Atomic doughnuts from single photons

Analysis of the interaction between a photon and an ensemble of some 3,000 atoms trapped between two mirrors has revealed a form of multi-atom quantum entanglement that has no counterpart in classical mechanics. See Letter p.439

James K. Thompson

What is the most that could happen when you analyse a single particle of light after sending it through a few thousand atoms? On page 439 of this issue, McConnell et al.1 demonstrate that the single photon creates a special quantum link between nearly all of the atoms, a link known as entanglement. The authors show that the particular ‘flavour’ of entanglement observed has no classical analogue — a first for such a large collection of atoms. Extending our ability to create entanglement in large systems may one day allow highly precise measurements of time, fields and accelerations, lead to new materials, and enhance our understanding of the transition from the quantum to the classical world.

In the quantum world, the act of measurement can profoundly change the state of the object being measured. McConnell and colleagues exploited this fundamental principle to create entanglement between almost 3,000 atoms that are laser-cooled to only a few ten-millionths of a degree above absolute zero. The atoms were levitated between two highly reflecting, weakly transmitting mirrors. Each of the atoms can be thought of as possessing an arrow, which corresponds to the orientation of the atom’s total quantum spin. All the arrows add up to make one big arrow that initially points in some direction, call it x, which lies on the equator of a sphere.

A weak pulse of light is injected through one of the mirrors and then detected after it leaks back out of the other mirror. The light also has an arrow attached to it, denoting its polarization (the direction of the light’s electric field). As the light bounces back and forth between the mirrors, it passes roughly 5,000 times through the atoms, each time being partially absorbed and then re-emitted back into the original pulse of photons (Fig. 1a).

If the total atomic arrow were pointing slightly north or slightly south of the x direction, because of quantum Heisenberg uncertainty in its orientation (Fig 1b.), then the polarization of the light would be slightly rotated clockwise or anticlockwise, respectively, when it was re-emitted. For each pulse of light sent through the mirrors, McConnell et al. checked to see whether they detected any rotated light. On most trials, they did not detect even one rotated photon. Failing was no problem. They just tried again until they finally detected that a single photon had been rotated. This told the experimenters that, on that particular trial, the total atomic arrow was not quite on the equator, but must have been pointing slightly north or south of x. The researchers verified that the arrow was no longer at the equator by making a second and much more precise measurement of the total atomic arrow’s north–south orientation.

The measurement apparatus fundamentally could not tell whether the polarization rotation of the single detected photon was clockwise or anticlockwise. With no further information, one would expect the measurement of a single photon to collapse the total atomic arrow into a quantum superposition state in which the arrow was simultaneously both north and south of the equator. But confirming with the precise measurement that the total atomic arrow does not lie...
on the equator was not sufficient to establish the superposition nature of the quantum state. To do this, the authors also performed experiments in which, after detecting the rotated photon, they then rotated the total atomic arrow about the $x$ direction by various amounts. They then made the precise north–south measurement. As predicted for a simultaneous north and south state, they observed a much lower probability that the arrow would be found on the equator than is possible for a classical arrow that is either just north or just south of the equator.

By measuring at different rotation angles, McConnell et al. determined the Wigner function — a quantum probability distribution of the direction in which the total atomic arrow points. The Wigner function looked like a two-dimensional doughnut centred on the $x$ axis (Fig. 1b), but rather than simply having an empty hole of zero probability at its centre, the centre of this doughnut had negative probability. This negative probability was a clear sign that the measurement of a single rotated photon collapsed the atoms into an entangled state. This is the first time that a negative Wigner function has been observed for such a large collection of atoms.

Several experiments have created entanglement between atoms using many photons to measure the north–south orientation of the total atomic arrow, producing large amounts of ‘quantum squeezing’ — enhancement in the sharpness of the atomic arrow needed for realizing better quantum sensors. McConnell et al. observed no improvement in the total sharpness of their atomic arrow.

However, the squeezing experiments carried out so far can be viewed semi-classically: quantum mechanics produces a certain magnitude of ‘noise’, after which the noise can be treated as arising from a fictitious classical source. In McConnell and colleagues’ work, the observation of a negative Wigner function demonstrates that any semi-classical description fails to capture their flavour of entanglement.

The authors also demonstrate that nearly all of the roughly 3,000 atoms must be involved in the generated entanglement, by using a multi-partite entanglement measure known as the entanglement depth, which has been applied in related work. It is unclear exactly how to interpret this particular measure because it does not provide information about the magnitude of the shared entanglement. However, showing that entanglement can be simultaneously shared among so many atoms continues to push the progression of the observation of quantum mechanics from the microscopic to the mesoscopic regime. It may one day help us to understand the transition from the quantum to the classical world of our everyday experience, in which we would never see arrows pointing both slightly north and slightly south at the same time.

In future work, the detection of two or more rotated photons may open the door to even larger amounts of entanglement, and to states that might be useful for quantum sensors.

Figure 1 | Creating highly shared entanglement. a. Vertically polarized photons (red) pass many times through atoms (blue) as the photons bounce back and forth between highly reflecting, weakly transmitting mirrors. The polarization of a photon is only very occasionally rotated to horizontal owing to quantum noise (uncertainty) in the quantum–spin orientation of the atomic arrows. Only horizontally polarized photons generate a click on a detector. b. The quantum probability distribution of the orientation of the total atomic arrow is represented by a region (purple disk) at the tip of an arrow on the equator of a sphere. McConnell et al. show that detecting just one horizontal photon (click!) changes this distribution to a ‘two-dimensional doughnut’, which has a positive outer region (purple) and a negative inner region (yelllow) — a hallmark of quantum entanglement between the atoms. The negative-probability filling means that, no matter how the doughnut is rotated about its axis, the probability of measuring the arrow on the equator is zero.
such as atomic clocks, magnetometers or accelerometers.

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Defiant daughters and coordinated cousins

Genetically identical cells can have many variable properties. A study of correlations between cells in a lineage explains paradoxical inheritance laws, in which mother and daughter cells seem less similar than cousins. See Letter p.468

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During the winter holidays, many of us are reminded of the complexities and challenges of family dynamics. Some traits, such as table manners or verbal tics, may run in the family; others, such as a passion for science or the law, might generate rebellion in the next generation. Repeated defiance could even cause behavioural traits to skip a generation, so that a child’s apparent rebellion turns out to be an unconscious copying of a grandparent. Rebellious cells are harder to imagine, but in this issue, Sandler et al.¹ (page 468) demonstrate that pairs of cousins (cells with a common ‘grandparent’) are more similar to one another than are mothers and daughters, in terms of the time it takes them to grow and divide.

Intuitively, if one cell in a population has more or less of a particular component than the population average, levels of that component will tend to deviate in the same direction in that cell’s daughters. Owing to subsequent random fluctuations, these deviations will decorrelate over time, such that compositions of genetically identical cells should become less correlated with each generation. Contrary to this expectation, observations¹,² indicate that the time it takes one cell to become two — its doubling time — can show a stronger correlation between cousins than between mother–daughter pairs (Fig. 1). It has been unclear whether this surprising result reflects the fact that cells born at different times are exposed to different conditions, just as the teenagers of the 1980s behaved differently from those of the 1990s. But the current study demonstrates that, under tightly controlled conditions, the phenomenon persists.

Simple inheritance laws seem to imply that this is impossible: if doubling times become uncorrelated in a single generation, how can they persist between cousins, which are separated by four generations of growth? Sandler and colleagues propose that an unknown factor that affects doubling times oscillates periodically in cells, such that cousins tend to be born in a similar phase, but mothers and daughters usually are not. A computational model showed this simple explanation to be consistent with the authors’ findings in a mammalian cell type called a lymphoblast. Sandler et al. then analysed their data using measures borrowed from chaos theory⁴, a field of mathematics that predicts seemingly random variation using non-random (deterministic) equations that merely amplify tiny changes in initial conditions. The results of this work further support the researchers’ hypothesis that the variation they observed arises from a simple dynamical system, rather than from a random process. Finally, they reanalysed published data⁵ for cyanobacteria, in which growth is coupled to circadian rhythms, and showed that cousins were indeed substantially more positively correlated than mothers and daughters.

Much of the variation in doubling times thus seems to reflect differences in the phase of an as-yet-unidentified internal oscillator, rather than stochastic factors, such as ‘noisy’ gene expression. A few decades ago, such a deterministic scenario might even have been the first guess. Differences between genetically identical cells were then often explained by nonlinear models, for example oscillations, chaos, or bistable switches. Noise was invoked only to explain infinitesimal perturbations that might eventually cause systems to diverge. Now the pendulum has swung the other way, and physiological heterogeneity is explained by random bursts of gene expression almost by default.

The problem is that both no-noise and all-noise views ignore the interconnectedness of random fluctuations and average dynamical

Figure 1 | Family values. When considering cellular inheritance, an intuitive model implies that each generation will display the previous generation’s behaviour plus some stochastic variation. The entire family tree can then be reconstructed from the correlation coefficient $\rho$, which describes how much each generation decorrelates from its predecessor. For example, correlations between sisters and between grandmother–granddaughter pairs, which are both separated by two generations, are $\rho^2$. Similarly, cousin–cousin correlations are $\rho^2$ because, to go from one cousin to another, we have to move two generations up in the family tree and two down again, connecting cousins through the common grandmother. Sandler et al.¹ report that the time each cell takes to divide strongly violates this model, because these times are, on average, more similar between pairs of cousins than between mothers and daughters.