Abstract

The metric dimension of an RNA graph is a graph-theoretic parameter that measures the minimum number of nucleotides required to uniquely identify the secondary structure of an RNA molecule. RNA graphs capture the connectivity between nucleotides, where vertices represent nucleotides and edges represent basepairing interactions. By studying the metric dimension of RNA graphs, researchers can gain a deeper understanding of RNA folding, RNA-RNA interactions, and other biologically relevant phenomena. In the context of graph theory, this abstract tries to give a general understanding of the metric dimension of RNA graphs. We look at how the metric dimension of RNA graphs is defined, its computational components, and how it affects RNA structure analysis. In addition, we address the techniques and approaches used in bioinformatics and computational biology to figure out the metric dimension of RNA graphs.