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COVER Dune crest in Kelso dunefield, Mojave Desert, California. Foreground ripples illustrate self-organization of fine sand bed into 10-centimeter wavelength ridges oriented perpendicular to wind during saltation. Upper lee face shows grain fall deposition of saltating grains, and subsequent failure as grain flow during later wind event, with wind blowing toward observer. See page 820. [Robert S. Anderson, California Institute of Technology, Pasadena, CA 91125]

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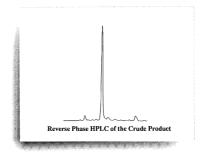
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This Week in

Science

Deficit delusion

◀ HE government's deficit is widely used and widely debated as a measure of fiscal policy, but it may also be viewed as an entirely arbitrary accounting device that depends on how the government labels its receipts and expenditures. A large deficit does not necessarily equate with loose fiscal policy nor a small one with tight policy. Kotlikoff (page 791) describes a way of measuring tightness or looseness of fiscal policy by analyzing in present value what each generation has to pay to the government. As an example, he uses the U.S. fiscal policy of the 1980s from the perspective of generational accounts. Younger generations lost from the changes in Social Security in 1983, but gained about the equivalent in present value from income tax cuts in 1986. Older generations came out even from the Social Security changes, benefited from the 1981 tax changes, but lost from the 1981 changes in investment incentives. A look at the October 1987 stock market crash shows that about \$1 trillion was redistributed from older generations, who held most of the stock, to younger generations, who can now purchase the same assets at a lower price. The result was the eqivalent of extremely tight fiscal policy.

Solving the phase problem

ONVENTIONAL methods of solving protein structure involve preparation of multiple isomorphous derivatives or use of coordinates of a similar structure for molecular replacement. Guss et al. have applied a method of multiple wavelength phasing to directly solve the structure of the basic "blue" copper protein (CBP) isolated from cucumber seedlings. The structure of this protein has been particularly recalcitrant to determination by classical methods. An x-ray diffraction technique, multiple-wavelength anomalous dispersion, was applied to solve the structure of this protein (page 806). In crystals that contain atoms with large

anomalous scattering effects (such as the Cu atom in CBP) the net observed intensity of Bragg reflections will be energy dependent and the differences in intensity at several x-ray energies may be used to derive the crystallographic phases. Bragg intensities were measured from two crystals of CBP at four x-ray energies generated by an intense polychromatic synchrotron source and the resulting data were used to prepare an electron density map. The initial phasing of the structure could then be determined at a resolution of better than 3 angstroms. There is an entire family of such proteins and the newly solved structure explains some of the previous spectroscopic and redox properties of these compounds.

Doing the hop

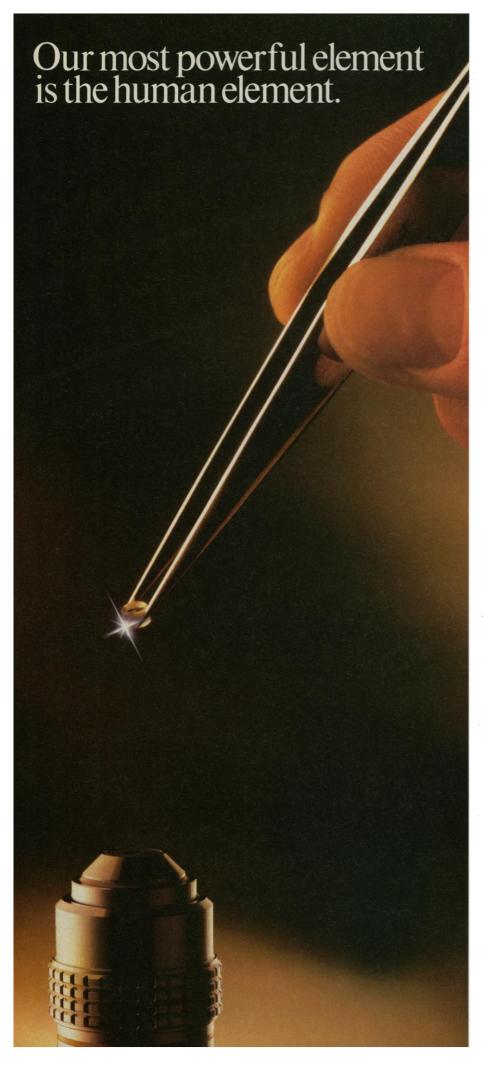
ALTATION or jumping is the dominant process by which sand-sized particles travel in wind. Most of the transport takes place in the first centimeter above the sand bed. Understanding the physics of blowing sand is important in studies of sediment transport on Mars, soil erosion by the wind, and such geomorphic features as ripples, sand dunes, blowouts, and ventifacts (stones worn, polished, or faceted by windblown sand). Anderson and Haff (page 820) have modeled most of the complex interactions in saltation, including initial aerodynamic entrainment of the particles, interactions between grains and the bed as the grains hit the bed at the end of a hop and rebound or splash out other grains, and the effect of the number of saltating grains on the profile of wind velocity. As the grains are entrained, they extract momentum from the wind, and eventually the number of grains being transported reaches a steady state. The profile of steady state mass flux decreases rapidly above the bed, in accord with wind tunnel results and observations of naturally blowing sand. From initial entrainment of grains to steady state, transport takes about 1 second or about the time it takes a particle to make three long hops.

Coagonists for the NMDA receptor

HEN messenger RNA extracted from rat brain is injected into frog oocytes, the oocytes express N-methyl-D-aspartate (NMDA) receptors that can then be studied more quantitatively than those in whole brains or slices. Kleckner and Dingledine (page 835) found that glycine is required for the activation of NMDA receptors by NMDA in oocytes. It was thought that glycine could only potentiate the activation of these receptors by glutamate agonists. Glycine, an abundant amino acid, is a common laboratory contaminant. When special precautions were taken to ensure low concentrations of glycine in laboratory materials, it could be shown that NMDA receptor activation was dependent on the presence of glycine. Thus the NMDA receptor-channel complex requires the combination of glycine and a conventional glutamate receptor agonist for activation. Glycine antagonists may prove useful in treating pathologies associated with NMDA receptor activation.

Wilms' tumor and aniridia

♦ HE association of Wilms' tumor with aniridia (complete or partial absence of the iris) and the fact that most children with both conditions have constitutional deletions on the short arm of chromosome 11 have led to the assignment of the WAGR (Wilms' tumor-aniridia-genitourinary-mental retardation) gene complex to that chromosome. The scarcity of molecular probes in this region of chromosome 11 has slowed the identification of the genes responsible for Wilms' tumor and aniridia. Davis et al. (page 840) identified two DNA segments that map to the WAGR region and separate the Wilms' and aniridia loci. By cytological studies, they established that a translocation event associated with aniridia was accompanied by deletion of DNA that presumably includes part of the aniridia locus. They deduced a linear map of the WAGR gene complex that should help identify genes in the WAGR locus.



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Regularizing "Pork"

espite the outcries of academic leaders, "pork barrel" science and engineering—the congressional practice of attaching pet projects to general agency appropriation bills—is becoming more common. Depending on definitions, estimates of the level of earmarked funding range from a quarter to over a third of a billion dollars a year, with between 40 and 50% attached to budgets of the Department of Energy.

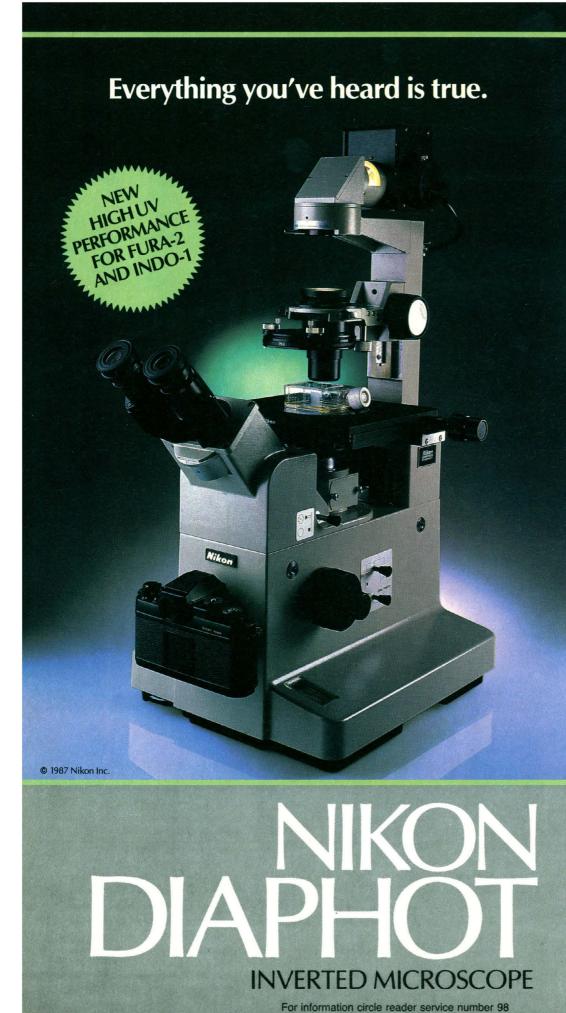
Opponents argue against this behavior on the grounds that it circumvents the peer review process, may result in the funding of projects that do not deserve support on technical merit, and leads to serious inefficiencies in the allocation of scarce federal resources. They also complain that the practice has adverse consequences for federal agency research programs. Funds sufficient to cover the special projects are often not provided in appropriations. Thus, "pork barrel" projects must be supported by curtailing planned programs in the agencies.

Proponents argue that, like other federal capital programs, "pork barrel" science and engineering projects are a way to spread the wealth. Although there have been exceptions, most of these projects have involved the construction of buildings and other facilities. Never easy to obtain, in recent years capital for such facilities has become especially scarce. Proponents argue that without the facilities constructed with earmarked funds, many universities cannot write competitive proposals to secure research support through normal peer review channels. Hence, federal research monies continue to go to a few leading research centers, and the rest of the country languishes. Given the economic importance now attached to science and technology, members of Congress are not prepared to sit back while the few regions of the country with the most accomplished research groups skim, what these legislators argue are, vital regional development resources.

Both arguments have merit. The practice shows no sign of abating. This suggests that it is time to move the discussion to a different level. If "pork barrel" science and engineering cannot be stopped politically, and arguably serves positive social ends, we should be trying to regularize the practice in a formal program, not terminate it. In recent months there have been several unsuccessful efforts to begin to do this. The University Research Facilities Revitalization Act (H.R. 1905), introduced by Representative Robert A. Roe (D-NJ), is stuck in committee. Similar language was inserted and passed in the trade bill that was vetoed. Both the House and Senate versions of the National Science Foundation (NSF) authorization act contain modest programs of competitive matching facilities grants, but so far funds have not been appropriated.

These efforts represent important first steps. But none of the current proposals will provide enough resources of the right kinds to stem the pork barrel tide. Ultimately we may need two programs, both requiring matching funds and supporting only capital costs. The first should fund facilities strictly on the basis of technical merit and could be appropriately administered by NSF. The second should fund facilities on the basis of a mixed consideration of technical merit and regional need. While NSF could coordinate the technical reviews, the actual funding decisions for this second program should probably be made by an interagency group housed administratively in some other agency, perhaps the Department of Commerce. Decisions in this second program will necessarily contain a significant political dimension. Giving this reponsibility to NSF runs too great a risk that political influences will spill over and contaminate other NSF decision processes.

Such a program would have the advantage of requiring Congress to make two explicit choices. First, it would have to choose the overall fraction of our nation's R&D expenditure that should be devoted to the construction of university research facilities. Second, it would have to choose what portion of these resources the nation should invest in the most costeffective pursuit of research output, and what portion should serve the important additional goal of developing regional R&D infrastructure. Clearly these choices are too important to be made in the piecemeal way that we now make them. Having established such a program, Congress will have to enforce discipline on its members to prevent continued attachment of individual projects. There is reason to believe that if the program is successful, and large enough, such self-discipline would be possible.—M. Granger Morgan, Head, Department of Engineering and Public Policy, Carnegie Mellon University, Pittsburgh, PA 15213



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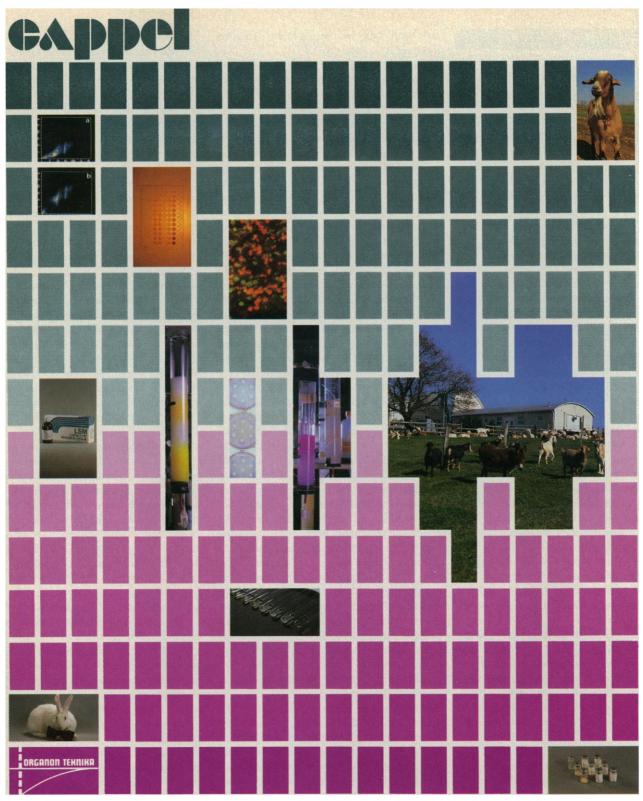


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Response: We explained the rationale behind our approach in the first paragraph of our article (1). Far from assuming the hypothesis before we started out, we feel that treating the emergence of modern Homo sapiens as an evolutionary event enables proper consideration of that event. Multiregional models can (and for some authors do) account for the evolution of "modern" features in geographically separate populations by parallel evolution, and it seems essential to diagnose what we mean by "modern humans" in an article which discusses the origin of modern humans. Too often other workers (including some authors of the above letter) have not made clear and scientific presentations of what they mean by "modern human," thereby preventing tests of their preferred evolutionary models. Thus they do not provide consistency of approach or genuine testability for their ideas. Without a clear conception of what they mean by "modern human," they are unable to provide appropriate data on ranges of variation in "modern humans," to recognize the earliest appearance of "modern humans" in any given area, or to establish the existence of evolutionary intermediates or hybrids, which should be essential components of multiregional—gene flow models.

Inextricably linked with these discussions are different or confused conceptions of what is meant by the term "species." One must have a conception of what is meant by the term "modern human," as well as an awareness of the limitations of the biological species concept as applied to fossils. It is evident from recent studies that neospecies may have very high or very low levels of morphological variation. In the case of extant primates, it seems that the use of skeletal variation alone would lead to a serious underestimate of species numbers (2).

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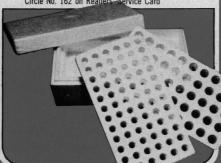
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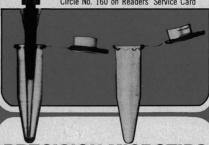
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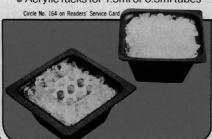
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sufficient for the formation of such a complex, which in turn might inhibit receptor function (28). By this view, hormone binding would derepress receptor activity by altering the conformation of the hormone binding region and disrupting the receptor-hsp90

It is now apparent that different segments of steroid receptors comprise functional domains that can operate independently of one another, or when placed into different molecular contexts. Thus, Green and Chambon (30) showed that replacement of the estrogen receptor DNA binding domain with that from the glucocorticoid receptor yields a chimeric protein that induces transcription from GRE's in response to estrogen; similar "finger-swap" experiments involving other receptor proteins have been reported (31). Picard and Yamamoto (12) demonstrated that the hormone binding domain of the glucocorticoid receptor functions as a ligand-dependent nuclear localization cassette when fused to β-galactosidase. Finally, we establish here that hormone-dependent transcriptional regulation is retained in chimeric receptor derivatives that contain a structurally distinct DNA binding domain and, conversely, that the enh2 region functions independently as an enhancement region in association with a heterologous DNA binding domain. Taken together, these results underscore the modular structure of steroid receptors, and suggest that these and other regulatory proteins might be evolving by independent reassortment of functional units, perhaps via exon shuffling.

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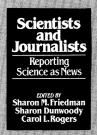
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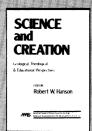
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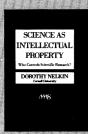
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The Gene-Splicing Wars: Reflections on the Recombinant DNA Controversy, Edited by Raymond A. Zilinskas and Burke K. Zimmerman.

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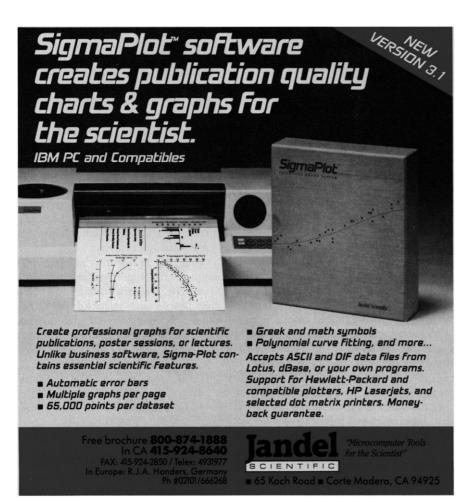
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