A reader urges caution about having confidence in a Nuclear Test Ban Treaty. Researchers assert that, mathematically, the physical properties of DNA are more like links of overcooked spaghetti than a chain of rigid uncooked pieces: "in reality, there are no hinges interspersed with rigid regions (unless perhaps one reduces to a single base pair–level description)." Phylogenetic analyses of whales are explored. The editor of the *Thomas A. Edison Papers* comments on the nature of Edison's workshops and research. Scientific journal prices are decried. And the ability of epidemiological studies to identify risks from silicone breast implants is questioned.

Confidence in Nuclear Deterrence

One must admire the determination and idealism expressed by Sidney Drell *et al.* (Policy Forum, *Science*'s Compass, 19 Feb., p. 1119) for trying to achieve the controversial political goal of a Comprehensive Test Ban Treaty (CTBT). However, the U.S. nuclear stockpile cannot be known to be free of unanticipated problems without experimental testing of the explosive itself. Changes creep into the system as time passes. "Confidence" is a relative, not an absolute, term. The consequence of mistaken untested confidence regarding a nuclear weapon issue could involve human lives. By analogy, in Drell's field, the complete testing of postulates at a high energy–physics facility is often required before wide acceptance is possible. Unanticipated results are not infrequent.

Recruitment and retention of top-notch scientists and engineers who are qualified to assess the amalgamation of the many technical fields that enter nuclear explosive performance will be difficult indeed unless they can test their work. To complicate the issue, any technical ambiguity in an assessment will have to stand up to enormous political pressures to postpone or ignore bad news ("clear warning signs of unanticipated problems").

It is not surprising that many have concluded that a CTBT is not in the U.S. national interest.

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DNA: Uncooked, *al Dente*, or *Scotti*?

A recent Random Samples contribution "Locked but not knotted" (12 Feb., p. 931) describes a mathematically interesting result about locked, unknotted hexagons. We believe, however, that the statement that DNA is like "chains or loops of linked rigid pieces, like bits of uncooked spaghetti joined by hinges," rather than the more familiar "overcooked spaghetti" is misleading.

Piece-wise linear models of polymers were introduced by Kuhn in the 1930s to provide a tractable model simpler than the continuous description that he knew was closer to reality. His approximation and subsequent refinements have successfully allowed relatively simple mathematical and numerical treatments of physical phenomena in DNA. However, the effective physical properties of DNA are relatively uniform along the backbone and, in reality, there are no hinges interspersed with rigid regions (unless perhaps one reduces to a single base pair–level description).

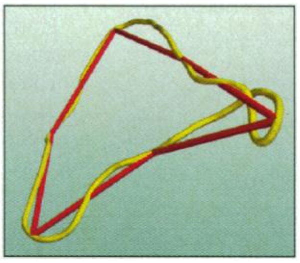

Fig. 1. DNA model.

Electron microscopy of DNA has shown that on the wide range of viewable length scales the double helix appears as a continuous curve (Fig. 1). Any such smooth curve (in yellow) can be well approximated by *n* line segments, with *n* sufficiently large (the case $n = 6$ shown in red seems inadequate). The question of how large *n* needs to be depends on the smoothness of the underlying curve, or whether the spaghetti is cooked *al dente* or *scotti*. For models of DNA, this smoothness depends on the number of base pairs represented by the continuous curve (2686 for the data shown).

We know of no realistic application involving a piece-wise linear model of a DNA loop where the number of links, *n*, can be as few as 6. Moreover, any conclusion that depends sensitively on *n*—for example, rigidity—for $n = 6$, which disappears for $n = 7$, cannot be physically pertinent for DNA.

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Response

The point of Stasiak *et al.* that DNA does not resemble a polygon of 6 or 7 rigid segments is absolutely correct. Such a model may be more realistic for an artificially synthesized polymer, and several mathematicians I spoke with suggested that this might be an interesting project for chemists to work on (similar to the synthesis of "rotaxanes," in which two loops are geometrically linked without being topologically linked). For DNA, the best model may indeed be one that depends on the details of how the spaghetti is cooked, as Stasiak *et al.* suggest.

The mathematical treatment of large molecules with a certain amount of rigidity is still very much in its infancy. If mathematicians continue to study models of molecules that are in some respects outdated or oversimplified, the reason is that there are still interesting questions about them that have not been answered. The mathematicians I spoke with felt that the shape presented by Jason Cantarella was a useful step toward understanding the effect of rigidity on conformation. The conclusion: Rigidity matters.—**Dana Mackenzie**

Whale Origins

In a recent book review (*Science*'s Compass, 12 Feb., p. 943) of the volume *The Emergence of Whales: Evolutionary Patterns in the Origin of Cetacea* (edited by J. G. M. Thewissen) (*1*), John E. Heyning writes, "[m]ost analyses of the morphological data indicate that perissodactyls (horses, tapirs, rhinos) form the sister taxon to cetaceans" and cites four phylogenetic analyses (*2*) of paleontological data. All of these predate work in the *The Emergence of Whales*. In fact, chapter 6 of the Thewissen volume (*3*) explicitly *supports* the idea that artiodactyls are more closely related to cetaceans than are perissodactyls on the basis of a maximum parsimony analysis of morphological data.

Again, on the subject of whether or not perissodactyls are the extant sister taxon of cetaceans, Heyning writes, "[i]n all the molecular analyses this potential relationship either has not been fully explored or, in some cases, has been excluded by the designation of perissodactyls as an outgroup." This statement is contradicted by a