On the theory of QTL detection

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In the case of a linkage analysis of a backcross population, Lander and Botstein (1989) and Cierco (1996) proved, under the assumption of a dense map with all markers informative, that the likelihood ratio test (LRT) statistic under the null hypothesis that there is no QTL versus the alternative is asymptotically (as the number of individuals tends to infinity) distributed as the square of an Ornstein-Uhlenbeck process on the chromosome.

In a first part, we generalize this result to a population with family structure. We obtain that the LRT statistics is asymptotically (as the number of individuals in each family tends to infinity) distributed as the square of an Ornstein Uhlenbeck Chi Square process (OUCS).

By simulations, we show that the dense map hypothesis is too strong. That's why, we extend the previous results to the case of a sparse map. We obtain that when the tests are only performed on markers, the limit process defined by the test statistic is a Discrete Ornstein Uhlenbeck Chi Square process. When the tests are performed anywhere on the genome, the limit process defined by the test statistic is the sum of the square of I independent gaussian processes with unit variance and covariance function equals to $\exp(-2d_{xy})$ where d_{xy} is the distance between the closest markers of positions x and y. This last result is obtained using the information of the closest marker of each position.

As all these results are asymptotic, we try to quantify, by simulation, the number of individuals required in each family to match the asymptotic hypothesis. Besides, we show that these theoretical results decrease highly the CPU time needed to calculate the threshold.

Finally, in the case of only one family, we obtain the limit process of the LRT statistic first under the alternative that there exists one QTL on the chromosome and then under the general alternative that there are Q QTLs on the chromosome. This last results allows us to propose a method to estimate the number of QTLs on the chromosome, their effects and their positions.