millionth of the strength of the Earth's field) and it has been used to repeat parts of the Stanton Drew survey. Preliminary results show that this instrument has potential for 'seeing' archaeological features in even more detail.

The Stanton Drew survey is a fine example of the use of magnetic surveying in archaeology, and the power of the technique to detect features that would otherwise go unnoticed. ☐

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Fluid dynamics

Diffusion in a different direction

David A. Weitz

Diffusion of particles or molecules in a fluid is an essential manifestation of thermal energy. It is seen in the familiar brownian motion of dust particles in a fluid or a gas, and it ensures the mixing of different molecules in a fluid. So mixing, at the shortest length scales, results from diffusion rather than convection. This is behind a standard method for measuring molecular diffusion coefficients: a sharp concentration gradient is established between two fluids, and the decay of this gradient as the two fluids mix determines the diffusion coefficient of one fluid in the second. Observers look in a direction perpendicular to the gradient (that is, with the interface edge-on), and the results are interpreted assuming a smooth relaxation of the concentration gradient. But that may not be valid: on page 262 of this issue[1], a team from Milan report unexpected spatial fluctuations in the concentration of two fluids mixing by diffusion.

The authors, Vailati and Giglio, take the unorthodox approach of looking along the direction of the gradient, so that no large-scale variation from the main concentration profile is seen. Rather than the expected uniform variation in concentration, they observe huge spatial fluctuations of the concentration perpendicular to the gradient. These fluctuations develop rapidly, and persist until the gradient has been completely relaxed. It is only by looking from this new perspective that they can observe these surprising fluctuations.

The authors use two fluids that can be placed, by a suitable choice of temperature, near a 'consolution critical point', at which they go from miscible to immiscible. The temperature is first lowered, making the fluids separate, with the heavier fluid on the bottom. It is then quickly raised above the critical temperature, making the fluids miscible. Diffusion relaxes the concentration gradient — but it also creates enormous fluctuations, in a direction perpendicular to the gradient, which are large enough to be seen from the variations they cause in optical phase change and in the pattern of scattered light.

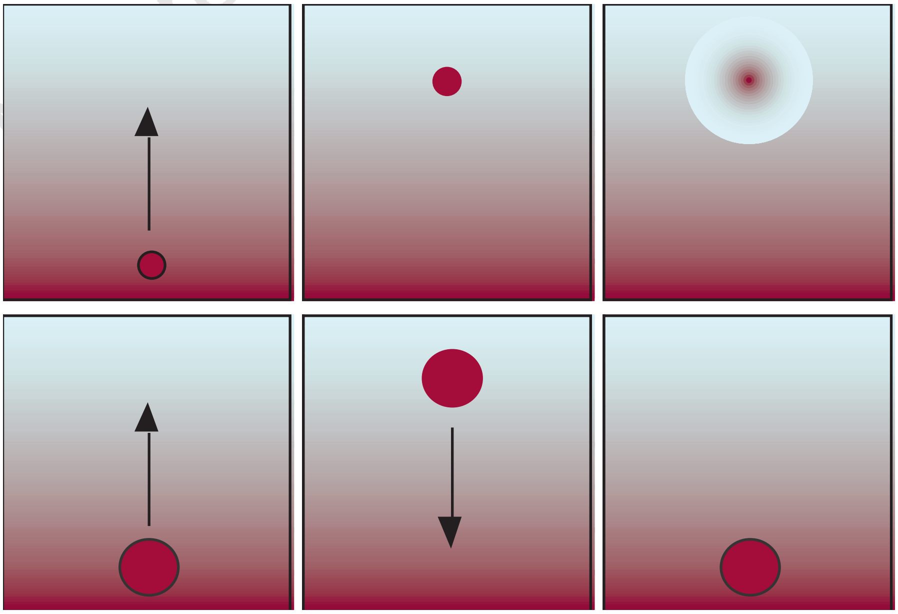

Figure 1 **How large fluctuations can occur in diffusion.** a, **A velocity fluctuation carries a small volume of one fluid into the other, along the direction of the concentration gradient. It relaxes by diffusion, leading to a large spatial fluctuation perpendicular to the gradient.** b, **Gravity limits the size of the fluctuations, because larger volumes do not have time to diffuse before buoyancy brings them back to their original position.**

Where do these fluctuations come from? The authors propose that naturally occurring velocity fluctuations transport small volumes of fluid along the gradient, which then relax most quickly by diffusion, leading to large-scale spatial fluctuations in the concentration perpendicular to the gradient (Fig. 1a).

In retrospect, it is perhaps not so surprising that a diffusive process can be so dominated by fluctuations. Diffusion is simply the continuum limit of a statistically random process, and if the large statistical fluctuations grow faster than any relaxation process, then highly disordered patterns can result. An example is the diffusion-limited accretion of particles onto a growing seed[2]. If the growth kinetics are controlled by diffusion, and if the particles are not allowed to relax once they strike the surface but instead are pinned onto the point of first contact, then they form highly disordered structures.

The structures produced by diffusion-limited aggregation are fractals, that is, they are scale invariant. They produce a light-scattering intensity that is similar in form to that from the diffusive fluctuations reported by Vailati and Giglio. In both cases, the scattering intensity is a power-law function of the scattering wave vector, reflecting the lack of any characteristic length scale. In both cases, a simple solution of the diffusion equation would lead to a very uniform structure. In both cases, the fluctuations dominate because they cannot relax quickly enough.

The fluctuations observed by Vailati and Giglio are limited in size only by gravity: if the volume transported by the velocity fluctuation is too large, then it is relaxed by convection due to buoyancy, rather than by diffusion — the displaced volume returns to its original location without contributing to the spatial fluctuations (Fig. 1b).

Traditional measurements do not have this unusual perspective, explaining why these fluctuations are typically not observed in diffusion coefficient measurements. More generally, the reason they have escaped our observation until now is probably that mixing is controlled by diffusion only on short length scales. On larger scales, either convection or stirring usually dominates.

By using buoyancy-matched fluids, the scale of the fluctuations could be greatly increased. Even more pronounced effects would occur if the experiment were carried out in space, in microgravity. Then, the length scale of the fluctuations could become truly macroscopic, easily approaching a millimetre. This would have profound consequences. It would radically alter any measurements that depend on diffusive motion — measurements of particle sizes and diffusion coefficients, for example, and of the behaviour of critical fluids. Indeed, any fluid measurements performed in space must be interpreted very carefully, to fully take into account the effects of the fluctuations.

Moreover, some manifestations of diffusive motion that are well established on Earth may be profoundly changed in microgravity. Even the mixing of fluids may be appreciably affected, by a change in the timescale of homogeneous mixing. Further surprises are probably to be found in diffusion-driven phenomena without gravity. ☐

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Virology

Illicit viral DNA

Robin A. Weiss and Paul Kellam

More than 20 years ago, the late Victor Zhdanov at the Ivanosky Institute of Virology in Moscow published a remarkable paper[1] claiming that complementary DNA copies of RNA viruses such as measles and polio occurred in retrovirus-infected cells. The observations raised eyebrows at the time, because promiscuous cDNA synthesis seemed to run counter to everything known about viral replication. But the data were neither confirmed nor refuted, and were soon forgotten.

On page 298 of this issue[2], Rolf Zinkernagel's group resurrects the issue posed by Zhdanov's results. Klenerman *et al.*[2] show that cDNA fragments of the RNA-replicating lymphocytic choriomeningitis virus (LCMV) form in mice and in murine and hamster cells in culture which express retroviral reverse transcriptase, the enzyme which uses an RNA template to synthesize DNA. The formation of LCMV cDNA is inhibited by azidothymidine (AZT), confirming that reverse transcriptase activity is involved. There is, of course, ample evidence for reverse transcription having occurred in evolution, with the formation of processed DNA or pseudogenes from RNA[3]. But the LCMV cDNA is a case of a non-retroviral RNA being caught red-handed in the act of seemingly illicit DNA synthesis.

Many viruses of animals, plants and bacteria carry their genetic information in the form of RNA. With the exception of retroviruses, they replicate through RNA intermediates, so that no viral DNA sequences are synthesized at any stage of the viral life cycle. LCMV is such a virus[4] (and belongs to the arenavirus family, which also includes the dreaded Lassa fever virus). The RNA in LCMV virus particles is composed of two 'ambisense' single-stranded molecules, large and small. Part of each molecule has the same coding sense as messenger RNA from which the viral proteins are translated, and part is complementary to mRNA. LCMV encodes and packages an RNA polymerase which makes complementary RNA from the genomic RNA template. The viral polymerase is not known to have reverse transcriptase activity. That is why it is so surprising that Klenerman *et al.* detect DNA sequences homologous to viral RNA.

When outlandish claims are based on detection through the polymerase chain reaction (PCR), the sceptic's initial reaction is to suspect false-positive data. After all, a laboratory in which cloned viral sequences are handled, or where reverse-transcriptase PCR is routinely used to detect viral RNA, is just the right environment for error, as we all know to our cost. But Klenerman *et al.* appear to have performed all the appropriate controls to guard against contamination.

One reason why they investigated the presence of cDNA was to try to solve an immunological puzzle — mice which have cleared all evidence of previous LCMV infection continue to show strong immune responses as if some viral antigen persisted in the animals. The authors therefore speculate that the cDNA might act as a naturally produced form of DNA vaccine that produces antigen. This is difficult to conceive for cDNA lacking promoter sequences for expression. However, if any of the cDNA sequences were to integrate downstream from cellular gene promoters or within an open reading frame, a low level of specific peptides might be expressed that would be sufficient to load major histocompatibility antigens in antigen-presenting cells, and thereby elicit an immune response.

Klenerman *et al.*[2] detected LCMV cDNA in mouse and hamster cells expressing reverse transcriptase activity. But it was not found in a variety of other cells without such activity, or in reverse-transcriptase-positive guinea-pig cells. Further work is required to find out whether retroviral reverse transcriptase is responsible for the LCMV cDNA synthesis, or whether some other cellular component in mouse and hamster cells confers a reverse transcriptase activity upon the LCMV RNA polymerase. One of the reverse-transcriptase-negative cell lines should be infected with amphotropic murine leukaemia virus and then superinfected with LCMV to see whether cDNA

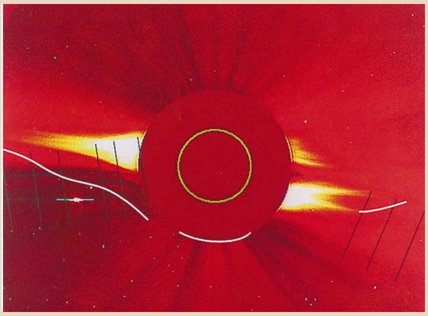
Solar physics

Galileo through the Sun's streamers

The Galileo satellite, on its tour of Jupiter's moons, has provided a remarkable bonus for solar physicists. In January, the Sun obstructed our line of sight to the distant probe. By monitoring radio signals from Galileo as they passed through the Sun's corona, astronomers have solved an old problem about the origin of the solar wind. It has long been known that the wind has two distinct components, slow and fast. But where on the surface of the Sun do they originate?

This image (Habbal, S. R. *et al.* *Astrophys. J.* 489, L103–L106; 1997) is a white-light view obtained using the Solar and Heliospheric Observatory (SOHO). The solar disk is blanked out, revealing the hot, inner coronal regions and filamentary structures known as streamers. Jupiter is the bright point to the left of the solar disk.

Galileo's apparent passage behind the Sun is marked by the straight black lines, which show where the slit of a spectrometer on SOHO was positioned to make ultraviolet measurements of the corona, simultaneous with the radio transmissions. The UV spectra give a rough indication of the Solar wind speed,



and the 94 $\mathrm{km\,s^{-1}}$ contour is shown in white. Scintillation of Galileo's radio signal also indicates wind speed, importantly with very high spatial resolution: on one occasion, the scintillation increased markedly (a sign of the slow wind), and, by no coincidence, a streamer stalk intercepted the line of sight to the probe at the same time. It seems that the slow wind comes from streamers, and the fast wind comes from the whole surface — not, as had been thought, only from the polar regions.

Eventually, these results may help solve the biggest mystery of the solar corona — the nature of its heating mechanism.

Karen Southwell