

Comparative Analysis of Machine Learning and Deep Learning Algorithms to Classify Cancer Based on Microarray Genes

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Abstract: *Cancer classification is a topic of major interest in medicine because it allows accurate and efficient diagnosis and facilitates a successful outcome in medical treatment. previous studies using large-scale RNA profiling and supervised machine learning (ML) algorithms to construct molecular-based classifications of carcinoma cells from breast, bladder, adenocarcinoma, colorectal, gastro esophagus, kidney, liver, lung, ovarian Human tumors have been classified. , pancreas, and prostate tumors. These datasets are collectively known as the 11 Tumor Database, although this database has been used in many works in the ML field, no comparative study of different algorithms could be found in the literature. On the other hand, advances in both hardware and software technologies have led to substantial improvements in the accuracy of solutions using ML, such as Deep Learning (DL). In this study, we compare the most widely used algorithms in classical ML and DL to classify tumors described in the 11 tumor database.*

Keywords: Dataset, Database, Algorithm, ML, DL, Cancer etc

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