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Open Science Phyloinformatics: Resources, Methods, and Analyses

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Deadline for manuscript submissions:
closed (28 February 2018)

Message from the Guest Editors

Phylogenetic research, today, is increasingly complex and data-intensive, placing increased demands on effective data sharing, analytical reproducibility, and knowledge synthesis. Large trees, vast datasets, and long multi-step analysis pipelines demand that biologists follow best practices in open access, sharing, and data integration. This Special Issue aims to assemble articles on phyloinformatic resources, tools, and research reports that exemplify best practices supporting open science reproducibility and/or demonstrate inference of broad-scale patterns through the integration of large datasets in phylogenetics.

mdpi.com/si/10929

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Message from the Editor-in-Chief

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