

## Microarray policy

More and more scientists are taking advantage of DNA microarray chip technology to further their research. PubMed can give a rough estimate of the growth and acceptance of this technology; a search for papers that contain the word "microarray" yields only 239 papers in 2000. In the next year the number increased almost four times to 808, and then almost doubled to 1,435 papers in 2002. The excitement that this technology has generated is similar to the immediate embrace of the polymerase chain reaction (PCR) when it was introduced in 1986 (PCR, by the way, has garnered over 150,000 publications to date).

As investigators became more familiar with microarrays, it was apparent that like any new technology, microarray systems share caveats and weaknesses of which to be mindful when designing, manipulating and interpreting experiments. Appropriate negative and positive controls and standards of best practice have fortunately emerged to help limit the introduction of artifacts when normalizing data or doing comparative analyses.

As discussed in an editorial in the 29 September 2002 issue of *Nature*, the enormous quantities of data generated by microarrays have presented new challenges to investigators, with regard to the proper way to record, referee, store and retrieve the microarray data associated with submitted articles. The *Nature* family of journals, including *Nature Immunology*, are now requiring authors who use these methods to also submit their data in a standard fashion and deposit them in public databases (GEO at [www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/) or ArrayExpress at [www.ebi.ac.uk/arrayexpress/](http://www.ebi.ac.uk/arrayexpress/)) upon publication, as is already accepted practice for nucleotide sequences and protein structures. To simplify matters, we are asking authors to follow the guidelines developed by the International Microarray Gene Expression Data (MGED) group, which is promulgating standards as to what constitutes the appropriate minimal information about a microarray experiment (MIAME).

Almost all papers submitted to *Nature Immunology* are now received through our online submission system, accessible through our homepage. Ironically, although the microarray community is computer-savvy and readily uses the web, these same authors cannot completely abandon snail mail yet. *Nature Immunology* will need five compact disks, each containing the completed MIAME checklist and attendant data tables. The author of any paper with microarray data is expected to download the checklist from the MGED website ([www.mged.org/Workgroups/MIAME/miame\\_checklist.html](http://www.mged.org/Workgroups/MIAME/miame_checklist.html)) and provide all the information requested in a format that will be accessible to others. Among other necessary information mentioned in the checklist are the quantitations of raw

images and tables of image analysis data, from both before and after data selection and transformation. The MIAME guidelines ask for quite a bit of information, presented in a standardized format. Although it may seem excessive, proper evaluation of the data set, or legitimate comparisons to other experiments, can hardly be made otherwise. Standardizing the collection of this information will enable the research community to properly search databases for experiments and data by many criteria, such as sample type, chip source or experimental condition. The last step for authors is the deposition of the data in GEO or ArrayExpress, in time for accession numbers or their equivalent to be included in the published paper.

What makes a microarray paper appropriate for *Nature Immunology*? There is a particular type of microarray paper that catches an editor's eye. These papers, like all interesting papers, do more than characterize a system or set of mRNAs: they provide new insights which are important to communicate to the broad community of immunologists. Investigations in this category sometimes commence by using microarrays in a "fishing expedition" concerning a process about which we know little. Surprising or unexpected initial observations are then followed up by a series of nonmicroarray experiments that bring fresh mechanistic insight to the immunologic process being examined. Having achieved this, a paper's priority for review is likely to be high. The order of events here is sometimes reversed, of course. Hypothesis-driven research can lead to a finding that then warrants investigation with microarrays. These careful analyses of changes over time or under altered conditions can also lead to increased understanding, and may be well worth considering for in-depth peer review. Thus, although there is no one type of paper that is sure to be reviewed by *Nature Immunology*, the underlying significance of the paper's ultimate message must be self-evident.

From the time of the introduction of the much-heralded Lymphochip, developed in the laboratories of Lou Staudt and Patrick Brown, immunologists have been cutting-edge users of microarrays. Currently, one cannot attend a conference without hearing about new, reliable, bigger arrays that are expected to expand research horizons for years to come. Immunologists have always had problems on hand that were ready to be made tractable by the latest technologies. Ten years ago, immunologists seized upon display libraries for peptide analysis, to find ligands for receptors and to improve antibody affinities and specificities *in vitro*. *Nature Immunology* readily supports the wise use of better technology, and will publish the most outstanding investigations that make use of it.