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Untangling Host-Symbiont Coevolutionary History in the High Throughput Sequencing (HTS) Era

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Deadline for manuscript
submissions:
closed (29 November 2024)

Message from the Guest Editors

In this Special Issue, we seek to bring together empirical, methodological, or theoretical papers that will advance our overall knowledge of host-symbiont coevolutionary history, especially on cutting-edge topics that utilize HTS data. HTS data include, but are not limited to, genomes/transcriptomes/epigenomes, multi-gene datasets, SNPs, or symbiont-associated microbial metagenomes. Examples of preferential topics include cophylogenetic methods, epigenetics, gene expression, genome architecture, genome evolution, hybridization, microbiomes, phylogenomics, phylogeography, phyllosymbiosis, population genomics, and transcriptomics.

The scope is very broad, and we encourage any submissions that are useful to the field of host-symbiont coevolution, including preliminary results or small-scale studies. Additionally, there is an updated deadline for submissions (29 November 2024). Please do not hesitate to inquire about whether an idea may fit in the Special Issue.



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Special Issue



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Message from the Editor-in-Chief

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