Microscopes have been used for more than 400 years to understand biological and biomedical processes by visual observation. Although science is the art of observing, science also requires measuring, or quantifying, what is observed. Research based on microscopy image data therefore calls for automated methods for quantitative, unbiased, and reproducible measurements. An automated approach is further motivated by the development of scanning microscopes and digital cameras that can capture image data in multiple spatial-, time-, and spectral-dimensions, making visual assessment cumbersome or even impossible.

High-throughput screening (HTS) is a technique for searching large libraries of chemical or genetic perturbants, to find new treatments for a disease or to better understand disease pathways. We present one such study where we characterize cancer stem cells (CSCs) by quantitative microscopy, searching for therapeutically relevant regulatory differences between patients. The aim is to elucidate mechanisms of action and enable accurate targeting of disease subgroups. Modeling disease by culturing cells allows for efficient analysis and exploration. However, many diseases and biological pathways can be better studied in whole animals—particularly diseases that involve organ systems and multicellular interactions, such as metabolism and infection. The worm Caenorhabditis elegans is a well-established and effective model organism, used by thousands of researchers worldwide to study complex biological processes. Samples of C. elegans can be robotically prepared and imaged by high-throughput microscopy, and we show how novel image-analysis algorithms are capable of scoring phenotypic changes in high-throughput assays of C. elegans. In particular, we show how computational methods can identify novel anti-infectives as well as genes involved in fat metabolism.

Finally, detection, diagnosis, and severity grading of cancer are traditionally based on the visual examination under a microscope of histopathological tissue samples. The current transition from visual examination of glass slides under microscopes to whole slide scanners and computer-aided image analysis, i.e., digital pathology, holds the promise of more objective cancer grading that will lead to better prognostication while at the same time reducing the pathologist's workload. We present recent advances in detection and spatial mapping of biomedical markers that may improve prognostication in the future.

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