

Fungal Trees Grow Faster With Computer Help

Researchers trying to determine the relatedness of organisms are finding it hard to keep up with the torrent of DNA sequence data gushing from biology's spigots. Now, two new computer programs are coming to the rescue, at least for biologists constructing the fungal family tree. One program, created by Frank Kauff of Duke Uni-

really tried to piece together where the discrepancies lie. That's where automated computer analyses will help, says Hibbett, a fungal systematist.

Among other fungal projects, Hibbett's lab focuses on mushroom-forming varieties, which make up an estimated 20,000 of the



Fast track. New computer programs are automating the classification of mushrooms and other fungi.

versity in Durham, North Carolina, and his colleagues, helps validate, assemble, and keep track of raw data from fungal DNA sequencing efforts. The other, developed by David Hibbett of Clark University in Worcester, Massachusetts, automatically retrieves fungal DNA sequences from the public archives and incorporates the data into an ever-improving phylogeny of this diverse group of microorganisms. Both efforts are part of the "Assembling the Fungal Tree of Life" project begun in 2003 and may be bellwethers of taxonomy's future. "It's great to have this all automated," says Michael Donoghue, a botanist at Yale University. "It means that progress can be made while we sleep."

Molecular studies now dominate fungal systematics, but the plethora of data they provide has not necessarily brought clarity. There are hundreds of published family trees for the fungi or their various branches, and many conflict with one another. Yet no one has

more than 70,000 known fungal species. To deal with the ever-growing number of DNA sequences for this group, Hibbett's program, which he dubbed *mor*, sifts through GenBank for newly deposited data on a single gene, called *nuc-lsu rDNA*, in mushrooms. If a researcher has deposited a new sequence of this gene for a species, the computer program compares it with other deposited copies of the gene for that species, weeding out any redundancies. It then compares the best version with the sequence of the gene in other species and uses the differences to adjust the branches of the fungal family tree. It even assigns names to new subgroups as needed. So far, *mor* has 2401 sequences representing 1899 mushroom species in 562 genera, Hibbett reported in Fairbanks, Alaska.

"It's one of the first attempts to automate large-scale phylogenetic analysis," says Roderic Page, a systematist at the University of Glasgow, United Kingdom.

FAIRBANKS, ALASKA—At Evolution 2005, from 10–14 June, evolutionary biologists, natural historians, and systematists shared results about fungi, mice, yeasts, and other organisms.

Although fungal experts may need that help more than most—these organisms are among the most diverse and the most difficult to sort out—Hibbett's approach should also be portable. "It's easy to see how it could be expanded to fit other organisms," says David Baum, a botanist at the University of Wisconsin, Madison. Adds Donoghue, "I'd love to have something like this for plants."

Kauff's program, dubbed WASABI for Web Accessible Sequence Analysis for Biological Inference, comes into play before fungal family trees are created. In essence, it ensures that such trees sprout from good seeds. The consortium working on the fungal tree of life project is sequencing eight genes in 1500 different fungi, and WASABI rates the accuracy of each newly submitted DNA sequence. The program also pieces together short fungal DNA sequences into ever longer ones and compares these so-called contigs with existing sequence information. This all happens automatically, providing researchers with one place to find refined data that originated from various consortium members. Finally, WASABI archives its manipulations and analyses of the raw information. "WASABI considerably reduces the time users would otherwise have to spend," verifying and piecing together sequences, says Kauff. "The speedup is many orders of magnitude."

Together with other consortium members, Hibbett and Kauff have already published one 588-species fungal tree, with all the major branches, such as the mushrooms, represented. The goal is to have the 1500 under study linked up in the proper relationships by 2006. Says Baum, "Fungal systematists are really leading the pack in terms of their critical use of cutting-edge analytical tools."

Color Genes Help Mice and Lizards

The light-skinned deer mice (*Peromyscus polionotus*) found along Florida's shoreline didn't always have such a bleached-out look. It took the beach rodents less than 5000 years to go from brown to blond; the darker look may have provided camouflage in the dense fields in which they used to dwell, but on the white sand, it would have made the mice a conspicuous meal for predators. At the meet-

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