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Joint Modelling of Genetic Linkage and Association

A joint modelling of genetic linkage and association within families having a remote common ancestor is presented. This joint modelling uses a likelihood approach that allows the inclusion of other covariates into the model for quantitative traits; for binary traits, a score test is proposed. The simulation study show that the joint test is more powerful than linkage or association test alone where both sources of variation are present. Furthermore, the proposed method also allows to test against specific alternatives. For example, against the significance of linkage given that there is no association and so on.