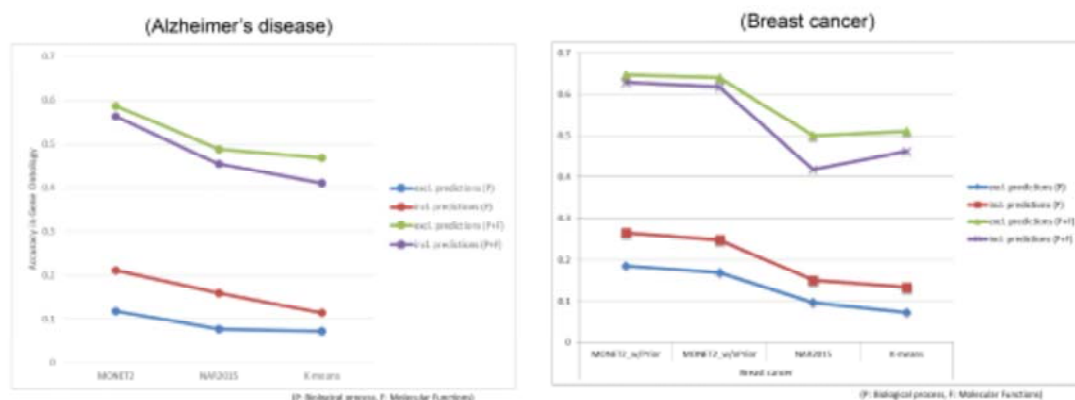


Development of HPC-based global gene regulatory network inference system for investigating Alzheimer's disease genes

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Inferring gene regulatory networks are important in investigating disease genes and to understand overall perspectives and mechanisms for diseases, global gene regulatory networks are needed. However, inferring global networks require tremendous computations and huge information content, and the inference without these requirements results in infeasible execution in reasonable time and inaccurate networks. To solve this problem, we had developed MONET technique, MODularized NETwork learning, in which computational burden can be overcome by divide-and-conquer strategy with High Performance Computing(HPC)-resources and insufficiency of information is tackled by integrating the existing biological information. In this study, we have developed MONET2, which extends to Homo sapiens and enables more accurate resulting networks by integrating multiple biological information from genomics, epigenomics, interactome, disease gene data, and so on. We used MONET2 to construct the global networks of Alzheimer's disease by incorporating more than eleven biological data sources in thirteen brain cell types. MONET2 enables the inference of accurate global networks in a feasible time by using parallel processing techniques based on HPC-resources of KISTI and we plan to open this method to the public like the first version of MONET which was developed as a plugin of Cytoscape.



<Test if the gene pairs have the same GO terms>

Excl. predictions: only include EXP, IDA, IPI, IMP, IGI, IEP, TAS types

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