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**ROBERT BEIKO**, Dalhousie University

*When Phylogenetic Trees Can't Agree: Building a coherent network of microbial gene sharing*

Just as it is possible to represent the branching relationships between organisms using a phylogenetic tree, we can also build trees for all the genes contained within a set of organisms. However, microorganisms can readily acquire genetic material from other microbes, even from donors that are distantly related. This process of lateral gene transfer or LGT allows microbes to exploit new opportunities in their environment, and can change the way they interact with other organisms including host organisms such as humans. In phylogenetic terms, LGT events often lead to topological differences between trees of microbial species and trees of the genes contained within their genomes. Many gene trees will disagree with each other as well, and different genes will be found in different subsets of microorganisms. How can we represent and interpret these divergent histories? Networks or graphs provide important generalizations of trees, but choosing the right data and the right representation is both critical and how to do so is not immediately obvious. We have developed methods that can reconcile trees through topological permutations that mirror the effects of LGT, and can generate a permutation path between two trees that suggests a plausible series of LGT events. These approaches allow us to appreciate the extent and impact of LGT, but there is still a need for methods that provide a clear view of evolution's role in shaping microorganisms.