Integrating trees and networks into reproducible data analytic workflows

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Résumé

Biomedical data often contain information from different sources or sources. Interaction networks and phylogenetic trees are omnipresent in biomedical and genomic data and their integration into longitudinal multivariate analyses can be challenging.

As examples, I will show how our group has developed software (phyloseq, structSSII and adaptivegPCA) that can incorporate phylogenetic trees into count abundance data and modulate the influence of the tree using tree-based regularization and testing.