

Developing an Information Theory of Quantitative Genetics [†]

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Quantitative genetics has evolved dramatically in the century since its foundation, and the modern proliferation of genetic data both in quantity and in type now enables new kinds of analysis beyond the scope of its theoretical foundations. We have begun laying the foundations of an alternative formulation of quantitative genetics based on information theory since it can provide sensitive and unbiased measures of statistical dependencies among variables, as well as a natural mathematical language for an alternative description of quantitative genetics. After all, genetics is fundamentally the science of information transfer between generations. Earlier work has applied information theory to descriptions of evolution and some aspects of population genetics. In our previous work we examined the information content of discrete functions, which are useful in describing genetic relations and applied this formalism to the analysis of genetic data. We describe a set of relationships that both unifies the information measures for these discrete functions and uses them to express key genetic relationships in genotype and phenotype data. We present information-based measures of the genetic quantities of penetrance, heritability and degrees of statistical epistasis. We analyze two- and three-variable dependencies for independently segregating variants, which captures a range of phenomena including genetic interactions, and two phenotype pleiotropy. Note however that this formalism applies naturally to multi-variable interactions and higher-order complex dependencies as well, and can be extended to account for population structure, genetic linkage and non-randomly segregating markers. We discuss our progress towards laying the groundwork for a full formulation of quantitative genetics based in information theory.



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