

1106-92-1907

**Heather Gronewald\*** (gronewah@southwestern.edu). *Computing Cophylogenetic Invariants.*

Phylogenetics is the study of evolutionary relationships among organisms. One method for reconstructing phylogenetic trees involves establishing phylogenetic invariants (polynomial relationships that vanish when expected pattern frequencies are substituted for variables) and then comparing expected and observed invariants. Cophylogeny is the study of concomitantly evolving organisms (e.g. a host and parasite). Huggins, Owen, and Yoshida suggest that existing methods for reconstructing host and parasite trees can exaggerate true differences between trees. We consider both the independent and pairwise reconstruction of trees, establishing classes of metrics for which independently inferred trees match pairwise inferred trees, and exploring methods for reconstruction that consider the cophylogenetic relationship. (Received September 15, 2014)