Summary

These works note that searching for a disease gene for many diseases might not exist. Instead, multiple genes work together to cause a disease, so looking at groups of genes might prove more useful. This is where gene set enrichment analysis helps by looking at groups of gene expressions and a phenotype.

Reaction

GSEA seems very powerful, letting us see connections that previous methods might miss. As demonstrated by the papers it is useful in many applications, such as diabetes, sex differences, and cancer.

Questions

How do we use this information that a group of genes work together?

Is the leading-edge subset of genes determined by just taking high scoring genes? How do we determine a cutoff if one should be applied?