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## Relative Expression Classification Tree. A Preliminary GPU-based Implementation

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The enormous amount of omics data generated from high-throughput technologies has brought an increased need for computational tools in biological analyses. Among the algorithms particularly valuable are those that enhance understanding of human health and genetic diseases. Relative eXpression Analysis (RXA) is a powerful collection of computational methods for analyzing genomic data. It finds relationships in a small group of genes by focusing on the relative ordering of their expression values. In this paper, we propose a Relative eXpression Classification Tree (RXCT) which extends major variants of RXA solutions by finding additional hierarchical connections between sub-groups of genes. In order to meet the enormous computational demands we designed and implemented a graphic processing unit (GPU)-based parallelization. The GPU is used to perform a parallel search of the gene groups in each internal node of the decision tree in order to find locally optimal splits. Experiments carried out on 8 cancer-related gene expression datasets show that the proposed approach allows exploring much larger solution space and finding more accurate interactions between the genes. Importantly, patterns in predictive structures are kept comprehensible and may have direct applicability.

**Keywords:** relative expression analysis, decision trees, GPU, CUDA.