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Saturday, January 20, 2007

Evolution - The hitchhiker's guide to altruism

Darwin explained how beneficial traits accumulate in natural populations, but how do costly traits evolve? In the past, two theories have addressed this problem.

The theory of hitchhiking suggests that genes that confer a cost to their bearer can become common in natural populations when they "hitch a ride" with fitter genes that are being favored by natural selection. Conversely, the theory of kin selection suggests that costly traits can be favored if they lead to benefits for relatives of the bearer, who also carry the gene.

"Animal traits are not always independent. For example, people with blond hair are more likely to have blue eyes," explains Andy Gardner (Oxford University). "This is a nuisance for natural selection, which could not, for instance, favor blond hair without also indirectly favoring blue eyes, and this is the idea of genetic hitchhiking."

Kin selection is similar, but here the genetic associations are between different individuals: "If I have a gene that makes me more altruistic, then I can also expect my relatives to carry it. So while the immediate effect of the gene is costly for me, I would benefit by receiving altruism from my relatives, and so the gene is ultimately favored," Gardner explains.

New research carried out at the University of Edinburgh and Queen's University, Canada shows that both processes are governed by the same equations. This reveals that kin

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selection can be seen as a special form of genetic hitchhiking, explain Gardner and his coauthors Stuart West and Nick Barton (University of Edinburgh) in the February issue of *The American Naturalist*.

The researchers built on a general framework for modeling hitchhiking first proposed by Barton and colleagues, showing how it can be used to describe social evolution and recovering the classical results of kin selection theory. This insight raises the possibility of using the tools of hitchhiking theory to explore social problems that have so far been too complicated to analyze using traditional kin selection techniques. [Source: University of Chicago Press]

Based on the paper:

The Relation between Multilocus Population Genetics and Social Evolution Theory

Abstract / Full Text

Evolution at multiple gene positions is complicated. Direct selection on one gene disturbs the evolutionary dynamics of associated genes. Recent years have seen the development of a multilocus methodology for modeling evolution at arbitrary numbers of gene positions with arbitrary dominance and epistatic relations, mode of inheritance, genetic linkage, and recombination. We show that the approach is conceptually analogous to social evolutionary methodology, which focuses on selection acting on associated individuals. In doing so, we (1) make explicit the links between the multilocus methodology and the foundations of social evolution theory, namely, Price's theorem and Hamilton's rule; (2) relate the multilocus approach to levels-of-selection and neighbor-modulated-fitness approaches in social evolution; (3) highlight the equivalence between genetical hitchhiking and kin selection; (4) demonstrate that the multilocus methodology allows for social evolutionary analyses involving coevolution of multiple traits and genetical associations between nonrelatives, including individuals of different species; (5) show that this methodology helps solve problems of dynamic sufficiency in social evolution theory; (6) form links between invasion criteria in multilocus systems and Hamilton's rule of kin selection; (7) illustrate the generality and exactness of Hamilton's Rule, which has previously been described as an approximate, heuristic result.

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Excerpt:

In this article, we highlight the social evolutionary interpretation of this multilocus methodology. In particular, we show how the quantitative genetical approach is exactly analogous to existing methodology used for social evolutionary problems and that it provides a straightforward guide to constructing and analyzing social evolutionary models of arbitrary complexity. Moreover, we demonstrate that multilocus theory may be used to solve problems of dynamic sufficiency in social evolution models so that we may examine coevolutionary dynamics of social evolutionary traits and describe the evolution of relatedness itself. We emphasize that no new methodology is developed but rather that this article is intended as a synthesis of multilocus and social evolution theory so that the results derived within each of these bodies of theory may be readily interpreted in terms of the other.

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