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Claudia Solis-Lemus*, solislemus@wisc.edu. *Identifiability of phylogenetic networks under the multispecies coalescent model.*

Reconstructing the Tree of Life from genomic sequences is challenging due to the variety of biological forces that shape the signal in the data, and many of those processes like incomplete lineage sorting and hybridization can produce confounding information. Here, we will present the mathematical proofs of identifiability of phylogenetic networks under the pseudolikelihood model in SNaQ. We establish that the ability to detect different hybridization events depends on the number of nodes on the hybridization blob, with small blobs (corresponding to closely related species) being the hardest to be detected. Our work focuses on level-1 networks, but raises attention to the importance of identifiability studies on phylogenetic inference methods for broader classes of networks. (Received August 30, 2021)