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Logic regression based methods in application to quantitative trait loci (QTL) data analysis

We consider a biological problem of locating multiple interacting QTLs. Logic regression is a regression method, specifically aimed at detecting high order interactions in SNP data. Considering the problem of detection of interacting QTL as a problem of multiple testing, we show theoretically that logic regression may lead to a larger power of detection an interaction than the standard methods based on a Cockerhams genetic model. Next we consider a procedure called logicFS (logic feature selection) in which the "best" model of a fixed dimension is estimated with simulated annealing, aimed at maximising the likelihood. The overfitting is prevented by aggregating the results of the analyses performed on many bootstrap replications of the original sample. The method can be applied both for binary and quantitative responses. We applied LogicFS for QTL mapping and compared it to the classical methods based on the standard linear models by computer simulations and real data analysis. We analysed two real QTL data sets. For both data sets logicFS was able to detect some interactions which were not reported in original papers and not detected by standard QTL mapping methodology. According to our results, logicFS can be successfully applied to identification of interacting QTLs.