

Impact of Interaction patterns on genetic association studies: an example of prostate cancer

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Abstract

It is commonly known that individual genetic variants or single nucleotide polymorphisms (SNPs) are not sufficient to explain the complexity of diseases' causality. It has been established that gene-gene/SNP-SNP interactions may have a higher impact on the causality of complex diseases than individual SNP effects. Despite many SNP-SNP interactions associated with cancers have been conducted, few of the results can be replicated. These inconsistent findings are partially due to inadequate statistical approaches. The conventional approach uses a hierarchical interaction model and treats SNPs as an additive mode is not sufficient. Our research team has developed two statistical methods: the SNP Interaction Pattern Identifier (SIPI) and the additive-additive 9 interaction-model approach (AA9int). In this talk, performance of these two statistical methods on evaluating SNP-SNP interactions associated with a binary outcome will be discussed. Application of using these new statistical approaches on evaluating SNP-SNP interactions on prostate cancer will also be presented.