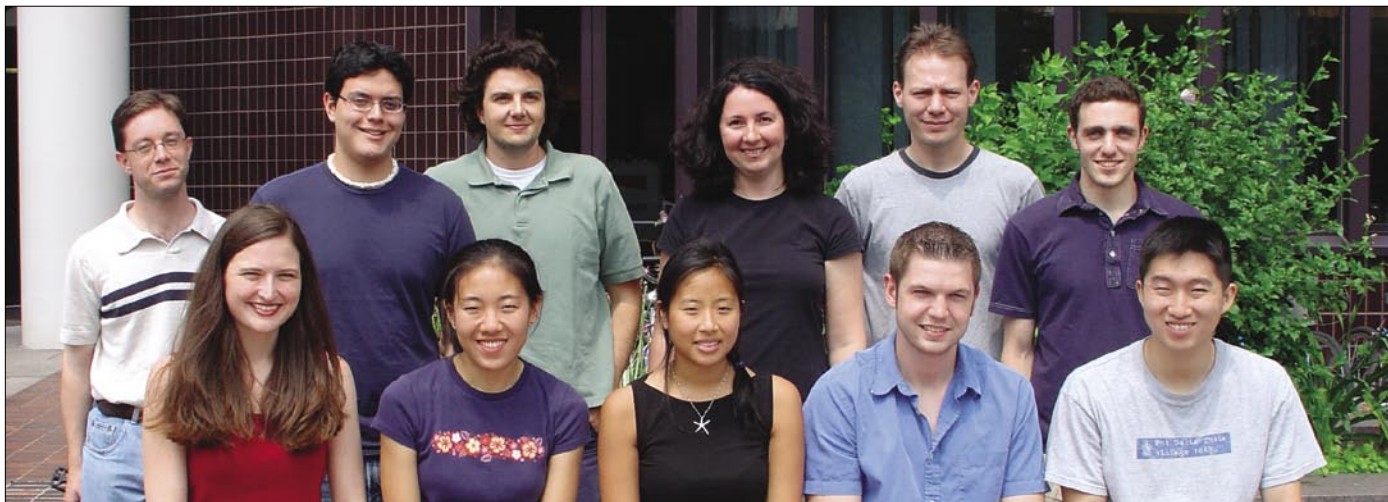


The CellProfiler™ Project Team

Whitehead Institute for Biomedical Research and The Computer Science and Artificial Intelligence Laboratory at Massachusetts Institute of Technology, Cambridge, MA, USA



The People: Front row from left: Anne Carpenter (Postdoctoral Fellow and Cofounder), Jun Liu (Undergraduate Student), Vicky Lay (Undergraduate Student), Mike Lamprecht (Programmer and Technician), and InHan Kang (Graduate Student). Back row from left: Adam Papallo (Data Analyst), Rodrigo Ipince (Undergraduate Student), David Sabatini (Principal Investigator, Whitehead Institute), Polina Golland (Principal Investigator, MIT), Thouis Jones (Graduate Student and Cofounder), and Chris Gang (Undergraduate Student).

The Research

Our interdisciplinary team develops software and data mining methods mainly to analyze large-scale image based biology experiments. We work primarily with David Sabatini's group, which, through the RNAi Consortium (TRC), is producing a large set of lentiviral RNA interference reagents to systematically knock down every gene in the human genome. Automation is used to prepare tens of thousands of cell samples, each with the expression of a different gene knocked down (reduced). Our main goal is to extract high-quality measurements of the cells in fluorescence microscopy images from each sample and identify samples with phenotypes of interest. This project rapidly reveals gene function and is aiding in functional annotation of the human genome. Anne Carpenter and Thouis Jones initially launched the CellProfiler™ project and specifically tuned it to analyze images from these high-throughput microscopy experiments.

www.cellprofiler.org

The Technique

We quickly realized that CellProfiler would be useful in applications beyond the large-scale microscopy experiments we were analyzing. Biologists frequently look at samples using plain sight—whether observing fluorescently stained cells, counting colonies, scoring samples, or making measurements. For a small number of samples, this analysis can yield rich and qualitative conclusions; however in many cases, automated analysis would be much preferred to produce quantitative, objective results and to avoid tedium. CellProfiler software is designed to meet this need so that biologists without training in computer vision or programming can quantitatively measure phenotypes from thousands of images automatically. The work described in our article is, for the most part, a departure from biological questions of immediate interest in our own laboratories. Instead, it describes our work of adapting and applying CellProfiler software to questions of interest outside our groups (i.e., various laboratories who have come to us for assistance). These collaborations are answering key biological questions and, at the same time, are helping to improve the software itself. CellProfiler is free and open-source, so that improvements and adaptations can be easily added to expand its usefulness to the scientific community.

CellProfiler™: free, versatile software for automated biological image analysis, p. 71.