

found for LBGs and starburst galaxies of the same age but one to two orders of magnitude higher than LBGs of similar masses. Their star-formation rate coupled with their densities of 2×10^{-5} galaxies per cubic megaparsec, two orders of magnitude higher than starbursts', mean the new galaxies are responsible for the majority of the stars produced by massive galaxies in the early universe.

The problem for theorists

Although the newly found ancient galaxies help explain the presence experimentally of so many, and such large, massive galaxies at lower redshifts, they present a problem for most galaxy-formation theories (see the article by Jeremiah Ostriker and Thorsten Naab, *PHYSICS TODAY*,

August 2012, page 43). Semianalytic models—those that tune simple phenomenological descriptions of astrophysical processes to match the abundance, clustering, redshift, and other observed properties of the galaxy population—underestimate the density of massive galaxies in the early universe by one to two orders of magnitude. And hydrodynamic simulations of galaxy merger rates predict no massive galaxies at all. Although previously observed LBGs and starburst galaxies already challenged those theories, the abundance and star-formation rates of the new galaxies render the disagreements harder to ignore.

"More and more observations show that a large population of massive galax-

ies and supermassive black holes has already been established in the young universe," says Wang. "In general, the young universe is more efficient in forming big things than we thought." To reconcile theory with observations, astronomers will need more accurate redshift measurements and better characterization of the physical properties for a larger sample of galaxies so they can put more stringent constraints on galaxy-formation models.

Heather M. Hill

References

1. T. Wang et al., *Nature* **572**, 211 (2019).
2. C. Schreiber et al., *Astron. Astrophys.* **618**, A85 (2018).
3. T. Wang et al., *Astrophys. J.* **816**, 84 (2016).

A molecular clock for testing fundamental forces

The vibrational frequencies of trapped ultracold molecules can serve as a check on what we think we know about the universe.

Gravity over macroscopic distances is well understood. The simple inverse-square law, proposed centuries ago by Isaac Newton, continues to accurately describe the force at scales across the non-relativistic regime, from laboratory-scale torsion balance experiments to the motions of stars and galaxies. It's been especially well tested at the scale of the distance from Earth to the Moon.

Short distances—microns or less—are another matter. In microscopic experiments, electromagnetic forces are so overwhelmingly dominant that the force of gravity at small scales has never been directly measured. All we have are upper bounds on its strength, some of which are astonishingly large. According to the best experimental constraint so far, the gravitational attraction between two objects 1 nm apart is no more than 10^{21} times what Newton's law says it is.¹

It's not so outlandish to imagine that the force of gravity could follow the inverse-square law over large distances but deviate from it over small ones. Theories of extra dimensions through which only gravity can propagate, for example, allow

just such a functional form. (See the article by Nima Arkani-Hamed, Savas Dimopoulos, and Georgi Dvali, *PHYSICS TODAY*, February 2002, page 35, and the Quick Study by Lisa Randall, *PHYSICS TODAY*, July 2007, page 80.) To help test and constrain those theories, experimenters have been working for decades to chip away at the possible parameter space of short-range non-Newtonian gravity. Their techniques include measurements of the Casimir force (see the Quick Study by Jeremy Munday on page 74 of this issue) and neutron scattering off atomic nuclei.

Now Columbia University's Tanya Zelevinsky and colleagues are adding a new experimental method to the mix with their ultraprecise measurements of molecular vibrations.² Because their experiment, shown schematically in figure 1, is similar to that of an atomic optical-lattice clock (see *PHYSICS TODAY*, March 2014, page 12), they call it a molecular lattice clock, even though precision timekeeping isn't among their immediate goals. Although theoretical details remain to be worked out, the researchers estimate that with their current experimental ca-

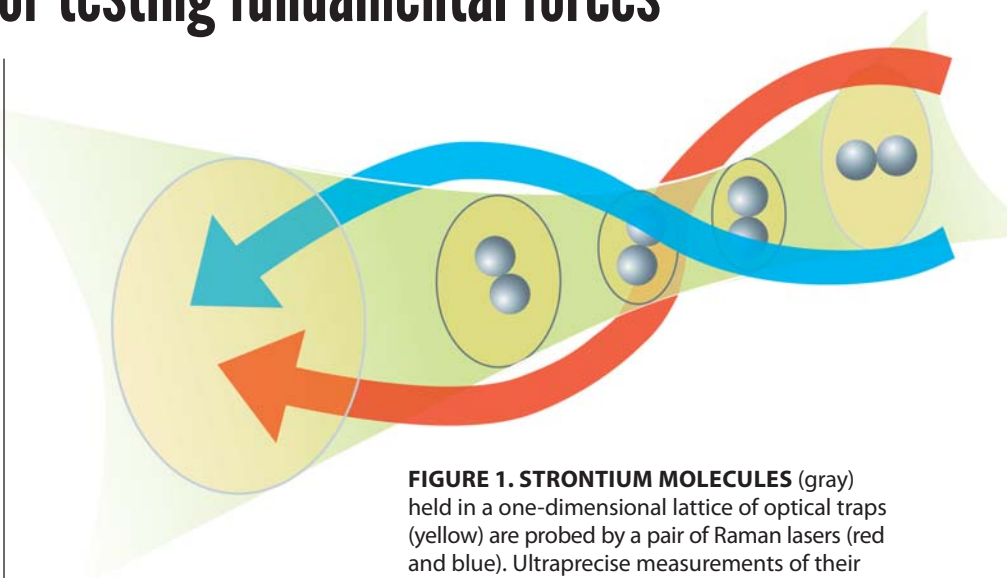


FIGURE 1. STRONTIUM MOLECULES (gray) held in a one-dimensional lattice of optical traps (yellow) are probed by a pair of Raman lasers (red and blue). Ultraprecise measurements of their vibrational frequencies reflect the fundamental forces acting on the nuclei and electrons.

pabilities—measuring a 25 THz vibrational resonance to within just 1 Hz—they'll be able to constrain predictions of nanometer-scale gravity to within 10^{18} – 10^{19} of its Newtonian value.

Cold-molecule spectroscopy

Relative to atoms, molecules are complicated. Not only can their electrons be excited into more energetic states, but their vibrations and rotations are also quantized. The resulting hierarchy of quantum levels lends itself to probing many aspects of fundamental physics (see the article by Dave DeMille, *PHYSICS TODAY*, December 2015, page 34). But it also makes molecules hard to control. Whereas it's straightforward to optically cool atoms to a fraction of a kelvin, doing the same for molecules means keeping track of a vast tangle of states to make sure the cooling lasers aren't inadvertently pumping energy into the molecules instead of pulling it out. (See *PHYSICS TODAY*, January 2010, page 9.)

Molecular-physics experiments don't always require ultracold samples; sometimes it suffices to use a molecular beam, in which collisions cool the molecules to a relatively balmy few kelvin. Zelevinsky and colleagues needed lower temperatures than that, though, so they used an established trick in the cold-molecule field. Rather than cooling the molecules directly, they first cooled a gas of atoms, then optically coaxed the atoms into diatomic bound states. (See the article by Debbie Jin and Jun Ye, *PHYSICS TODAY*, May 2011, page 27.)

That approach is limited to the elements compatible with cold-atom techniques, though, so their molecule—the strontium dimer, Sr_2 —isn't one that's often found outside of cold-molecule experiments. It's held together not by a covalent bond but by the weaker van der Waals force, so it's an order of magnitude larger than a covalently bound molecule such as nitrogen or oxygen, and its binding energy and vibrational-level spacing are accordingly smaller. Otherwise, it behaves much like any other diatomic molecule.

To probe the energy difference between two vibrational states, shown in blue and orange in figure 2, the researchers use Raman spectroscopy, a two-photon process that connects the two states by way of a higher-energy virtual state. The difference between the Raman laser frequencies can be stabilized to better than

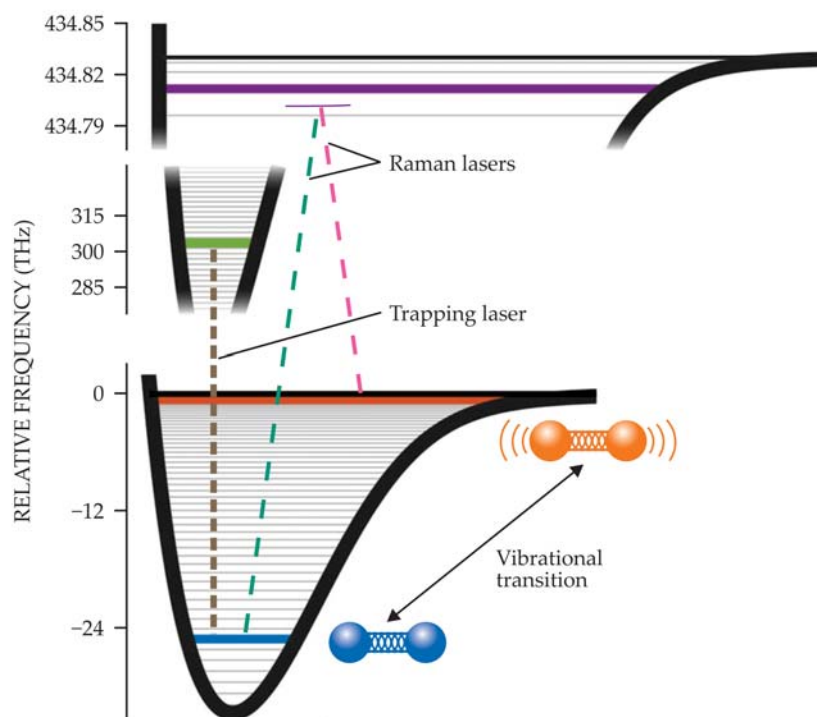


FIGURE 2. IN THE HIERARCHY OF MOLECULAR QUANTUM STATES, each electronic state (thick black curves) contains a series of vibrational levels (horizontal lines). To probe the frequency of the vibrational transition between the levels marked in blue and orange, Tanya Zelevinsky and colleagues use a pair of Raman lasers that drive the transition by way of a higher-energy virtual state (thin purple line). To eliminate both Doppler broadening and AC Stark shifts, they optically trap the molecules at a so-called magic frequency that's nearly resonant with yet another excited state (green solid line). (Adapted from ref. 2.)

0.1 Hz. The technique's precision is thus limited by molecular, not optical, effects.

Magic trapping

One potential source of uncertainty comes from Doppler broadening. Molecules moving toward or away from the source of the Raman lasers are excited at slightly different frequencies. Cooling slows their relative motion, but even at 2 μK , the molecules move enough to broaden the resonance by 30 kHz. So the researchers confine the molecules to a one-dimensional optical lattice formed by the standing wave of a near-IR trapping laser, shown in yellow in figure 1.

Lattice trapping eliminates Doppler broadening, but it introduces its own problem. Through the AC Stark effect, the trapping laser field separately shifts each vibrational state's energy by an amount that depends on the state's frequency-dependent electric polarizability and the trapping light's intensity. Molecules in different parts of the lattice can have their transition energies shifted by differ-

ent amounts, and the overall resonance can be broadened by tens or hundreds of kilohertz.

Fortunately, the cold-atom community had already worked out a solution: Set the trapping laser to a so-called magic frequency at which the two states have the same polarizability. The Stark shifts then cancel, and the transition frequency can be measured with high precision.³

It's not always possible to find a convenient magic frequency, especially for a pair of molecular vibrational states, whose polarizabilities tend to parallel each other without crossing. The exception is for frequencies close to a resonance between one of the states of interest and a higher-energy electronic state (shown in green in figure 2). Near-resonant fields make a molecule's polarizability fluctuate rapidly as a function of frequency, so crossing points become plentiful.

But near-resonant trapping is risky, because the trapping laser can slowly excite molecules out of the vibrational state of interest and into the higher-energy

metastable state. The excitation's slow destruction of the sample isn't such a problem: The researchers' spectroscopic technique requires them to destroy and re-form the sample for every data point anyway, and the process takes only a few seconds. What's worse is that the near-resonant excitation degrades the coherence lifetime of the vibrational transition. Because the sharpness of a spectroscopic line is fundamentally limited by the transition coherence time, any-

thing that reduces the lifetime of either state cuts down on the measurement precision.

Zelevinsky and colleagues went for it anyway. With their near-resonant magic trapping, they obtained a coherence time of 30 ms, corresponding to a resonance linewidth of 32 Hz. For a transition frequency of 25 THz, that's a quality factor of nearly 10^{12} , a record for any vibrational measurement. Still, it's several orders of magnitude less than has been

achieved in atomic measurements—where quality factors have reached 10^{16} —and less than Zelevinsky was hoping for. “We were surprised that the near-resonant trapping shortened the coherence time as much as it did,” she says. “There’s clearly something that’s not very well understood, and we take it as our new challenge to figure it out.” Because the molecules have so many excited states, there are many more near-resonant magic frequencies to explore that could perform better.

The hunt for new physics

A linewidth of 32 Hz doesn't mean that the measurement precision is limited to 32 Hz. Zelevinsky and colleagues estimate that with a reasonable integration time, they can find the center of the line to within 1 Hz. That's enough for them to start making meaningful measurements of fundamental forces. Strontium has several stable spin-0 isotopes that range in mass number from 84 to 88. Looking at each of them in turn should allow the researchers to isolate what observable effect, if any, gravitational mass has on interatomic forces.

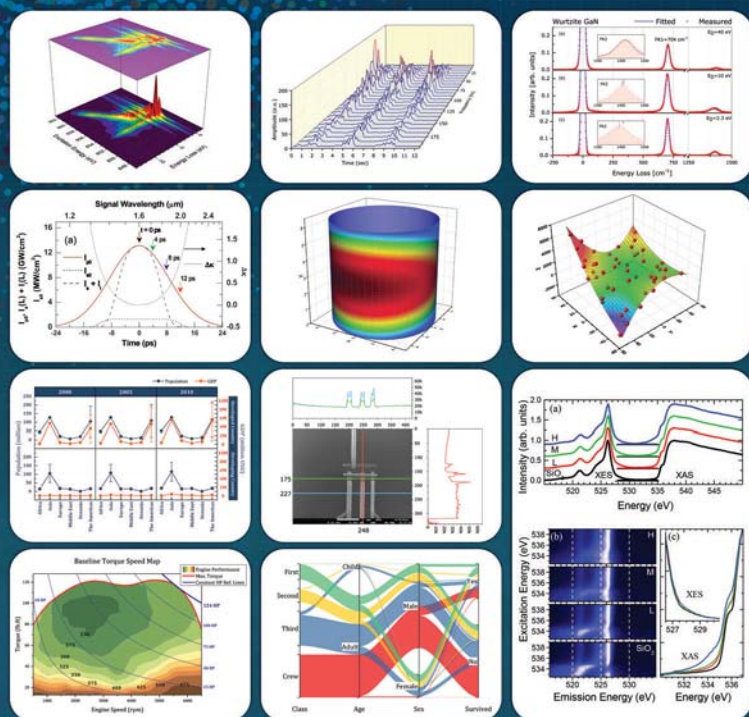
Before they do those experiments, though, they want to have a good handle on all the other ways vibrational frequencies can depend on mass. Heavier nuclei have more inertia, so they respond more sluggishly to the forces of the surrounding atoms (see, for example, *PHYSICS TODAY*, September 2018, page 17). To help isolate the influence of gravity, the experimenters are working with theorist Robert Moszyński and colleagues at the University of Warsaw to calculate contributions to that isotope effect that are usually ignored, including the effects of relativity and coupling between nuclear and electronic motion.

Non-Newtonian gravity isn't the only fundamental-physics measurement the experimenters have in their sights. They're also interested in testing the stability of the proton-electron mass ratio over time.⁴ The ratio could change if, for example, the strong nuclear force is not constant: The proton, unlike the electron, is not a fundamental particle, and its mass depends on how its constituent quarks interact. So far, there's been no sign of such a drift in the proton mass, but as Zelevinsky explains, “It's not strictly ruled out, and therefore scientists are actively looking for it, since there are many things

New Version!

ORIGIN® 2019

Graphing & Analysis



Over 75 New Features & Apps in Origin 2019!

Over 500,000 registered users worldwide in:

- 6,000+ Companies including 20+ Fortune Global 500
- 6,500+ Colleges & Universities
- 3,000+ Government Agencies & Research Labs

For a **FREE 60-day**
evaluation, go to
OriginLab.Com/demo
and enter code: 2876

OriginLab® 25+ years serving the scientific & engineering community

about the universe we know we don't understand."

If the proton–electron mass ratio does change, one natural place to look for it is in molecular vibrational frequencies, which straightforwardly depend on both bond stiffness (a consequence of the quantum mechanical behavior of electrons) and nuclear inertia. Most constraints to date have come from astrophysical spectra of distant galaxies, which are

sensitive to small fractional drifts in the ratio (on the order of $10^{-16}/\text{yr}$) averaged over billions of years.⁵ But the ratio doesn't necessarily drift at a constant rate. To complement the astrophysical constraints, Zelevinsky and colleagues are working toward an Earth-based measurement that has comparable precision but is focused on the present-day drift rate.

Johanna Miller

References

1. Y. Kamiya et al., *Phys. Rev. Lett.* **114**, 161101 (2015); C. C. Haddock et al., *Phys. Rev. D* **97**, 062002 (2018).
2. S. S. Kondov et al., *Nat. Phys.* (2019), doi:10.1038/s41567-019-0632-3.
3. J. Ye, H. J. Kimble, H. Katori, *Science* **320**, 1734 (2008).
4. T. Zelevinsky, S. Kotochigova, J. Ye, *Phys. Rev. Lett.* **100**, 043201 (2008).
5. See, for example, J. Bagdonaitė et al., *Science* **339**, 46 (2013).

A folding protein gets caught in the act

Time-resolved NMR spectra paint a picture of structural transformation with millisecond resolution.

To transform from linear chains to three-dimensional structures, *in vivo* proteins somehow navigate tortuous free-energy landscapes. Their final configurations must be just right for them to function properly; protein misfolding is thought to underlie some allergies as well as neurodegenerative diseases such as Parkinson's and Alzheimer's.

X-ray crystallography and NMR are well-established methods for accessing the detailed structure of a protein's final folded configuration. Gathering dynamical information about the folding process itself requires real-time techniques such as fluorescence, circular dichroism, and hydrogen exchange; acquiring information that quickly, however, comes at the expense of structural detail. Molecular dynamics simulations are also a valuable tool for studying protein configurations (see *PHYSICS TODAY*, December 2013, page 13), but because of computational limitations they fail to capture either the complete atomistic detail of real proteins or the complete process of folding.

Now Jaekyun Jeon, Robert Tycko, and coworkers at the National Institutes of Health in Bethesda, Maryland, have introduced a new way to track a protein's folding.¹ Their experimental setup, shown in figure 1, can start and stop the folding process quickly enough to trap proteins in transitory configurations. With the help of a signal-enhancing NMR technique, the researchers generated 2D spectra to track the formation of helices and dimers by melittin, a protein found in bee venom.

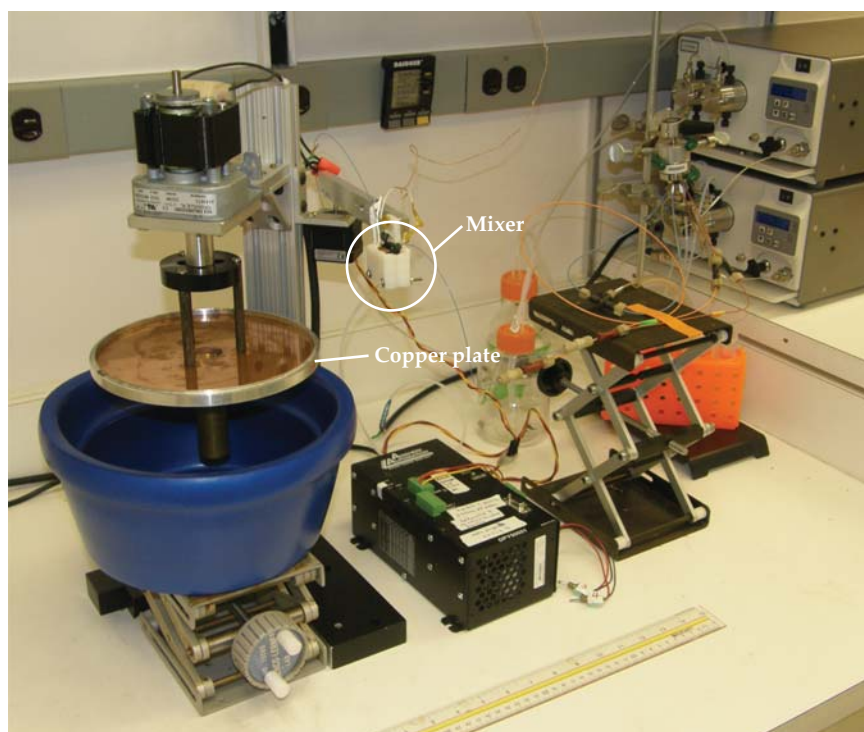


FIGURE 1. A RAPID-MIXING DEVICE starts and stops the protein-folding process with millisecond resolution. The mixer combines two pumped solutions, producing a high-velocity jet that freezes when it hits a liquid-nitrogen-cooled rotating copper plate. The frozen samples are subsequently analyzed using solid-state NMR. (Adapted from ref. 1.)

Their data, which have both high spatial and temporal resolution, challenge the previously accepted picture of melittin's structural development.

One moment in time

Melittin is a small protein—a peptide—with only 26 amino acids. At low pH, the peptides are linear chains, but in neutral to high pH, each peptide forms a bent helix. The helices form antiparallel dimers, which pair to make tetramers, melittin's native configuration.² The entire transi-

tion happens in less than 10 ms, so whether those steps happen concurrently or sequentially has been hard to discern.

Tycko's group developed a rapid mixer to change the solution's pH and initiate the protein-folding process. It mixes two solutions in just 1.6 ms—not quite instantaneous on the protein-folding time scale, but fast enough to capture a narrow spread of folding times. Although it's conceptually simple, the mixer is a critical part of their technique. "We've been working on these kinds of experiments