

## Power to the people

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The National Human Genome Research Institute of the National Institutes of Health is delighted to sponsor this special supplement of *Nature Genetics*. The primary aim of this supplement is to provide the reader with an elementary, hands-on guide for browsing and analyzing data produced by the International Human Genome Sequencing Consortium, as well as data found in other publicly available genome databases. The majority of this supplement is devoted to a series of worked examples, providing an overview of the types of data available and highlighting the most common types of questions that can be asked by searching and analyzing genomic databases. These examples, which have been set in a variety of biological contexts, provide step-by-step instructions and strategies for using many of the most commonly-used tools for sequence-based discovery. It is hoped that readers will grow in confidence and capability by working through the examples, understanding the underlying concepts, and applying the strategies used in the examples to advance their own research interests.

One of the motivating factors behind the development of this *User's Guide* comes from the general sense that the most commonly-used tools for genomic analysis still are *terra incognita* for the majority of biologists. Despite the large amount of publicity surrounding the Human Genome Project, a recent survey conducted on behalf of

the Wellcome Trust indicated that only half of biomedical researchers using genome databases are familiar with the tools that can be used to actually access the data. The inherent potential underlying all of this sequence-based data is tremendous, so the importance of all biologists having the ability to navigate through and cull important information from these databases cannot be understated.

The study of biology and medicine has truly undergone a major transition over the last year, with the public availability of advanced draft sequences of the genomes of *Homo sapiens* and *Mus musculus*, rapidly growing sequence data on other organisms, and ready access to a host of other databases on nucleic acids, proteins and their properties. Yet for the full benefits of this dramatic revolution to be felt, all scientists on the planet must be empowered to use these powerful databases to unravel longstanding scientific mysteries. As pointed out by Harold Varmus in the Perspective, free accessibility of all of this basic information, without restrictions, subscription fees or other obstacles, is the most critical component of realizing this potential. It is our modest hope that this *User's Guide* will provide another useful contribution.

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