to the origin. The excellent linear correspondence found here verifies nearly complete elongation and demonstrates the validity of OCM. Selected images of maximally extended DNA molecules corresponding to the sizes used in the plot are presented in Fig. 2(*a–e*). Because it is a good approximation to assume that a DNA molecule reaching its most extended state is straight, the apparent contour length is close to the actual contour length. This combination of contour measurement coupled with complete stretching and transient fixation through hook formation forms the physical basis of OCM.

An intercalating fluorochrome, such as ethidium bromide, can unwind a DNA helix and thus increase its contour length[8]. OCM begins to quantify this effect. For the yeast chromosomal DNA molecules, the measured contour lengths are from 4 to 14% longer than the lengths calculated assuming B DNA (0.34 nm per base pair) and using sizes determined by physical mapping[9]. The measured contour length for lambda DNA is 16.5 μm, which matches the length calculated using 48.5 kb. Size discrepancies may also be due to electrophoretic stretching and accompanying distortion of the helix, particularly in larger molecules.

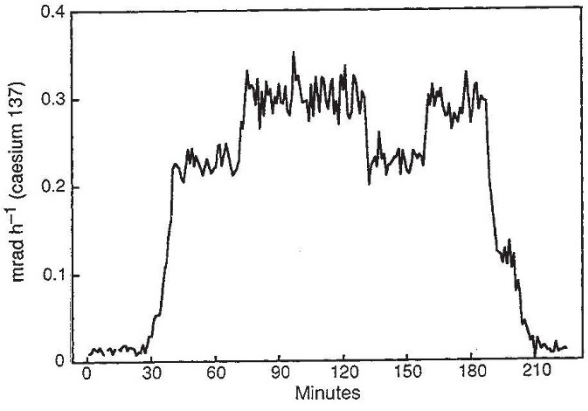
Size determinations of large DNA by OCM are very precise, with an estimated precision of approximately 6%, which is equivalent or superior to most pulsed electrophoresis size determinations. In sum, OCM offers a rapid and precise new methodology for sizing large DNA molecules.

Xuan-Hui Guo
Edward J. Huff
David C. Schwartz
Department of Chemistry,
New York University,
New York,
New York 10003, USA

1. Schwartz, D. C. & Cantor, C. R. *Cell* **37**, 67–75 (1984).
2. Carle, G. F., Frank, M. & Olson, M. V. *Science* **232**, 65–68 (1986).
3. Schwartz, D. C. & Koval, M. *Nature* **338**, 520–522 (1989).
4. Smith, S. B., Aldridge, P. K. & Callis, J. B. *Science* **243**, 203–206 (1989).
5. Deutsch, J. M. *Science* **240**, 922–924 (1988).
6. Zimm, B. H. *Phys. Rev. Lett.* **61**, 2965–2968 (1988).
7. Smith, S. B. & Bendich, A. J. *Biopolymers* **29**, 1167–1173 (1990).
8. Berman, H. M. & Young, P. R. *Ann. Rev. biophys. Bioengng.* **10**, 87–114 (1981).
9. Link, A. J. & Olson, M. V. *Genetics* **127**, 681–698 (1991).

In defence of radioactive journals

SIR — Those concerned about even minuscule doses of radioactivity will take no comfort in the revelations of Singh and Taylor (*Nature* **356**, 293; 1992) concerning the ionizing radiation emitted by the fine clays used to manufacture the glossy papers used in many magazines and journals. Singh and Taylor calculate that a person standing 0.4 m in front of a seven-shelf bookcase filled with issues of *Nuclear Physics* receives a dose of about 0.6 μrad h^{-1}.



Background radiation received aboard a commercial aircraft flying from Pittsburgh, Pennsylvania, to San Antonio, Texas. The two highest peaks correspond to an altitude of 10,670 m; the two secondary peaks to an altitude of 9,450 m. The cluster at 0.1 mrad h^{-1} near 195 min resembles what is typically observed when an aircraft levels off during its descent. (Instrument: RadAlert (International Medcom, 7497 Kenney Road, Sebastopol, California 95472.))

Because of the threat that the worst offenders may be banned by zealous regulators, I propose that journal publishers counter by publishing dose rates to which both their readers and regulators are subjected by everyday activities.

Consider, for example, flying aboard a commercial aircraft. For several years I have passed the time flying between cities by recording the background count indicated by a small Geiger counter. On long flights, I use a Geiger counter connected to a palmtop computer. While flying from Pittsburgh to San Antonio last December (see figure), I was subjected to 500 times the dose rate received during my last visit to a library. The dose rate received from a bookcase loaded with radioactive journals is less than the thickness of the trace plotted in the figure. During a recent flight to and from Hawaii, the dose rate was somewhat smaller, but the exposure time was several times longer.

Publishers can appease regulators by suggesting that anxious readers avoid an hour of aircraft travel for every 500 hours spent in a library. Frequent flyers can relieve their anxiety by declining the magazines passed out by flight attendants. Those who insist on reading while flying should be advised to hold the magazine rather than resting it on their lap. Flyers who are troubled more by boredom than by cosmic rays might take up the entertaining hobby of logging the background count as they fly.

Forrest M. Mims III
Science Probe, Inc.
433 Twin Oak Road,
Seguin,
Texas 78155, USA

More on bear droppings

SIR — We note with interest that the polymerase chain reaction (PCR) is increasingly being used to analyse unconventional material[1,2]. The use of the method to analyse bear droppings reported by Höss *et al.*[2] marks an advance in the study of wild animal behaviour. We would like to comment on two aspects of their work.

First, we are impressed by the demonstration of plant DNA in the bear droppings. But, given the sensitivity of the PCR method, the amplification of plant genetic materials does not necessarily imply that an animal has fed on plants, but could mean that it has ingested a herbivore that has just fed on grass. This 'Russian doll' effect could theoretically go some way back into the food chain.

Second, Höss *et al.* demonstrate the potential of applying PCR analysis of excrement to the study of genetic variability and population size. The mitochondrial sequences derived from three Brenta bear droppings (which differed from the American brown bear and the Romanian brown bear samples) reported by Höss *et al.* were identical to each other. Höss *et al.* alluded to the possibility that this is a reflection of the small population size or inbreeding, which may need statistical analysis, as an alternative explanation is that a single bear has deposited droppings in three different places. One way to address this issue is to establish the identity of the individual animals, for example by PCR-based sex determination or DNA fingerprinting. This information could allow the movements of individual animals to be followed by tracking the droppings.

Y.-M. D. Lo
J. S. Wainscoat
Nuffield Department of Pathology and Department of Haematology,
John Radcliffe Hospital,
Oxford OX3 9DU, UK

1. Sidransky, D. *et al. Science* **256**, 102–105 (1992).
2. Höss, M. *et al. Nature* **359**, 199 (1992).