

Korean team develops algorithm for diseased genes

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A new study, affiliated with Ulsan National Institute of Science and Technology (UNIST), South Korea has recently presented a novel statistical algorithm, capable of identifying potential disease genes in a more accurate and cost-effective way. This algorithm has also been considered as a new promising approach for the identification of candidate disease genes, as it works effectively with less genomic data and takes only a minute or two to get results.

In the study, the research team presented the novel method and software GSA-SNP2 for pathway enrichment analysis of GWAS P-value data. According to the research team, GSA-SNP2 provides high power, decent type I error control and fast computation by incorporating the random set model and SNP-count adjusted gene score.

The research team expects that their GSA-SNP2 is able to visualize protein interaction networks within and across the significant pathways so that the user can prioritize the core subnetworks for further studies. With this algorithm, the researchers can easily identify new drug targets, thereby deepening the understanding of diseases and unlock new therapies to treat it.