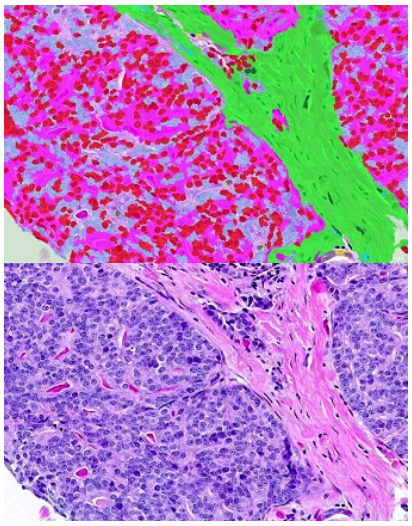
Automated Pathology Gives Accurate Predictions

Image-processing software developed by researchers at Stanford University has successfully predicted survival of breast cancer patients based on microscopy images of tissue samples (Sci Transl Med 2011;3:108–33). The researchers hope that, with further development, computerized pathology will provide more objective, reproducible tumor grading in the clinic.

Intra-observational variability among pathologists is a known problem. In one study, for example, a group of 6 pathologists given standardized criteria agreed on tumor grade in only 58% of cases (Am J Surg Pathol 1992;16:1133–43). Analytical software promises to be more consistent and to discern features too subtle for the human brain to detect.

"We deliberately took an unbiased approach," says Daphne Koller, professor of computer science at Stanford University, who led the project. Previous software was designed to spot features that human pathologists believed to be significant, and focused only on the cancerous epithelial tissue, not the surrounding stromal tissue. The Stanford group developed a large set of image features related to both types of tissue and allowed the software to determine which ones were significant based on patient survival.

Starting with a group of images from 248 breast-cancer patients from the Netherlands Cancer Institute, Koller's group first developed the software to measure 6,642 features, including cell-nucleus shape and the spatial relationships between cells from each tissue type. The software analyzed how these measurements related to one another, then weighted the measurements based on the associated survival data. The software was validated using tumor images from a second group of 328 patients from the Vancouver General



The microscopy image of a breast-cancer tissue sample (bottom) has been labelled by image analysis software (top) to identify typical epithlial cell nuclei (red), atypical epithelial nuclei (light grey), epithelial cell cytoplasm (purple), stromal matrix (light green), and stromal nuclei (dark green).

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Hospital. Prognostic scores generated by the software were strongly associated with survival in this test group.

"This is the way we should go; this is the future," says Aysegul Sahin, chief of breast pathology at MD Anderson Cancer Center, who was not involved with the research.

Whether analyzed by a computer or by a person, tumor morphology alone can only tell doctors so much about an individual's cancer and how to treat it, she says. Sahin says the real promise of automated pathology is to combine image analysis with data about gene expression levels and treatment outcomes. Koller's group is now developing the software in both directions, in part through a collaboration that draws on data from The Cancer Genome Atlas.

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