Aula 11 – Multiple interval mapping (MIM)

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Materials and Methods

The genotypic and phenotypic information from a F_2 *Mimulus* population was used to construct a genetic map using the OneMap v.2.0 (Margarido et al. 2007; version under development) a package for R. The trait under consideration for QTL mapping is "pv" (trait 8) of the data set. To perform the multiple interval mapping (MIM) of QTLs related to this trait the data set and the genetic map were loaded into the R/qtl package for R software (Broman et al., 2003). The first step of the analysis was to choose the best available model (model selection). This was done by performing a stepwise method using the Haley-Knott approximation considering epistatic interactions between them and also refining the QTLs positions after each modification of the model. The criterion for model selection was the BIC criterion. This procedure was implemented using the stepwiseqtl function of the R/qtl software package.

The penalties used in the BIC criterion were calculated through 1000 permutations of the genome also using the Haley-Knott approximation (Haley & Knott, 1992). Initially the number of QTLs was not known a priori. To solve our problem we made the following procedure. First we use the stepwise function to find the best model for the trait that was chosen (pv), than based on the results for stepwise function the makeqtl function was used to estimate the QTLs effects and refine the QTL position aiming identified QTL by refineqtl function. Finally the best model was fit to estimate the QTLs effects.

References

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