

综述

## 多QTL定位的压缩估计方法

章元明

南京农业大学作物遗传与种质创新国家重点实验室/国家大豆改良中心, 南京 210095

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摘要

本文综述了多标记分析和多QTL定位的压缩估计方法。对于前者, Xu (Genetics, 2003, 163: 789-801) 首先提出了Bayesian压缩估计方法。其关键在于让每个效应有一个特定的方差参数, 而该方差又服从一定的先验分布, 以致能从资料中估计之。由此, 能够同时估计大量分子标记基因座的遗传效应, 即使大多数标记的效应是可忽略的。然而, 对于上位性遗传模型, 其运算时间还是过长。为此, 笔者将上述思想嵌入极大似然法, 提出了惩罚最大似然方法。模拟研究显示: 该方法能处理变量个数大于样本容量10倍左右的线性遗传模型。对于后者, 本文详细介绍了基于固定区间和可变区间的Bayesian压缩估计方法。固定区间方法可处理中等密度的分子标记资料; 可变区间方法则可分析高密度分子标记资料, 甚至是上位性遗传模型。对于上位性检测, 已介绍的惩罚最大似然方法和可变区间Bayesian压缩估计方法可供利用。应当指出, 压缩估计方法在今后的eQTL和QTN定位以及基因互作网络分析等研究中也是有应用价值的。

关键词 [Bayesian分析; 上位性; 多QTL模型; 数量性状基因座; 压缩估计](#)

分类号

## Shrinkage Estimation Method for Mapping Multiple Quantitative Trait Loci

ZHANG Yuan-Ming

Section on Statistical Genomics, State Key Laboratory of Crop Genetics and Germplasm Enhancement/Chinese National Center for Soybean Improvement, Nanjing Agricultural University, Nanjing 210095, China

### Abstract

<P>In this article, shrinkage estimation method for multiple-marker analysis and for mapping multiple quantitative trait loci (QTL) was reviewed. For multiple-marker analysis, Xu (Genetics, 2003, 163: 789-801) developed a Bayesian shrinkage estimation (BSE) method. The key to the success of this method is to allow each marker effect have its own variance parameter, which in turn has its own prior distribution so that the variance can be estimated from the data. Under this hierarchical model, a large number of markers can be handled although most of them may have negligible effects. Under epistatic genetic model, however, the running time is very long. To overcome this problem, a novel method of incorporating the idea described above into maximum likelihood, known as penalized likelihood method, was proposed. A simulated study showed that this method can handle a model with multiple effects, which are ten times larger than the sample size. For multiple QTL analysis, two modified versions for the BSE method were introduced: one is the fixed-interval method and another is the variable-interval method. The former deals with

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markers with intermediate density, and the latter can handle markers with extremely high density as well as model with epistatic effects. For the detection of epistatic effects, penalized likelihood method and the variable-interval approach of the BSE method are available.</P>

**Key words** [Bayesian analysis](#); [epistasis](#); [multiple QTL model](#); [quantitative trait locus](#); [Shrinkage estimation](#)

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通讯作者 章元明 [soy Zhang@njau.edu.cn](mailto:soy Zhang@njau.edu.cn)