Anne Carpenter: Imaging Breakthrough by Necessity

Title: Postdoctoral researcher, Whitehead Institute for Biomedical Research

Education: PhD, University of Illinois, 2003

Recommended by: William Hahn, David Sabatini

Anne Carpenter never meant to get into software development, but her goals for doing genome-wide screens left her with little choice. Her goal when she joined David Sabatini's lab was to find all the genes that regulate cell size, but "it turned out at the time that we could not find any commercial software that could accurately analyze the images of cells that would be produced in this type of project," she says. The problem: Carpenter would be using Sabatini's living-cell Drosophila technology, and at the time, imaging software wasn't optimized for correctly analyzing and determining the size of Drosophila cells. So she started writing her own solution, and managed to find a collaborator at MIT to help out. The result is CellProfiler, "an open source, freely available software package for high-throughput cell image analysis."

The software has become so popular that Carpenter runs a small group within Sabatini's lab to work with external scientists who are performing the type of genome-wide RNAi screens that Carpenter originally had in mind. "We're routinely helping people with a couple of screens a month now," she says. "We're able to almost all the time get the image analysis to work well, so biologists aren't spending months and months scoring by eye." That also fit in nicely with Carpenter's longtime interest in automation and quantification. "For quite a while I was a little frustrated by the fact that we'd look at images" by eye and qualitatively score them, she says. "It's so rare for biologists to find tools that will help them to be quantitative."

Currently a postdoc, Carpenter is just now determining her next step in the field. She expects that to be a position within academia, but knows for certain that "this unique ability to do almost any image-based screen that people would want to do" will be a key focus of her work in the coming years. "Another major focus of my future research will be really mining that data for all it's worth," she adds. "You've actually got a whole lot of information present in the images that is usually ignored" when scientists look for one particular phenotype. Carpenter believes comprehensive data mining of these images could lead to identification of new gene families, for instance. "I'll be moving a little bit more toward the systems biology level to mine this data," she says.

Looking ahead

The rate-limiting step for high-throughput imaging is currently the microscope part of the equation, says Carpenter; at this point, sample prep and other steps are quite robust. She'd like to see "a higher-throughput robotic microscope" that would help push the field

forward. She also says that more sophisticated data mining will be a critical component in getting better and more comprehensive information out of images.

Publications of note

Carpenter's key paper explaining the software and its utility has been submitted but not yet published. In the meantime, several collaborators who have used CellProfiler have published papers that include their findings from Carpenter's software, such as "A lentiviral RNAi library for human and mouse genes applied to an arrayed viral high-content screen" in Cell from David Root's group at the Broad Institute.

And the Nobel goes to…

Carpenter says if she could one day win the Nobel Prize, she'd like it to be for "generating a gigantic data set of all the genes knocked out and their phenotypes, analyzed in a number of ways that would include image-based data, transcriptional data, proteomics data — and using that data set to … get a lot of information about the genome and the networks that control how cells function."

— MWS