community Assembly in Arid Ecosystems." *iMeta* 1: e2. <https://doi.org/10.1002/imt2.2>
28. Zheng, Xin, Likun Wang, Linhao You, Yong-Xin Liu, Michael Cohen, Siyu Tian, Wenjun Li, and Xiaofang Li. 2022. "Dietary Licorice Enhances In Vivo Cadmium Detoxification and Modulates Gut Microbial Metabolism in Mice." *iMeta* 1: e7. <https://doi.org/10.1002/imt2.7>
29. Huang, Yina, Jinxin Liu, Hein Min Tun, Catherine Stanton, Tingtao Chen, Hani El-Nezami, Hua Wei, Mingfu Wang, and

- Qinglong Wu. 2022. "Gut Microbiota Insights into Human Adaption to High-Plateau Diet." *iMeta* 1: e6. <https://doi.org/10.1002/imt2.6>
30. Chen, Yuzhu, Jian Li, Yufeng Zhang, Mingqian Zhang, Zheng Sun, Gongchao Jing, Shi Huang, and Xiaoquan Su. 2022. "Parallel-Meta Suite: Interactive and Rapid Microbiome Data Analysis on Multiple Platforms." *iMeta* 1: e1. <https://doi.org/10.1002/imt2.1>
31. Michel-Mata, Sebastian, Xu-Wen Wang, Yang-Yu Liu, and Marco Tulio Angulo. 2022. "Predicting Microbiome Compositions from Species Assemblages through Deep Learning." *iMeta* 1: e3. <https://doi.org/10.1002/imt2.3>
32. Dufault-Thompson, Keith, and Xiaofang Jiang. 2022. "Applications of de Bruijn Graphs in Microbiome Research." *iMeta* 1: e4. <https://doi.org/10.1002/imt2.4>
33. Wang, Zhenghong, and Yi Song. 2022. "Toward Understanding the Genetic Bases Underlying Plants Mediated "Cry for Help" to the Microbiota." *iMeta* 1: e8. <https://doi.org/10.1002/imt2.8>
34. Yang, Pengshuo, and Kang Ning. 2022. "How Much Metagenome Data is Needed for Protein Structure Prediction: The Advantages of Targeted Approach from the Ecological and Evolutionary Perspectives." *iMeta* 1: e9. <https://doi.org/10.1002/imt2.9>