mean flux in each spectral channel.

Space-based radio emissions, on the other hand, show up as horizontal stripes, localized in position and weakly dependent on frequency. To remove them, the researchers used a matrix-algebra technique, called a principal component analysis, to decompose their data into a sum of components, each the product of a function of frequency times a function of position. The strongest components, they figured, probably represented the unwanted synchrotron sources. They removed those and retained only the weaker components that contained most of the hydrogen signal. The result is shown in figure 2b.

That done, the researchers calculated the cross-correlation of their data and the DEEP2 galaxy density. The two were correlated up to length scales of 40 Mly—quantitatively similar to the DEEP2 data's autocorrelation. That means that the extracted signal measures much the same thing as the galaxy survey: The teasing out of the hydrogen contribution was a success.

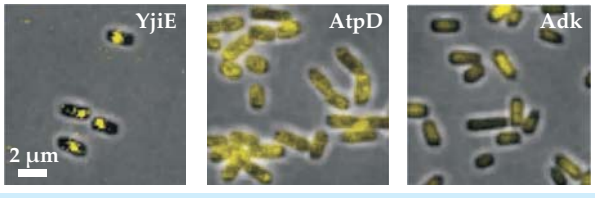
There's a long way to go, though, before intensity mapping can provide any

physics update

These items, with supplementary material, first appeared at http://www.physicstoday.org.

Muonic Lamb shift. Willis Lamb's 1947 measurement of the tiny splitting between the 2*s* and 2*p* states of atomic hydrogen gave a crucial impetus to the development of quantum electrodynamics (QED). That "Lamb shift" from the Dirac hydrogen spectrum is a 4-μeV increase in the 2*s* energy level due primarily to vacuum fluctuations of the electromagnetic field. Now Randolf Pohl (Max Plank Institute for Quantum Optics, Garching, Germany) and coworkers at the Paul Scherrer Institute (PSI) in Switzerland have finally measured the analogue of the Lamb shift in the muonic H atom—a proton orbited by a μ^- instead of an e^-. Muons live only microseconds, but they are 200 times heavier than electrons, and their atomic orbits are correspondingly tighter. The muonic Lamb shift is about 200 meV, and its precise value is particularly sensitive to the proton's finite size. The PSI experiment was accomplished with precision laser excitation of μ^- p atoms created by an intense μ^- beam stopping in a small volume of H_2 gas at very low pressure. The team measured the muonic Lamb shift to a part in 10^5 and compared it with elaborate QED calculations that parameterize the proton's finite size with an effective charge radius R_p. They find an R_p about 4% smaller than that measured, with less precision, by conventional H spectroscopy and e^-–p scattering experiments. The discrepancy is 5 standard deviations. Either the proton really is smaller than previously thought, argue Pohl and company, or there's something wrong with the QED calculations or their input constants. But the proton is a quark composite whose size and shape are quantum-chromodynamic manifestations beyond the purview of QED. Several QCD theorists suggest that at the extraordinary precision achieved by the PSI experiment, it may not be possible to describe proton-size effects adequately with a single length parameter. (R. Pohl et al., *Nature* **466**, 213, 2010.) —BMS

The noisy expression of genes into proteins. Genetic information is transcribed from DNA to RNA and translated from RNA to make proteins. Because each step entails a modest number of molecules, gene expression, as the DNA-to-protein conversion is termed, is inevitably noisy: Identical genes in identical cells don't yield identical numbers of proteins. But how noisy? Sunney Xie of Harvard University and his collaborators have used single-molecule fluorescence microscopy and microfluidics to find out.



They started by modifying the DNA of *Escherichia coli* to create 1018 different strains of the single-celled bacterium. In each strain, the code for a yellow fluorescent protein (YFP) was inserted after the gene for a different protein. To see the rate at which one gene is expressed in one cell of one strain, you'd illuminate the cell with a laser and measure the YFP emission through a microscope. To gather gene-expression statistics for a sample of cells from all 1018 strains, the Harvard team sent streams of cells through channels cut in a microfluidic chip and imaged them. The figure shows sample images for three proteins, YjiE, AtpD, and Adk. Ninety-six strains could be processed at once at a total throughput of 160 cells per second. The team found that the least abundant proteins appear at 10^{-1} molecules per cell; the most abundant, at 10^4 per cell. Gene expression is indeed noisy, but with a twist. As you'd expect, the least abundant proteins have the largest cell-to-cell fluctuations. But for proteins whose mean abundance is 10 per cell or higher, the expression noise saturates, presumably because the various molecules that mediate gene expression inside a cell are in limited supply. (Y. Taniguchi et al., *Science* **329**, 533, 2010.) —CD

Space buckyballs. The field of nanotechnology is in part rooted in the 1985 Nobel Prize–winning laboratory synthesis of buckyballs—the soccer-ball-shaped carbon molecule C_{60}—by Rice University chemists Richard Smalley and Robert Curl and their collaborator, University of Sussex chemist Harold Kroto. The synthesis was guided by Kroto's hypothesis that complex carbon chains could naturally form in the interstellar medium of aging carbon-rich, hydrogen-poor giant branch stars. Now, 25 years later, Jan Cami at the University of Western Ontario and his colleagues have reported the clearest evidence yet of such complex carbon structures in space. The research team analyzed IR spectroscopic data—collected by the *Spitzer Space Telescope*—of the circumstellar region of a planetary nebula known as Tc 1. As the image shows, the spectrum contains several prominent peaks of C_{60} (red arrows) and peaks of the rugby-ball-shaped C_{70} (blue arrows); both molecules were uncharged and in the solid phase. Previous spectra of other carbon-rich planetary nebulae indicated strong emission peaks of volatile polycyclic hydrocarbons, which were completely absent in the monitored region of Tc 1.