From the Editor

Our annual meeting

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The end of each year brings an opportunity to both look forward to the coming year and reflect on the past year. For the editors at *BioTechniques*, this means another series of year-end editorial meetings where we try to identify shifts in the landscape of methods development in an effort to understand the needs of our readership. These meetings can be very interesting, but also very contentious. While our manuscript submission numbers in specific fields and categories provides solid data for discussion, what these figures really tell us about overall trends and interest levels in a particular methodology is always debatable. Sometimes we are off target, and other times we hit the mark. But no one regrets taking part in these meetings. With all this in mind, I thought it would be interesting to give readers a glimpse into what we have learned, or think we have learned, about methods trends for 2012 and beyond.

The article submission story

For me, nothing is more telling when it comes to methods or techniques needs than patterns in the manuscript submissions we receive. This is not to say manuscripts we accept, rather all those we receive. Researchers work in a variety of specialized fields, so their methods needs can vary dramatically. But does a spike in submissions related to a certain methodology or technique really say anything about science in general? In 2012, we noted several trends in our manuscript submissions that might point directly at trends in research in general.

First, there was a marked increase in submissions relating to new applications and methodologies of so-called third-generation sequencing systems. Although not surprising on the surface as DNA sequencing continues to be a hot topic, I suspect this trend speaks volumes to the future of DNA sequencing in general. First, these submissions fall in line with a general pattern of articles in the scientific literature aimed at expanding the scope of next-gen sequencing applications. Sequencing platforms have demonstrated the capacity to rapidly sequence large quantities of DNA in a cost-effective manner. Although this base application is critical to advancing genetics, genomics, and personalized medicine, methods developers are making efforts to harness the power of sequencing in other application areas as well. Metagenomics, transcriptome analysis, and even antibody generation have benefited greatly from NGS in recent months. As an example, in this issue

of *BioTechniques*, a group of researchers from the Wellcome Trust Sanger Institute describe a new approach for direct sequencing of circular DNA that could enable rapid pathogen detection or new diagnostic applications in the future. While this direct sequencing approach is still clearly in its infancy, such articles are indicative of the future — additional optimization could make direct sequencing a viable option for more NGS applications (rapid virus identification during outbreaks and single cell analysis for example), saving both time and money. Refinements and novel applications in DNA sequencing were not the only trends observed in 2012 — we also noted a swell of methods articles relating to enhancement in real-time quantitative PCR. qPCR can be challenging, especially when it comes to data normalization and analysis. A number of manuscripts this year examined strategies to enhance the robustness of qPCR, indicating that researchers continue to be interested in obtaining quantitative measurements to make biology more precise.

Citations speak

Whether you love the impact factor or hate it, observing patterns in citation counts for articles does provide another window into how quickly and widely a particular method is adopted. Looking back a single year is difficult as citations for an article generally begin to accumulate 6-12 months following its publication. But still, examining recent citation patterns can expose trends just like submissions numbers. For example, we have published several articles on the bimolecular fluorescence complementation (BiFC) assay in the past two years which have been highly cited and accessed. These articles generally dealt with refinements of the core methodology and expansion of the BiFC reagent toolkit; the high citation numbers are likely an indication of the growing interest in applying more robust protein interaction assays in the lab.

Now, tell us what you think. What trends do you see in the lab and within your field? Share your thoughts with us at bioeditor@biotechniques.com and we will follow-up with another editorial in the coming months.

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