

Editorial

The number of organisms with completed genome sequences continues to grow rapidly, and the past year has seen the completion of several major eukaryotic genomes, including those of the chicken and rat as well as the first chimpanzee chromosome. The addition of new species, such as *Drosophila pseudoobscura*, the pufferfish *Tetraodon nigroviridi* and the nematode *Caenorhabditis briggsae*, all of which have close relatives whose genomes had already been sequenced (*Drosophila melanogaster*, *Takifugu rubripes* and *Caenorhabditis elegans*, respectively), has allowed further demonstrations of the power of comparative genomics for genome annotation and evolutionary studies. While the advantages of free and unfettered access to sequence data are evident from the ever-increasing number of studies that make use of public sequence databases, the question of how to give access to publications of genomic and other scientific data continues to be the subject of much debate.

Following an overwhelming vote by the US House of Representatives urging the National Institutes of Health (NIH) to develop an Open Access strategy, NIH invited comment on its plans to enhance access to the research that it funds. Under the NIH proposal, NIH-funded researchers would have to provide electronic copies of the final accepted versions of each of their manuscripts, for archiving along with any supplementary information in PubMed Central [<http://www.pubmedcentral.nih.gov>]. Six months after publication of the research in question - or sooner if the publisher agrees - the provisional copies will be made publicly available at no charge to readers. NIH is now submitting a final version of its policy to the US Congress.

Genome Biology heartily supports the NIH proposal, which brings us one step closer to the immediate availability of all peer-reviewed research free of charge. Indeed, as Open Access pioneers, BioMed Central and *Genome Biology* already provide PubMed Central with final full text and PDF versions of all research articles immediately on publication, and we encourage all publishers to follow suit. In an ideal future, the electronic version of each research article would be the final and definitive form - easily archived, centrally searchable and available at the click of a mouse to all who would read it, be they scientists or members of the public. Of course, print would still play an important role, but printed articles will no longer constitute the historic record of the work. And moving away from the printed article in favor of its online incarnation makes sense for other reasons too: electronically, researchers can display all relevant data instead of an edited subset, and moving images and other web-only

formats can be easily integrated. It will no longer be possible to represent a complete research article accurately on the printed page.

As many readers know, *Genome Biology* has always presented its research articles in a way that differs from traditional journals: each printed issue serves to draw readers' attention to the definitive online content on the journal's website (or in central archives such as PubMed Central), where original research articles are freely available to all readers and no restrictions apply on the number of pages or the kinds of datasets that can be presented. In the world of genomics the rapid and easy publication of large datasets has been particularly important. Many researchers have taken advantage of *Genome Biology's* Open Access policy, and the number of submissions of original research articles to *Genome Biology* (and the number of such articles published) has risen continually since the journal's launch. *Genome Biology* and its publisher, BioMed Central, are committed to building a sustainable Open Access business model. This should primarily ensure that research articles are immediately and permanently available online without charge, as well as being deposited into permanent repositories - both of which provide far more efficient ways of disseminating, retrieving, and searching for scientific information. For this reason, in 2003 the journal introduced a standard processing charge that is levied on research articles accepted for publication, so as to cover the costs associated with making the article freely and universally accessible online (see [<http://genomebiology.com/information/about/apcfaq.asp>]).

Genome Biology urges other funding bodies and policy makers to follow the lead of the NIH, the Science and Technology Committee of the UK Parliament, the Howard Hughes Medical Institute, The Wellcome Trust and the signatories of the Berlin Declaration [<http://www.zim.mpg.de/openaccess-berlin>], and to encourage the researchers they fund to publish their results in a way that promotes public availability of scientific information. At the same time, it should be recognized that we still have a long way to go before every research article is free for anyone to read online on the day it is published: even articles describing the genome sequences of important organisms are still submitted to journals that restrict access to the analysis and description of the genomic data, so that only subscribers can read the analysis. You can play your part in overcoming these restrictions by submitting your next important article to *Genome Biology*.

E-mail: editorial@genomebiology.com