The times they are a-changin'

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Published online: 2 March 2011
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Recently, we have seriously changed our laboratory facilities in my department. The building is only 6 years old and was designed according to our own wishes. We changed several of our “wet” laboratories to rooms full of computers. The obvious reason: we are gathering data at such a high speed and in such large quantities in only limited experiments that indeed we need less pipettes, but more chips. We are not the only ones. Looking at the results of the quarterly literature search in this issue of the *Journal of Hematopathology*, one can see that bioinformatics is increasingly shaping our scientific world. There is a lot of interest in systems biology, the method by which computer modeling tries to understand life in all its forms. This approach results in many new insights and will certainly affect our work as pathologists in due time. Nevertheless, it is also clear that huge datasets need clever understanding and the trained eye of a pathologist is not nearly surpassed by the new possibilities in recognizing disease in tissue.

The role of pathologists in this field of research cannot be underestimated. There are still cancer biologists who do not realize that when one investigates tumors on gene expression, that much of the signal actually comes from

non-tumor cells. The fact that these are often referred to as bystander cells, stresses the importance of looking at slides: it is obvious that those cells are a crucial part of the tumor, and we know for instance that gastric mucosa-associated lymphoid tissue lymphomas need *Helicobacter Pylori* recognizing T cells to survive. It should therefore come as no surprise that expression array experiments that combine tumor tissue samples with cell lines result in clustering of the cell lines.

Nevertheless, not only can we support cancer research by using our skills, we can also learn a lot from the results. Especially new markers that delineate disease entities come out regularly and also new entities arise making classifications schemes longer and longer. It is nevertheless good to realize that rarely, if ever, one marker defines a tumor entity. Modern classification combines clinical, morphological, immunophenotypical, and genetic criteria to define an entity. But is this sufficient? Increasingly, we need to provide information on molecular pathways that may be altered in tumors in order to facilitate the clinician in the selection of targeted therapies. Are we moving to a new type of classification that incorporates such data?

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