SCORE TEST FOR LINKAGE IN GENERALIZED LINEAR MODELS

J.J.P. Lebrec, H.C. van Houwelingen

Leiden University Medical Center, Leiden, The Netherlands

Email: *j.j.p.lebrec@lumc.nl*

We derive a test for linkage in the Generalized Linear Mixed Model (GLMM) framework, it provides a natural adjustment of the test for marginal covariate effects. The method boils down to the score test of a quasi-likelihood derived from the GLMM, it is computationally inexpensive and can be applied to arbitrary pedigrees. In particular, for binary traits, relative pairs of different nature and individuals with different covariate values can be naturally combined in a single test that takes the dependence between pairs into account. In the case of sib-pairs, the approach gives some insight as to how different versions of the so-called Haseman-Elston regressions, routinely used for continuous phenotypes, can be adapted to binary phenotypes. As illustration of our method, we use published population migraine data to obtain estimates of the marginal effect of sex. By simulating a putative locus in sib-pair data, we quantify the potential gains obtained when taking sex into account in the linkage test and we show how both affected and discordant pairs are combined.