

Similitude, similarity, and scaling

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Abstract

An exceptionally rich and colorful literature, drawn in almost equal parts from pure mathematics, from the sciences, and from the technologies, has grown up over the years, which bear in different ways on the topics under discussion. It is the intent of the present paper to survey this far-flung literature, point out some of the commonalities and interrelationships which underlie it, and briefly indicate how it has been and can be applied. To my knowledge, this kind of review has not been attempted before.

Introduction

The issues with which this conference is concerned are by no means confined to Ecology. On the contrary, they are manifestations of deep epistemological problems which concern the entire scientific enterprise; problems which have never been resolved, or even, in my opinion, effectively addressed as such. The relation of system to model, and of model to data, are the real problems at issue here. Our proximate concern is with Ecology, but the answers we seek are not to be found therein.

Where, then, should one look when one addresses such problems? Where are answers to be found? In my view, they are not to be found in any one place; they involve diverse but cognate experiences drawn equally from formalisms (*i.e.*, from mathematics), from physics, from biology, and even from technology. Consequently, the answers themselves, if we can find them, will in themselves not pertain to any one discipline. It will require a further theoretical development to bring them specifically to bear on particular disciplinary problems, *i.e.*, to apply them.

In what follows, I will limit myself to one aspect of these problems, namely, to the circle of ideas

generally referred to as *Similitude*. A study of similitude will, I hope, serve two distinct and important purposes for us: (a) the specific results arising therefrom will be interesting, pertinent, and important in their own right, and (b) they will be sufficiently typical to serve as a guide to the more general questions of which similitude represents a particularization.

Basically, the situation we envisage is the following. We suppose ourselves given a system S , and a model M of that system (for a fuller discussion of what this means, cf. *e.g.*, Rosen 1985). Suppose first that we 'operate' on the model M , *i.e.*, that we *deform* M in some specific, allowable way to produce a new object δM . Under appropriate circumstances (namely, when we can likewise regard M as a 'deformation' of δM), we may express the relation between M and δM as one of *similarity*. The question is: Can we find a corresponding deformation δS of S , such that the relation between δM and δS is the same as that which previously existed between the undeformed system S and the undeformed model M ? If so, then we can likewise say that S and δS are similar.

For instance, suppose M is such that we can multiply everything in it by fixed numbers, *i.e.*, change

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the scales of measurement which associate magnitudes in the system \mathbf{S} with magnitudes in the model M . Can I then correspondingly enlarge or contract the magnitudes in \mathbf{S} , with respect to the original scales, such that the new system in the new scales looks exactly like the old system in the old scales?

Or, to give another kind of example, consider the problem commonly referred to as ‘lumping’ of magnitudes. In an ecological context, suppose that in my model M , I amalgamate a number of individual species under a single collective noun, like ‘predator’. In effect, I am going from my original situation to another, at a coarser level of discrimination, and hence with fewer magnitudes. The question is whether there is a new ecosystem δS , of which δM is a model.

In general, situations of this kind fall within the province of Stability Theory. Stability is the study of effects of perturbations, or modifications, or changes, in one part of a system on the properties or behaviors of other parts. In the present case, we study the effects of changes in a model on the relation between that model and the system \mathbf{S} which it models. Similitude or similarity thus expresses a kind of stable relation between system and model, as we shall see in detail below. This kind of stability is of central importance, but so too is instability or bifurcation.

We can of course turn things around, and ask whether an operation on the system \mathbf{S} , resulting in a deformed system δS , can be offset by an allowed or canonical deformation δM of the model M . For instance, we can ask whether δS can be modelled by a change of scales in M . This is the same kind of stability question as before, but one which in a sense interchanges the roles of M and \mathbf{S} , and hence interchanges dependent and independent magnitudes.

A pregnant special case: The van der Waals equation

The ideas involved in our analysis are individually simple, but there are a moderate number of them, which have to be borne in mind simultaneously. Accordingly, instead of starting at the greatest generality and working down to particulars, we shall

start with some simple particulars and work up. The example I like to use for this purpose is non-biological; it involves the characterization of the family of equilibria of non-ideal gases, governed by an equation of state, called the van der Waals Equation.

Before we begin, we may note that thermodynamic equations of state, like the Ideal Gas Law, or the van der Waals equation which generalized it, already bear interestingly on the topics of this conference. It is worth mentioning them explicitly here, because they tie equations of state more directly to ecological interests, and make our example more pertinent than it might otherwise appear.

It was learned very early to characterize the behavior of simple thermodynamic systems, like gases, in terms of a small number of measurable quantities; specifically, the pressure P (measured with a manometer), the temperature T (measured with a thermometer), and the volume V . These are the thermodynamic *state variables*. It was discovered that, at *equilibrium*, the values of these quantities were not independent, but satisfied a definite relation. On the basis of curve-fitting, using limited ranges of temperatures and pressures available at the time, this relation was expressed as

$$PV = rT,$$

the Ideal Gas Law. This law is a simple example of an equation of state; the relation satisfied by the otherwise independent thermodynamic state variables under conditions of equilibrium.

It was obvious that the Ideal Gas Law could not be correct for all temperatures, volumes, and pressures. The hyperbolic relation it posits leaves no room for liquification of gases, which always occurs when temperatures are low enough, and pressures are high enough. Stated another way, the Ideal Gas Law does not allow for a phase transition.

Van der Waals modified the Ideal Gas Law in an interesting way, by taking into account the atomic microstructure of gases. Basically, he argued that the *measured* quantities P , V , which appear in the equation of state, are not the relevant ones. For

instance, since the gas is composed of particles which are extended in space, the measured volume V must be diminished by the volume occupied by the particles themselves, and is consequently smaller than what we measure. Likewise, since the particles themselves interact with each other, through net attractive forces between them, the pressure we measure with a manometer (*i.e.*, the ambient pressure) is less than that actually 'seen' by the gas itself. He expressed the 'real' pressure and the 'real' volume in terms of the corresponding measured quantities, and proposed a new equation of state, of the form

$$(P + a/V^2)(V - b) = rT,$$

which is the van der Waals equation. Here P , V , T are the measured quantities, as before, but there are two new *parameters*: a quantity a , which measures the attraction between particles, and b , which measures their individual volumes.

This replacement of quantities we actually measure by quantities we should be measuring is an early example of what is called *renormalization*. I commend this procedure to your attention, as it indicates most sharply what I have long contended, that there is nothing sacred about measurements or data *per se*; data acquires significance only insofar as it sheds light on the processes being observed. Indeed, in the case of the van der Waals equation, the quantities we should be measuring are not even directly accessible; it requires an underlying microscopic theory to make them manifest.

This leads to the next point. The relations between thermodynamics and an underlying microscopic theory has many ecological parallels. For instance, mathematical ecology since the days of Volterra and Lotka is based on Mass Action. Mass Action is itself derived from a microscopic viewpoint, and is in fact closely related to the van der Waals equation. The relation between microscopic and macroscopic scales (if I may call them such here) has itself been lifted into a purely ecological context, mainly in the work of Kerner (1957, 1959). But these issues are not our main concern; they are mentioned here because they are in fact important in their own right, and to indicate that our example

from Thermodynamics is in fact a natural one to use in the present context.

Returning to the van der Waals equation itself, we see that it posits a cubic relation between pressure and volume at a fixed temperature. Accordingly, we can see intuitively that the behavior of a gas at equilibrium depends on whether this cubic relation has one real root or three real roots. The gas/liquid phase transition resides precisely here. For pointing this out, van der Waals received the Nobel Prize in 1910.

The van der Waals equation comprises an early instance of what Thom (1975) called the *cuspid catastrophe*. A good discussion of this has been given by Fowler (1972), who has translated the language of thermodynamics into Thom's terminology. Some salient points of this are worth going into here.

The first point involves a classification of the thermodynamic state variables into two different types. One of these types are called *control variables*, and it consists of the pressure P and the temperature T . Because these are specified by ambient conditions with which the gas is equilibrating, we will later call them *environmental variables*. When these are specified, the remaining variable V is determined at equilibrium, according to the van der Waals equation. In catastrophe theory it is generally called a *behavior variable*; later, we shall call it a *phenotype*. Thus, we have two independent dimensions of control, and one (dependent) dimension of behavior in this case; in geometric terms, the surface of equilibria specified by the van der Waals equation is a pleated surface of behaviors as a function of controls. As we see in Fig. 1, the pleat in this surface lies above, and is determined by, the cusped curve in the control space. Algebraically, this curve separates the region corresponding to one real root from that corresponding to three real roots of the van der Waals equation. The cusp point on the curve gives three coincident real roots; every other point on the curve (fold points) gives a pair of coincident real roots. The phase transition arises from making the controls cross this curve.

The details are not important for us now. What is important is that the cuspid curve specified by the van der Waals equation has partitioned the control space into four disjoint regions, which

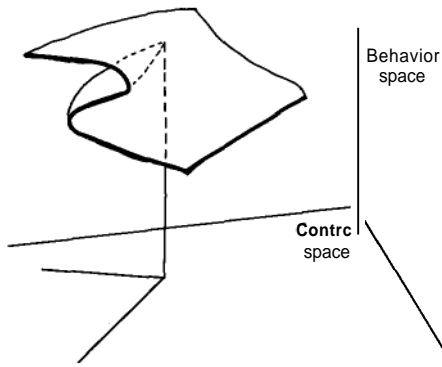


Fig. 1. Van der Waals Equation: Surface of Equilibrium Points.

cover that space. Specifically, we have:

- a. The controls *outside* the curve.
- b. The controls *inside* the curve.
- c. The controls *on* the curve, excluding the cusp.
- d. The cusp of the curve.

The first two of these regions are open sets; given any control in either of them, there is a whole little circle of controls around this point which does not cross the curve. The third is not open; an arbitrary change of controls will take us off the curve (either inside it or outside it), but very special changes of controls will keep us on the curve. As to the cusp itself, any non-zero change of controls will take us off it. We generally refer to controls of the first two types as *stable*; the latter two as *unstable*.

The stable regions are characterized by the fact that a small enough, but otherwise arbitrary, *change* in controls does not change the behavior, in the following precise sense: There is a coordinate transformation on X itself (*i.e.*, on the behavior space), depending only on the control values involved, which makes the new behavior in the new coordinates look exactly like the old behavior in the old coordinates. That is, *within* each of these four distinct regions, we can offset a change of controls by means of a change of coordinates (*i.e.*, of scale) in the behavior space. But *between* these regions, we cannot.

We may say, suggestively, that as long as we stay within any one of these regions, all behaviors are *similar*. But the behaviors corresponding to different regions are dissimilar. Going from region (a) to region (b) in control space is the phase transition

itself. Region (c) and region (d) correspond to different kinds of metastable situations. Regions (c) and (d) comprise the *bifurcation points*, separating two dissimilar regimes of behavior.

The four regions (a), (b), (c), and (d) can be thought of as comprising equivalence classes of an equivalence relation on control space, connoting regions of similar behavior. And as we have seen, similarity means precisely that we can completely compensate for a change of control by means of a change of scale (a coordinate transformation) of behavior alone.

It might be remarked explicitly that in general, a bifurcation in behavior of the kind we have been considering corresponds intuitively to the making or breaking of a constraint at a more microscopic level. For instance, the liquid/gas phase transition corresponds microscopically to an Ising lattice in which neighboring states are highly correlated (the liquid) or highly uncorrelated (the gas). Likewise, in the exactly analogous case of the buckling of beams, or of failure modes of structures in general, the constraint is rigidity. At the macroscopic level, the bifurcation manifests itself by (a) the destabilization of the original steady state, and (b) the simultaneous appearance, as if from nowhere, of new steady states, to which the system then appears to discontinuously jump.

What we have said so far is only a part of the story of the van der Waals equation. So far, we have left out of account the parameters (a , b , r) which enter into that relation. Let us see what happens when we bring them into the picture.

Intuitively, the values assigned to these parameters characterize what *kind* of gas we are dealing with. The state variables are common to all gases, but the parameters denote a particular *species*. Accordingly, we may call them the *genome* of a gas. Bringing them explicitly into our discussion as potentially variable (or ‘mutable’) magnitudes allows us to compare the behaviors of different species of gas, not merely, as we have done so far, the different behaviors manifested within a single species. This is a quite different kind of question, but still entirely within the province of the van der Waals equation itself. Let us then briefly consider where this leads us.

Interspecific aspects: The law of corresponding states

When we bring the genomic parameters into consideration, the van der Waals equation becomes a relation involving six arguments:

$$\Phi(P, T, V, a, b, r) = 0.$$

The first three arguments (P, V, T) are the thermodynamic state variables, which we have further subdivided into environmental ('control') variables, and phenotype ('behavior'). In this suggestive terminology, the van der Waals equation, or indeed any equation of state, expresses phenotype as a function of genome and environment.

So far, we have considered stability and bifurcation of behavior with genome held fixed. Now we want to investigate stability of behavior with respect to genome.

We have seen that the van der Waals equation isolates for us a distinguished point; the cusp point in control space, and the behavior which corresponds to it. This is, in a sense, the point of maximal singularity. Let us denote it by

$$(P_c, T_c, V_c),$$

and call this state the *critical state* of the gas. Intuitively, it is that unique equilibrium state at which the cubic relation specified by the van der Waals equation has three coincident real roots.

The critical point of a gas is determined by its genome alone. In fact, it is an easy exercise to compute that

$$P_c = a/27b^2; V_c = 3b; T_c = 8a/27rb \quad (1)$$

We see here explicitly the twin phenomena of *pleiotropy* (the same 'gene' affecting several characters) and *polygeny* (the same character being affected by several 'genes'), even in this completely abiological situation. It is convenient to *normalize* the original state variables P, V, T in terms of this critical point; *i.e.*, to introduce new state variables \mathbf{a}, ω, τ defined by

$$\mathbf{a} = P/P_c, \omega = V/V_c, \tau = T/T_c.$$

This, it will be noted, is just a change of scale, into new units defined by the critical point itself; in these units, the critical point always receives the coordinates (1, 1, 1).

We can do this for any gas satisfying the van der Waals equation. In particular, suppose we are given two different species of gas, with genomes (a, b, r) and (a', b', r') respectively; we can think of the second as a 'mutation' of the first. Suppose (P, V, T) and (P', V', T') are particular states of these two gases. We shall call these states *corresponding* if

$$\begin{aligned} P/P_c &= P'/P'_c; V/V_c = V'/V'_c; \\ T/T_c &= T'/T'_c. \end{aligned} \quad (2)$$

That is, corresponding states of different gases receive the *same* normalized coordinate values \mathbf{a}, ω, τ , each now measured in its own intrinsic scale. Then it is easy to verify that *the van der Waals equation is invariant to* (a) replacement of a given genome (a, b, r) by a new (mutated) genome (a', b', r'), and (b) replacement of a given state (P, V, T) of (a, b, r) by the *corresponding* state (P', V', T') of (a', b', r'), defined by (2).

Indeed, if we rewrite the van der Waals equation itself in terms of normalized state variables, we find it assumes the form

$$(\mathbf{a} + 3/\omega^2)(3\omega - 1) = 8\tau$$

in which no parameters at all are explicitly visible. This is called the *dimensionless form* of the equation, for reasons we shall discuss in a moment.

The Law of Corresponding States is embodied in the relations (1). Explicitly: Given any species (a, b, r) of gas, and any state (P, V, T) of that gas (measured in neutral units), then for any other species of gas (a', b', r') there is a unique *corresponding state* (P', V', T'), defined by (1), with the properties we have indicated. The relations (1) are relations of *similitude*. The Law of Corresponding States then asserts, in effect, that all these gases are *similar*; any change or mutation in species can be annihilated by an appropriate change of scale in the state space.

In effect, we are now thinking of the space \mathbf{A} of

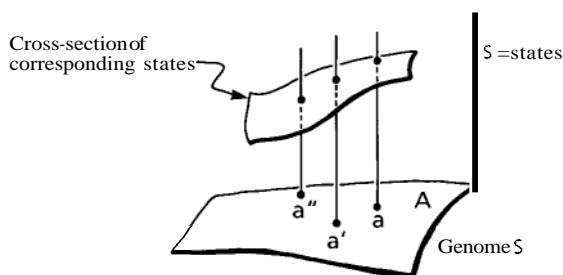


Fig. 2. Law of Corresponding States (Schematic).

all genomes (a, b, r) as a ‘control’ space, and the state spaces as ‘behavior’ space. In contradistinction to our previous analysis, there is now no bifurcation at all; all species of gas at this level behave absolutely alike. Accordingly, we need in effect to study only one species of gas; the data we obtain can be transformed into *corresponding* data for any other gas, by applying the transformation (1).

Let us look at the situation geometrically, using a diagram (see Fig. 2) analogous to Fig. 1. We have a base space A , the space of genomes (a, b, r). Above each point in the space, we have a copy of the state space $S = (P, V, T)$, which we can call a *fiber*. The whole thing constitutes a *fiber space*. Given any point on a fiber, there is a corresponding point on every other fiber. The totality of these corresponding points, one for every species of gas, fill out a *cross-section* of the space, as indicated in the figure.

It will be noted that these non-intersecting cross-sections define an equivalence relation on this fiber space. Specifically: A point in this space is a 6-tuple

$$(a, b, r, P, V, T).$$

Two such 6-tuples are *equivalent* precisely when they satisfy (1) above, *i.e.*, the genomes are arbitrary and the states are corresponding. This is the similitude relation, made completely explicit. The scaling laws themselves constitute a complete set of invariants for this equivalence relation.

Since this relation is so basic, we will look at it algebraically as well as geometrically. In effect, we started with a single relation (the van der Waals equation), involving six arguments:

$$\Phi(a, b, r, P, V, T) = 0.$$

We have essentially rewritten this single relationship as a three-parameter family

$$\Phi_{abr}(P, V, T) = 0$$

of relations involving three arguments. That is, we now treat the genomes (a, b, r) as *coordinates in a function space*; a set of addresses at which individual functions Φ_{abr} reside. The Law of Corresponding States says that this three-parameter family is a stable family, with the consequences we have seen.

It is also important to note that, if we were to try to pull out another argument (*i.e.*, one of the state variables themselves) and use it as a parameter, thereby converting the original van der Waals equation to a four-parameter family of functions of two arguments, the resulting family *cannot be stable*. It necessarily bifurcates; in effect, the bifurcations we studied previously (the phase transition) would now manifest itself directly. Thus the Law of Corresponding States, which holds for three (or fewer) parameter families, fails for four parameter families. This is a most significant fact.

Let us further remark that, according to our analysis, *the van der Waals equation satisfies D’Arcy Thompson’s Principle of Transformation* (cf. D’Arcy Thompson 1917). This principle asserts, in my own paraphrase (cf. Rosen 1962) that *closely related species are similar*. Since ‘closely related’ pertains to distances between genomes, and ‘similar’ pertains to phenotypes or behaviors, this assertion is highly non-trivial. In the case of the van der Waals equation, the assertion holds without qualification. But this is a very special situation, as we shall now see; in general, the Principle of D’Arcy Thompson cannot be true.

Dimensional analysis and its generalizations

The Law of Corresponding States, which asserts that all van der Waals gases are models of each other, is actually a special instance of scaling or scale modelling in general. The theory of scale modelling underlies the widespread invocation of

surrogate systems, which among other things permeates biology, *e.g.*, in the employment of laboratory animals as model humans, or in the extrapolation of data from one kind of ecosystem to another. As we noted, the first one to draw attention to this circle of ideas, albeit in evolutionary and developmental contexts, was D'Arcy Thompson. But these ideas have a much longer history, going back to Galileo (no less), and before him to Archimedes and Euclid.

A historical survey of these ideas is remarkably rich and varied, but far beyond our present scope. We wish to mention here only one thread in this tapestry, namely, the ideas of *dimension* which were first systematically stated by an applied physicist named Buckingham (who worked for the National Bureau of Standards), but which go back at least to Fourier. Buckingham (1914) framed Principles of Similitude (of which the relations (1) above are an explicit example) in terms of 'dimensional' ideas in his well-known Π -theorem; he wrote his paper in disgust over a preceding paper by R.C. Tolman (1914), who had claimed, in effect, that if all magnitudes in the universe were doubled, no one would know it.

Fourier pointed out that physical magnitudes are not simply pure numbers, but come along with an additional characteristic which he called 'dimension'. These associated 'dimensional' characteristics have an algebra of their own, distinct from any numerical values associated with them. The algebra of these 'dimensions' must be respected in any purported relation among physical magnitudes; this is the substance of Fourier's 'Principle of Dimensional Homogeneity'. Indeed, the mathematical idea of a 'pure number' is a rather recent one; the Greeks, for example, had no such idea, and even today, in many languages (*e.g.*, Japanese) numerical magnitudes are invariably associated with a complicated system of counters or tokens which embody Fourier's assertion.

Fourier's Principle, which sharply limits the mathematical expressions which may describe physical relations, appears almost magical in the way it allows one to do physics, for instance, without knowing any physics (beyond the 'dimensionalities' of physical magnitudes, and their al-

gebra). This is at the root of Buckingham's Theorem.

As Fourier already showed, if we have a set of numerical magnitudes or 'dimensional' quantities, then the 'dimensions' of some of them can be constructed from the 'dimensions' of others by mere algebra. In particular, we can choose a *fundamental* set of these magnitudes; a subset of them such that (a) the magnitudes in the fundamental set are dimensionally independent, and (b) all the remaining magnitudes (called *derived*) have 'dimensions' which can be constructed algebraically from those in the fundamental set. If these magnitudes are related (*e.g.*, through the laws governing the operation or behavior of a material system) then this classification into fundamental and derived has deep significance for the relation as well.

Rather than go through the details of Buckingham's analysis in this limited space (cf. *e.g.*, Rosen 1978), we merely remark that, in our treatment of the van der Waals equation, the parameters we called genome constitute a fundamental set in the above sense, and the state variables P, V, T are derived. Our normalization (1) defines new, *dimensionless* variables \mathbf{a} , w , τ , in terms of which the original relation can be re-expressed in parameter-free, dimensionless terms (the parameters, of course, have disappeared into the *scales* in which the derived magnitudes are now measured). The Law of Corresponding States, as embodied in (1) above, generalizes into Buckingham's Principle of Similitude.

Dimensional Analysis has played a major role in both physics and technology. But it is still limited. It has worked well in physics, because the magnitudes entering into descriptions of material systems tend to be of disparate dimensions, and hence the conclusions drawn from Buckingham's Theorem tend to be highly non-trivial. It has played no such role in biology, where many magnitudes are of the same 'dimensions'. Thus, for example, we can learn much about a harmonic oscillator through 'dimensional' ideas, but we can draw no such conclusions about, *e.g.*, a Volterra oscillator, even though the underlying mathematics of both are closely related.

Nevertheless, Buckingham's Theorem can be

generalized far outside of its original ‘dimensional’ context. Briefly, we can invoke the idea we have already seen above, of expressing a single relation involving N arguments as an equivalent r -parameter family of relations in $N-r$ arguments. Under very general circumstances, it turns out that there is a number r_0 such that: (a) an r_0 -parameter family can be found which is stable, but (b) every (r_0+1) -parameter family bifurcates. The r , magnitudes which parameterize a stable family play the role of the *fundamental* magnitudes of Buckingham; the arguments in these relations are accordingly the *derived* magnitudes. In this way, the Buckingham Theorem, and the Principles of Similitude which come from it, can be applied to situations far removed from ‘dimensional’ ones.

Let us now see what these ideas mean in a more biological context. In the preceding section, we classified the arguments of a relation (*e.g.*, a system law) into genome, environment, and phenotype. We now have a second way of classifying these arguments, namely, into fundamental ones and derived ones. These two modes of classification are different, and independent. It so happened, in our analysis of the van der Waals equation, that the genomic parameters also constituted a fundamental set; hence the Law of Corresponding States as an embodiment of the Principle of Similitude in that case. But there is no reason to expect this to be true in general. In particular, if we can find a fundamental set which is properly included in genome, then there must be bifurcating genomes; mutations leading to species behaviors which cannot be removed by mere change of scale. In this situation, the Law of Corresponding States fails for genome-parameterized families. With it, D’Arcy Thompson’s Principle of Transformation fails for such families; we can have ‘closely-related’ species, indeed *arbitrarily* closely-related species, which are dissimilar. In an evolutionary context, this looks like Macro-evolution. If so, it is fundamentally different from Micro-evolution, which stays *within* a similarity class, and is hence governed entirely by similitude.

Applications

In the preceding, we have reviewed only a very few of the more salient aspects of similitude, similarity,

and stability. What we have seen all boils down to the study of equivalence relations on metric spaces. From the equivalence relations, we get the similarity; from the metric, we get an idea of closeness, or approximation. It is the interplay between the two which is the subject of study. A situation is stable if all nearby situations (in terms of the metric) are similar to it (in terms of the equivalence relation). As we have seen, when situations are similar, the quantitative differences between them can be transformed away. If a situation is not stable in this sense, then arbitrarily small deformations of it (*i.e.*, arbitrarily good metric approximations) can lie in quite different similarity classes; what is important is *how* the deformation is made.

There are obviously many ways in which this circle of ideas bears on the subject of the present conference. For instance: The separation of arguments in an equation of state, into genomic, environmental, and phenotypic, inherently separates the possible behaviors of systems described thereby into a number of discrete levels. If, for instance, we vary environment with genome held fixed, the relation obtained thereby between change of environment and change of behavior can be looked upon as an adaptation of an individual ‘species’ of system to that change. As we have indicated above, if the resultant adaptations are inter-transformable, then the adaptation does not involve a change of constraints; otherwise, such a change (reminiscent of a phase transition) must occur. Likewise at the genomic level; here, similarity means that, within a similarity class, a change of genome can be offset by a corresponding change in environment; between similarity classes, this is no longer true. Thus, the response of, *e.g.*, an ecosystem to imposed perturbations can be resolved at these different levels, where they assume quite different significance.

It should be remarked explicitly that, although our example of the van der Waals equation concerned systems at equilibrium, our treatment is perfectly general. There is nothing to prevent an equation of state, in our sense, from describing general dynamical situations, *i.e.*, situations in which some of the arguments of the equation of state are derivatives, fluxes, or rates of change. Indeed, this is what is tacitly done when ideas of similarity are mani-

fested in terms of structural stability of dynamical systems.

A second area of applications involves the relation of sampling to the system being sampled. Sampling involves an idea of metric approximation. The problem, of course, is the compatibility of this kind of approximation with the underlying similarity structure. It is a different kind of question from assessing the response of an actual system to a particular perturbation; rather, it involves the perturbation of the whole formalism which models the system. Thus, the question is the extent to which an approximation to a model remains a model. As far as I know, such questions have never been treated at the appropriate abstract level which I believe is required. Nevertheless, such a treatment will involve precisely the same circle of ideas as we have indicated above.

Finally, there is the question of the extent to which ecosystems are models of each other, *i.e.*, the extent to which data pertaining to one system can be transformed into data about another. This, too, involves a circle of formal issues which have never been suitably addressed. In our discussion of stability and bifurcation, we regarded these as, in a sense, all-or-none concepts; a phenotype was either stable or it was not. But the issue is more delicate than that. We have already alluded, in our discussion of the van der Waals equation above, to formal analogs of the biological phenomena of pleiotropy and polygeny. For instance, looking at the relations (1) above, which define the critical values of state variables in terms of the genomic parameters, we see that the parameter a is expressed in both P , and T , (*i.e.*, is to that extent pleiotropic); conversely, the value of P , involves the expression of the two parameters a and b (polygeny). Thus, a 'mutation' involving a alone will not require us to transform every state variable in going from states of the original system to corresponding states of the 'mutated' system. More generally: When we perturb the value of any fundamental quantity, we can partition the derived quantities into two classes: those whose values need to be transformed by an appropriate similarity transformation, and those which do not.

Still more generally, even if such a 'mutation' takes us from one similarity class to another (a situ-

ation which does not arise in the van der Waals equation, where there is only one similarity class), we can still identify a class of derived variables whose values remain intertransformable. The size of this set gives a measure of the 'degree of stability' or 'degree of bifurcation' arising from our 'mutation'. These degrees of similarity seem to underlie the classifications familiar from biological taxonomy; *e.g.*, different species in a genus are 'more similar' than species from different genera within an order, etc. In this sense, the extent to which one species can be employed as a model or surrogate for another depends heavily on both (a) *how* the species differ at the genomic level, and (b) the effect of this specific genomic difference, through pleiotropy and polygeny, on those derived magnitudes in which we are particularly interested. Questions of this kind, as I have indicated, all await detailed study.

To conclude, we should mention certain caveats which must be borne in mind, even when two systems we wish to compare are known to be within a similarity class. The first involves an explicit recognition that data pertaining to one of them can only be transformed into *corresponding* data about the other. If two systems are not in corresponding states, their data do not intertransform (or at least, not according to the ideas we have discussed so far). Thus, even if similarity obtains, there are severe limits imposed on our ability to extrapolate data from one system to another. It is ironic that the care with which data are gathered is not always matched by any corresponding care in the extrapolation of that data.

Our last caveat involves the effect of extraneous material constraints on our considerations of similarity and scaling. Such constraints are well known in technology, where scale models are widely used to investigate, *e.g.*, the hydrodynamic and aerodynamic characteristics of ships and aircraft. Namely, in these situations, if scaling is to be exact, then *every* derived quantity must be scaled, including such things as surface tension and buoyancy. But since we must use water, and air, for both the scale model and the prototype, we introduce thereby an error into the scaling laws themselves, which need not be small or negligible in general. Likewise

in biology and ecology; we must assess the effects of any departure from inter-transformability arising from our (or Nature's) inability to scale everything.

Our discussion above has barely scratched the surface of the issues raised in this conference, but it is hoped that we have indicated something of their true amplitude and scope. As we stated at the outset, these issues far transcend Ecology, or indeed any individual science; they are at root epistemological in character. We hope to have indicated that concepts from similarity can play a pivotal role in elucidating such issues, and we have hinted at a possible program for doing so. But it is probable that the very scope of these problems places them outside the purview of any one approach or any one individual or any one group. It would be interesting to return in 100 years, to another such conference, and see what fruits our present labors have borne.

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