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Steven Kelk, Simone Linz* (s.linz@auckland.ac.nz), **Georgios Stamoulis** and **Wim van Wersch**. *Exploiting phylogenetic networks to compute the tree bisection and reconnection distance between two phylogenetic trees.*

The reconstruction of a phylogenetic tree typically requires a search through phylogenetic tree space, a space that grows exponentially with the number of leaves in a tree. Tree space is commonly searched by using modification moves on phylogenetic trees such as the extensively-studied tree bisection and reconnection (TBR) move that locally modifies a phylogenetic tree and induces a metric on phylogenetic tree space. To understand the connectivity of this space under TBR moves, it is natural to ask for the smallest number of TBR moves required to transform one tree into another. This question also plays a crucial role in quantifying the dissimilarities between two phylogenetic trees, e.g. a reconstructed tree and ‘the true’ tree. In this talk, we investigate how phylogenetic networks can be leveraged to obtain faster algorithms for computing the TBR distance between trees. We present new data reduction rules, explore their mathematical underpinnings, and demonstrate their practical impact. (Received August 29, 2021)