Mus Musculus Aging Genes' Topological Analysis and Prediction

Kai Feng, Yuan-Chun Zhou, Jian-Hui Li and Yan-Hui Li

Computer Network Information Center, Chinese Academy of Sciences

Abstract:

An important task of aging research is to find genes that regulate lifespan. Wet-lab identification of aging genes is tedious and labor-intensive activity. Developing an algorithm to predict aging genes will be greatly helpful. In this paper, we systematically analyzed topological features of proteins encoded by Mus musculus aging genes versus those encoded by non-aging genes in protein-protein interaction (PPI) network and found that aging genes are characterized by several network topological features such as higher in degrees. Based on these features, an algorithm was developed to detect aging genes genome wide. With posterior probability score describing possible involvement in aging higher than 0.8, 110 novel aging genes were predicted. Evidence supporting our prediction can be found.