

CORRESPONDENCE

Falklands story

SIR — The history given by Asociacion Argentina Para el Progreso de las Ciencias (*Nature* 10 June, p.450) is in error.

The islands were discovered by the English navigator John Davis, inventor of the backstaff and double quadrant, in 1592. Hawkins was there in 1594.

Commodore Byron took the islands for England in 1765 on the basis of this prior discovery and when the naval garrison was withdrawn in 1774 it left a plaque claiming full sovereignty and allowing Spain to maintain its settlement until 1806.

In 1816 the new United Province of Rio de la Plata having overthrown the Spanish yoke claimed to succeed Spain and a local governor was installed by them in the Falklands in 1828. In 1833 Britain expelled the Argentine soldiers and again raised the Union Jack in the Falklands.

The British prime minister said in 1834 that the British were not prepared to permit any other state to exercise a right as derived from Spain that Britain had denied to Spain herself.

The present conflict does not have its origin in Grytviken, but in the recent naked aggression by Argentina. What was said in 1834 by the British prime minister still stands.

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Burning question

SIR — Most cosmologists feel that the evidence currently available suggests that the Universe originated with a big bang and is now in an expansion phase. One of the more important questions presented by such a scenario is whether or not the Universe will recontract to its primordial super-massive germ. The physical evidence required for resolution of this issue is not yet available.

There is, however, a source which provides the answer clearly and unequivocally. In II Peter 3; 10 it is stated: "But the day of the Lord will come as a thief in the night; in which the heavens shall pass away with a great noise, and the elements shall melt with fervent heat, the earth also and the works that are therein shall be burned up."

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Whence high IQs?

SIR — In *Nature* of 20 May, A.M. Anderson in his comments¹ on the article in the same issue by R. Lynn entitled "IQ in Japan and the United States shows a growing disparity"², refers to the increase in educational opportunities in Japan since the 1930s, perhaps implying that this increase might be partly responsible for "the Japanese IQ increase", even though Lynn argues against it. While agreeing with Anderson that no intelligence test can be totally culture-free and, therefore, the performance in any such test cannot be unreservedly taken as a true measure of a person's intelligence³, I suggest that what has been found in Japan may indeed be true of all countries where a large proportion of the population has been deprived educationally and socially, over many generations and where people have

overcome this deprivation through rapid democratization of education.

Where opportunities for education and access to knowledge and information, have been limited, education (or lack of it) tends to run in families, with only an extremely small proportion of either class (the educated or the educationally deprived) changing over to the other class. In India, for example, I estimate that education is a hereditary prerogative of between 12 and 20 million persons (2–3 per cent of the population) representing less than 4 million small families and half-a-million "large" families — large in the sense of Indian "joint" families⁴. Probably, less than 10,000 persons every year (out of a total population of 680 million) enter the educationally privileged class from the under-privileged, changing the complexion of neither class.

For those who are educated, the day-to-day problems of survival are lessened. The survival of the uneducated, on the other hand, depends on their possessing abilities which would allow them to cope with the adverse environment in which they must live. Thus the uneducated of today would, as a result of evolutionary pressures, come to possess more "native" (that is inherited) intelligence, than the educated ones on whom by and large these pressures have not operated.

Since the intelligence tests cannot give a true indication of the native intelligence of a person who has been socially, culturally and economically deprived in early childhood, when the cultural patterns are often irrevocably fixed, the above-mentioned difference between the native intelligence of the long-deprived and the long-privileged would show up only when the two groups have had equal opportunities and a comparable environment to live in from the very beginning. A consequence of such a situation would be an apparent rise in the average intelligence of a population where there has been educational deprivation of a large population for a long period, as such deprivation disappears — as has happened in Japan since the 1930s.

If what I have said above is true, one could make two predictions: (1) what has been found in Japan should be found to be also true of other countries and populations where there has been democratization of education on a large scale in a relatively short time; and (2) the average IQ of those who have moved up from a traditionally educationally deprived state should be higher than of those who have been educationally privileged for generations due to circumstances of birth. We must, in that case also, conclude that in the United States, real democratization of educational and related opportunities has not occurred to the extent to which it has in Japan. The fact that the differences in IQ were found by Lynn even at the age of 6 could be merely an indication of the improved environment in Japan, in which the children were brought up to that age, as a consequence of the true educational status of the parents having improved across the population in the earlier generation(s).

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1. Anderson, A.M. *Nature* 297, 181–182 (1982).

2. Lynn, R. *Nature* 297, 222–223 (1982).

3. Bhargava, P.M. *Bull. Atomic Sci.* 26, 40 (1976).

4. Bhargava, P.M. *New Quest* 15, 147 (1979).

Sequence software

SIR — In the article "Europe leads on sequences" (*Nature* 15 April, p.596), the problem of the collection of nucleic acid sequences is discussed. While it is a crucial problem, it is not the only one. Once collected, the sequences should be easily and quickly accessible to a large number of users, the mode of interrogation of the data base should be manifold, flexible and selective, and the answers should be immediate. Otherwise, the enormous effort required to set up a sequence library would be partly nullified by its limited use. At present, access to the data by most European users occurs by means of magnetic tapes, requested and sent by mail, containing all the sequences and related information stored in the library. The recipient of the tape then needs to read the entire tape on his own computer before the required information can be extracted. This procedure is time consuming and inefficient.

We have developed, on a computer Digital VAX/VMS 11-780 (Physics Institute, GNCB, Bari), an interactive software system for the retrieval and analysis of nucleic acid sequences. This system, which works in real time, offers a large number of options both for perusing and for analysing the data. No specific computer knowledge is required since the users, connected with remote terminals through telephone lines, are guided throughout their work. The main novel feature of the system is the mechanism of data retrieval, which is accomplished through the use of forty keys. Each key can be used alone or in combination with others. Among the available keys are: sequence code, bibliographic citations (journal, year of publication, personal communication), date of entry into the library, number of base pairs, function and biological source. Among eukaryotes, the selection can be made by kingdom, phylum or division, class, genus and species. An analogous selection is offered for prokaryotes. Viral nucleotide sequences can be retrieved by using the virus name, the genus, the family or the host. Biological groups of particular interest can also be selected, for example protozoa, bacteria, algae, fungi, lichens, higher plants, invertebrates and vertebrates. The outputs can be tailored to specific needs, through a choice of what to print and on which output device.

To test our software, we used sequences from a collection of about five hundred, kindly given to us by Dr Greg Hamm (European Molecular Biology Laboratory, Heidelberg) and by Dr Kurt Stüber (Genetics Institute, Cologne). These data were reorganized in order to make them compatible with our software. In planning the system, we took into consideration the fact that precise requirements and standards for a nucleic acid sequence library do not yet exist. Therefore, we incorporated into the software design provisions for great flexibility in terms of additions, deletions and changes.

This system is available to the scientific community upon request and without cost. We hope that it will become a useful research tool.

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