torsional oscillation of the star can, in principle, produce the required amplitude of phase modulation, but it would be nearly impossible to reproduce the apsidal motion and the Einstein delay. Moreover, this object would still be very special, since no other radio pulsar is known to exhibit a similar behaviour.

In short, it requires quite a cosmic conspiracy for any physical mechanism (other than the motion in a binary system) to produce a pulsar signal with a phase modulation that accurately mimics an eccentric binary orbit with two relativistic corrections.

D. BHATTACHARYA
R. A. M. J. WIJERS
Astronomical Institute,
University of Amsterdam,
Roetersstraat 15, NL-1018 WB,
The Netherlands

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Early tetrapod hearing

SIR—I should like to respond to the comments in Scientific Correspondence[1,2] on my recent Letter on the stapes of the early tetrapod Acanthostega[3]. This bone is pierced by a stapedial foramen, clearly marking it as a stapes rather than a fish hyomandibula[4]: a more certain basis for distinction than inferred function[1].

Second, neither the hyomandibula of osteolepiforms (the group of lobe-finned fishes presumed ancestral to tetrapods) nor the stapes of Acanthostega have direct connections with the jaws. The suggestion[2] that this decoupling in Acanthostega is a major difference from the osteolepiform condition is therefore untrue.

Third, we need not accept that osteolepiforms had a tympanic membrane[2], with the implication that an open spiracle is incompatible with an air-filled spiracular pouch. Spiracles can be closed, and a pouch with a functional spiracle might also act as a middle ear cavity. The existence of a basilar papilla in the extant coelacanth Latimeria[2] suggests that an auditory function for the inner ear is a primitive feature of lobe-finned fishes, in association with an air-filled spiracular pouch with or without a membranous closure.

JENNIFER A. CLACK
University Museum of Zoology,
University of Cambridge,
Downing Street,
Cambridge CB2 3EJK, UK

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When is random random?

SIR—The intelligentsia is not on speaking terms with itself. Ochs[1] correctly cautions against sloppy use of the term 'random', but seems unaware of the work of mathematicians on this problem over many years. If each event in a set is selected with equal probability, say the toss of a fair coin, the selection is indeed random. But the probability of a 7 in a fair throw of two dice is not the same as that of a 2, yet the process is clearly to be considered random. Thus there is more randomness in a sequence of heads or tails from the toss of a fair coin than in a sequence of throws of two dice. Clearly a more sophisticated definition of randomness is required than one finds in a dictionary.

Suppose we wish to send to our little green friends on a planet near Arcturus the value of π. We could start sending the digital sequence in the decimal representation of π, but that would take an infinite time and an infinite amount of information, for there is no pattern among these digits. But π is a transcendental number, and we could send one of the algorithms from which it is calculated, not necessarily the shortest, letting our little green friends do the rest. Thus it is clear that π and all other transcendental numbers have a finite amount of information, namely, that in the algorithm by which they are calculated.

In the case of a sequence of heads and tails generated by the tossing of fair coin, there is no algorithm which can shorten the sequence. We must simply send the sequence itself. Such random sequences are known as Bernoulli chains or strings. On the other hand, the probability distribution in the tossing of two fair dice may be used to shorten the sequence of numbers generated. This is because some information is lost when the numbers on the faces of the two dice are added and only the sum is recorded. (We cannot know from the sum, especially in the case of 7, the exact faces which were uppermost.)

Thus we can measure the amount of randomness in a sequence by the length of the algorithm, in bits by which we can describe it to our little green friends. This fact emerged from the initially independent work of Solomonoff[2], Kolmogorov[3], Chaitin[4] and Martin-Löf[5] on the foundations of probability theory. Sequences which cannot be described by an algorithm shorter than the sequence itself have the greatest measure of randomness. Because any computable number can be described by an algorithm which is finite in length, no computable number is random[6]. It is impossible to prove that any given sequence was generated by a random process.

The current state of the theory is due to Chaitin[6]. I suggest that this literature be consulted by those who are interested in the proper use of the term 'random'. Ochs[1] repeats a common mistake in that he attempts to squeeze meaning out of words such as 'chaotic, unpredictable, uncertain, arbitrary, undetermined'. 'Arbitrary' and 'undetermined' do not mean 'random'. Words are merely names of mathematical functions and take their meaning from the mathematics, not the other way around.

HUBERT P. YOCKEY
1507 Balmoral Drive,
Bel Air,
Maryland 21014, USA

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Cold shock and DNA binding

SIR—Goldstein et al.[1] have recently described a gene from Escherichia coli that is induced in response to low temperature, giving rise to a cold-shock protein (csp) CS7.4. No similarity between CS7.4 and any other protein was noted by these authors. But when this sequence is compared with Gen-Bank v62 using the program SEQFT[2], a striking similarity with a conserved region of human DNA-binding proteins is revealed. The human proteins DbpA, DbpB (ref. 3) and YB-1 (ref. 4) share a region of conserved sequence which closely matches the entire deduced sequence of CS7.4.

The function of CS7.4 is unknown, with suggestions varying from antifreeze protein to a role in initiating translation. It has also been suggested that the protein is autoregulatory, interacting with its own gene promoter[1]. DbpA and DbpB are DNA-binding proteins of unknown specificity[3] but YB-1 has

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csp   MSGKMTGIVKWFNADKGFGFITPDDGSKDVFVHFSAIQNDG---Y-KSLDEGQKVSFTIESGAKGPAAGNVTSL        1-70
dbpa  LATKVLGTVKWFNVRNGYGFINRNDTKEDVFVHQTAIKKNNPRKYLRSVGDGETVEFDVVEGEKGAEAANVTGP      157-230
dbpb  IATKVLGTVKWFNVRNGYGFINRNDTKEDVFVHQTAIKKNNPRKYLRSVGDGETVEFDVVEGEKGAEAANVTGP       95-168
ybl   IATKVLGTVKWFNVRNGYGFINRNDTKEDVFVHQTAIKKNNPRKYLRSVGDGETVEFDVVEGEKGEEAANVTGP       55-127
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Alignment of deduced amino-acid sequences of CS7.4 (csp)[1], DbpA and B[3] and YB-1[4]. Sequence positions are indicated. Residues which are identical between the prokaryotic and eukaryotic proteins are marked with an asterisk; conservative changes are marked with a dot.