maximizing information gain. When navigating in turbulent odour plumes, it seems that the rate of information acquisition could have a similar role to that of the concentration gradient in chemotaxis.

Although the simulated infotactic trajectories resemble their biological counterparts, the control mechanisms underlying the similarities in trajectories might well differ. In moth flights, for example, the temporal regularity of the turns, whether expressed in zigzagging upwind or in casting, suggests the existence of an internal oscillatory mechanism, known as self-steered counterturning[9]. Search models based on counterturning produce trajectories similar to those observed for moths in wind-tunnel experiments[7,8], and might also to some extent account for the complex 'Lévy-flight' patterns characteristic of insect flights in field studies[10].

But Vergassola *et al.* did not develop their search algorithm on the basis of control mechanisms specific to moths. They considered the problem of olfactory search as sufficiently universal that maximizing information gain allows any searcher to track a chemical plume efficiently to its source. This hypothesis is plausible, because many animals, including crabs and birds, exhibit zigzagging trajectories very similar to those of moths, even though these are probably subject to completely different control mechanisms[3]. In infotaxis, crosswind casting and zigzagging upwind can be viewed as parts of a behavioural continuum ranging from pure exploration to pure exploitation.

The authors' work[2] is intriguing in several respects, and will certainly foster future research. Perhaps the most direct implication is the potential use of infotaxis in robotic search applications, in part because computationally efficient algorithms that update a source probability map in real time are already available for on-board implementation[11]. ■

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ATOMIC PHYSICS

The social life of atoms

Maciej Lewenstein

In a trail-blazing experiment 50 years ago, it was observed that photons from far-off stars bunch up. But in fact there's a more general distinction among free, non-interacting particles: bosons bunch, and fermions 'antibunch'.

Counting individual quantum-mechanical objects such as the particles of a complex many-body system — whether photons, electrons, atoms or something else — is an efficient way to learn about the properties of both the system and of the particles being counted. Fifty years ago, Robert Hanbury Brown and Richard Twiss[1] published the results of the paradigmatic experiment of this sort, in which they counted joint detections, in two separate detectors, of photons from distant stars. The two-photon correlations clearly showed that the photons liked to arrive bunched up in groups. Jeltes *et al.*, whose results appear on page 402 of this issue[2], use less well-travelled particles for their investigations — ultracold helium atoms. But they are able, for the first time in the same experiment, to compare and contrast the Hanbury Brown–Twiss (HBT) effect for both 'bosonic' and 'fermionic' particles.

Although the original HBT effect can easily be understood within the framework of classical physics, explaining it in quantum-mechanical terms is more tricky. It requires acknowledging that photons are particles of integer spin, or bosons. These particles are far more gregarious than their fermion (half-integer-spin) cousins, and the bunching phenomenon can be described as the result of constructive interference of the quantum-mechanical probability amplitudes of two (bosonic) photons reaching the detectors. This explanation led Roy Glauber[3] to formulate modern photon-counting theory within the framework of quantum electrodynamics, the quantum field theory of the electromagnetic force. The result was the birth of modern quantum optics, an achievement crowned by a Nobel prize for Glauber in 2005.

Atoms of the helium isotope ^{4}He are also bosons, because they consist of a total of six half-integer-spin particles: four nucleons (two protons and two neutrons) and two orbiting electrons. Experiments with ultracold, metastable ^{4}He have not only famously allowed the observation of Bose–Einstein condensation (the phenomenon of many bosons all adopting the same quantum state), but have also opened the way to precise time-resolved and position-sensitive counting experiments in atomic systems. These helium atoms have a very long lifetime if unperturbed, but can be detected with almost perfect efficiency in microchannel plate and delay-line detectors.

The first direct observation of the bunching of ^{4}He atoms — the atomic HBT effect — came two years ago[4]. The same authors are part of the team that has now seen[2] the analogous effect in ^{3}He atoms, whose two electrons and three nucleons (only one neutron this time) make them fermions. Fermions obey the Pauli exclusion principle, so unlike bosons they do not like being in the same place at the same time. What Jeltes *et al.*[2] observe in the case of ^{3}He, therefore, is not the bunching characteristic of bosons, but 'antibunching' resulting from the destructive interference of the fermions' probability amplitudes.

The measurement of the HBT effect gives insight into the 'pair-correlation functions', a measure of the probability of finding two atoms at a certain distance apart, and therefore of how an atomic system is put together. Jeltes and colleagues' experiments were performed with dilute, practically non-interacting clouds of atoms in a state of thermal equilibrium. The

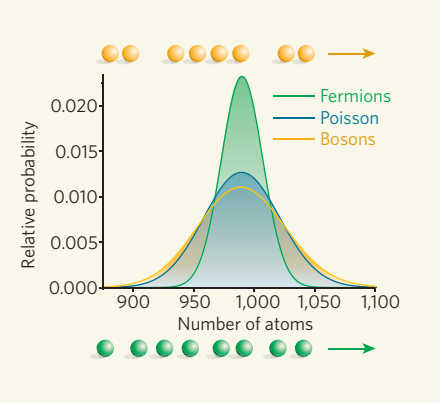
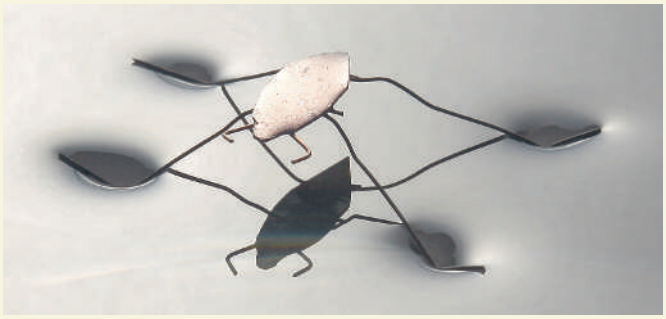


Figure 1 | Bunch, antibunch. Simulated distributions of the number of atoms detected in a certain time-window after 1,000 are released from an atomic trap at low temperature. If the arrival times of the atoms at the detectors were truly random, they would conform to a Poisson distribution (blue). In fact, bosons prefer to bunch, so in the time-window of any one detection event, significantly more or fewer than the mode number can arrive: the counting distribution (yellow) is broader. For fermions, the converse is true: they antibunch, arriving more regularly spaced than purely randomly, and so produce a taller, narrower counting distribution (green). (Figure courtesy S. Braungardt, U. Sen, A. Sen (De) & R. J. Glauber.)

SURFACE CHEMISTRY

Repellent legs



The glossy, water-repellent leaves of lotus plants (*Nelumbo nucifera* and *N. lutea*) have inspired many synthetic superhydrophobic surfaces. But the best of these are difficult to make, and can be very fragile. Steven Bell and colleagues now describe a simple method to prepare robust superhydrophobic surfaces of high quality (I. A. Larmour *et al. Angew. Chem. Int. Edn* doi:10.1002/anie.200604596; 2007).

The secret of lotus leaves' water-repellency is the double roughness of their surfaces — caused by the presence of nanohairs on microbumps — coupled with a waxy coating. The authors recreate this double roughness by coating metal substrates with a textured layer of another metal, simply by immersing them in a metal-salt solution. Scanning electron microscopy shows that the deposited metal forms flower-like structures (0.20 to 1 μm across) that are made up of smaller crystallites (about 60 to 200 nm in size), simulating the complexity of lotus leaf surfaces.

Dipping the substrates in a solution of a chemical surface-modifier, HDFT, supplies a monolayer of hydrophobic molecules. These molecules are highly fluorinated, just like the Teflon lining of non-stick frying-pans. The resulting surfaces show almost perfect super-hydrophobicity: a drop of water on a perfectly water-repellent surface forms a contact angle θ of 180°, and the surfaces produced by this method have θ values consistently greater than 170°.

The approach is so simple that it can be applied to metal objects of any reasonable size or shape. The authors again turned to nature for inspiration. Pond skaters (*Gerridae*) use superhydrophobic legs to walk on water. Bell and colleagues made a model pond skater from copper (pictured), with legs that had been treated with silver and HDFT. Despite having ten times the mass of a real pond skater, the metallic insect was able to rest comfortably on the surface of water.

The authors suggest that their method will aid research into superhydrophobic surfaces. This should hasten the arrival of practical applications, such as reducing turbulent flow in water-bearing pipes.

Andrew Mitchinson

ultimate goal is to measure the pair correlations, or perhaps higher-order correlations between more than two particles, for various strongly correlated, interacting quantum systems. Such measurements are technically demanding, but the authors show how a significant step can be made towards that goal by using an atomic lens. This is a laser that forces atoms away from its axis, 'defocusing' the atomic clouds, spreading them out in space and so significantly increasing the resolution for detecting the position of individual atoms.

The atomic-lensing method should allow the observation of, for instance, the antibunching that a one-dimensional gas of bosons undergoes because of 'fermionization' as a result of increased atom–atom repulsion in a confined space. Analysing the raw data obtained from atom detectors, one should also be able to extract the full atomic counting distribution. For non-interacting bosonic atoms in thermal equilibrium, this distribution should be broader than a Poisson distribution (Fig. 1); for non-interacting fermions, it should be narrower.

Direct counting of atoms at high resolution is so far possible only with metastable helium atoms, which limits the application of the method. Alternatives are in development. The pair correlations of a Bose–Einstein condensate that was split into two interfering parts was measured a few years ago[5]. The detection of single atoms passing through a high-quality optical cavity is possible, and was also used[6] to measure bosonic counting statistics and the bosonic HBT effect.

Another powerful method for measuring pair-correlation functions is noise interferometry. This is particularly useful for ultracold gases in an optical lattice[7], a perfect periodic potential made by interfering laser beams. When this optical potential is strong, bosonic atoms cannot tunnel from lattice site to lattice site. They form instead a 'Mott insulator' state with a fixed number of bosons per site. The images obtained when these bosons are released from the lattice are noisy and blurred, indicating a lack of phase correlation. Analysing the noise correlations in a sequence of such images has been used to assess, for example, the pair-correlation functions of the Mott-insulator state of bosonic rubidium-87 atoms[8]. A band insulator of polarized fermionic potassium-40 atoms in a lattice has also been constructed[9]. This is a state in which atoms completely fill the lowest energy band; as in the Mott insulator, there is no possibility of tunnelling, and no site-to-site phase coherence. Whereas noise interferometry in a bosonic Mott-insulator system produces a periodic sequence of peaks (Fig. 2) indicative of bunching, here it leads to a series of dips, equivalent to fermionic anti-bunching.

These noise interferometry investigations and atom-counting experiments such as those of Jeltes and colleagues[2] will continue to supply fascinating information on the physics of strongly correlated quantum many-body systems and their constituents. As our methods develop, so our prying into the private and social lives of particles will become ever more pervasive. ■

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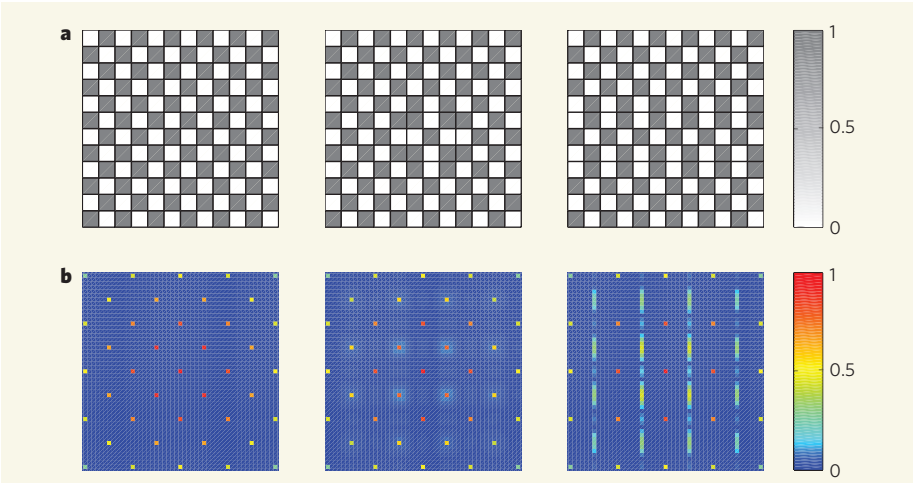

Figure 2 | Noise assessment. 'Noise interferometry' is a particularly efficient way of assessing spatial structures. **a**, A two-dimensional, dipolar Bose-gas Mott-insulator state held in an optical lattice, for example, ideally forms a chequer-board state of alternating filled and vacant sites at low temperatures and half filling[10] (left diagram; dark sites indicate presence of an atom). In practice, various kinds of defects occur (adjacent squares filled or unfilled; middle and right diagrams). **b**, Noise interferometry converts this spatial pattern into an easily identifiable interference signal, a characteristic series of peaks equivalent to a bunching behaviour.

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STRUCTURAL BIOLOGY

Pass the protein

Jean-François Trempe and Jane A. Endicott

Modifier proteins, such as ubiquitin, are passed sequentially between trios of enzymes, like batons in a relay race. Crystal structures suggest the mechanism of transfer between the first two enzymes.

Proteins are essential for all cellular processes, but their activities must be tightly controlled. One way of doing this is to covalently attach a small protein such as ubiquitin, or other ubiquitin-like proteins (UBLs)[1,2] such as NEDD8 and SUMO. For example, many proteins that control cell division must be degraded at precise points during the cell cycle. The initial step in this process is achieved by tagging the protein with ubiquitin.

Despite the variety of UBL functions, the enzymes that attach UBLs to proteins are remarkably similar, and share the same general mechanisms of action[3]. But how do these enzymes work? On page 394 of this issue, Huang *et al.*[4] describe the structure of an intermediate protein complex that forms during the process of attaching UBLs to proteins*. This structure gives valuable insights into the mechanism by which UBLs act in cell-signalling pathways.

UBLs become attached to proteins in a series of reactions catalysed by a trio of enzymes — described generically as E1, E2 and E3. The UBLs are first activated by E1, using energy derived from adenosine triphosphate (ATP) molecules. In this step, one end of the UBL becomes adenylated — that is, covalently attached to adenosine monophosphate — to generate a reactive intermediate that binds tightly to E1's adenylation active site (A-site). The UBL is then transferred to another active site within E1, the T-site, where it becomes attached to a cysteine amino acid. This relatively stable E1~UBL adduct transfers its UBL cargo to a cysteine in the next enzyme of the sequence, E2. The resulting E2~UBL adduct then interacts with the third component of the cascade, the E3 enzyme. This acts as a bridge between the E2~UBL adduct and the protein receiving the UBL, and thereby provides substrate specificity to the pathway.

What do we know about the molecular details of these reactions? The crystal structures of two E1–UBL complexes have been determined[5,6]. In each case, a single UBL molecule binds within a cleft from which the flexible UBL tail extends, so that the end of the tail is positioned close to the A-site of E1 (Fig. 1a). But although these structures suggest mechanisms by which an E1 enzyme can recognize and activate its particular UBL, they do not reveal how the activated UBL is transferred from the A-site to the T-site.

We also know something about how an E1 enzyme passes its UBL cargo to an E2. The E1 enzyme for NEDD8 consists of two proteins, called UBA3 and APPBP-1. The structure of a complex between the E2 enzyme of NEDD8 and a fragment of UBA3 has been determined[7]. Intriguingly, when this structure is superimposed on the structure of an entire E1–UBL complex, the E1 and E2 active-site cysteines are remote from each other — too far apart for a direct transfer of the UBL from one to the other. So how is this hand-over effected?

The answer lies in Huang and colleagues' crystal structure[4], which depicts a complex formed from two NEDD8 molecules, E1, E2 and an ATP molecule associated with a magnesium ion. In this structure, the E1 enzyme is folded into three domains that create a large central groove; the groove is divided into two clefts by a 'crossover' loop, which connects two of the domains. One NEDD8 molecule, here designated UBL(T), is covalently attached to the active cysteine of E1 at the T-site; the other NEDD8 molecule binds to the same part of the cleft that was occupied by the UBL in the singly loaded E1 structures described above[5,6]. On the basis of their structure, Huang *et al.* propose that a change in conformation of the protein complex allows the UBL to be passed from E1 to E2.

Central to this conformational switch is a region of UBA3 known as the ubiquitin-fold domain (UFD). In the previously determined structures that are loaded with just one UBL, this domain occupies the position of UBL(T), but in the doubly loaded structure[4] it is rotated 120° away from the T-site (Fig. 1b). The E2 enzyme binds to the UFD in this rotated position, so that the active cysteine of E2 lies enticingly close to the UBL-loaded cysteine of E1. Rather elegantly, this conformational change also alters the affinity of E1 for E2, creating an affinity switch: E1 doubly loaded with NEDD8 displays high affinity for E2, whereas singly loaded E1 does not.

But the story does not end there. As the E2 binding sites for E1 and E3 are mutually exclusive[8], the E2~UBL adduct must dissociate from E1 in order to associate with an E3. Does it jump, or is it pushed? The answer is possibly the latter. Following the discharge of UBL from the T-site, E1 reverts to its singly loaded

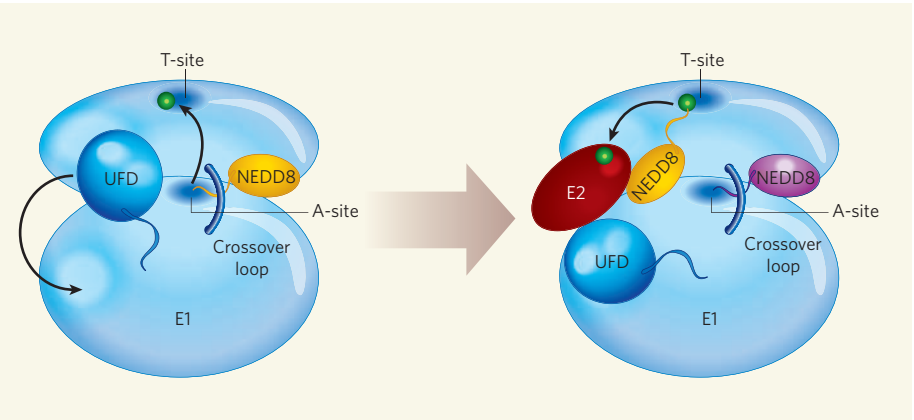

Figure 1 | A protein conformational switch. a, Before they become attached to a target protein, ubiquitin-like proteins such as NEDD8 are transferred from an E1 to an E2 enzyme. Crystal structures show that the tail of a NEDD8 protein (yellow) that is bound to E1 passes under a 'crossover' loop; the tail's end reacts with adenosine triphosphate (ATP) at the ATP-binding site of E1 (the A-site). The NEDD8 molecule is then transferred to a cysteine amino acid at the 'T-site', and a region of E1 known as the ubiquitin-fold domain (UFD) changes position. **b,** Huang *et al.*[4] propose that the combined conformational changes create a surface to which an E2 enzyme binds with high affinity. A second NEDD8 molecule (purple) now also binds to the A-site. The first NEDD8 molecule (yellow) is then transferred to a cysteine in the active site of the E2 enzyme. The positions of the active cysteines in E1 and E2 are marked by green circles.

*This article and the paper concerned[4] were published online on 14 January 2007.