

Editorial

In the world of genomics, 2002 saw a number of organisms joining the ranks of those claiming sequenced genomes, including fission yeast, rice, mosquito, sea squirt, mouse, and prokaryotes almost too numerous to mention. The focus on comparative genomics has become increasingly evident, and future priorities for sequencing that have been announced include organisms from many branches of the tree of life. In focussing on the biology beyond the genome sequences themselves, we have also been engaged by the proliferation of techniques for genome-wide analysis. These allow analysis not only of transcripts but also of proteins, their interactions with one another and their post-translational modifications. The field continues to develop and evolve.

In keeping with its own promise to evolve in response to the needs of readers, *Genome Biology* is making a number of practical changes with the beginning of 2003. Readers of articles online may already have noticed the introduction during this year of links to related articles, a facility to e-mail an article's details to a friend, and a link to allow downloading of the article's reference directly to citation-management software. Now, we have added to the online toolkit the ability to post comments about an article, and we continue to work on tools to make online submission and peer review easier and more efficient. Our commitment to providing immediate, world-wide, barrier-free, open access to the full text of all original research articles continues unabated, and we are also making freely available all articles of all types two years after publication (both on *Genome Biology's* own site and within public repositories such as PubMed Central [<http://pubmedcentral.org>]).

In recognition of the fact that the developing field of 'functional genomics' depends on new technologies to drive it forwards, the original research articles we have published in 2002 have included a growing number of descriptions of analytical and experimental methods and freely available software tools. From this issue of *Genome Biology* onwards, such articles will be designated 'Method' or 'Software', respectively, and will be included within the 'Refereed research' section of the journal [<http://genomebiology.com/refres/>]. The criteria by which

such articles are judged, like those for more traditional research articles, take into account the extent to which each article is likely to impact the field and affect the course of future studies. A further change to the types of articles published sees the replacement of individual 'Paper reports' with selected evaluations of articles by members of Faculty of 1000 [<http://facultyof1000.com>], a literature-awareness tool that highlights and reviews the most interesting papers published in the biological sciences, based on the recommendations of a faculty of well over 1000 selected leading researchers. Like *Genome Biology*, Faculty of 1000 is published by BioMed Central.

Readers of the print issue may notice a leaner look and feel, as increasing numbers of articles include material online that it does not make sense to attempt to reproduce in print. And as part of an ongoing desire to make online access and linking as efficient as possible, this issue of *Genome Biology* sees the introduction of a new, simpler system of article numbering that is more in line with that used by other online journals, including all of those published by BioMed central (see [<http://genomebiology.com/citation.asp>] for further details).

A final change for 2003 is to the Advisory Board, from which a handful of founder members are retiring this year. We are tremendously grateful for their help and support in the journal's early years, and are delighted to take the opportunity to welcome aboard several new members, who bring new strength in their areas of expertise. As we begin 2003, the vibrant future of open-access science publishing seems even more assured now that the Public Library of Science has announced its intention to publish journals, using a similar model to BioMed Central (see [<http://publiclibraryofscience.org>]). We look forward to continuing to meet new challenges, both in the interpretation and understanding of huge volumes of genomic information and in providing the means for disseminating results and offering access to the broadest audiences possible.

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