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The improved method to infer global gene regulatory network for investigating disease genes using High-Performance Computing resources

Younghoon Kim[1]

[1] *Department of Supercomputing Applications,*
Korea Institute of Science and Technology Information (KISTI)

In order to investigate disease genes and understand the global mechanisms of diseases, gene regulatory networks are needed and global gene regulatory networks need to be prepared. However, the methods to infer the global gene regulatory networks are a few, because there are many hurdles such as tremendous computational burden to calculate the network scores and hugh information content needed for network inference. So far we have developed global gene regulatory method named MONET (MOdularized NETwork learning). This method can solve those problems and secure high-quality gene networks by divide-and-conquer strategy with High Performance Computing(HPC)-resources and information integration strategy. In order to improve our method, we incorporate new databases such as STRING and HumanNet(v3) into MONET method, because biological information contents are very important for high-quality network results. By the databases integration the information contents are greatly increased and the coverage of the resulting networks is improved.