A Logistic Regression Model for Measuring Gene-Longevity Associations

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The logistic regression model is a popular model for data analysis in epidemiological research. In this paper we employ this model to analyze genetic data collected from gene-longevity association studies. This new approach models the probability of observing one genotype as a function of the age of investigated individuals. Applying the model to genotype data on the TH and 3’ApoB-VNTR loci collected from an Italian centenarian study, we show how it can be used to model the different ways that genes affect survival, including sex and age-specific influences. We highlight the advantages of this application over other available models. The application of the model to empirical data indicates that it is an efficient and easily applicable approach for determining the influences of genes on human longevity.