nature genetics
supplement september 2002

Spreading the word

doi:10.1038/ng961

There was a time, not too long ago, when the wisdom of genome-sequencing projects was up for discussion. Would they be too expensive, draining funds from other areas of the life sciences? Would they be worth the trouble? Not much more than 15 years have passed since those early debates, and the importance of sequenced genomes to biology and medicine has now gained wide acceptance. This is in part owing to the relatively rapid fall in the cost of sequencing, followed by the undeniably important insights gained from the annotation of several bacterial genomes, and those of a few of our favorite eukaryotes. The news has been so relentlessly upbeat that one might even have expected some 'genome fatigue' to set in, especially given the saturation coverage of the publication of the drafts of the human genome sequence 18 months ago. Not so, however; witness the recent jockeying by different groups for inclusion of 'their' model organism in the next round of sequencing projects. The honeymoon goes on.

And yet there are important issues to be addressed. One is the concern surrounding any bestseller—that it will have far fewer actual readers than one might expect. At first glance, this would seem not to apply to the human genome. After all, one is hard pressed these days to pick up a copy of *Nature Genetics*, or any genetics journal, and not find evidence that sequenced genomes inform many of the most important advances. A survey published last year by the Wellcome Trust, however, found that only half of the researchers who were using sequence data were fully conversant with the services provided by the freely accessible databases.

There is also the concern that genome sequencers might be victims of their own success. As computational biologist David Roos recently put it, "We are swimming in a rapidly rising sea of data…how do we keep from drowning?" And if geneticists and bioinformaticians are struggling to stay afloat, what of the non-geneticists who are eager to exploit the sequences but are relative newcomers to the tools needed to navigate all of this information?

It is with these questions in mind that we present *A User's Guide to the Human Genome*. Written by Tyra Wolfsberg, Kris Wetterstrand, Mark Guyer, Francis Collins and Andreas Baxevanis of the National Human Genome Research Institute (NHGRI), this peer-reviewed how-to manual guides the reader through some of the basic tasks facing anyone whose work might be facilitated by an improved understanding of the online resources that make sense of annotated genomes. The directors of these online resources—Ewan Birney of Ensembl, David Haussler of the University of California, Santa Cruz and David Lipman of the National Center for Biotechnology Information—have served as advisors during the development of this guide, ensuring a balanced and accurate treatment of their respective web portals. The online version of the guide will also evolve, with an initial update scheduled for April, 2003.

As noted by Harold Varmus in his eloquent perspective on *A User's Guide* and the public databases it examines, one of the important legacies of the Human Genome Project is its ethos of open access to the data. In this spirit, and with the generous sponsorship of the NHGRI and the Wellcome Trust, the online version of this supplement will be freely available on the *Nature Genetics* website.

Alan Packer
Nature Genetics