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LETTERS

Tenure for Foreigners in Japan

Alun Anderson's article "Japanese academics bemoan the cost of years of neglect" in the special issue devoted to *Science* in Japan (23 Oct., p. 564) mentions the small number of foreign faculty members at Japanese national universities (p. 569) but could be somewhat misleading. As I have discussed elsewhere (1), the reason Japanese universities have hired only an infinitesimal number of foreign faculty, and in most cases have given them only term appointments (whereas all Japanese citizens, at any level, have tenure), is not "[g]overnment regulations" that "are not exactly welcoming," but rather discriminatory internal regulations adopted by the individual universities. Also the new law was adopted in 1982, not 1987, as the article states.

Fortunately Tokyo University is a notable exception. To my knowledge, I was the first foreign faculty member to be hired with tenure by any Japanese national university (in 1984). Since then I have been running a productive research group in global seismology and have not been treated unequally in any way by the university. The most recent data available indicate that six of the eight foreign faculty members at Tokyo University are tenured. (It would be better, of course, if all were.) Our president, Akito Arima, has forcefully advocated hiring foreign faculty with fully equal terms of employment (2). It is regrettable that Kyoto University, Tsukuba University, Osaka University, and many others have refused to follow suit and have adopted discriminatory internal regulations that categorically forbid granting tenure to foreign faculty.

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Sequencing and Computer Time

I read with interest the recent correspondence between Geoffrey J. Barton and Steven A. Benner *et al.* (Letters, 18 Sept., p. 1609) about the computer time required to compare each sequence in the current data banks with every other. My name is invoked by Benner *et al.* as an "expert in the field" who believes (or has somehow led others to believe) that ex-

haustive data bank comparison is "thought to be essentially impossible." In support of this view, a piece of mine in *Nature* is cited (1).

I would like to point out that I have never held such a view nor, more important, does my *Nature* piece give any support to the notion. Indeed, it makes no mention of the data bank alignment problem, but deals with a technique to cluster proteins in peptide hyperspace.

I would not normally raise such a matter except that much of my research over the past years has been the complete antithesis of what Benner *et al.* seem to believe. As long ago as 1987 I compared the, then quite small, National Biomedical Research Foundation data bank (4000 sequences) against itself (2) [repeating the exercise on a slightly larger version in 1989 (3)].

More recently, we aligned the SWISS-PROT data bank (4) in order to derive a new amino acid exchange matrix (5). We completed this comparison in 1 CPU (central processing unit)—day on a moderate-sized workstation using a conventional Dynamic Programming algorithm [Needleman and Wunsch (6) type], compared with the 400 CPU-days taken by Benner and his co-workers (7). We achieved this by applying a simple prefilter based on peptide composition to avoid calculating alignments for pairs of sequences that could not possibly be related within the confidence limits we had set. Clearly, a simple heuristic can save a lot of unnecessary computation.

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Dividing Up the Neocortex

In a Perspective by Carla J. Shatz (9 Oct., p. 237), my view of the mechanism of cortical parcellation was not accurately represented. The protomap hypothesis suggests that post-