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Visualization of plant Regulomics Network in Graph using Neo4j

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Abstract

Plants have highly interacted with the environment through phenotypically. The phenotype of plants controls via epigenome by DNA methylation, histone modification, small RNAs like (miRNAs/siRNAs), transcription factors and repetitive elements. These all regulatory factors work together in various stress conditions of plants for the protection or survival. The regulators perform their function in the module of a mechanism at TGS or PTGS. Some regulators may be activated or deactivated according to their action of the mechanism. Such type of interaction briefly called Regulomics which control or regulate the genotype through epigenomics. In, various types of interaction have been considering for the case studies. Most important interactions related to small RNAs and DNA methylation for their expressional silencing of key genes in various pathways. The possible interaction of miR-Gene, miR-TF, TF-miR, TF-Gene and Gene-Gene is mostly found in the complex network of plants. Need to provide a dynamic, interactive, systematic and versatile visualization technique to provide a comprehensive platform to view such complex interaction graph networks for plants. Graph based interaction networks visualization available for regulomics contains various interactions. For these Neo4j have been emerging NoSQL based graph tool to visualize versatile networks in graphical as well as user defined formats. We provide the graph based big-data networks in various plants like Thale cress, Soyabean, Maize, Rice, Populus, medicago, tomato, etc. Each plants network has more than ~30,000 nodes and their edges or relationships. It has been very fast and friendly for users. This facility provides vital impact for plant sciences in the area of network interaction in future.

References

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