

# Statistical functional mapping for genetic control of programmed cell death

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## Abstract:

The development of any organism represents a complex dynamic process which is controlled by a network of genes and environmental factors. Traditional mapping approaches that analyze phenotypic data measured at a single time point are too simple to describe the genetic control of the development process. A general statistical mapping framework called functional mapping, has been developed for mapping quantitative trait loci (QTL) that underlie variation of a complex dynamic trait. In this study, I extend the principle of functional mapping to study the relationship between gene actions and a physiological cell suicide process, programmed cell death (PCD). PCD occurs during the development of most organisms. The biological mechanisms of PCD can be mathematically described as exponential growth for the first stage and polynomial death for the second stage. The developed model incorporates this unique PCD features into the functional mapping framework to localize genes that affect this process. Different modelling strategies are derived to model the mixture proportions for various genetic designs. A series of stationary and nonstationary models are applied to model the covariance structure among the phenotypes at different time points. The model is statistically investigated through simulation studies and validated by a real example for tiller number in rice. Our model provides a quantitative and testable framework for assessing the interplay between genes and organism developmental patterns.