Method of the Year 2008: cast your vote!

You can now nominate candidates and vote online to help select the Method of the Year 2008.

When *Nature Methods*' editors sat down last year to select a Method of the Year, it was with the firm intention of making this affair a yearly tradition. It is now time to gear up for the Method of the Year 2008, and this year, we are asking for your opinion. You can nominate candidate methods as well as vote and comment on posted suggestions on the new website— http://www.nature.com/nmeth/votemoy2008.

The Method of the Year event is a celebration of methods development and innovation because we think that methods developers should have their share of the limelight. It is also a fun opportunity to assemble Commentaries, technical information and news items about a method we consider particularly important among the developments that we, as editors, continuously observe across a broad range of disciplines. But we also wanted to take the pulse at the bench and see what you, with firsthand experience, think of recent methods developments. This online voting and nomination process is your opportunity to speak up. We will weigh our decision in light of the popular vote.

We are interested in methods that have come into their own in 2008 and have had a proven impact but also in your views on burgeoning methods which, while they are not quite ready for prime time, are worth watching.

To nominate a candidate method, you must reference a paper or a webpage describing the method, so that other viewers can see exactly what you mean and express their opinions. It is perfectly fine to put forward your own development, as long as you are upfront about your personal interest.

With one click, you can vote for or against a candidate method and, should you wish to, you also have the ability to post comments. All you need is a free nature.com account. (You do not need a subscription to the journal.) Go to http://www.nature.com/nmeth/votemoy2008 and vote away!

We look forward to hearing about your Method of the Year!

Target practice

A constant influx of new methods keeps research on microRNA biology fast-paced and can provide divergent vantage points.

The field of microRNA (miRNA) biology is now a little over a decade old, and shows very little sign of flagging vigor. In particular, the adoption of new methodology by scientists in the field continues apace.

miRNAs post-transcriptionally regulate gene expression, typically by destabilizing mRNA or repressing its translation. The role of these regulators in development and disease is now well established, but there is still much to be learned. Central to the effort to understand miRNA function is the identification of the messages that they target.

The first miRNAs were uncovered by genetic analyses in *Caenorhabditis elegans*, and their targets were accordingly identified as suppressors of loss-of-function miRNA mutants. Then, with the early observation that miRNAs pair to complementary sequences in the 3′ untranslated regions of the messages they regulate, computational methods for target prediction soon began to fly fast and furious. Variably based on sequence features, evolutionary conservation, RNA structure and thermodynamic considerations, the prediction algorithms are still evolving and gaining in power. However, *in silico* methods are still not sufficient to unambiguously identify functional targets.

In the past few years an assortment of new technologies has been applied to the question of miRNA target prediction. Gene expression microarrays, for instance, have been used to examine miRNA effects on cellular mRNA levels. This has allowed the identification of sequence features enriched within affected messages—information that has been incorporated into the newest wave of target-prediction algorithms.

Microarrays, however, are only informative about effects at the mRNA level. Taking the analysis to the protein level with the application of quantitative proteomics, the laboratories of David Bartel and Nikolaus Rajewsky, each in collaboration with mass spectrometry experts, have now added to the list of techniques used in this field (see Research Highlight, p. 753). The two groups have independently determined what