Boolean AIGenebra: A Nature-Inspired Framework for the Analysis of Cancer Genes

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Euclidean distance metric based analysis, including regression and clustering, is good at detecting symmetrical relationships between variables, such as “if gene A was high, then gene B was low” and “if gene B was low, then gene A was high.” Asymmetrical relationships, however, are characteristic in many genes found in nature. This can be illustrated as “if gene A was high, then gene B was low. However, when gene B was low, gene A could have been high or low.” Such asymmetrical relationships play a vital role in gene regulation and cell differentiation, which could lead to tumorigenesis. The student’s research effort has developed and validated a Boolean state-space analysis tool to detect potentially cancer causing genetic relationships by analyzing 27,000 genetic expression experiments and mutation data from 4,700 cancer tumors. The six types of Boolean relationships harvested could be used to look for genes that play a role in the crucial intermediary stages of tumor growth, as well as to study cancer pathways, which could identify new genes to target for drug therapies.

Awards Won:

European Organization for Nuclear Research-CERN: Third Award $500