

Generalized Linear Model for Mapping Viability Selection Loci

Shizhong Xu

Department of Botany and Plant Sciences, University of California

Abstract

Viability selection will cause fitness related genes to deviate from the expected Mendelian segregation. These loci are called viability selection loci. Molecular markers closely inked with these viability loci will show distorted segregation. Using the distorted markers, we can locate the viability loci. In this study, we develop a generalized linear model to map the viability selection loci using genome-wide high density marker information. Parameters of the generalized linear model are estimated using the Lasso method. A real life example is used to demonstrate the generalized linear model.