

the numbers of both predator and prey increase and decrease, sometimes leading to extinction of first prey and then predator. Altering the form of the functional response can, in some circumstances, prevent extinction<sup>1</sup>.

Fryxell *et al.*<sup>1</sup> examine how group living in prey, in predators and in both kinds of species influences the shape of the functional response and the interaction between predator and prey populations. They show theoretically that gregarious living in either the prey or the predator species reduces the rate of prey consumption by each predator. Intake rates are lowest when both species live in groups. If prey lives singularly, an increase in the number of prey will lead to a linear increase in the likelihood that a predator will encounter a meal on its daily wanderings. However, if the prey forms clumps, there will be large holes in the landscape through which a predator can roam without finding something to eat. Group living in prey therefore decreases intake rate. When a predator does find a group of prey, it encounters an embarrassment of riches and quickly becomes satiated. The intake rate of predators is reduced if they live gregariously because each individual searches the same area and then has to share the prey that it kills.

Fryxell *et al.* primarily use data from surveys of lions preying on wildebeest in the Serengeti National Park, Tanzania, to reach their conclusions for a system where both predator and prey live gregariously. They show that the consequence of both species living in groups is a predicted reduction in the food-intake rate per lion of 90% compared with the rate when lions forage solitarily. This is an enormous amount, and is equivalent to the decrease in food availability that results if the migratory wildebeest is present in a lion-pride territory for only a fraction of each year. The authors also examine the consequence of such a large reduction in intake rate on the dynamics of the lion and wildebeest populations. They predict that, if both species shunned group living and wandered the plains singly, the dynamics of both populations would be highly unstable, with both predator and prey likely to become extinct. In contrast, if both predator and prey live in groups, it is much more likely that both populations will persist.

But the question of why lions live in groups remains. Fryxell *et al.* argue that the benefits primarily accrue from territory defence and the communal protection of young against males that can kill cubs when they take over a pride<sup>5,6</sup>. However, an argument familiar to most ecologists is that lions live gregariously because group hunting is required to bring down large prey. Fryxell *et al.* accept that group hunting does allow lions to attack and kill the formidable Cape buffalo, but they also state that: "Most individual lions refrain from contributing to group hunts." This carefully worded statement does not rule out the possibility that substantial benefits arise from group hunting, and it flags one of the problems of parametrizing functional responses. It is challenging to work

out individual intake rates accurately across different sizes of predator and prey groups for a range of prey densities, especially for species with such complex social arrangements as those seen in lions. I would be interested to know whether functional responses derived entirely from observations on the feeding of individual lions would yield similar conclusions to those obtained by Fryxell *et al.* using survey data.

This work<sup>1</sup> shows that extending the functional response to include some realistic natural history helps to explain why the inevitable extinction of predators and prey, predicted by some simple population models, is not observed in the wild. The paper will stimulate researchers who have obtained functional responses using detailed observational data

on group-living predators. And it should encourage theoreticians to examine how other aspects of animal behaviour might affect the predictions derived from simple population models. ■

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## ATTOPHYSICS

# At a glance

David M. Villeneuve

**Measurements on the attosecond timescale had been limited to the dynamics of electrons in an atomic gas. But a record has now been set in a quite different context — the photoemission of electrons from a surface.**

The quest for faster and faster time-resolved measurements has reached a new level: Cavalieri *et al.* report (page 1029 of this issue)<sup>1</sup> that they have measured a delay of 100 attoseconds in the emission of electrons ejected from a surface irradiated by light. This is not just the experiment with the best time resolution yet; it is also the first time that attosecond metrology has been applied to a solid, rather than a gaseous, system.

It was only in the 1990s that the trend to ever faster measurements produced laser sources with pulse durations below 5 femtoseconds (a femtosecond is 10<sup>-15</sup> seconds). This is the timescale of the motion of atoms within molecules. Femtochemistry, in which a chemical reaction is followed through its transition state, became big news<sup>2</sup>. But that is now old hat. The attosecond (10<sup>-18</sup> seconds) is the timescale of the motion of electrons within atoms: an electron takes about 150 attoseconds to orbit a hydrogen atom.

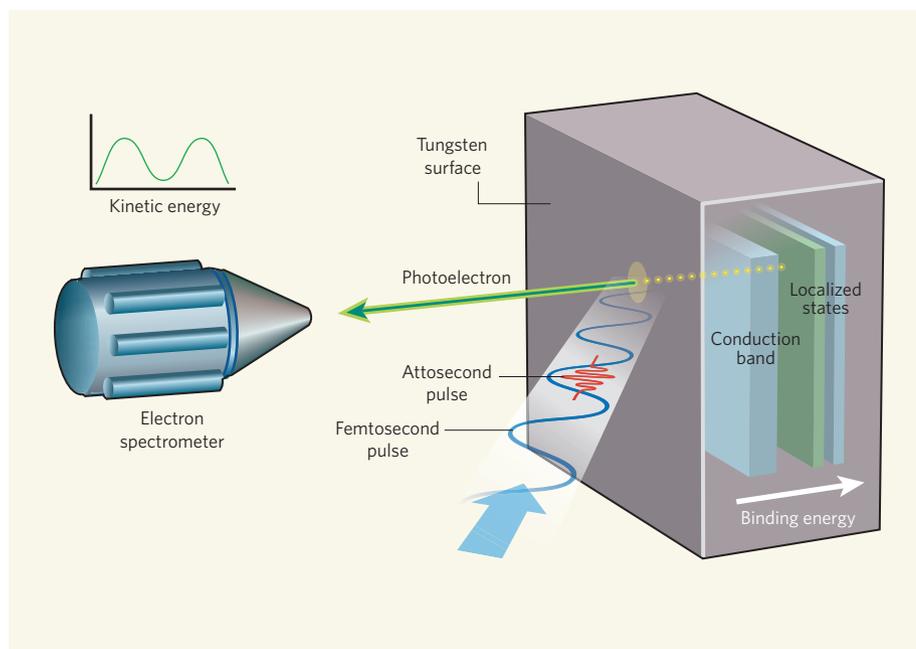
Attosecond pulses are created when intense laser pulses of femtosecond duration are focused into a gas sample. A process known as high-harmonic generation<sup>3</sup> then kicks in to produce light at a range of frequencies that are precisely phased together, creating a train of very short, coherent pulses. In the past few years, the technology has evolved to the point where single pulses just 130 attoseconds long can be produced with tabletop-sized laser systems<sup>4</sup>. These pulses are so short that their frequency (and thus energy) lies in the extreme-ultraviolet or soft-X-ray

portion of the electromagnetic spectrum.

Attosecond metrology has previously been applied to samples of atomic gases to observe excitation processes of electrons such as shake-up and Auger decay<sup>5</sup>. These are essentially 'pump-probe' measurements: an attosecond pulse excites the system, and the intense optical laser field that generated the pulse follows it and is used to sweep up the charged products — much as an oscilloscope streaks an electron beam across the screen to resolve an electrical pulse.

Cavalieri *et al.*<sup>1</sup> focus their 90-electronvolt extreme-ultraviolet pulse at an angle on a tungsten metal surface (Fig. 1, overleaf). The lower-frequency optical pulse that created the attosecond pulse follows along the same path, but its passage can be delayed in steps of 300 attoseconds. Electrons liberated through the photoelectric effect by the first pulse are detected by a spectrometer that measures their kinetic energy. The optical laser field pushes these photoelectrons' energy up or down, depending on the precise position of both the attosecond pulse and the photoelectron in the laser field's cycle.

By varying the time delay between the pulse and the optical field, and measuring the shift in the up and down motion of the energy spectrum, the authors could precisely measure the emission time of the photoelectrons. They were able to distinguish electrons coming from different energy states in the surface, observing that electrons from the more deeply bound core states in the surface were emitted



**Figure 1 | Fast light on a dark place.** In Cavalieri and colleagues' set-up<sup>1</sup>, an extreme-ultraviolet, attosecond pulse is produced from an optical femtosecond laser field, and dislodges electrons from a tungsten surface through the photoelectric effect. The kinetic energy of the electrons, measured in a spectrometer, determines the energy level from which they were ejected. The authors observe a delay of around 100 attoseconds between electrons emitted from the energetically shallow conduction band of the metal and those emerging from deeper localized states.

around 100 attoseconds after those from the conduction band.

The authors' great triumph is to apply the streaking technique to a metal surface, rather than a gas sample. This required an optical field of intermediate strength — intense enough to modify the energy of the

photoelectrons significantly, but not so intense as to create photoelectrons directly.

When it comes to sources of soft X-rays of high brightness, synchrotrons still reign supreme. But the pulse duration of synchrotron light is in the picosecond range, and thus much too slow to observe the dynamics of fast

electrons. Next-generation free-electron-laser facilities, such as FLASH at the DESY research centre in Hamburg, Germany, have pulse durations of around 50 femtoseconds, and will allow images to be obtained of molecular structures during chemical reactions, or protein structures to be determined<sup>6</sup>. The final kilometre of the SLAC linear accelerator at Stanford University is also being converted into a source of femtosecond X-ray pulses, the Linac Coherent Light Source, or LCLS.

But quite apart from the reduced cost, attosecond pulses produced from tabletop lasers have one significant advantage over these very expensive pulsed-X-ray facilities — they are exquisitely synchronized with the laser pulse that produces them. In our facility in Ottawa, we have found that attosecond pulses produced in two separate sources by the same laser are synchronized to even better than an attosecond — in the zeptosecond ( $10^{-21}$  second) range. By contrast, free-electron sources have significant timing 'jitter' that limits their resolution in pump-probe experiments. And, as any physicist living out of a suitcase will tell you, working in one's own laboratory is far preferable to travelling to a distant facility.

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## BIOCHEMISTRY

# Indifferent chaperones

Eckhard Jankowsky

**How do nonspecific enzymes that help to correct RNA folding identify misfolded structures among similar, properly folded RNAs? It seems that careful discrimination has little to do with it.**

Most RNAs adopt defined three-dimensional structures that allow them to function properly. But RNAs also often misfold into inactive structures, which can persist for a long time<sup>1</sup>. Fortunately, RNA chaperone proteins give misfolded RNAs the opportunity to refold correctly<sup>1,2</sup>. However, many RNA chaperones are nonspecific, and correctly folded and misfolded RNA structures tend to be very similar. On page 1014 of this issue, Bhaskaran and Russell<sup>3</sup> describe the way one RNA chaperone, CYT-19, confronts this challenge.

CYT-19 is a member of the large group of DEAD-box proteins — enzymes that are involved in almost all aspects of RNA

metabolism<sup>4</sup>. The name DEAD-box comes from the amino-acid sequence (D-E-A-D in single-letter code) of one of the evolutionarily conserved motifs in these proteins. DEAD-box proteins are often called RNA helicases, because they can unwind short RNA duplexes using ATP as an energy source. But in contrast to canonical helicase enzymes, which unwind duplexes by travelling along the nucleic-acid strands, DEAD-box proteins do not move on the RNA duplexes but load directly to double-stranded regions and then pry the strands apart<sup>5</sup>.

Among the targets of CYT-19 are misfolded group-I intron RNAs, which are catalytic RNAs

that excise themselves from, and subsequently rejoin the ends of, a larger precursor RNA. It is thought that CYT-19 unwinds one or more of the short helices that are the building-blocks of larger RNA structures<sup>6</sup>. Like most DEAD-box helicases, CYT-19 unwinds duplexes indiscriminately and, given that the correctly folded and misfolded group-I introns form almost identical helices, it was not clear how CYT-19 distinguishes between these structures. The general assumption was that, somehow, CYT-19 unravels only the misfolded structures to promote correct folding.

Bhaskaran and Russell<sup>3</sup> make the remarkable observation that CYT-19 unfolds both correctly folded and misfolded structures. However, misfolded RNAs are disassembled at a faster rate. Consequently, at any given time, the misfolded group-I intron RNAs have a better chance of unfolding and refolding correctly (Fig. 1, overleaf).

But why are misfolded RNAs disassembled faster than the correct structures? The authors show that mutated group-I introns that are functional but cannot pack all their helices together in the ultimate higher-order