

Fence Methods in Genetic Applications

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Abstract

Gene mapping techniques play a vital role in identifying the genes that are associated with a trait. Furthermore, gene mapping elucidates how these genes function interactively in their relation to each other and to environment, and hence contribute the variation of the phenotypes. Gene search is practically a long process, and, as an important first step, the goal is usually to identify the genomic area(s) that harbor genes attributed to the trait. For many simple traits, strong correlation between the phenotype and markers have been established. However, for complex traits to which many genes are attributed, the contribution of a particular gene is quite small. This leads to the difficulty in detection of the genomic region(s) near such gene(s) due to fairly weak correlation(s) between the markers and phenotypes. Several statistical methods have arisen to take advantage of the availability of numerous informative markers, hoping to map the genes more successfully in complex traits. Model search strategies play an important role in finding such susceptible genes simultaneously. Fence method [21] was motivated by a number of limitations of traditional information criteria in selecting optimal models. The goal of this project is to bring this method to genetics applications, hoping the method is able to detect the specific genome region that is tightly linked to genes attributed to complex traits.