# Elastic-Degenerate Strings in Bioinformatics: Motivation and Open Problems

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As the volume of biological data grows, effectively managing and efficiently storing this data becomes a key challenge in bioinformatics. While processing, data structures with different representations are built to acquire better answers in a meaningful amount of time and with minimal memory consumption. One of the promising representations of highly similar sequences is the elastic-degenerate string (EDS), a mathematical concept that allows multiple sequences to be stored in a compact space. Although the concept of EDS has been around for many years now, a number of open problems remain unsolved due to struggles with biological meaning and the computational complexities of the algorithms. The biggest potential and ongoing application of EDS lies in manipulating data for population studies, pangenomics and other studies based on variant callings or sequence alignments. This talk provides an overview of the current state of the art, as well as the main challenges associated with processing such representations.