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*The Bourque Distances for Mutation Trees of Cancers*

Mutation trees are rooted trees in which nodes are of arbitrary degree are labeled with a mutation set. These trees are used in computational oncology to represent the mutational history of tumours. Classical tree metrics are of limited use for the comparison of mutation trees. One reason is that mutation trees inferred with different methods or for different patients often contain different sets of mutation labels. We generalize the Robinson-Foulds distance into a set of distance metrics called Bourque distances for comparing mutation trees.