

Incorporation of Gene Information for Conducting Meta-analysis

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Abstract:

Meta-analysis can be defined as “the statistical analysis of a large collection of analysis results from individual studies for the purpose of integrating the finding” (Glass 1976). For human genetic linkage studies, the integration could be pooling marker data, estimating allele sharing among related individuals, or combining LOD scores or p-values across studies to obtain a consensus. The consensus can be evidence for linkage to a QTL or estimate of genetic variance. Just as individual linkage studies have challenges (i.e., power of the linkage test, sample size, ascertainment bias, population admixture, etc.); meta-analysis, too, has many challenges: publication bias, time-lag bias, same complex disease, different phenotype and among-study heterogeneity (i.e., differing sample sizes, denseness of marker maps, environmental factors, population substructure, ascertainment schemes). In this presentation, I review existing meta-analysis for human linkage studies in terms of a meta-analysis spectrum consisting of five. Level 1 encompasses the realized situation in which meta-analysis is completed using information only obtained from published sources. The spectrum proceeds to level 5 and details the ideal situation in which raw data from numerous linkage studies are available to the researcher. For each level, existing meta-analytic procedures are discussed as well as their advantages and disadvantages.