**FIGURE 19-3** Example of chromatic-aberration correction. Study of the topology of the genes *ABL* (green) and *BCR* (red) in human cell nuclei (blue). The genes are visualized using the FISH technique. Image data (*a, c*) and analysis results overlaid over the image data (*b, d*) are shown. Uncorrected images (*a, b*) are compared with the images corrected for chromatic aberration (*c, d*). Only part of the whole image is shown. The nuclei are about 10 μm in diameter. The analysis results are visualized in yellow: the *ABL* genes are shown as triangles, the *BCR* genes as circles, and the nuclear boundaries as closed curves. Note that one of the *ABL* genes is out of the nucleus before correction, whereas after correction it gets into the correct place. Consequently, this gene was rejected from the analysis without correction, whereas after correction it was safely detected. Note also that the *ABL* and *BCR* genes coincide in the right nucleus before correction, but are well separated after correction. This means that, without correction, the right nucleus is wrongly classified as Philadelphia (Ph)-positive (carrying the t(9;22) translocation), whereas after correction it is correctly classified as Ph-negative (no t(9;22) translocation present). Reprinted from Kozubek and Matula (2000).