Entropy in Newtonian physics and evolution

Prof.Manjula Katageri
Asst Professor of Physics
Govt First Grade College, Navanagar
Bagalkot

ABSTRACT

Our systems models of living systems postulate a boundary that separates order and information within a biological system from the entropy of its environment. While useful, that model denies a role for entropy within biological evolution. This paper will seek to define a concept of biological entropy and demonstrate , via a thought experiment, its relevance for the evolution of complex living systems. Biological entropy reflects the inherent phenotypical variability of a species and is proposed as an evolutionary vector that parallel's Chaisson's energy flow density.

The paper proceeds by defining entropy in observational terms as a condition where no observer can differentiate states or patterns within a defined state space. It proceeds to propose a concept of biological entropy that is a measure of the phenotypical state space of a human being. For the purposes of this experiment, the genome is subdivided between the genetic state space required to be human, healthy, and alive, the genome, and a second state space of genetic variation that contributes to each person's uniqueness, the 'phenome.' The thought experiment assumes a sociobiologically trained observer who is challenged, on the basis of genetic information, to predict the behavioral differences between two individuals. This challenge is demonstrated to be identical to that which was defined as observational entropy.

Biological entropy, expressing the inherent variability of the 'phenome' is proposed as a vector parallel to energy flow density. Both concepts are anchored in thermodynamics. It is suggested that the number of genes and modes of reproduction of organisms can be investigated to produce an evolutionary progression that is similar to that of energy flow density.

The paper seeks to demonstrate an alternative path to understanding the indeterminancy of biological phenomena and the necessary limits to prediction. The goal has been to demonstrate a creative space for the freedom of humanity based on thermodynamic principles without appeal to mysticism or emergent characteristics of systems.

Keywords: phenome, Genetic Entropy , evolution, thought experiment, energy flow density

Introduction

The purpose of this thought experiment is to reincorporate the concept of entropy into a systems view of biological evolution and, thereby, define a necessary potential space for human purposefulness and creativity. Since the boundary between what is understood as human and animal is fuzzy, the exercise must allow for what might also be seen as "freedom" in animals. The inspiration for this paper came from Eric J. Chaisson's presentation at last year's ISSS meeting in Monterey. By relating the thought experiment to his evolutionary vector – Energy Flow Density – we will find that what differentiates humans from other species is their complexity and argue that that very complexity is a result of what we might label as '*biological entropy*.' Biological entropy may also be understood as an outcome of non-equilibrium thermodynamics (Prigogine, 1997).

We will adopt a systems perspective to define entropy in observational terms and proceed to imagine what the biological equivalent of such entropy might be in genetic terms. The essence of the thought experiment will be to assume two human beings from one set of parents, postulate a zoologically and genetically trained sociobiologist, and ask whether genetic information can provide sufficient information to distinguish the potential behaviors of these two human beings. The core argument, to be demonstrated, is that that observer will be faced with a situation indistinguishable from what, in other circumstances, would be defined as entropy. This approach owes much to my understanding of Weinberg's work explicating general systems theory (1975). The concept of biological entropy will be used to suggest that living system complexity is better understood as an expression of variability rather than information or order. A vector, parallel to Chaisson's energy flow density will be proposed for biological evolution.

The thought experiment will be revisited by loosening the constraints on our sociobiologist and allow many more variables to be utilized to predict the behaviors. However, we will see that appeal to more variables necessarily exacerbates the challenge of predicting behaviors. Finally, we will propose a scientific perspective, related to systems, that allows for both a measure of predictability along side freedom and creativity.

Objective

Through this paper we propose to phyiscale volution in Newtonian physics model and understand effects of entropy

Living Systems and Entropy

Our theories about the nature of living systems derive from the pioneering work of
Bertalanffy (1968) who extended Schrodinger's argument about living systems feeding on "negantropy. "

> "But entropy…is a measure of disorder; hence negative entropy or information is a measure of order or of organization since the latter, compared to distribution at random, is an improbably state."

Thus, general systems theory was able to bridge through physics, biology, to organization. This proved fruitful but at a cost of limiting our ability to address significant living system phenomena. Our models of living systems suggest a boundary between order, a property of systems, and disorder or entropy, a property of environments. The concept of the living systems as excluding disorder and entropy and exhibiting self-regulation and stability is simplistic. Nor does it appear to be a valid extension of Shrodinger's logic. He argued that atomic level phenomena remain probabilistic and that, in the final analysis, all clockworks are clouds. Stability is a statistical outcome of large numbers of random events at the atomic level. The order, or law like behavior, we observe in living systems is based on that stability.

> "An organism must have a comparatively gross structure in order to enjoy the benefit of fairly accurate laws, both for its internal life and for its interplay with the external world.(p18) (Shrodinger, 1992)

The point is that systemic behavior of living systems does not emerge from the exclusion of entropy and disorder from within but from the statistical effects of very large numbers of interacting biological elements. The artificial and simplistic dichotomization that systems theory postulates between order and entropy conceals the many rich ways that biological processes may *embrace* entropy.

What is entropy?

We begin our thought experiment by seeking an observational operationalization of the concept of entropy. How could we discover entropy via observation? How could an observer "see" entropy?

Let us start with a liter of gas at standard temperature and pressure populated by Avogadro's 6.02×10^{23} molecules. One way to define entropy or disorder is to assert that no conceivable observer could see enough to determine the path of any particular molecule. Alternatively, no specific pattern of molecular interactions can be observed, i.e. that no set of forces exist within the gas that can segregate the paths of a given subset of molecules into an identifiable pattern. The energy of the molecules is so randomly distributed that no conceivable measuring device can be triggered to identify a particular state from the indefinitely large number of potential states. From Prigogine's (1997) perspective, no resonance can emerge from the gas to produce recognizable structure among the motions of the molecules.

As long as the space occupied by this liter of gas is either perfectly insulated from its surroundings or at the same temperature as those surroundings, no net energy will flow across the boundaries of the space. The gas is at equilibrium, a statistical concept, but its constituent molecules are likely to be at many different energy levels and move in countless directions.
Equilibrium, then, is not a state of rest within the liter of gas but the average condition of the gas as seen by an observer. Thermodynamic equilibrium suggests that the gas would be at its lowest level of energy with respect to its environment. Observational equilibrium suggests that, however great the variations in energy and motion among molecules, they are indistinguishable to an external observer.

The level of entropy in the space is defined by Boltzmann's equation as
$E = k \log D$ where D is equal to the number of potential states of the gas within the space.

Therefore, entropy is a condition of disorder in a state space that denies an observer the possibility of distinguishing between states within the state space. Observationally, all states are equivalent and only average properties of the entire state space are observable, for example: pressure, temperature and volume.

Our question becomes?

Can we formulate an equivalent concept of biological entropy?

Biological Entropy

Medical blood testing exemplifies the statistical nature of biological processes. A sample of blood is taken as a valid representation of the blood in the body and tested for various electrolytes and constituents. The results are sample averages which are extrapolated to infer population averages. The data is a probabilistic estimate of the blood population. However, given the vast number of molecules involved in even a small sample, that estimate is accorded great validity. In practice, whatever entropy may characterize our blood, it is assumed to be controlled within narrow limits as defined by a medical observer.

However, for our purposes, we need a more far-reaching concept of biological entropy, one that can be related to the predictability of major behavioral differences. In our thought experiment, let us look at the phenotypical variety within the human species.Human beings have more than 50,000 gene pairs combining a selection from the pairs of their parents. Genetic biologists are mapping those genes. They are seeking to map all of them but tend to divide them into two groups, those that are definitive of the human genome and "junk genes." Implicitly, we have a partitioning of the gene pool into a genomic 'order' and a phenotypic 'disorder.' The genes critical in defining the genome, i.e. those that make us human, represent order. The remainder combine to make us unique.

Therefore, for the purposes of this thought experiment, we may assert:

The genome, human being, is defined by a subset of genes and gene states which, if absent, mean that the organism dies or is not human.

The genome, therefore, defines a state space within which human genetic variety is displayed as phenotypes.

These assertions depart from conventional understandings of genotypes and phenotypes. The genome is thought to include the entire genetic ensemble while the phenotype is said to emerge from the interaction between the genome and the environment. For this thought experiment, we are partitioning the genome between those genetic states required to be human and those genetic states that lead to uniqueness. That is what seems to be implied by the notion of "junk genes." Let us define "phenome" as a term representing genetic variability prior to environmental influences.

The "phenome," then, is one of an indefinitely large number of genetic states that can be exhibited within the state space defined by the genome.

It follows that our notion of biological entropy might be related to the phenotypical variability of a species.

Human Phenotypical Variety

An estimate of the state space of human phenotypical variability may be computed as follows. Let us assume 50,000 genes although some estimates are 100,000. Further let us assume that we would expect 10 genes to flip in selections within pairs for every thousand genes. In other words, every sperm cell would differ from another cell by 10 genes for every 1000. One percent of the genes would differ but which one percent cannot be defined. How many potentially different sperm could one man produce? We would have, potentially, 10^{50} different sperm cells. Note that this is a conservative estimate of the state space since we have not considered the equal variability contributed by the female. For the purposes of this thought experiment, let us simplify by assuming the above 10^{50} as a useful estimate of genetic variability deriving from the combined contribution of female and male parents.

The first instance of biology embracing entropy, understood as unpredictability, emerges from the above estimate. In mating, a single sperm succeeds from among 400 million available. Why is biology so lavish with its resources to require the loss of 400 million sperm that one might succeed? The classic Darwinian argument is natural selection, the fittest sperm wins the race. However, we can suggest an alternative principle.

Every one of those sperm cells is unique.

The evolutionary value of expending 400 million sperm cells makes sense if they inject rich variety into the genetic stream. It is extremely probable that each of those cells is different. They are a selection of 4×10^8 from among 10^{50} possibilities. It is all but inconceivable that any two sperm would be identical.

We may partition these 10^{50} possibilities between the human genome and 'phenome.' Let us arbitrarily assume that the genomic requirement is 10^{27}, that is that to be human, alive, and healthy requires 10^{27} gene states. That leaves 10^{23} gene states for the expression of human phenotypical uniqueness. *(We have purposefully computed this to honor Avogadro.)*

A Sociobiological Zoologist Observer

Let us assume a competent scientist who is a sociobiologically trained observer (*Observer).* He, the gender seems fitting for this experiment, is trained to see and map all of the important genetic information associated with the human genome. While *Observer* may be able to identify particular junk genes, the interactions among such genes are inaccessible within his research models and are seen as irrelevant to his explanatory paradigm.

We will confront *Observer* with two different observational challenges.

Experiment One:

> *We have 400 million sperm in a test tube alive, energetic, and available for insemination without any degradation in potential or quality. An egg is to be made accessible to all of these 400 million sperm in the normal manner. Observer knows the genetic make up of each of these sperm cells and the egg.*
>
> *The challenge*
>
> > *Predict the phenotypical characteristics of the expected offspring.*

Note that we expect a normal healthy human offspring. We expect to be able to predict whatever the genome requires. The challenge is to further delimit the phenotypical possibilities.

Experiment Two:

> *We have two human offspring of the same parents who are both either male or female. Observer is given complete genetic samples from each of these individuals, including their gender, and no other information about them. These individuals are healthy typical examples of the genome, i.e. their* 10^{27} gene *states have emerged quite successfully.*
>
> *The challenge:*
>
> > *Predict the phenotypical behaviors of these individuals, i.e. what behavioral patterns may be rooted in their genetic 'phenome?' . How will their behaviors differ?*

Biological "Gas"

The second experiment asks our *Observer* to predict the outcomes of the interactions among 10^{23} genetic states. While this is more structured than Avogadro's gram-mole of gas in the liter, the essential characteristics of the challenge are the same. *Observer* is confronted with what we defined as observational entropy.

The second experiment may be characterized by a paraphrase of Boltzmann's equation:

$$\text{Genetic Entropy} = k \log D$$

Where k would have to be defined for genetic material and D represents the number of potential genetic states within the state space defined by the 'phenome.' In honor of Avogadro, we have arbitrarily defined $D = 10^{23}$.

In what way is this experiment different than that of the observer of our liter of gas? Our *Observer* can no more distinguish outcome states than the earlier observer could predict paths of molecules.

The first experiment is somewhat simpler than the second if only because the range of possibilities has been greatly reduced by limiting sperm to 400 million. However, the question of which sperm will succeed evokes our observational definition of entropy above. "*no conceivable observer could see enough to determine the path of any particular molecule."* And it is evident that neither can our *Observer* predict the path of any sperm to success. This is again an expression of biological entropy.

Finally, we might combine these two experiments and ask of our *Observer* to both predict the outcomes of the sperm pool and then the resulting phenotypical differences between two individuals emerging from two fertilized eggs, assuming there were two available. Thus, the full extent of biological entropy becomes more apparent. Each of these experiments defines entropic state spaces and their combination presents a state space with vast entropic potential.

Therefore,

> *Biological entropy may be understood as a condition of genetic uncertainty or disorder within a genetic state space that denies an observer the possibility of distinguishing between phenotypes within that state space. Observationally, all potential state spaces are equivalent and only average genotypical properties of the entire state space are observable.*

The observer can determine that this emerging biological entity will be human, male or female, and a variety of other general characteristics of the individual.

A Link to *Energy Flow Density*

This paper was inspired by the work of Eric Chaisson and his presentation on the "Cosmological Imperative" at the 1999 Asilomar meeting of the society. Chaisson develops a cosmological vector that characterizes the evolution of the cosmos from the big bang through to complex cultural entities. That vector is the *energy flow density* of matter in bodies in the universe.

Chaisson's model begins with the period after the Big Bang when the universe is understood to be "an exceedingly large, isotropic gas cloud" dominated by radiation and "flooded with photons…ensuring a non-structured, undifferentiated,

(virtually) informationless, and highly uniform blob of plasma "(p. 14) "…matter and radiation were intimately coupled to each other – thermalized and equilibrated." (Chaisson, 1998, p16)

In effect, we had a completely entropic universe which exhibited a single directed evolutionary force: It is expanding. Matter cooled more quickly than radiation during this expansion and electrons were bound into atoms. What had been a fog of entropic, and essentially homogeneous radiation and matter, become differentiated as atoms formed. But, matter is still simple by present standards as most of the complex elements had not yet been created.

As complex elements are formed in stars, matter assumes a greater variety of forms until we get to those "clumps of matter" that are life forms. At this point, the slow evolutionary increase in the *energy flow density* rapidly accelerates with the evolution of increasingly complex life forms. 'Clearly [free energy rates densities] has increased steadily as more intricately ordered structures have emerged throughout cosmic history (Chaisson, 1998, p18).

Chaisson has eschewed attempting to quantify the degree of order of such structures in terms of "tricky empirical values of negentropy" or "slippery interpretations of information content" preferring the simpler principles of non-equilibrium thermodynamics (Prigogine, 1997)

A purpose in this paper is to propose a measure of order that is consistent with thermodynamics and can potentially be verified by simple data. It emerges from the thought experiment developed above.

> *The complexity of a living system, understood as its biological information content, can be measured by the number of potential states available to it within a state space defined as alive.*

The information content of organisms is not measured by their order but by their inherent variability. It is not their predictability that represents complexity but their unpredictability. Energy flow density, Chaisson's vector, evolves along with increasing variability of "clumps of matter." That suggests a parallel biological evolutionary vector.

> *A biological vector is postulated that would be mapped from the number of genes in organisms coupled with their mode of reproduction to compute their inherent potential phenotypical variability.*

It appears reasonable to assume that such a computation should map along the same vector that Chaisson develops in that segment that is the domain of living systems. Simple organisms have many fewer genes than more complex organisms.

Cosmic Evolution Revisited

The result of cosmic evolution is the polar opposite of the homogeneity of the early universe. We have evolved "clumps of matter" that exhibit cosmic variability within systemically functioning organisms. Since this may seem a grand exaggeration, some computations are in order.

At Asilomar, I asked Eric Chaisson whether his cosmology could account for the emergence of himself to explain it us. Our sciences have yet to be able to explain our capacity to discover and explain the universe in scientific terms, a feat that Popper (1972) argued was an event of infinitesimal probability. So let us demonstrate a quantifiable measure of evolutionary complexity using Eric as an example.

How many potential Erics were there? How many potential behaviors could any of those potential Erics exhibit?

Sociobiologists have argued that, in principle at least, human behavior is determined by combinations of genetic information and human experience. It is as if each of us is simply a deal from two mixed 'decks of cards,' the first our genetic make up and the second whatever learning has been encoded in the neurons in our brains. Systems thinkers might ask, "How big are those 'decks of cards?'"

How big was the genetic deck of cards from which the unique person we know as Eric emerged? Let us limit the computation to a single sperm and egg and forget about those other 400 million "clumps of matter." To further simplify, let us assume that 10^{50}, the estimate we used for just the sperm variability, represents the combined potential genetic variability of the fertilized egg. I have heard, but cannot document this estimate, that 10^{50} is a number larger than the number of atoms in the known universe. *We need a cosmologist to confirm that.*

How big is the learning deck of cards? We are blessed with an estimated 100 billion neurons which weave a web of interconnections that vary from one per neuron to as many as one thousand. The number of potential states of our brain, as an estimate of our learning, might be conceptualized as the number of potential paths through that system. While many different computations might be ventured, we are again faced with a number which is most probably greater than the number of atoms in the known universe.

Now, our sociobiologist has argued that our behavior is determined by some combination of these all but infinite shuffled decks of cards. One must wonder what possible meaning can be assigned to the word "determined" with respect to such extreme variability. The potential, and we should add, the evident uniqueness of Eric Chaisson, must defy any deterministic explanation.

What might this mean if mapped against the cosmological evolution described by Chaisson?

Cosmic evolution starts with a vast equilibrated, undifferentiated blob of plasma and evolves towards a small highly complex, and ordered living systems with a repertoire of genetic and behavioral variety greater than the number of atoms that emerged when matter first began to dominate the universe.

It is in that sense that we might argue that evolutionary biology embraces entropy.

Multi-Disciplinary Approaches

It might be argued that a multi-disciplinary approach might increase the predictability of human behavior. It has long been the agenda of the systems approach to act as a bridge between the many scientific disciplines.

We can most certainly expand the observational sets that can be used to describe the behavior of a human being. However, as observational sets increase, so, too, must the relevant state spaces. Since the size of state spaces expands combinatorially, each additional observational set of variables must, necessarily, exacerbate the challenge. The state space expands faster than the ability to determine outcomes within the state space.

Whither the Human Sciences?

We can continue with our classical scientific methods. We can place our subjects in carefully delimited laboratories and severely limit their behavioral state spaces so we can execute controlled experiments. We might grow multiple clones artificially for such purposes. The classical experimental method operates by collapsing state spaces and forcing entropy out beyond experimental walls. Thus, it seems that generations of rats bred in our laboratories always appear much dumber than those creatures in our back yards. In essence, we create conditions where behavioral and genetic variability can be denied. Hopefully, no human society will allow such experimentation. From such a restricted purview, not much will be learned.

Alternatively, we might restrict our domain of inquiry to just those characteristics shared by all human beings and use statistics to seek out the natural laws shaping the state space within which human variability is exhibited. These laws may further delimit the state space but, given phenotypical variety, cannot eliminate what we have called biological entropy. The domain of variability will remain very large indeed.

We might adopt a Structuralist perspective as proposed by Piaget (1970). This view of science has come and gone as a fad mainly at the hands of the humanities and the social sciences. It appears particularly appropriate as a paradigm for scientific progress in the face of the evident variability and creativity of human behavior. It allows for that freedom that conventional scientific models deny. Moreover, it is related to the systems perspective.

Piaget argues in a little book, *Structuralism*, that there are deep structures in our minds that are pattern generators capable of an indefinitely large number of outcomes all governed by these patterns. In effect, the deep structure defines a state space within which a great variety of behaviors, actions, and expressions are possible. In the structuralist model, science progresses by identifying deep structures as evidenced by patterns. This would require an enlargement of the systems perspective and what we define as systems understanding.

To demonstrate, we may take the notion of goal directed behavior as developed by an early systems biologist, Sommerhoff. Sommerhoff developed the directive correlation model of biological goal directed behavior and a mathematical model of Bertalanffy's equifinality. Ross Ashby (1968) alternatively formulated this model as *requisite response variety*. Ashby bridges between Sommerhoff's work and general systems theory. However, Sommerhoff was a determinist and defined the goal directed behavior accordingly. He assumed that the combination of environment and living system response variety must lead to determined outcomes. As we have argued above, such an agenda must fail from an observational perspective.

However, we can relax the deterministic assumption. The author did so in investigating the nature of human work. So relaxed, the directive correlation model becomes a domain of pattern generation which closely resembles the logic of language defined by Sauserre (1959), the patterns of sensorimotor control identified by Piaget, and other examples of structuralist models. The advantage of such models is that they delimit what is predictable, patterns, from what is free and variable. Such partitioning will be increasingly necessary in science if we are to make progress in the face of such cosmic variability as has been identified above.

Conclusion

We have developed an alternative path to Karl Popper's "indeterminist" view of science (1972) . In effect, the necessary interplay between order and variability *within* biological systems of any complexity limits the possibilities of precise predictions of genetic or behavioral outcomes unless such systems have been artificially constrained in laboratory settings.

The conflation of order and variability, the expression of biological entropy, assures an irreducible domain of potential freedom in which human phenotypes can exhibit purpose, choice, control, and produce knowledge such as our sciences. This assertion does not deny such potential to other animal species but that freedom cannot be discovered within conventional scientific paradigms. In this paper, we have sought to demonstrate a model that can encompass our own existence and activity as scientists.

My goal has been to argue for a creative space for our humanity without appeal to mysticism or to imagined emergent characteristics of whole systems. Similar to Chaisson's work, I wanted thermodynamic principles to supply space for freedom.

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