Outlook

In "predicting" genes, protein functions, and structures, it is helpful to define our terms precisely and be honest about our achievements. Otherwise, we will continue to be baffled by paradoxical new prediction methods that yield >80% error rates. Gene identification, structure prediction, and functional inference are nontrivial computational tasks, but with the relentless accumulation of sequence data, improvements continue to be made in all areas.

Nature functions by integration, and the adoption of a more holistic view of complex biological systems is an essential next step for bioinformatics. To get the most from genomic data, we need to take account of information on the regulation of gene expression, metabolic pathways, and signaling cascades. Proteins do not work in isolation but are involved in interrelated networks. Unraveling these networks and their interactions will be vital to our understanding of normal and pathologic cell development, and will help us create an integrated mapping between genotype and phenotype.

Genomics-based drug discovery is heavily dependent on accurate functional annotation. Toward this end, bioinformatics will need to deliver highly integrated, interoperable databases (and data "warehouses") that allow the user to reason over disparate data sources and ultimately enable knowledge-based inference and innovation. The more genome annotation is automated, the greater will be the need for collaboration between software developers, annotators, and experimentalists. And the more data we have to handle, the more rigorous we must be in our thinking (and writing) if we are to make sense of the complexities. Sequence-structure-function bioinformatics does not yet yield all the answers, but a future holistic approach should help fuse today's glimmerings of knowledge into a new dawn of understanding.

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17. Single-letter abbreviations for the amino acid residues are as follows: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.

TECHSIGHTING

SOFTWARE

Conquering by Dividing

The average personal computer spends much less than half a day actually performing useful computations. Many users, concerned about the vulnerability of expensive electronic components to the constant cycling of the power on and off, leave their systems on continuously. It is staggering to imagine the enormous, unused computing resources of several million PCs left running unattended. One popular approach to tapping this computing power is the Search for Extra-Terrestrial Intelligence (SETI) project (*1*), which breaks giant computing problems into pieces that can be solved on personal computers in their spare time.

Popular Power Worker
Popular Power, Inc.

San Francisco, CA
Free
www.popularpower.com

Popular Power, Inc. is a company offering a new twist on this theme. Like SETI, a company computer feeds pieces of large computing problems to networked personal computers via their software program, Popular Power Worker, for idle-time operation. Popular Power's approach differs, however, in providing a variety of computing problems to work on. These include nonprofit projects with no financial incentive to the personal computer owner, as well as commercial jobs that will eventually pay users for tasks performed on their machines.

The current version of the Popular Power Worker runs only on Windows and Linux systems and is officially in pre-release form. The preliminary status of the software is readily apparent; numerous bugs, frequent crashes, and difficulties in installation plague the program currently. If information at the company Web site is accurate, personal computer owners interested in Popular Power's computing model may find dealing with the problems of the early release worth their while. Users of the pre-release software are promised priority of access to commercial computing jobs after the official version is released. Popular Power Worker can be downloaded for free from the company's Web site, and it installs as a screen saver, which starts the program running when it becomes active. Future versions of the program for Macintosh and Solaris systems are planned.

The benefits of the Popular Power scheme for distributed computing tasks do not accrue solely to the user whose computer is used. The flexible nature of Popular Power's design provides access for businesses, scientists, and anyone with massive computing projects to computing power that is potentially far greater than they would gain from a fixed piece of hardware. Personal computer users might be able to select which commercial job to run through Popular Power Worker depending on the return offered by the originating contractor. A key to the success of the computing model is likely to be the price Popular Power demands for acting as the interface between the computing project creators and the personal computer users.

In summary, the current version of Popular Power Worker is still in the testing phase and users may find the software unstable. Tech-savvy personal computer enthusiasts are best suited to test the current pre-release product. The remaining users are advised to wait at least for the official release of the software.

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TECHSIGHTING

SOFTWARE

Eyes on the Skies

J-Track, J-Track 3D, and J-Pass
NASA

Free
http://liftoff.msfc.nasa.gov/realtime/JTrack/Spacecraft.html

The orbital space above Earth contains an astonishing collection of man-made satellites. Tracking all of these objects is no small task. Liftoff is a NASA Web site that provides several software tools to locate, track, and identify Earth-orbiting satellites. At the Web site, three programs are available: J-Pass (identifies satellites passing overhead); J-Track (allows one to track orbiting objects); and J-Track 3D (allows one to view satellites orbiting Earth from a perspective far away in space). Each of these platform-independent applications is written in Java and is accessible from both Internet Explorer and Netscape

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