

[P22] Network of Human Disease Genes from Association Studies*Jeehye Choi, Korea University*

Until recently, studies on genetic mutations were biased to those with Mendelian inheritance. More common, however, would be non-inherited mutations, the properties of which have not yet been characterized from network perspective. With this motivation, here we classify human disease genes into three classes, which are genes with lethal mutations, with Mendelian-inherited mutations, and with mutations identified by association studies. We compare their properties in the context of human interactome and transcriptome, focusing on distinct network features of the association-studied genes and their implications to understanding of diseases from non-inherited mutations.