Skew–Normal Composite Interval Mapping

Elisabete Fernandes

CEMAT, Portugal

Email: ebfernandes@fc.ul.pt

António Pacheco

CEMAT and Instituto Superior Técnico, Universidade Técnica de Lisboa, Portugal

Email: apacheco@math.ist.utl.pt

Carlos Penha-Gonçalves

Instituto Gulbenkian de Ciência, Portugal

Email: cpenha@igc.gulbenkian.pt

Abstract: The composite interval mapping, CIM, (Jansen and Stam, 1994; Zeng, 1994) combines interval mapping (IM) with multiple-marker regression analysis, which controls the effects of quantitative trait locus (QTL) on other intervals or chromosomes onto the QTL that is being tested and thus increases the precision of QTL detection. This approach makes use of the assumption that the quantitative phenotype follows a normal distribution (Kruglyak and Lander, 1995). Many phenotypes of interest, however, follow a highly skewed distribution, and in these cases the false detection of a major locus effect may occur (Morton, 1984). An interesting alternative is to consider a skew-normal mixture model in CIM, and the resulting method is here denoted as skew-normal CIM. This method, which is similar to CIM, assumes that the quantitative phenotype follows a skew-normal distribution for each QTL genotype. The maximum likelihood estimates of parameters of the skew-normal distribution are obtained by the expectation-maximization (EM) algorithm. The proposed model is illustrated with real data from an intercross experiment that shows a significant departure from the normality assumption. The performance of the skew-normal CIM is assessed via stochastic simulation. The results indicate that the skew-normal IM has higher power for QTL detection and better precision of QTL location as compared to CIM.

Key words: Composite interval mapping (CIM), Interval mapping (IM), Quantitative trait locus (QTL), Skew-normal distribution, Expectation-maximization (EM) algorithm

References:

[1] Jansen, R.C. and Stam, P. (1994). High resolution of quantitative traits into multiple loci via interval mapping. *Genetics*, Vol.136, p.1447-1455.

[2] Kruglyak, L. and Lander, E.S. (1995). A Nonparametric approach for mapping quantitative trait loci. *Genetics*, Vol.139, p.1421-1428.

[3] Morton, N.E. (1984). Trials of Segregation Analysis by Deterministic and Macro Simulation. *In*: Chakravarti, A. (Ed.), Human Population Genetics: The Pittsburgh Symposium. Van Nostrand Reinhold, New York, p.83-107.

[4] Zeng, Z.B. (1994). Precision mapping of quantitative trait loci. *Genetics*, Vol.136, p.1457-1468.