Statistical modeling of genotype-phenotype relationship through gene family analysis

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Quantitative genetics aims to understand the genetic bases of traits (phenotype) coded by many genes, or complex traits. This kind of trait includes most traits of interest in medical science (e.g. complex diseases), animal and plant breeding (e.g. growth, productivity) and evolutionary biology (e.g. life-history traits). Gene families have extraordinary importance in elucidating genome architecture and dynamics: they combine the study of traits at pathway level with the evolutionary mutational divergence and selection trajectories. We propose an Ornstein-Uhlenbeck model to study genotype-phenotype mapping and the relations of genes within large families of duplicated genes scattered in the human genomes. This model is also suitable to investigate patterns of speciation. We discuss our model in the context of the infinitesimal model (Fisher 1918), the recent omnigene model and we describe a tutorial of a related software.

References

R. A. Fisher. The correlation between relatives on the supposition of Mendelian inheritance. Proc. Roy. Soc. Edinburgh 52 (1918), 399-433.