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Automated analysis of tissue microarrays

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Analysis of histological sections of disease tissues has traditionally relied on pathologist-based scoring. In an Advanced Online Publication in Nature Medicine Camp *et al.* describe techniques to automate the analysis of tissue microarrays that contain hundreds of tumour tissue sections arrayed on glass slides (*Nature Medicine*, 21 October 2002;doi:10.1038/nm791). Their approach, nicknamed AQUA (Automated Quantitative Analysis), involves a set of algorithms that can distinguish subcellular compartments and quantitatively assess protein localisation. Validation experiments demonstrated that the AQUA methodology is at least as good as conventional pathologist-based evaluation. Camp *et al.* used this technique successfully to assess estrogen receptor immunohistochemistry of breast carcinoma samples and nuclear beta-catenin expression in colon cancer.

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