A Novel Approach to Genetic Interaction Research with an Integrated Repository of Gene Regulatory Networks

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Gene regulatory network (GRN) studies reveal crucial pathways behind debilitating genetic diseases. While GRNs have previously been found via biological experimentation (bGRNs), recent developments in high throughput technologies have expedited the process via computational prediction of GRNs (cGRNs), providing an untapped class of GRN information. However, without a centralized source for cGRN information, cGRN experiments are inaccessible for researchers, withholding many benefits of cGRN studies. This project provides an innovative online repository and analytical search engine to increase access to GRN information for genomic research. The repository integrates bGRNs and cGRNs in a unified, heavily connected property graph in the Neo4j graph database. The efficient, scalable query engine allows users to issue various complex, criteria-specific graph traversal queries across 2.62 million interactions spanning over 70,000 biomolecules, with an example query for a length 11 pathway between specific genes involved in GBM cancer executing in 1.73 seconds against the 178 quadrillion theoretical length 11 paths. These computationally intensive queries are facilitated via a novel breadth-first approach that eliminates excess computation. Researchers can explore query results in the user interface via dynamically generated graph visualizations and access annotations from integrated repositories (e.g. PubMed, UniProt). Ultimately, this repository provides researchers with unprecedented access to cGRN information and analytical tools which can further GRN studies by expediting research of cGRNs and facilitating hypothesis of novel GRN interactions and pathways through the unique overlay of bGRN and cGRN webs, providing benefits which can be translated to cancer prevention.

Awards Won:
Third Award of $1,000