

The G-Matrix as One Piece of the Phenotypic Evolution Puzzle

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In quantitative genetics, a single term, the genetic covariance matrix (G-matrix), is used to encompass all important associations between traits, whether due to pleiotropy or gametic disequilibrium. As noted by Polly (2008) some quantitative geneticists have argued that the G-matrix is a sufficient descriptor of the ways in which underlying development influences phenotypic evolution, while many other researchers find these models unsatisfactory. To see why G-matrix models are sufficient sometimes, but not always, we need to look to a more general formulation, phenotype landscape theory, of which quantitative genetics is one special case.

A phenotype landscape is a plot of some trait as a function of a set of underlying genetic or environmental factors. Such landscapes have recently started to be constructed for particular traits, either through the synthesis of detailed developmental studies (Nijhout et al. 2006) or through Quantitative Trait Locus analysis (Rice 2008). Evolution on the landscape is described by a set of vectors, termed Q vectors, each of which corresponds to a different set of interactions between the underlying factors or a different property of the shape of the distribution of underlying variation. There are potentially a very large number of Q vectors, and an exact description of how a population evolves over a phenotype landscape requires specifying all of them. One of these vectors, Q_1 , describes the effects of directional selection on an uncurved landscape in terms of only the variances and covariances of the distribution of underlying genetic variation. Q_1 is thus essentially the same as the G-matrix model.

The fact that the G-matrix is only one of many terms that jointly describe phenotypic evolution raises the question of why it is ever useful by itself. The answer is

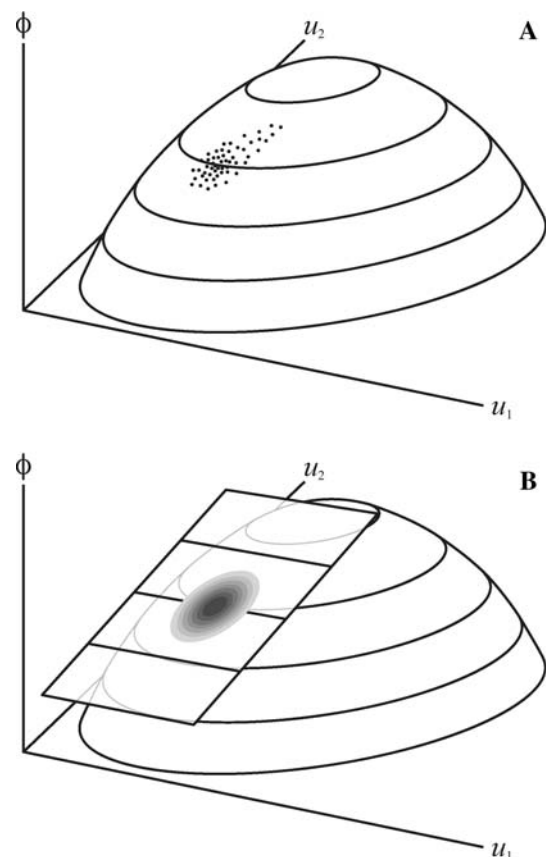


Fig. 1 What G-matrix models see. (a) A nonlinear phenotype landscape representing a trait, ϕ , as a function of two underlying genetic factors. The cloud of points on the surface represents a population, each point corresponding to an individual. (b) G-matrix models consider a tangent plane and treat the population as a multivariate normal distribution

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illustrated in Fig. 1. G-matrix models consider a local linear approximation to the phenotype landscape. We can think of this as a plane that is tangent to the landscape at the point corresponding to the population mean. These models also replace the actual distribution of variation within the population with a multivariate normal distribution. So long as the landscape is locally smooth, then for a very small region it will be well approximated by an uncurved plane. If, in addition, the joint distribution of parent and offspring phenotypes is close to multivariate normal, then G-matrix models provide a good approximation of short term evolution.

Figure 1 also illustrates why G-matrix models are of little value for the study of long term evolution. As the population moves over the landscape, the slope and local geometry changes (i.e., the genetic architecture changes) in ways that could not be predicted from the initial linear

approximation. G-matrix models are thus a useful tool for addressing some questions in phenotypic evolution, but they are at best one piece of a much larger puzzle if we are interested in long term evolution or evolution of developmental processes.

References

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