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Charles Semple* (charles.semple@canterbury.ac.nz), School of Mathematics and Statistics, University of Canterbury, Private Bag 4800, Christchurch, 8140, New Zealand. *Building networks with caterpillars.*

A well-known result in mathematical phylogenetics says that every rooted phylogenetic tree is recoverable from (determined by) its set of induced subtrees on three leaves. This result typically underlies those algorithms for reconstructing and analysing phylogenetic trees that take, as input, a collection of smaller phylogenetic trees on overlapping leaf sets and output a parent tree that ‘best’ represents the input. Collectively known as supertree methods, these algorithms are practical and widely used in tree reconstruction. As an initial step towards developing analogous algorithms for reconstructing phylogenetic networks, to what extent is a phylogenetic network recoverable from its induced subtrees? What about its induced pairwise distances? In this talk, we investigate these questions, and discuss some surprising and unexpected results for the class of normal (phylogenetic) networks. (Received August 30, 2021)