Professor Lee Insoo’s Research Team
Finds a New Way to Study Human Diseases

Like a social network service such as Facebook and Twitter, genes working in human bodies are functionally wired together for cooperation. Prof. Lee’s research team has previously developed one of the world’s largest networks of human genes, dubbed “HumanNet” (www.functionalnet.inetbio.org), which connects more than 16,000 human genes with a half million cooperative relationships (see the figure below). To develop this network, his team used Big Data mining approaches analyzing more than 50 million data points about biological molecules. This network has proven useful in various human disease studies such as discovery of disease genes and classification of cancer patients. More recently, his team demonstrated that HumanNet can find nonobvious connections between human disease systems and laboratory organism phenotypes. Laboratory organisms are indispensable for human disease research, because they have many disease systems evolutionarily conserved. However, finding disease systems from laboratory organism is often prohibitively difficult due to their seemingly unrelated phenotypes. To overcome this hurdle, his team developed a new HumanNet-based software, MORPHIN (model organisms projected on a human integrated gene network; http://www.inetbio.org/morphin), to find hidden disease systems from various laboratory organisms such as yeast, worm, fly, fish, frog, mice, and rat. For example, using MORPHIN, his team found that worm genes regulating ‘fat associated bodies’ are associated with human disease ‘hyperhomocysteinemia.’ This connection between worm phenotype and human disease was not detectable by any previous methods. This finding was also validated by independently reported clinical implication of association between hyperhomocysteinemia and Type 2 diabetes.

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