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Advice for a Better OTA

NOW THAT A SERIOUS EFFORT TO RESTORE THE U. S. Government's Office of Technology Assessment (OTA) has begun, some anomalies in the structure of this much lamented institution need to be addressed (News of the Week, "Memo to Congress: Get better advice" by D. Malakoff, 22 Jun., p. 2229). In the past, the advice from OTA was valuable to Congress, but even more valuable to policy researchers. From their point of view, OTA's location in Congress was a great advantage, because it kept OTA's focus on policy and enforced political neutrality.

This location, however, also led to some problems. OTA never set forth a basic analytic approach to technology assessment. Each study was a unique effort. Its documentation focused on procedures such as how to relate to congressional clientele, how to constitute an advisory committee, and how to present the final results. Consequently, there is no manual from which the aspiring and newly appointed technology assessor can learn the basic intellectual framework underlying the craft: what constitutes an assessment, how one goes about doing one, what techniques are the most useful, and what are the hallmarks of quality. Another problem is that OTA left no direct academic legacy. It drew on the expertise of many individuals, but left behind no institutions that can carry on technology assessments in its mold. Its alumni will soon reach retirement age, leaving a legacy of valuable reports but no students to succeed them. And lastly, the OTA tended to neglect the international dimension of the issues it addressed. This was understandable at the time, but would be a serious anachronism today.

We need a 21st-century OTA, one that retains the laudable features of the previous OTA, but that addresses the institutional issues outlined above. It should have a clear mandate to establish an intellectual methodology and build departments and research teams in universities in different parts of the country. And a new OTA should also place its analyses in an international context by examining the international aspects of the problems it addresses, and by comparing U.S. domestic problems with their counterparts in other countries. In this way, technology assessment could this time become a recognized academic discipline and research activity that could survive any future political vicissitudes.

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Comparing Human Genome Mapping Data

A PRESENTATION GIVEN BY ONE OF US (COLIN Semple) at the joint Cold Spring Harbor Laboratory/Wellcome Trust Conference on Genome Informatics (8 to 12 August, Hinxton, UK) is the topic of a News of the Week

report, "Less can be more, U.K. study finds," by B. Shouse (17 Aug., p. 1238). Semple's presentation compared the relative coverage and rates of misassembly across several draft human genome assemblies for a region of chromosome 4p linked with bipolar affective disorder. The assemblies examined included releases from the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/), the University of California at Santa Cruz (http://genome.ucsc.edu/), and the public release from Celera Genomics (CG) (http://public.celera.com/). There were inaccuracies in the article relating to the data analyzed, the results presented, and the attributed collaborators in this work, and we wish to set the record straight.

First, this work was performed by Colin Semple in collaboration with Kathryn Evans and Stewart Morris in the laboratories of David Porteous in the Molecular Medicine Centre, University of Edinburgh.

Contrary to the report by Shouse, we have not undertaken large-scale sequencing of the region; rather, our group constructed a contig of BAC/PAC clones across the region (*1*). The comparisons between draft genome assemblies exploited the high-resolution physical mapping data from this contig. Each assembly was assessed with respect to the proportion of International Human Genome Sequencing Consortium (IHGSC) sequence data included from the region (constituting our estimate of coverage) and also for the number of deviations from the marker order seen in the contig (our estimate of the rate of misassembly). The region examined was estimated to be 5.8 megabases in size, not 6.9, as stated in the article. An important conclusion from the presentation was that the available assemblies vary widely by both measures. No conclusions were drawn, or could be drawn, as to the total amounts of sequence from the region produced by CG and IHGSC. The next generation of common, complex disease mapping studies will rely on linkage disequilibrium mapping using accurate, high-resolution maps of regions conferring susceptibility. Detailed descriptions of these regions cannot be derived from an inaccurate assembly of the available genomic sequence. Thus, our data emphasize that, until a region of interest is covered by finished sequence, a high-resolution physical map of the region is indispensable to correct the misassemblies present in all publicly available draft human genome assemblies.

Shouse also says that "Celera's approach of breaking the whole genome into random fragments for sequencing yielded better data than the map-directed approach used by [the Human Genome Project]." However, this is a false dichotomy because CG used mapping and sequence data from IHGSC in the production of their published assembly. Therefore, our comparisons, which only examined the published CG assembly, shed no light on the issue of whether it is better to start with a clone-based physical map of the genome or with whole-genome shotgun sequencing.

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CORRECTIONS AND CLARIFICATIONS

RESEARCH ARTICLE: "Resilient quantum computation" by E. Knill, R. Laflamme, W. H. Zurek (16 Jan. 1998, p. 342). In both the legend and the text discussion of Fig. 1, the double exponents in the expression $c^{(2h-1)}p^{(2h)}$ were omitted. The correct expression is $c^{(2^h-1)}p^{(2^h)}$.