

## **Analysis of microscopy data using CellProfiler and CellProfiler Analyst**

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CellProfiler is free open-source software designed to enable biologists without training in computer vision or programming to quantitatively measure phenotypes from thousands of images automatically. It was launched in 2006 and has been cited in more than 1500 published papers. It interfaces with ImageJ/Fiji plugins, and Ilastik, broadening the possibilities of problem specific solutions.

I work part-time at the Imaging Platform of the Broad Institute in Boston, developing algorithms for CellProfiler. My own lab at Uppsala University in Sweden is focused on algorithm development for microscopy image analysis with applications in biomedicine. It is part of SciLifeLab, which is a national facility for advanced research in biomedicine. As such, researchers in need of ways to quantify their microscopy data often contact us. Here, CellProfiler has become the primary tool for helping non-computer-science researchers getting started with their own data analysis. At the same time, CellProfiler is a key tool in our own research on primary cell cultures from glioma patients, and our development of methods for spatially resolved gene expression profiling. Raw data and analysis results from our large-scale experiments are stored on a web-accessible database, allowing collaborators to explore and analyze the high-dimensional image-derived data without having their own local copies of the data. We use CellProfiler Analyst for this data exploration, including its machine learning tools for identifying complex and subtle phenotypes.

I will present some of our ongoing projects using CellProfiler, and discuss recent developments in CellProfiler and CellProfiler Analyst.