CORRESPONDENCE

Fewer academics could be the answer to insufficient grants

SIR — The rejection of high-quality grant proposals is a problem endemic to universities throughout the world. I suggest that it arises from separating the employment of academics from the central bodies who provide grant funding.

Consider the country of Euphoria. It has just four universities, each of which employs ten academics of comparable quality, and one national funding body. Each academic submits two grants per year, only one of which is rated fundable. So each academic is awarded one grant per year. Into this happy state enters the ambitious new president of the Euphoric University of Fulchester. He makes his mark by doubling the number of academics in his institution. Now Euphoria has 100 grants submitted per year, but still only 40 grants available. Fulchester will get 16 of these and the other universities will now get only eight each.

This is a rational action by the new president, as the rewards from obtaining six additional grants are so great that it is worth hiring the 10 new staff. Euphoria loses overall, however, because its taxpayers and students are now paying to employ 10 extra staff, with the same amount of research being done. The other four universities also lose, as they are now receiving two fewer grants. The incentive will be for them to act in a similar way until Euphoria stabilizes, with many more excellent grants being submitted than can be funded.

This situation naturally arises in an environment in which employing academic staff is separated from obtaining research funding. We would be better off having fewer academics and using the savings to fund more grants, because then more research could be done for the same national expenditure. Such action has to be taken by governments, as universities currently have the freedom to over-staff and are rewarded for doing so under the present system.

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Working together to put molecules on the map

SIR — We applaud the call in your Editorial 'A place for everything' (*Nature* **453,** 2; 2008) for researchers to record the latitude and longitude of their data, in order to place all biological samples in proper spatial (and temporal) context. We agree that this minimum information guideline should apply to all biological samples taken from the natural environment, and note the pressing need for relevant molecular data to be tagged with geographical location.

The International Nucleotide Sequence Database Collaboration — comprising the DNA Data Bank of Japan, the European Molecular Biology Laboratory and GenBank — already offers the option of recording latitude and longitude coordinates. This qualifier, among others, was requested by the Consortium for the Barcode of Life to provide the geographical origin of molecules it uses to identify organisms. The "minimum information about a genome sequence" guideline published by the Genomic Standards Consortium (*Nature Biotech.* **26,** 541–547; 2008) calls for this critical field to be mandatory for all genome and metagenome submissions, along with altitude or depth and time of sampling.

Other molecules that are equally critical to tag with this information are the vast number of other marker genes, especially 16S and 18S ribosomal RNA sequences, that are being generated globally from a diverse range of habitats. This registration becomes all the more relevant as ultra-high-throughput sequencing of these molecules continues to be more widely applied. Core to these efforts are projects such as the Environment Ontology and Gazetteer initiatives, which describe environments and place names, respectively. Combined, these resources will support the consistent annotation and retrieval of environmental information associated with an organism or biological sample.

These projects all highlight the growing importance of community-driven initiatives in developing improved standards for reporting experimental data. We look forward to the day when it will be commonplace to view collections of molecules 'on the map', so to speak, such that questions relating to their global and local abundances, distributions, environments and functions can be properly addressed. Getting to this point will require: increased awareness; higher expectations for the quality and quantity of descriptive data recorded; improved standards, ontologies and databases; proof of the value of downstream analyses; and widespread practical changes, such as use of hand-held devices for recording real-time contextual information (and, in the future, for generating data) in the field.

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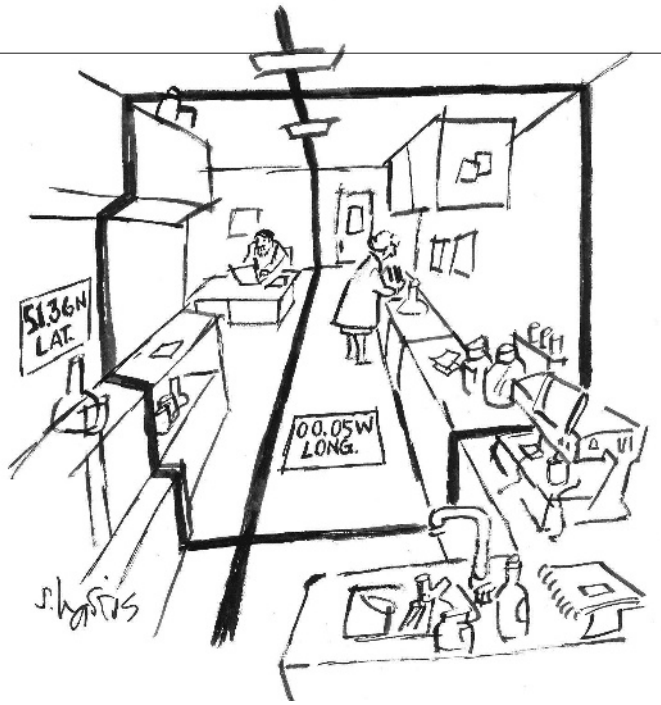
This letter was also signed by the following, whose addresses can be found at http://gensc.org:
Norman Morrison, Frank Oliver Glöckner, Renzo Kottmann, Guy Cochrane, Robert Vaughan, George Garrity, Jim Cole, Lynette Hirschman, Lynn Schriml, Ilene Mizrachi, Scott Federhen, David Schindel, Scott Miller, Paul Hebert, Sujeevan Ratnasingham, Robert Hanner, Linda Amaral-Zettler, Mitchell Sogin, Michael Ashburner, Suzanna Lewis, Barry Smith, Genomic Standards Consortium (GSC), International Nucleotide Sequence Database Collaboration (INSDC), Consortium for the Barcode of Life (CBOL), International Census of Marine Microbes (ICoMM), Environment Ontology Consortium (EnvO)



Decoherence does not get rid of the quantum paradox

SIR — In his Essay 'Lifting the fog from the north' (*Nature* **453,** 39; 2008), Maximilian Schlosshauer describes how the process of