Physics began with the study of simple models that became more complicated as they became more realistic. Biology has followed the opposite path but the two disciplines are now converging in the study of complex systems

Statistical physics and biology

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The relationship between biology and physics has often been close and, at times, uneasy. During this century many physicists have moved to work in biology. Amongst the most famous are Francis Crick (the joint discoverer of the DNA double helix with Jim Watson), and Max Delbrück and Salvatore Luria (Nobel prize-winners for their work on mutations). However, after these scientists changed their research field, they worked in the same way as other biologists and used their physics training to a reduced extent.

An intermediate discipline is biophysics, but here physics is often used as a tool to serve biology (a similar situation exists in biochemistry). In both cases, chemistry and physics provide explanations of what is happening at the lowest level, that of molecules and forces, but these are used in a biological framework.

The situation is now changing and scientists are using physics methods and developments in theoretical physics, such as statistical mechanics, to study certain fundamental problems in biology. This phenomenon arises from reasons common to both disciplines.

Current physics

One cycle in the history of physics has finished and a new one with different problems is emerging. One of the key problems in physics has been to discover the fundamental laws of nature, that is the elementary constituents of matter and the forces between them. Twenty years ago the structure of the components of the nucleus (protons and neutrons) and the origin of nuclear forces were unknown. Intense debates took place about whether quarks were the constituents of the proton and there was no clear idea of the nature of the forces between these hypothetical quarks.

Now almost everything is known about quarks and their interactions. The laws of physics, from the atomic nucleus to the galaxy, appear to be firmly worked out and most scientists do not expect the future to hold many surprises. However, at scales much smaller than the atomic nucleus and as large as the entire Universe, many things are still not understood. In some cases we are still in almost total ignorance. In physics possibly the greatest mystery still to be unravelled is the origin of gravitational forces and their behaviour over very short distances. This is a difficult problem, since the crucial experiments may involve particles with energies many billions of times greater than currently produced in the laboratory. But, within the range that affects normal human activities, from the physics of elementary particles to the study of stellar evolution, we have a satisfactory formulation of the laws.

However, a knowledge of the laws that govern the behaviour of the constituent elements of the system does not necessarily imply an understanding of the overall behaviour. For example, it is not easy to deduce from the forces that act between molecules of water why ice is lighter than water. The answer to such questions can be obtained from statistical mechanics. This discipline, which arose in the late 19th century from the work of Boltzmann and Gibbs, studies systems of many particles using probability methods rather than by determining the trajectories of the individual particles.

Statistical mechanics has provided the fullest possible understanding of the emergence of collective behaviour. We cannot say whether a few atoms of water will form a solid or a liquid and what the transition temperature is. Such statements only become precise when many atoms are being considered (or, more accurately, when the number of atoms tends to infinity). Phase transitions therefore emerge as the effect of the collective behaviour of many components – for example, the transition in which a normal metal suddenly becomes a superconductor – as the temperature is lowered. Statistical mechanics has been used to study a variety of phase transitions from which a range of collective behaviours emerge.

The predictive capabilities of statistical mechanics has increased greatly over the last 20 years, both through refinements of the theoretical analyses and through the use of computers. In particular, interesting results have been obtained from the study of systems in which the laws have been selected by chance – so-called disordered systems.

Effects of computers

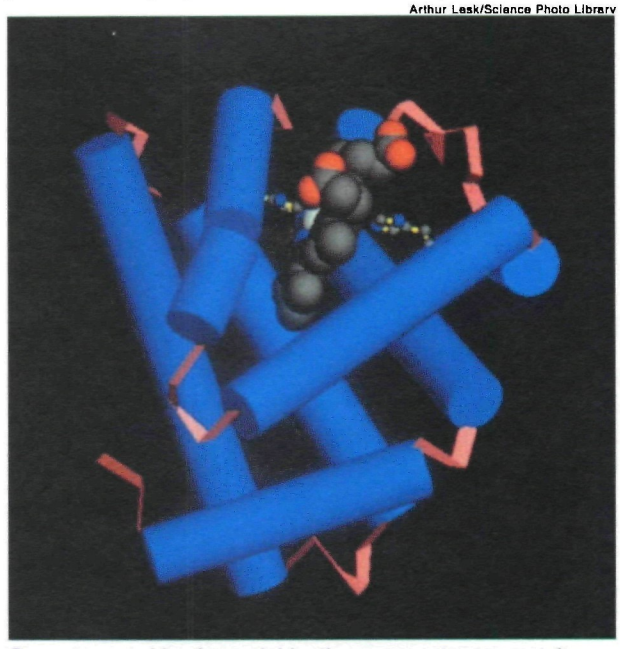
The computer has produced great changes in theoretical physics. Current computers can perform about a billion operations a second on seven figure numbers, and tasks that were once considered impossible have now become routine. If one wanted to calculate theoretically the liquefaction temperature of a gas (argon, for example) and one already knew the form of the forces between the atoms, then one had to make very rough approximations and only under the above conditions could a prediction of the liquefaction temperature be produced by simple calculations. However, the prediction would not agree with the experimental data (typically the error was about 10%). The only way to improve the agreement between the predictions and experiment was to remove the approximations gradually. This theoretical approach, known as

perturbation theory, produced highly complex expressions and tedious calculations which could be done by hand or, if necessary, by computer.

The new approach, which spread in the 1970s, together with the intensive use of computers, was to cease making approximations on the motion of particles and instead to calculate their trajectories exactly. For example, we can simulate the behaviour of a certain number of argon atoms (let's say 8000) inside a box of variable dimensions and observe what happens – whether the argon behaves as a liquid or as a gas. The computational load of such a simulation is enormous. The trajectories of 8000 particles have to be calculated and these have to be followed for long enough for them to overcome the dependence on the initial configuration. Such an approach could not even be imagined without a computer.

One of the reasons for the interest aroused by the simulations is that systems that do not exist in nature, but which are simpler from a theoretical point of view, can also be simulated. Simulations thus become the prime laboratory to examine new theories that could not be verified directly in the real, and too complex, world. Obviously the final aim is to apply such ideas to real cases but this may be done only after the theory has been sufficiently strengthened and has gained in confidence from being matched against simulations.

Arthur Lesk/Science Photo Library



Computer graphic of myoglobin, the oxygen-storage protein found in muscle. Biology must now move forward from a knowledge of the basic biochemical constituents of organisms to an understanding of such systems' overall behaviour

Complex systems

Computers have played a fundamental role in the development of modern theories of disordered systems and complex systems. For complex systems the situation is delicate since this is a newer field with interdisciplinary characteristics – it has connections with biology, information technology, system theory and ecology. It is also a fashionable field, despite the fact that anyone who tries to define "complex" finds it hard to do. Sometimes its sense of complicated is emphasised, meaning that it is composed of many elements (a nuclear power station is a complex system insofar as it is composed of many thousands of different pieces). At other times the sense of incomprehensible is stressed (the atmosphere is a complex system in that one cannot make long-range forecasts). Often every speaker at conferences on complex systems uses the word complex with a different emphasis (see Livi *et al.* and Peliti and Vulpiani in Further reading). The real problems emerge when, having declared that a given system is complex, one wishes to use this statement to obtain results and not restrict oneself to saying that the system is complex and therefore no prediction is possible.

The aim of a theory of complex systems is to find the laws which govern the overall behaviour of such systems. These are phenomenological laws which cannot be easily deduced from the laws that govern the individual components. For example, the behaviour of individual neurons is probably well understood but it is far from clear how ten billion neurons, linked by a hundred trillion synapses, form a brain that thinks. As we have already seen, the emergence of collective behaviours is a phenomenon that has already been much studied by physics in other contexts: the interaction of large numbers of atoms and molecules is responsible for phase transitions (of the water–ice kind). Nevertheless, for complex systems, the overall behaviour of the system is not as simple as that of water, which, at a given temperature, may be in one, or at most two, states (if one ignores the critical point).

If we assume that a complex system must display complex behaviour, then most of the systems studied in the past by physicists have displayed simple behaviour and cannot be regarded as complex. However, physicists, with the aim of understanding the behaviour of some disordered systems, for example the spin glasses (alloys of gold and iron that display anomalous magnetic behaviour at low temperature), have recently begun to obtain results on the properties of relatively simple systems which display complex behaviour (see Mézard *et al.* in Further reading). The techniques used during this research were more general than one might expect given their rather esoteric origin and are now being applied to the study of neural networks.

Frequently the study of complex systems has been advanced either by analysis or by computer simulation. Moreover, these two approaches can be combined synergistically. Computers enable simulations of complex systems of moderate complexity to be carried out so that quantitative and qualitative laws can be extracted from these systems before tackling truly complex systems. The mixture of analytical results from simpler systems and numerical simulations performed on systems of intermediate complexity is very effective.

A profound understanding of the behaviour of complex systems would be extremely important. Attention has been focused on systems composed of many elements of different types which interact on the basis of more or less complicated laws and in which there are many feed-back circuits that stabilise the collective behaviour. In such cases a traditional reductionist point of view appears to lead nowhere. An overall approach, in which the nature of the interactions between the constituents is ignored, also appears to be useless in that the nature of the constituents is crucial in determining the overall behaviour.

The emerging theory of complex systems takes an intermediate point of view. It starts from the behaviour of the individual components, as in a reductionist approach, but incorporates the idea that the minute details of the properties of the components are irrelevant and that the collective behaviour does not change if the laws governing the conduct of the components are changed slightly. The ideal would be to classify the types of collective behaviour and to see what position a system would occupy in this classification if the components were changed (see Rammal *et al.* and Parisi 1992b in Further reading). In

other words, collective behaviours should be structurally stable and therefore susceptible to classification, unfortunately a much more complicated one than that made by Rene Thom of the Institut Hautes Etudes Scientifiques, Paris, in the book *Structural Stability and Morphogenesis* (1975, Benjamin, Reading, MA).

Spin glasses: complex system exemplified

The theoretical study is not carried out on an individual system, but instead we study a whole class of systems simultaneously, which differ from each other in a random component. This approach may be understood more easily if I give a concrete example. Imagine a group of people in a room who know and either like or dislike each other. Suppose we divide them at random into two groups and then ask each person whether they want to move from one group to another (the person will answer yes or no according to their preferences). If a person says yes they change groups immediately. After the first round, some people will still not be satisfied. Some of those who moved (or who did not move after the first round) might wish to reconsider their own position after the moves made by others. A second round of changes is made and so on until there are no further requests from individuals. In a further stage, we could try moving not just individuals but whole groups of people, since a change of group may only be attractive if made in the company of others, until a state of general satisfaction is achieved.

The fact that after a finite number of rounds all the requests from individuals have been satisfied depends crucially on the hypothesis that we have assumed that relationships of like or dislike are symmetrical, i.e. that if Caio likes Tizio then Tizio likes Caio. We could have asymmetric situations: Caio likes Tizio but Tizio cannot bear Caio. If such relationships are common then the procedure above will never achieve a stable state – Caio pursues Tizio, who flees, and the two never stop. It is only when the relationships are symmetrical that the desires of the individuals are all directed towards the same objective – the optimisation of general satisfaction.

Obviously, the final configuration will depend upon the relationships between the various people and the initial configuration, and it cannot therefore be calculated directly without such information. Nevertheless, we can calculate approximately the general properties of this process (for example, how many rounds will be needed before everybody is happy) on the basis of the distribution of friendships and dislikes being random. More precisely let us suppose that we know the probability distribution of friendships. For example, the probability that two people selected at random will be friends is p, where p is a number between 0 and 1. We need to establish whether this relationship model is true or if the real situation is more complicated (for example, we could introduce degrees of dislike and suppose that people in real life who live near each other have stronger relationships, whereas those who live far apart are more indifferent). Once we have achieved an accurate model of the probability distribution of likes and dislikes, we can make predictions for the system. These will be purely in terms of probability and will become increasingly accurate (that is with a decreasing relative error) as the system becomes larger and the number of components tends to infinity.

In this situation, probability is used differently from how we are used to. Whilst, classically, it was supposed that the dynamics by which systems evolved were so complicated that one could assume that the configurations were entirely random (like a coin being tossed), in the case that we are studying, the laws that govern the system themselves are chosen at random before the dynamics are studied.

The symmetrical system corresponds exactly (from a mathematical point of view) to the spin glasses of physicists. If we were to replace the words "like" and "dislike" by "ferromagnetic" and "antiferromagnetic" and we identify the two groups with spins oriented in different directions we would produce a precise description of spin glasses. At low temperatures a physical system develops so as to minimise the temperature and this dynamic is very similar to the optimisation process described above, provided that physical energy is identified with general dissatisfaction. In the last decade, spin glasses have been studied intensively and we can now answer many of the questions that have been raised.

Possibly the most interesting characteristics of these systems are that many different equilibrium states exist (if we move just one person at a time) and that it is difficult to find the optimum configuration, in respect of a change of an arbitrarily high number of people. Spin glasses are one of the best known examples of those optimisation problems (termed "NP completeness problems" for reasons that need not be discussed, see Garey and Johnson in Further reading) whose optimum solution can be found only after a high number of passes (which increases exponentially with the number of elements in the system).

The presence of many different equilibrium states may be regarded as one of the most typical characteristics of complex systems (at least in one meaning of the word). A system which does not change with time is not complex whilst one that can assume many different forms is certainly complex. The unexpected discovery made in the last 10 years is that the complexity emerges naturally from the disorder of the laws of motion. To obtain a complex system we do not have to force ourselves to choose particular laws. They can be chosen at random but with well determined probability distributions. This result has opened up a new perspective in the study of complex systems. It is a new and fascinating field in which results are obtained slowly, partly because of the newness of the field and partly because of the need to use new mathematical tools. For example, the replica theory, which has been used to obtain the most interesting results, has no mathematical proof at present.

Detail of spin glasses

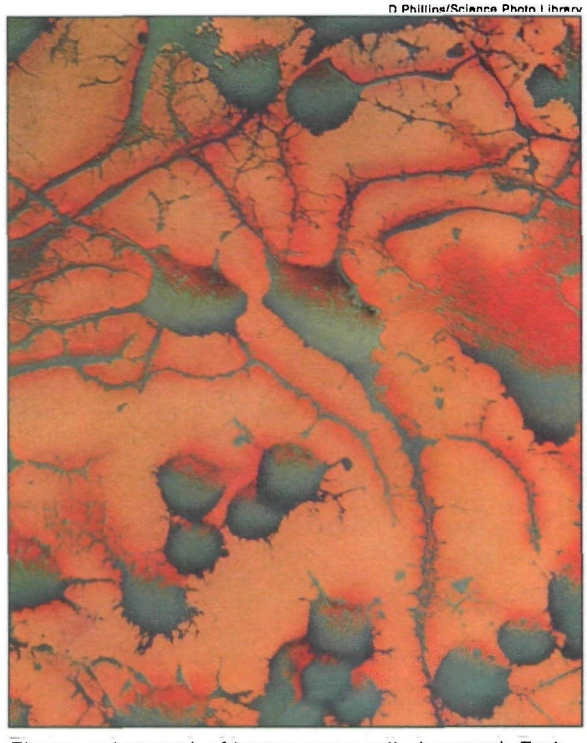
Spin glasses may be regarded as an overall optimisation process in which the minimising function corresponds to the system energy. I will now lay out in precise form some of the results that have been obtained on spin glasses (see Mézard et al. in Further reading).

More precisely we may consider a system described by N variables, s_i (i varies from 1 to N), which can have two possible values (1 or −1) corresponding to the two possible spin orientations (using the language of the analogy above, they correspond to the two possible changes of group). For every possible pair (i, k) a variable $\mathcal{J}_{ik}$ is introduced, which is chosen at random (1 or −1). The energy E is given by the sum for all the pairs of $\mathcal{J}_{ik}s_is_k$. If $\mathcal{J}_{ik}$ is negative, the minimisation of the contribution to the energy E of the pair (i, k) is obtained by choosing the same values for the two spins, s_i and s_k. If, on the other hand, $\mathcal{J}_{ik}$ is positive, the minimisation of the contribution of the pair (i, k) to the energy E is achieved by selecting opposite values for the spins s_i and s_k.

Different choices of $\mathcal{J}_{ik}$ correspond to different systems.

The theory of spin glasses provides accurate estimates on the behaviour of systems within the limits where N tends to infinity. Many of the properties become independent of the choice of these variables for practically all realisations of the system. In particular, the minimum energy can be approximated by $-0.7633\ N^{3/2}$.

The process of successive minimisation described above corresponds to choosing sequentially for each i, the variable s_i so as to minimise its contribution to the energy. If one starts from a random configuration this evolution results in a final energy proportional to $-0.73\ N^{3/2}$ and therefore markedly greater than the minimum. A procedure of sequentially searching for the minimum, carried out on one variable after another, cannot therefore attain the overall minimum but merely a local minimum, that is a configuration whose energy will not decline by changing one individual spin at a time. The fact that the evolution of the system becomes stalled in a local minimum is also connected with the existence of many local minima. The total number of different local minima increases as $2^{0.3N}$ (almost in line with the total number of configurations, which rises as 2^N).



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Electron micrograph of human nerve cells (neurons). Each neuron consists of a cell body (green) with branching processes extending from it. The arrangement of neurons in the brain is an excellent example of a disordered system

The calculation of the energy minimum is not simple and is based upon several hypotheses which, though reasonable, have not been proven rigorously. To calculate the minimum energy one must calculate simultaneously the number of configurations with energy close to the minimum, and the correlations existing between the difference in energy and the distance between two configurations defined as the percentage of different spins. A detailed analysis shows that the configurations with energy close to the minimum can be classified in a tree classification similar to that used in biology. This totally unexpected result demonstrates the enormous richness and complexity of such an apparently simple system. A more detailed description would take us too far from the subject of this article, but see Parisi 1992b in Further reading.

The dilemma of biology

Biology faces several problems which result from spectacular recent successes. Developments in molecular biology and genetic engineering have provided a detailed understanding of the basic biochemical mechanisms. In many cases we know the identity of the molecules on the cell membrane that receive a message (in the form of a chemical transmitter) sent by other cells, and how this message is transmitted to the cell nucleus via the activation of a chain of chemical reactions. We can often identify the genes that code for a particular character or which control the growth of an organism or the development of limbs. The human genome project has been launched with the aim of determining the sequence of human DNA. This colossal project will cost roughly one billion dollars.

The difficulties of exploiting these results to the full lie in the enormous differences that exist between the knowledge of the underlying biochemical reactions and the understanding of the overall behaviour of living organisms. Consider one of the simplest living organisms, *Escherichia coli*, a small bacterium little more than a micron in length that is present in large numbers in the human intestine. *E. coli* contains about 3000 different types of protein which interact extensively with each other. Some proteins play essential roles in the cell's metabolism, other proteins regulate the production of these proteins either by inhibiting their synthesis (suppressors) or stimulating it (operons). The synthesis of operon or suppressor proteins is itself controlled by other proteins. There is little doubt that within a few years the complete list of the proteins of *E. coli* will be available. It might even be possible to know the functions of each of these proteins and the mechanisms that control their synthesis. We could envisage that in a few decades we might have an enormous computer program which could successfully simulate the behaviour of a real *E. coli* cell in terms of the total amount and spatial distribution of each kind of chemical.

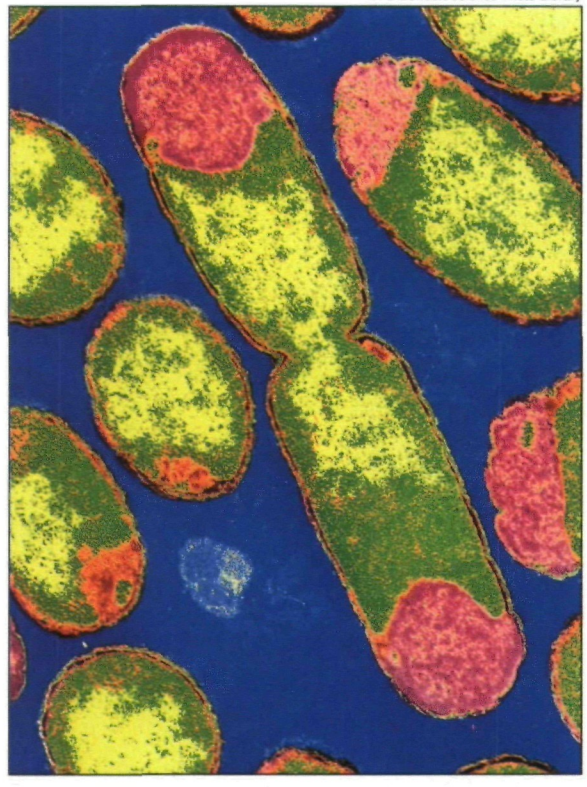
However, it is not clear that such knowledge would be sufficient to understand how the living organism functioned. We could eventually understand the various feed-back circuits but it does not seem that such an approach would enable us to grasp the underlying reasons by which the system behaves overall as a living organism. In other words, even if we succeed in modelling a unicellular living organism with a system of differential equations with N variables (the appropriate value of N for a single cell is not clear, but would be between 10^4, the number of different chemical substances, and 10^{12}, the number of atoms), we would still have to deduce the overall characteristics of the behaviour of the system with more sophisticated techniques than numerical simulations. It is the same problem as in statistical mechanics, where a knowledge of the laws of motion does not directly imply an understanding of the collective behaviour. One could therefore postulate that once the techniques of molecular biology had reached a sufficiently detailed level of knowledge of the molecular phenomena, an understanding of the collective behaviour (and therefore of life) should be obtained by using techniques similar to those of statistical mechanics.

The same problem presents itself at a higher level in the study of the vertebrate brain. We might soon know all the functional details of the behaviour of individual neurons but this information alone would not enable us to understand how several billion such neurons, linked in a disordered manner, form a brain that can think.

A similar approach could be taken for many biological systems, for example the study of the dynamics of protein synthesis in the cell, ontogenesis, natural evolution, and hormone balance in mammals (see Kauffman in Further

reading). A characteristic of all these systems is that they comprise many different types of elements which interact amongst themselves on the basis of more or less complex laws. Consider all the effects that a hormone can have on the production of other hormones. Furthermore, such systems have many feed-back circuits that stabilise the collective behaviour (the production of a given hormone is set by homeostatic mechanisms). In such cases, the traditional reductionist point of view does not appear to lead anywhere. The number of hormones, for example, is so high that the interactions of each hormone with the others cannot be determined fully and therefore a precise model of the system cannot be constructed. An overall approach, in which the nature of the interactions between the components is ignored, would also not seem to be appropriate. The hormonal system behaves in a different way from a cell (a cell divides in two, the former does not) and the differences in the nature of the components are crucial to determining the differences in overall behaviour.

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Electron micrograph of *Escherichia coli*. Even if we eventually manage to model this unicellular organism numerically, more sophisticated techniques will be necessary to deduce overall system behaviour

The problem that biology must confront is how to move forward from a knowledge of the behaviour of the basic constituents (proteins, neurons etc) to deducing the system's overall behaviour. Fundamentally, this is the same kind of problem that confronts statistical mechanics and this is why attempts are being made to adapt to biological systems the same techniques that were developed to study physical systems composed of many components of different types with laws chosen at random. The theories of the complex behaviour of disordered systems could thus be used to study biological complexity (see Anderson, and Kauffman and Levin in Further reading).

Chance and necessity

A proposal to study the laws that govern the interactions between the various components can make a biologist nervous. A first reaction is for them to regard the entire programme as idiocy put forward by someone with no clear idea of the nature of biology. The main objection is that existing biological systems result from a natural selection over many millions of years and that the components of a living organism have therefore been selected carefully so that it functions. It is not clear whether the probability methods of statistical mechanics (in the sense that the laws of motion have been chosen by chance) could be successfully applied to living organisms, in that components that have been selected for a purpose have not been chosen by chance.

The objection is not as strong as it may first appear. To state that something has been chosen by chance does not mean that it has been chosen *completely* by chance but on the basis of laws that are in part deterministic and part random. The real problem is to understand whether the chance element in the structure of a living organism is crucial to its proper behaviour.

Much depends upon the underlying structure of the living organism, although a major disagreement exists over this point between the various approaches. The cell is often seen as a large computer with DNA representing the program (software) and the proteins representing the electrical circuits (hardware). If this idea was not wide of the mark there would be no point in using statistical mechanics to study biology, just as there is no point in using it to study a real computer. A computer is built to a design and the connections are not made at random but in accordance with a firm layout. A living organism is not made in a totally random fashion but equally it is not designed on paper. They have evolved via a process of random mutation and selection.

These two aspects are crucial to the study of protein dynamics. On the one hand it is clear that proteins have a well defined purpose and have been designed to achieve it. However, proteins have initially been generated in a random manner and perhaps some of the physical properties of proteins (particularly those which have not been selected against) still reflect the properties of a polypeptide chain with elements chosen at random along the chain.

This marriage of determinism and chance can be found if we study the development of a single individual. For example, the brains of two twins may appear completely identical if not examined under the microscope. However, the positions and connections of the neurons are completely different. Individual neurons are created in one part of the cranium, migrate to their final position and send out nerve fibres that attach themselves to the first target that they reach. Without specific signals on the individual cells such a process is inevitably unstable and therefore the slightest disturbance leads to systems with completely differing results. The metaphor of the computer does not seem adequate in that the description of the fine detail (the arrangement and connection of the individual elements) is not laid down in the initial design. Moreover, the number of bits of information required to code the connections in a mammal brain is of the order of 10^{15}, far greater than the 10^{9} bits of information contained within DNA.

The arrangement of the neurons and their connections in the brain is an excellent example of a disordered system, in which there is a deterministic, genetically controlled component (all that is the same in the brains of two twins, i.e. the external form, weight, possibly the hormonal balances) and a chance element which differs from twin to twin. Our attitude to the methodology that should be used to achieve an understanding of the behaviour of the brain changes completely depending upon whether we consider the variable (and therefore chance) part to be a non-essential, non-functional accident or if we think that some character-

istics of the variable part are crucial for proper function.

The need to use techniques from the statistical mechanics of disordered systems also stems from the fact that biological systems interact extensively with the outside world and that this interaction has both a deterministic and a chance component. For example, the faces of the people that we know have a constant component (they are faces) and a variable (chance) one, the characteristics of each individual. It has perhaps not been fortuitous that the greatest success in biology of the use of the statistical techniques of disordered systems has been the study of neuronal networks and their capacity to function as memories, to memorise and to subsequently recognise several types of input (see Hopfield; Amit; Parisi 1992a in Further reading). The chance nature of the events being memorised reflects the random nature of the growth of the synapses between the various neurons and therefore a disordered synaptic structure. In this field, various models of associative memory have been constructed, whose dynamics are well understood theoretically, and a sufficient level of analysis has been reached to begin to compare the predictions of the theory (which has been made increasingly realistic) with the experimental data from recording the activity of individual neurons.

Convergence

The attempt to bring together physics and biology described here entails a change in the outlook of both the physicist and the biologist. As a result of training, the theoretical physicist tends to be more concerned with general principles (for example, in seeking to understand how a system that only distantly resembles *E. coli* could be regarded as living), whereas the biologist remains wedded to what is; that is, to understand the real *E. coli*, not a hypothetical system that could not be produced in nature.

Physics has a strong simplifying tradition and tends to concentrate on certain aspects whilst neglecting other elements, even essential ones. Modern physics was born with Galileo, who founded mechanics by ignoring friction, despite the fact that friction is an essential part of everyday life. The object that is not subject to any forces and which moves in a uniform straight line (as in Newton's First Law) is a purely abstract concept (leaving aside billiard balls).

Physics was born with a backward step, with the renunciation of the aim of understanding everything about what is, and with the proposal to study just a small, and initially tiny, corner of nature. Physicists were well aware that they were studying an idealised, simplified world. Niccolò Tartaglia, the 16th-century Italian mathematician who published the first book on projectiles, wrote: "Here we will study the motion of objects subject to the force of gravity, ignoring friction: and if real cannon balls do not follow these laws, so much the worse for them; it means we will talk no more of them." This step backwards, this break with the tradition of attempting to understand the real in its entirety, has enabled physics to provide a solid base for all the subsequent structures to be built on.

The same kind of backward step was made when the techniques of statistical mechanics were introduced to study neuronal networks (see Hopfield in Further reading). The physico-mathematical techniques then available only enabled systems to be studied where the interaction was symmetrical – where the influence of neuron A on neuron B was equal to that of neuron B on neuron A. In this case, the system behaves extremely simply and neither oscillations nor chaotic behaviour are possible. This symmetrical hypothesis is false from a physiological point of view. Nevertheless, its introduction allowed the problem to be seen in a form that could be studied in detail. Subsequently, by using the advances made in such study, the symmetry hypothesis could be removed and a relatively realistic model of neuronal networks built.

The tendency of physicists is to simplify clashes with the biological tradition of studying the living organism as it is observed, not how it could or should be. Without certain evidence of exobiology, we only have this Earth at our disposal and thus one of the physicist's objectives, that of identifying the constant characters in all possible living forms, is empty in the eyes of a biologist, who only knows the few kingdoms that exist on Earth. Physics is an axiomatic science (axioms selected by experiments), in which all the laws are deducible, even if with difficulty, from a few basic principles, whilst biology is a historical science, in which the products of history on this planet are studied.

These different concepts of science make the collaboration of physics and biology problematic but not impossible. The new way of using physics in biology is making the laborious first steps and it will be many years before we know if it will be successful. The advances are slow, because most problems, even after they have been cast in mathematically precise terms, are technically difficult and have still not been resolved theoretically.

I am convinced that the introduction of probability techniques to study living matter will be crucial in the near future, particularly in those systems in which the existence of a random element is essential. The true unknown is whether this phenomenon will only occur in some fields, or whether the techniques of mathematical physics based on the study of disordered systems will become the conceptual framework for understanding the dynamics of living organisms, particularly at the system level.

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