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MODELS AND SCIENTIFIC EXPLANATIONS *

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1. Models of Explanation and the Structure of Theories.

Theories have traditionally been treated as axiomatic systems, consisting of a formally defined set of statements, the "fundamental laws" of the theory, closed under some implication relation. The interpretation of the system comes only with the application of a selected subset of the terms, the "observation vocabulary", to empirical or observable phenomena; in Ernst Nagel's words, "the fundamentel assumptions of a theory constitute a set of abstract or uninterpreted postulates" (Nagel 1961, p. 91; cf. Carnap 1956).

Explanation was correspondingly understood as deduction, or as Carl Hempel puts it, as "deductive subsumption under laws or theoretical principles" (1964, p. 291). In the familiar schematic form, explanation in the "Deductive-Nomological" (D—N) form, as elaborated by Hempel and Paul Oppenheim, can be represented as follows :

$C_1, C_2, \ldots C_i$	Statements of Antecedent Conditions
$L_1, L_2, \ldots L_j$	General Laws
E	Phenomenon to be explained

Hempel and Oppenheim laid down four conditions which any explanation, whether deductive or inductive, ought to meet (cf. Hempel and Oppenheim 1948, pp. 247—248) :

(1) The explanation must have correct logical form.

When the explanation is of the D—N variety, the form was one of

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logical entailment; when of an inductive form, a weaker relation was allowed (cf. Hempel 1962 and 1965).

(2) The premises of the explanation must be true.

Without this condition being met, we have something that is no more than a potential explanation.

(3) There must be at least one lawlike generalization occurring essentially among the premises.

If each of these laws is a universal generalization, the explanation is of the D—N variety, if even one is a statistical generalization, it is of an inductive variety.

(4) The explanation must have premises with empirical content. Most importantly, it must be possible to determine what antecedent conditions hold, and what consequences ensue.

Neither the axiomatic view of theories nor that of theoretical explanation has proven to be without its problems. Perhaps the most salient problems concerning theoretical explanation have centered on the view of *statistical explanation.* Hempel defended the view that statistical explanations are but species of deductive explanations, in which at least one of the laws essentially involved are statistical laws. He tells us that "while a deductive explanation shows that, on the information contained in the explanans, the explanandum was to be expected with 'deductive certainty', an inductive explanation shows only that, on the information contained in the explanans, the explanandum was to be expected with high probability" (Hempel 1966, p. 59). In both cases, the function of explanation was to show that the event to be explained was naturally tobe expected, or could have been reasonably expected, in light of the relevant laws and conditions.

Wesley Salmon has pressed that the requirement that statistical, or probabilistic, explanations should render the effect more likely than its absence is one that is not generally met. The following case is representative. The explanation for pulmonary tuberculosis is, in part at least, contact with the tubercle bacillus. That is to say, if we propose to explain why a person contracts pulmonary tuberculosis, we must do so in terms of prior contact with the bacillus. This is true even though it is also true that most infections by the bacillus are countered effectively by the body's defenses, and that most contacts with the tubercle bacillus do not result in any infection at all. Contact with the bacillus is certainly causally relevant, even though such contact does not make contraction of pulmonary tuberculosis especially likely. Salmon has accordingly offered a formalization of statistical explanation according to which, given a factor that is statistically relevant to a specified effect, we know what "degree of expectation is rational" (Salmon, 1965, p. 78). Where "$P(A.C_1,B)$" represents the probability that a member of C_1 will be a member of B((C_1 is a subset of A), and where the goal is to explain why a particular object x, which is a member of A, is a B, the schema provided by Salmon may be given as follows :

(I) $P(A.C_1, B) = p_1$

$P(A.C_2, B) = p_2$

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$P(A.C_n, B) = p_n$

where

(II) $A.C_1, A.C_2, ..., A.C_n$ is a partition of A such that :
  (i) there is no partition of any $A.C_i$ into subclasses C_α and C_β and $P(A.C_\alpha, B) \neq P(A.C_\beta, B)$; and
  (ii) there are no i and j, $i \neq j$, such that $P(A.C_i,B) = P(A.C_j,B)$.

and

(III) $x \in A.C_k$.

it follows that :

(IV) The probability that x is/will be in B is p_k.

There are conditions of adequacy, analogous to those which apply to the Hempelian schema, applying to the S—R model :

(1) The explanation must have the correct logical form. That is, it must be capable of being regimented in the format provided above.

(2) The principles in the explanation must be true.
That is, the clauses given in Condition (I) must represent the *objective probabilities* for their respective reference classes (It does not matter whether these probabilities are treated as limiting

frequencies, with Salmon, or as propensities.)

(3) There must be at least one principle occurring essentially in the explanation.

That is, there must be some clauses in Condition (I) necessary for carrying through the explanation.

(4) The explanation must appeal to all the relevant classes within the reference class.

That is, the partition on A must be exhaustive and homogeneous in the sense specified in Condition (II). The corresponding condition imposed by Hempel is the requirement that the reference class be maximally specific (cf. Hempel 1965, pp. 394 ff.), and requires, intuitively, that the choice of a reference class relative to which probabilities are assessed should take into account all the information available which is of explanatory relevance. Unless some such condition is imposed, the condition of testability will be violated because there will be no determinate reference class with respect to which probability assignments can be made.

Several comments are in order. First, non-statistical, deterministic, explanations are no more than limiting cases of the above schema in which the probability is 1, and the initial reference class, A, is homogeneous with respect to B. Second, insofar as the *logical* structure is concerned, it does not matter whether x is an instance or a class of instances. The schema can therefore be extended beyond the single-case paradigm. Third, the S—R model is simply an extension of the Hempelian model which allows that "[an] explanation does not show that the event was to be expected; it shows what sorts of expectations ould have been reasonable and under what circumstances" (Salmon, 1965, p. 79). Alternately, it may be taken to show the *degree of causal influence* which the subclasses of A exert with respect to B (cf. Salmon 1975).

2. *Models and Theories : Pragmatics.*

The axiomatic view of theories has hardly fared better. Though some scientific theories can be treated as axiomatic structures, and though others can be partially axiomatized, it does seem clear that many cannot be cast in an axiomatic form, or cannot be so cast in a way that is useful either philosophically or scientifically. Thus, Freudian psychology, much of evolutionary theory, theories of development and gene expression, as well as theories of motivation and learning appear, for one reason or another, to be unreceptive to formal axiomatization (see Suppe, 1974, pp. 62 ff. for a useful discussion of this point).

One alternative to the axiomatic view which has gained some credibility is what is called the "semantic view of theories" (cf. Suppes 1967, Sneed 1971, Suppe 1972 and 1974, van Fraassen 1972 and 1980, Stegmüller 1976, and Giere 1984; for applications to biological theory, Beatty 1980a and 1980b, Thompson 1983, and Lloyd 1984). As its proponents explain it, on this view, a *presentation* of a theory is a specification of a set of abstract structures, what are intuitively its models, and an *application* of a theory is an interpretation of it applied to the actual world. The goal in presenting a theory is to define a family of models, each member of which exemplifies the same abstract structure, and which vary at most in their assignments of values to variables and parameters. Many population models in evolutionary ecology use only a variable for population size at a time, $N_i(t)$, for each of the relevant species in constructing a state description. It is assumed that this variable, together with values for reproduction, migration, and mortality, will be adequate to predict the future growth of the population. Alternately, to use an example developed by Ron Giere (1984), we can take a Newtonian system to be one which satisfies the three laws of motion, together with the law of universal gravitation; the models within the family would be determined by assignments of specific values for the variables, including the number of point masses within the system, and their respective values for location, mass, and velocity. Varying values for these latter variables would define distinct models within the family. The application of a theory is accordingly the identification of some natural system as, at least approximately, one of the models within the family. The system consisting of the earth, moon, and sun, e.g., approximates a three-body Newtonian system, and that simple model can be used in predicting their behavior. Analogously, population size can be used to predict future growth, so long as other factors (e.g., age structure, sex ratios) are relatively insignificant variables.

It does not matter for my purposes if there is a *principled* difference between the semantic view of theories and its axiomatic, "syntactic", rivals. There are *practical* differences between the approaches which make it preferable, for our purposes, to adopt the semantic view of theories. Most importantly, the class of cases which I shall be most concerned with, from evolutionary theory and evolutionary ecology, are standardly presented in a format which is very close to that adopted by advocates of the semantic view of theories. It will therefore involve us in a minimum of interpretation.

The models in terms of which a theory is presented are *ideal* systems. Presenting a *family of models* involves specifying the controlling parameters, the dimensions of variation, and dynamic principles. Given determinate assignments to the parameters and system variables, the dynamic principles provide a function from state-assignments to other state-assignments in the state-space. Viewed in terms of the potential applications of the theory, the articulation of a family of models involves the specification of the significant controlling variables in the domain for which the model is designed and to which it is intended to be applied. Other influences are assumed to be negligible, at least for the level of predictive and explanatory accuracy the model is designed to attain. Whether explicitly or implicitly, the articulation of a family of models will incorporate idealizations fixing the boundary conditions within which the family of models is developed. Newtonian mechanics commonly assumes the objects within its domain are point masses, and its application to real systems depends on the assumption that distances between objects are sufficiently great that real size is a negligible factor, and forces other than gravitational forces do not have significant effects. Relying on $N_i(t)$ as a predictor of population growth assumes that alternative influences are also negligible (in this case, they often are not).

The introduction of idealizations is clearly motivated by the need to obtain analytical tractability. As William Wimsatt has urged, they are essentially heuristic devices, geared to promoting economy in problem solving (see Wimsatt 1980 and 1981; also Michod 1981). Whether the case at hand is one of calculating the effects of gene interaction and linkage on fitness, or one of providing solutions to equations in celestial mechanics, in the absence of idealizations computational complexity will bar a solution to the problems posed even when they involve relatively small numbers of independent variables.

A simple case from evolutionary theory will illustrate the point. Biological models are often developed under the assumption that traits are controlled by single loci, with limited numbers of alleles, and which enjoy considerable independence. It has long been recognized that these single-locus models are unrealistic in a variety of ways. Traits are not generally under the control of single loci, the spatial relations of genes affect their expression, and linkage insures that genes affecting different traits will share a common fate. The ubiquity of these 'beanbag' models in biological theorizing is thus not a matter of their being regarded as realistic models. The gain from the assumption of a one-locus system is, rather, a practical one. By restricting the number of variables to be considered, one effects a simplification of the problems posed, and renders them analytically tractable. Wimsatt makes the essential point :

> "Similar advantages accrue for similar combinatorial reasons if problems of evolutionary dynamics can be treated in terms of the frequencies of individual alleles, with no epistatic interactions and no probabilistic associations between alleles at different loci due to linkage or assortive mating rather than in terms of the gametic or zygotic frequencies required if these assumptions do not hold. Here the simplification occurs in the number of dimensions in the phase space required to adequately describe and predict evolutionary changes" (1980, pp. 222–223).

We can see the advantage gained by working with the one-locus model most clearly by contrast with more complicated cases. Suppose the problem is to predict the relative frequency of variants in the population, for *two* alleles at each of *two* loci. The relevant variables are simply the relative frequencies of the alleles. The crucial parameter values will be the relative fitnesses assigned to each variant in the population. If we assume that there is no assortive mating, that there is perfect Mendelian segregation, and that there is no epistatic interaction, then it is possible to predict the future state of the system, given assignments of relative fitness to the alleles, as a function of two variables. For each locus, the frequency p of one allele is sufficient to determine the frequency of the second allele of that locus (viz., $1 - p$). Given lack of linkage and epistatic effects, the relative frequencies of genes at the other locus do not matter, and so the problem of projecting gene frequencies resolves into two independent problems. The assumptions of this model permit unproblematic predictions of subsequent states of the system from an initial assignment of frequencies and fitness values. It is possible to elaborate on this relatively simple case, and work in the last decade has seen substantial research on a limited number of models for two and three locus systems, with and without interaction. Nonetheless, this extension comes at considerable cost. For example, if we assume that *none* of the three idealizing assumptions hold, then the dynamic problem is one of predicting the future state of the system based on the relative frequency of zygotic classes. For the case of two alleles at two loci, this means that the subsequent state of the system is a function of no less than eight independent variables, specifying the frequencies of the zygotic types (there are nine possible genotypes), together with the associated fitness assignments. There is, as far as I know, no *general* solution to a problem of this dimensionality.

The contrast with the one-locus model is illuminating. In this case, the complexity of the problem is not appreciably affected by the adoption of the simplifying assumptions. If we again assume there is no assortive mating, perfect segregation, and lack of interaction, the state of the system is a function of but one variable; viz., the frequency of one allele at that locus. Without any of the three assumptions, we must again use zygotic frequencies as the units of analysis, but since there are but three possible zygotes (corresponding to the two homozygotes and the heterozygote), the state of the system is a function of two variables. The assumption of one-locus control thus leads to considerable simplification, and allows a treatment of systems that are otherwise biologically more realistic.

This sort of case is typical. In the analysis of population structure, multiple-species systems, and even social behavior, it is often assumed that the systems are "decomposable", and therefore that complex problems can be resolved into subproblems and solved independently. The crucial points to be made about such assumptions are two. *First*, they are *essential* in the sense that it is not feasible in practice to provide detailed explanations outside the imposed boundary conditions. Though, as we have seen in the case above, one idealization (viz., one-locus control) can be traded off against others (viz., there is no assortive mating, perfect segregation, and lack of interaction); but it is not feasible to dispense with them altogether. *Second*, they are *unrealistic* in the sense that the conditions they impose are rarely, if ever, met in actual cases. Again, though it is possible to vary the idealizations in such a way that particular dimensions fitting actual cases are met, it is not possible in general to construct or deploy a model which is realistic on all the relevant dimensions Simultaneously.

3. Models and Theories : Adequacy.

The adequacy of a family of models as explanatory structures will depend on a number of factors. Among many that might be considered, two are particularly noteworthy. The first concerns the limitations on the empirical applicability of the models. The second concerns what can be demanded of the dynamic principles.

If we are to apply models in explaining actual phenomena, we must, first of all, be able to attain realistic estimates of the values of the state variables and parameter values. If we view the dynamic principles as functions from states to states within a multi-dimensional state-space, then the problem is essentially one of obtaining reliable estimates for parameter values and for those variables which determine one's position within the phase space. In many cases, this is an extremely difficult undertaking. It was, e.g., an important achievement of evolutionary biology in this century to determine the amount of genetic variability in natural populations and the rate of genetic mutation; these values are, in turn, critically important in assessing different models of population structure and their impact on evolutionary change. A brief consideration of two related cases will serve to illustrate the methodological and theoretical difficulties which attend the assessement of empirical adequacy.

Within the literature on sociobiology, one of the more powerful analytical tools involves the application of game theory to evolution. It is assumed that we can evaluate behavioral strategies with respect to their relative optimality, and determine which, if any, of these strategies are evolutionarily, stable. John Maynard Smith pioneered the application of this tool in examining both aggressive behavior and sexual differences. A simple and standard example from his work will suffice. Let us suppose that a *Hawk* is any individual willing to escalate the level of violence in competing for any given resource, at least until she suffers serious injury. A *Dove*, correspondingly, is any individual that will avoid escalation, even if it means abandoning the contested resource. A Hawk will obviously succeed in any contest with a Dove, since she will escalate the level of violence when the Dove will not. Maynard Smith saw that this alone does not show that a Hawk is more "fit" than those with alternative strategies. What is important is whether a strategy is an *Evolutionarily Stable Strategy;* that is, whether, in a population in which a given strategy is universally adopted, any alternative strategy is superior. If the strategy is an evolutionarily stable one, no alternative would allow an individual to do better than the dominant strategy. Within specifiable limitations on the benefits (for acquiring the resources in question) and the costs (either in time wasted in competition, or from injury), it can be shown that neither a pure Hawk nor a pure Dove strategy is stable: in a population of Doves, a Hawk will enjoy unlimited success; and in a population of Hawks, a Dove will at least manage to avoid serious injury (for detailed treatment, see Maynard Smith 1975 and 1976).

It is frequently asserted that the particular parameter values (in this case, the values attached to benefits and costs) make no difference to this outcome. That is simply false. What the models give us are a family of curves for relative fitness values. Though the general shape of the curves is uniform, their location relative to the axes varies with parameter value assignments. Assuming that an individual who fails in a competition gains nothing in compensation and, further, that the cost of wasted time in conflicts between Doves is negligible, then a pure Hawk strategy will be stable provided that the magnitude of the benefit for a 'win' exceeds the magnitude of the cost for a 'loss'; that is, as injury costs go down, the stability of a Hawk strategy goes up. A pure Dove strategy will, correspondingly, be increasingly stable as the ratio of the benefit for a 'win' to the cost of an 'injury' approaches zero; that is, as injury costs go up, the stability of a Dove strategy goes up accordingly. In presentations of the models, values for these parameter values are assigned which are 'intermediate' in character, and that guarantees the result that neither pure Hawk nor pure Dove strategies are stable. What is crucially important is that there seems to be no valid reason for thinking that one range of values for these parameters is more realistic; indeed, one is hard pressed even to say what empirical measures would be relevant.

The difficulty here is not that the models are indeterminate. They are not. It is, rather, that we lack any objective criteria for estimating or assigning realistic parameter values, or even ranges of realistic parameter values. In the absence of such criteria, any hope of applying the models developed is clearly a vain one.

This sort of obstacle is reasonably common in using optimality models to estimate relative fitness (for further discussion, see Richardson 1984). Defining an optimality model requires specifying, among other things, the strategies available and an optimality criterion.

Consider the latter first. In the case of the actual systems to which optimality models are applied, there is rarely a single dimension which is to be optimized, and it is common for it to be impossible to optimize all the dimensions at once. E.g., one can discuss the efficiency of foraging strategies in birds, but it must be kept in mind that it is also necessary to engage in defense of the nest; since any time invested in the latter task will mean that foraging must be restricted, it follows that both dimensions cannot be optimized simultaneously. Moreover, even though the dimensions are not independent, the measures of optimality along these dimensions are incommensurable.

The second limitation on optimality models concerns lack of information concerning the available strategies. George Oster and E.O. Wilson explain :

> "The formulation of a mathematical optimization model requires an exhaustive specification of the allowable strategies. That is, the set of strategies must be just as complete as the set of states. ... This requirement makes it very difficult to apply optimization models to evolutionary processes. The reason is clear. The fundamental source of new adaptive strategies is mutation and recombination; natural selection acts only to delete the least "fit" individuals. There is no way to anticipate what new strategies can be generated by these genetic processes (1978, p. 298).

In some cases, it is possible to get a reasonable estimate of the available alternative strategies. In the case of foraging strategies in the social insects, as Oster and Wilson explain, there is substantial diversity available in the 10,000 or more available species. As a result, we can get what appears to be a reasonably complete set of available strategies. This is, however, the exception rather than the rule. In general, we have little more insight into the range of realistic options than we do into even the basic configuration of the optimality functions. The explanatory adequacy of the models is correspondingly in doubt.

The concerns over empirical adequacy does not exhaust the problems we face. R. C. Lewontin suggests that "the problem of constructing an evolutionary theory is the problem of constructing a state space that will be dynamically sufficient, and a set of laws of transformation in that state space that will transform all the state variables" (1970, p. 8). Even allowing that our characterization of the state of a system will not be exact, the requirement of dynamic sufficiency is essentially that our models must have sufficient dimensions to predict subsequent states of the system within the limits of tolerance. This appears to be an excessively ambitious expectation. As systems become increasingly complex, the relevant variables increase in number. As we have seen, it becomes impossible to incorporate them all. The most typical biological cases are in this category. The moral indicated would appear to be that we must settle for *dynamic relevance* rather than requiring dynamic sufficiency; that is, we should expect that our models would predict changes only statistically. The correponding methodological quandry is simply how much accuracy we should expect of our models.

4. A Puzzle for the Theory of Explanation.

We can close with a simple puzzle. We have seen that the idealizations incorporated into explanatory models are essential to the practical utility of those models, and to their application to actual biological systems. These idealizations, however, are assumptions which are, and are known to be, unrealistic. Yet the models of scientific explanation assume that the explanatory principles incorporated into the model are *true*. If we modify the criteria for adequacy in such a way that we require either that the principles be well-confirmed, or that the relevant reference classes in probabilistic claims be "epistemically homogeneous" (cf. Salmon, 1970, p. 80), we are in no better position. For we already *know* the idealizations are unrealistic. What is evidently required is a modification of the theory of explanation which allows for approximate fit of models to the world, or, equivalently, for truth of *invariant* assumptions across *families* of related models. Whether such modifications, incorporating a condition requiring the truth of *robust* assumptions (cf. Wimsatt 1981), will suffice in accounts of scientific explanation is a question we will leave for further examination.

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