shifting, it would seem eminently preferable to *eliminate* it.

With respect to a potential solution to the bandshift problem, I note that this kind of problem is not unique to DNA fingerprinting. Whether samples are correctly identified is often tested chromatographically in many fields, for example, identical samples are required to have identical retention times on high-performance liquid chromatography or gas chromatography, or identical retention values on thin layer chromatography. To obviate any "bandshift" problems in these analyses it is common practice to co-inject or co-spot a mixture of the two samples as well as to compare separate chromatograms or lanes. Similarly, co-electrophoresis of a mixture of the two DNA samples in a single lane of the gel [flanked on either side by lane(s) containing the individual samples] would eliminate the bandshift problem. In the mixed lane, each sample would experience the *same* set of factors affecting migration, whether it be sample load, impurities, gel or field inhomogeneities, and so forth. Thus, no correction factors are required and the criterion for a match would reduce to the finding, under visualization with each probe, of band correspondence in the two individual lanes and only single bands with no discernible band broadening for each band in the mixed lane. Conversely, in the event significant broadening or a doublet is observed at any of the bands, one could be quite certain that the two samples are nonidentical.

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The problem of bandshifting in Southern blots of genomic DNA digests is not unfamiliar to researchers. However, the solution that Lifecodes opted for is somewhat puzzling. Since DNA does not migrate as a linear function of fragment length in agarose gel electrophoresis (migration is inversely proportional to the log of the molecular weight), it seems overly simplistic to apply a single percentage correction to all the bands in a given lane of the gel. A simple yet better solution would be to spike each DNA sample with a set of marker fragments, for example, Hind III–digested λ DNA, and use these internal markers to calculate fragment sizes in each lane of the gel separately by linear regression. The bands from 0.5 to 1.0 micrograms of marker DNA would be visible above the background smear of genomic restriction fragments by ethidium staining. Alternatively, nanogram quantities of the markers could easily be detected by means of autoradiography by stripping and reprobing the blots with a λ-specific probe. Cross-hybridization between human probes and the marker would not be a problem as long as the human probe sequence was separated from its prokaryotic vector DNA. This method obviates the need to use several monomorphic probes in order to correct for the nonlinear bandshifting over the length of the gel.

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Erratum: In the report "The response of living cells to very weak electric fields: The thermal noise limit" by J. C. Weaver and R. D. Astumian (26 Jan., p. 459), figures 2 and 3 on page 461 were inadvertently interchanged. The captions were correct.