

Genetic Mapping attempts to home in on the positions on the genome that are causative for a phenotype of interest such as disease susceptibility. The more that could be learnt about the genotype→phenotype function, the more valuable this will be. The widespread redundancy in the genetic architecture presents a problem in this context, as many phenotypes will only be detectable by multiple events in different parts of the genomes. This could be solved by including more positions in the assumed genotype→phenotype function. How could networks help with mapping? The object is to use network properties to map genes to characters and also make statements about which sets of genes will not work as a group and should not be considered as a combination in a mapping study.