between conflicting data^{1.8} and in stimulating further investigation.

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GENERAL

Entropy and Evolution

CAMPBELL's expressed aim^1 is "to describe the entropy pump whereby the species of living matter not only prevent a drop into a position of greater positive entropy at each generation, but may in fact acquire more negen-tropy as their reproduction continues". This is attempted by recourse to the example of a codfish laying a million eggs the entropy content of whose genomes shows a normal distribution about a mean value in accordance with the second law of thermodynamics. On one tail of this distribution curve will be a small percentage of eggs with an entropy content equal to or less than that of the parents. There follows the crucial sentence: "These parents. There follows the crucial sentence: remarkable ones are most likely to grow up and repeat the reproductive process". What follows in Campbell's communication is unexceptionable provided that this sentence is true. But what is the evidence that those eggs which are "most likely to grow and repeat the repro-ductive process" are those whose genomes have a lower entropy content than those of the parents? It is at this point that the author merely evades one of the most important questions at issue in the earlier correspondence²⁻⁴. The genome may be regarded as a series of DNA molecules functioning as templates. The thermodynamic entropy content of these molecules is a function of the arrangement of the atoms, conventionally expressed as $k. \log D$ where k is the Boltzmann constant and D is a measure of the atomic disorder. A single alteration in the relative positions of adjacent nucleotide bases could convert a crucial part of the genome code to nonsense so that its capacity to support development was lost, but this could occur without an increase, indeed even with a decrease, in the thermodynamic entropy content of the genome molecules⁵. Stated in a more general way, this is the problem of the relationship between the amount of developmentally meaningful organization in the genome (we will call this the information content) and its entropy content. There are two problems here: first, the definition and quantization of the information content of the genome and, second, the nature of its relationship to the thermodynamic entropy content. One avenue of enquiry which offers hope in this situation would seem to be the information theory analogy.

Szilard⁶ pointed to the formal similarity between the equations defining information

$$H = -\sum_{i=1}^{i=n} \operatorname{pi} \log \operatorname{pi}$$

(where $0 \le pi \le 1$, $\Sigma_1^n pi = 1$ and pi is the relative probability of the *i*th symbol generated by a source), and entropy defined in statistical terms as

$$S = - \underset{i=1}{\overset{i=n}{k\sum}}$$
 pi log. pi

(where $\sum_{i=1}^{n} p_{i} = 1$ and pi is in this case the probability of an idealized physical system being in the state i of n possible equivalent states).

The work of Shannon⁷ and Brillouin⁸ showed the fundamental relationship between information and entropy defined in these terms. It is the unwarranted extrapolation of this relationship to biological systems which leads to erroneous conclusions, although the warning was admirably given by Brillouin himself⁹: "The present theory of information completely ignores the value (or meaning) of the information handled, transmitted or processed. This point has been very carefully emphasized throughout this book. Many other writers seem not to have realized the importance of this restriction, and many misunderstandings about the possibilities of the present theory resulted from this situation". This is the biological problem because, as I have said, different arrangements of equal members of nucleotides may have the same thermodynamic entropy but a different value in the context of the development and viability of the organism. It may be that, as Lwoff⁵ has supposed, this functional order cannot be measured in terms of entropy units and is meaningless from a purely thermodynamical point of view. But this may be an over-pessimistic view. For example, one possibility which seems worth exploring arises from possible analogy with the work of Carnap and Bar-Hillel¹⁰, who have applied techniques of symbolic logic to define the information content of a sentence. Now if for a very simple organism such as Mycoplasma, one came to know the complete nucleotide sequences and the limits of their physical variation within each operon consistent with successful replication and development, and the essential sequence of operon functions necessary for development, it might be possible to define the information content of the organism in terms of the number of base sequences commensurate with reproduction and development. From this it is conceivable that one might obtain a "content measure" bearing at least a qualitative similarity to the information equation of statistical thermodynamics. If this were achieved one would then in effect be saying something in thermodynamic terms about what marked off the living from the non-living. This may seem a long shot, and indeed ignores the whole question of essential extra-genomic factors11, but in any event until this or other possible approaches to the problem are explored we cannot with any confidence pronounce on either the direction or the magnitude of the thermodynamic entropy changes involved in the acquisition of the "fuller informational systems" which are the products of evolution. This being so, it would seem premature to speak of an "entropy pump".

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