QTL EXPRESS: RAPID AND USER-FRIENDLY MAPPING OF QUANTITATIVE TRAIT LOCI IN LIVESTOCK

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INTRODUCTION

We have developed fast, efficient and robust linear regression methods to map QTL in simple and complex pedigrees of relevance in livestock (*e. g.*, Haley and Knott, 1992; Haley *et al*., 1994; Knott *et al*., 1996; Visscher *et al*., 1996; Knott *et al*., 1998; George *et al*., 2000). QTL Express makes these QTL mapping tools immediately available to the wider scientific community via a web-based user interface.

COMPUTING METHODS

We follow a robust two-step procedure for QTL mapping, by firstly determining the identity-by-descent (IBD) probabilities at specific chromosomal locations from multiple marker data, and secondly fitting a statistical model to the observations and IBD coefficients. Populations that are currently suitable for QTL Express are half-sib outbred populations and F_2 populations derived from crosses between either inbred or outbred lines. Sib pair analysis for full-sib families will be implemented shortly.

Linear models are fitted to phenotypic data using a general linear model, *i. e*., allowing for additional fixed effects and covariates that explain trait variation. For the genetic component in the linear model, a single QTL or a two QTL model is fitted. Additional QTL can be fitted through the use of cofactors. For populations derived from crosses, the model for the QTL can be specified in terms of an additive and a dominance effect, with the option of an interaction between the QTL and a fixed effect. Additionally, for outbred line crosses, the QTL model can include a parent-of-origin effect (*e. g.* imprinting).

For the crosses between inbred or outbred lines producing F_2 populations, QTL are mapped that explain genetic variation between the founder lines. Implicitly, the founder lines are assumed to be fixed for alternative alleles at the QTL. This assumption can be tested in a cross between outbred lines by including an interaction between the QTL and family. For the half-sib population structure, QTL are mapped that explain within-family variation, with the evidence for QTL segregation accumulated across the common parents (Knott *et al*., 1996).

Permutation tests to set chromosome significance thresholds (Churchill and Doerge, 1994) and a bootstrap procedure to estimate the confidence interval of a QTL location (Visscher *et al*., 1996) are implemented.

EXAMPLE

The data set consisted of 693 progeny in 20 half-sib families. In Figure 1a the test statistic for one QTL at the given location versus no QTL, an F-ratio with 20 degrees of freedom in the numerator and 657 degrees of freedom in the denominator, is shown across the linkage group. In Figure b, the absolute t-values for each family indicate the strength of evidence for a QTL at the location estimated in the across-family analysis.

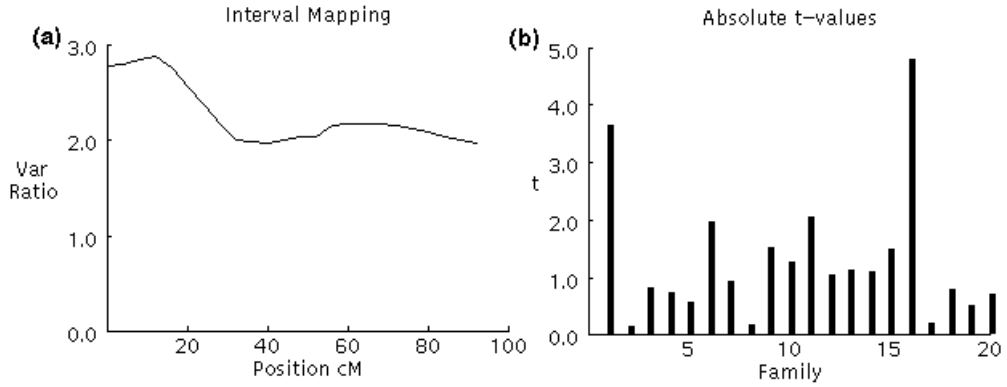

Figure 1: Example of graphical output from QTL Express. (a) Results from fitting a single QTL model, (b) Individual test statistics per half-sib family

AVAILABILITY

QTL Express is a free QTL mapping service available now at http://qtl.cap.ed.ac.uk.

COMPUTING ENVIRONMENT

The QTL Express site uses Java servlets. All numerical analysis, graphics and HTML output is handled by classes produced and executed by a 1.1.8 Java Development Kit compiler and virtual machine respectively. The QTL Express web site is a small server farm based on Intel i386 machines running Linux.

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