

Procedure and tool to determine genetic associations. The method allows to identify, without the need for predictive hypothesis, genes that influence, either individually or preferably collectively, the appearance of any phenotypic trait shared by several groups of individuals; groups in each of which the characteristic appears in a different context as they can be different diseases, a different reaction to the same treatment or different manifestations of the same disease. For each phenotypic context, a study is carried out of cases and controls, giving rise to associations of genes or combinations of genes with statistical significance. These associations are filtered, eliminating those that also appear when comparing controls versus controls. Of the remaining associations, those that have appeared in all the cases and controls are selected, preferably rationalized, and are validated by analysing their presence in larger groups.