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## Getting a handle on data

**B**ioinformatics arose as a field where people wrote their own software or taught themselves how to use the tools that were publicly available. As genomics data piled up, so, too, did programs to mine them. Scientists wanting to learn how to use the latest tool to explore the most recent data have been playing catch-up ever since.

But the educational obstacles appear to be getting even more daunting. More kinds of data — such as protein expression and structure — are accumulating, and programmers are now writing new tools to characterize them and integrate them with the old data. As a result, experienced bioinformaticians must constantly upgrade their skills, and neophytes must work harder to enter the field. More and better training for both groups seems necessary.

Several approaches show promise. Workshops are a start, but their quality tends to be inconsistent (see page 6). There is also evidence that the quantity of such workshops is lacking. One recent workshop at a bioinformatics institute in Europe that had 25 slots received 170 applicants (see page 4).

One alternative? Create a better ongoing dialogue between the people who write the software and those who use it. The US National Institutes of Health (NIH) has launched just such a scheme — bioinformatics experts plan to train small scientific groups from each of the NIH's 22 institutes (see page 7). But this approach has its limitations — for now, the programme applies only to scientists who conduct intramural research, not those who are funded to perform research outside NIH facilities. But if it is adopted by a wider community, such ongoing dialogues between developers and users could create better software, and result in more people who can exploit all the available features.

**Paul Smaglik**  
*Naturejobs* editor



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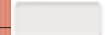
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