



100 YEARS AGO

The result of this inquiry is to prove the existence of a small number of more or less isolated hereditary centres, round which a large part of the total ability of the nation is clustered, with a closeness that rapidly diminishes as the distance of kinship from its centre increases. The materials are derived from the replies to a circular which I sent with a blank schedule, to all fellows of the Royal Society, asking for the names and achievements of their "noteworthy" kinsfolk in each degree of near kinship as specified in the schedule. Noteworthiness was defined as including any success that was, in the opinion of the sender, at least equal in its way to that in which the honour of a fellowship of the Royal Society is held by scientific men. Returns are still dropping in, and now exceed two hundred. They continue to be very acceptable, but I judged it best to content myself with the number received up to a date when I could conveniently work at them, and to publish the preliminary results without delay... the experience gained through this inquiry has strongly confirmed an opinion expressed in my lecture on Eugenics before the Sociological Society... that it would be both feasible and advantageous to make a register of gifted families. Francis Galton
From *Nature* 11 August 1904.

50 YEARS AGO

The chromosomes of *Mus musculus* have a high chiasma frequency, and for this reason very loose linkages are to be expected. Many of the problems of linkage and independence in this species may therefore have to be solved by cytogenetic methods rather than the breeding techniques of formal genetics. Among them is the question whether linkage group VII is carried in the pairing segment of the sex chromosome... With the object of obtaining evidence on questions such as this we have induced a number of translocations in the mouse, using X-rays, and have identified linkage groups in eleven of them... Translocation 78 thus offers a means of settling the question whether linkage group VII is sex-linked. The translocation and the sex bivalent should be cytologically recognizable in primary spermatocytes; it should therefore be possible to establish their chromosomal independence or interdependence. T. C. Carter, Mary F. Lyon & Rita J. S. Phillips
From *Nature* 14 August 1954.

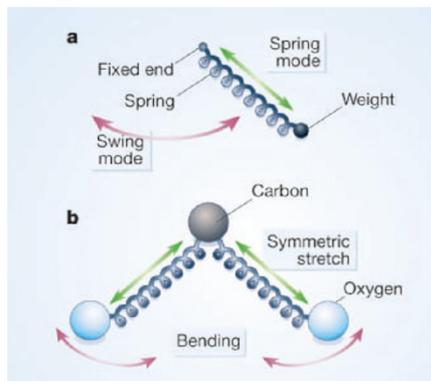


Figure 2 The swing-spring. The swing-spring can stretch like a spring and swing like a pendulum (a), and can be used as a simple model for the carbon dioxide molecule (b).

which is simpler than the exact Hamiltonian but is still a good model.

The quantum energy-momentum lattice of the molecule consists of the eigenstates of this Hamiltonian, that is, the pure vibrational modes. For a fixed energy, these modes correspond to two classical 'constants of motion' — angular momentum and a quantity related to the rotational symmetry. The eigenstates can be characterized by two quantum numbers, which are integers, so these eigenstates form a regular planar lattice like a chessboard.

However, there is an extra quantum number, related to another classical variable, called the 'action'. The new phenomenon

here is that, because of monodromy, the action is defined only locally and cannot be consistently extended across the entire lattice. For fixed quantum numbers in the lattice, this additional quantum number can take on infinitely many values, at equally spaced points at right angles to the chessboard. The simplest structure of this kind is a three-dimensional cubic lattice — an infinite stack of chessboards, vertically above each other. Monodromy implies that the totality of all sets of quantum numbers does not form a cubic lattice. Instead, it has a single topological defect where the regularity of the lattice structure breaks down.

This analysis is important because it suggests, and supports, a general principle. The most significant features of the quantum-mechanical description of a classical system occur at its singularities. The singularities introduce defects into the ensemble of quantum eigenstates, but they also organize the structure of those defects. Everywhere else, quantization works just as in previous, simpler examples. The authors suggest several directions for future progress, mostly to develop the growing use of nonlinear dynamics in the understanding of quantization. But the most tantalizing is the possibility of detecting quantum monodromy experimentally. Maybe we will soon be able to see how Schrödinger's cat turns itself upside down. ■

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Cognitive science

Rank inferred by reason

Sara J. Shettleworth

Pinyon jays seem to work out how to behave towards an unfamiliar jay by watching it in encounters with members of their own flock. The findings provide clues about how cognition evolved in social animals.

Susan is taller than Billy. Peter is taller than Susan. Who is taller, Billy or Peter? Knowledge about pairs of objects linked by relationships such as 'taller' or 'stronger' permits conclusions to be drawn about novel pairs (here, Billy and Peter) — a process known as transitive inference. Monkeys, rats and some birds can solve transitive-inference tasks in the laboratory¹, but why would this ability evolve? A plausible answer is that transitive inference is an evolutionary adaptation in certain kinds of social group. For example, suppose I know from bitter experience that Bob always beats me in contests (that is, he dominates me). I now observe some new individual, Andy, dominating Bob. If I reason, "Andy dominates Bob, and Bob dominates me, therefore Andy will dominate me", I can avoid fights by deferring to Andy when we meet. But there

has been no well-controlled evidence that animals actually use transitive inference in social situations. In the study reported on page 778 of this issue, Paz-y-Miño and colleagues² provide this.

In effect, the authors staged the Andy-and-Bob scenario using pinyon jays (*Gymnorhinus cyanocephalus*; Fig. 1), a highly social member of the crow family. These birds live in large, permanent flocks with clear pecking orders. Paz-y-Miño and colleagues created groups of captive pinyon jays that were previously unknown to each other, and allowed stable dominance relationships to develop in each group. Then jays from each group were allowed to observe individuals from other groups interacting over a peanut, and later interacted with some of those same birds. In the experiment, the observer saw a relatively dominant bird from



Figure 1 Pinyon jays — watching and learning.

its own group ('Bob' in our scenario) losing encounters with a stranger from another group ('Andy'). To ensure that the stranger would not be seen only to dominate others, the observer also watched the same stranger losing contests with another stranger. As a control, other observer birds watched a stranger both winning and losing to members of the stranger's own group, an experience that should give observers no information on whether the stranger will be able to dominate them.

If pinyon jays infer social status transitively, observers should behave more submissively in their first encounter with the stranger in the experimental condition than in the control — and this is what Paz-y-Miño and colleagues⁷ observed. To act in this way, the observers must first have identified both the individuals they watched and their roles in the observed encounter, and then retained this information for later use. Thus, their behaviour implies a more complex set of cognitive skills than that implied by another recent report of birds' sensitivity to a generic social relation (whether mated or not) between unfamiliar individuals present³.

It is noteworthy that the animals in this study are birds. The idea that the demands of a complex social life might drive the evolution of cognition was originally proposed to explain the apparently high intelligence of monkeys and apes⁴. However, other mammals, such as hyenas and elephants, and some birds also form long-lasting groups of identifiable individuals with differentiated social roles. Long-term field studies indicate that social complexity has shaped cognition in a similar way across species^{5,6}, but in field work it can be difficult to know all the animals' relevant experiences. The experimental approach of Paz-y-Miño and colleagues² will serve as a model of how manipulating

the experiences of captive animals can provide firm conclusions.

If transitive inference is used in social life, species with more complex societies should be better at it. Laboratory studies using an abstract transitive-inference task provide some support for this idea. First, animals are taught the relative reward value of five or more pairs of colours⁷ — red is better than green, green is better than blue, and so on. Then they are tested with novel pairings. Monkeys behave in such tests as though they are reasoning by transitive inference, whereas pigeons do not¹. But this finding need not reflect a difference in sociality between monkeys and pigeons because they differ in so many other ways. More relevant is a recent comparison of pinyon jays with the closely related, but less social, western scrub jay⁸. Pinyon jays perform more like monkeys in the abstract task than do scrub jays.

Members of the crow family, such as New Caledonian crows⁹, western scrub jays¹⁰ and ravens, feature in recent reports of remarkable cognitive abilities including making and using tools, episodic-like memory and forms of social learning. Each of these abilities is thought to reflect a species-specific adaptation, for example to extract prey or retrieve stored food. Comparisons of different species

in similar tasks are necessary to test whether such abilities are in fact associated with the ecological factors supposed to select for them. Nevertheless, such findings underline the importance of viewing animal intelligence as consisting partly of species-specific adaptations, rather than being an entirely undifferentiated 'general intelligence'. So, comparative psychology can provide experimental support for the idea that cognitive modules have evolved for solving different kinds of task — an idea so popular, but often untestable, in human evolutionary psychology⁵. ■

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Human genetics

An expression of interest

Nancy J. Cox

The baseline level of gene expression varies from person to person, but how is this determined genetically? The answer may improve our understanding of complex traits, including some genetic diseases.

On page 743 of this issue, Morley and colleagues¹ report how they successfully determined the genomic locations of genetic determinants that influence the variation in levels of gene expression between people. How was this accomplished, and why is it important?

In searching for the genetic basis of a measurable trait, or phenotype — height or eye colour, for example — geneticists start by identifying people with variation in that trait. In the simplest situations, the variation is traced to a single gene, and particular variations in the sequence of that gene are shown to determine the observed phenotypic variation.

A less tangible, but no less significant, trait is the baseline level of gene expression. Much of our progress so far in understanding the basis of rare genetic diseases has come through identifying changes in gene sequence that change the nature of the encoded protein, so that it is insufficiently or inappropriately functional. But changes in the amount of protein produced might also

affect the health of an organism. This amount is determined in part by gene expression — or how much messenger RNA (mRNA) is transcribed from the relevant DNA sequence — and the relative abundances of mRNA for many thousands of genes can now be routinely assessed for any accessible tissue. But gene expression is generally regulated by DNA regions outside the parts of genes that actually encode proteins, and there is much that is not yet understood about this process. In particular, little is known about how variation in DNA sequences might affect the variability in baseline levels of gene expression among individuals — the topic of Morley and colleagues' investigations¹.

Thus, their studies stand squarely at the crossroads of some of the most challenging questions in human genetics. Among the most pressing of these questions are: how can we identify regulatory elements? Does variation within regulatory elements have the same frequency spectrum as the variation that occurs within genes and