EDITORS'CHOICE

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ECOLOGY

Migration-Based Monitoring

Counts of birds passing traditional hawk-watching sites provide a means for estimating population trends in migrant raptors. To gauge the effectiveness of such efforts, Farmer *et al*. explore the degree to which the existing network of sites could sample the autumn tracks of 57 adult ospreys (*Pandion haliaetus*). Birds from four breeding areas across the United States were fitted with satellite transmitters. An average of 1.5 relocations per day were observed per bird. To analyze flight trajectories, the authors identified migration paths that connected locations with 3-km- or 6-km-wide corridors. Across North America, 12% of the narrow and 23% of the broader pathways intersected one or more active watch sites; these values rose to 21 and 36% in the eastern region (through which the majority of the continent's population probably passes). Models that assume a conditional random walk between consecutive positional fixes estimate that 95% of the birds' utilization distributions cross at least one observation area. Disparities in mean regional detection probabilities for individuals (east, 34%; midwest, 5.8%; northwest, 4.7%) reflect the relative distribution of hawk watches. The satellite tracks also show southbound ospreys concentrating along narrow fronts and avoiding large water crossings. These results suggest that migration counts do offer a practical means of monitoring populations of the North American osprey and perhaps many other hawks. — SJS

Auk **127**, 863 (2010).

BIOCHEMISTRY

Acting Like Actin

In a dividing cell, DNA must be replicated and accurately partitioned between the two daughter cells. In eukaryotes, microtubules, which are linked to the centromeric DNA by kinetochores, separate the replicated chromosomes with the help of motor proteins. Prokaryotic plasmid-partitioning systems are similar in that they involve an adaptor protein that links DNA to a filament-forming protein; however, no motor proteins are involved, and nucleotide-hydrolysis dependent filament dynamics are responsible for movement. To gain insight into the segregation of the *Bacillus thuringiensis* pBToxis plasmid, Aylett *et al*. determined the structure of two protofilaments of the tubulin/FtsZ-like protein, TubZ, which mediates plasmid segregation. A combination of crystallography and electron microscopy revealed that instead of forming tubulin-like straight protofilaments that organize into microtubules, TubZ forms twisted double filaments that can bundle, reminiscent of structures formed by ParM, an actin-like prokaryotic partitioning filament. That two disparate proteins have evolved to perform a similar function using similar superstructures suggests strong evolutionary constraints on partitioning systems. — VV

Proc. Natl. Acad. Sci. U.S.A. **107**, 19766 (2010).

EVOLUTION

Good for You, Good for Me, Too

In most examples of cooperative breeding, reproductive individuals are assisted by closely related helpers. Although helpers sacrifice their own ability to reproduce, they obtain an indirect fitness benefit from improving survival in their kin (kin theory). Increasingly, however, cooperative breeding has been revealed among unrelated individuals. In greater anis (*Crotophaga major*), multiple pairs of birds will cooperate to build nests and raise and defend young. Riehl has now shown that these pairs are relatively unrelated, thus cooperation cannot be explained by kin theory. Instead, she finds that the individual fitness of all the pairs is increased when pairs cooperate, despite initial reproductive competition generated during egg-laying. Three pair groups were able to obtain and defend prime nesting sites better than two pair groups, and pairs attempting to breed alone failed in all observed instances. Furthermore, there was no cost to individual fitness on the basis of the number of eggs laid, most likely because females changed their laying order across years. In unrelated cooperative breeders, what's good for "the many" is most likely also good for "the one." — SNV

Proc. R. Soc. London Ser. B 10.1098/rspb.2010.1752 (2010).

GEOCHEMISTRY

Reflecting on Mica

Trace metals in soils and sediment predominantly exist as either tiny mineral grains or mobile aqueous ions in pore water. In both cases, adsorption and desorption reactions at the surface of mineral grains control their fate and transport through the subsurface. Because the size of ions and strength of the surrounding hydration shell are highly variable, predicting the way in which metals are distributed even at one specific mineral/water interface is challenging. To systematically address this question, Lee *et al.* measured—using an X-ray reflectivity technique sensitive enough to determine the thickness of a single layer of water—the

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manner in which divalent metal ions adsorbed on a hydrated muscovite surface. As expected, metal ions with weak hydration shells lost water and bound tightly to muscovite within just 2.5 Å; stronger hydration shells remained intact, pushing other metal ions further out (3.5 to 4.5 Å from the surface). The reflectivity profiles also revealed, surprisingly, an unexpected additional broad layer of metal ions 5 to 10 Å away from the mineral surface. Computational models of similar interfaces may need to be adjusted to account for this extended layer. — NW

Langmuir **26**, 16647 (2010).

PHYSICS

Hiding in the Pseudogap

When cuprate superconductors, which can conduct electricity without resistance up to temperatures on the order of 150 K, were first discovered almost 25 years ago, it was expected that the explanation for their extraordinary properties was around the corner and would lead to even higher transition temperatures T_c. Today this mechanism remains a mystery; however, most researchers agree that the so-called pseudogap region, which lies above T_c but is characterized by a non-zero excitation gap that disappears at a higher temperature T^*, is key to understanding the entire phase diagram. Along the doping axis, the pseudogap region borders an antiferromagnetic phase, the remnants of which can be detected by neutron scattering as a resonance centered around the corner of the Brillouin zone. Li *et al.* use polarized neutron scattering to detect another magnetic excitation that is present at all wave vectors and, surprisingly, has an integrated spectral weight an order of magnitude higher than that of the resonance. Because the studied compound, $HgBa_2CuO_{4+\delta}$, is thought to be representative of the cuprates, and the new magnetic excitation appears at the same T^* determined from prior transport and neutron diffraction measurements, it is tempting to interpret this result as a corroborating piece of evidence that a true phase transition, rather than a crossover, takes place at T^*. — JS

Nature **468**, 283 (2010).

CLIMATE SCIENCE

The American Sink

Understanding how fast the concentration of carbon dioxide in the atmosphere will rise as we continue to burn fossil fuels depends on how well we know what fraction of emissions is absorbed by the sea and by the terrestrial biosphere. Studies have suggested that North America constituted a terrestrial carbon sink during the past several decades, although how much carbon it has accumulated remains debatable. Crevoisier *et al.* have now estimated land-atmosphere fluxes across North America during the period from 2004 to 2006 by balancing the inflow and outflow of carbon dioxide from the troposphere, using a simple budgeting approach and vertical profiles of atmospheric carbon dioxide to construct the distribution over the continent in three dimensions. They find that the coterminous United States provided a moderate sink and that the distribution of carbon uptake agrees well with agricultural and climate patterns during that time. Their technique thus also provides a potential independent method to link regional carbon uptake to climate drivers. — HJS

Proc. Natl. Acad. Sci. U.S.A. **107**, 18348 (2010).

SIGNAL TRANSDUCTION

Cell as Corporation

Systems biology provides insight into the complex regulatory networks within a cell, with the hope that such analysis will yield insight into how biological control systems work and how they may be modified for therapeutic benefit. Some network models suggest that the extent of connectivity of a transcriptional regulator indicates the essentiality of that protein in that system. Bhardwaj *et al*. propose an alternative view. They organized transcription factors in yeast or bacteria in a pyramidal hierarchy and then used information regarding the effects of the various factors on cell fitness to determine that the importance of a transcription factor is more related to its placement in the hierarchy than to its total direct connectivity to target genes. Thus, proteins at the top of the hierarchy exerted the greatest influence over cell fitness. The relative ease of testing network perturbations in biological systems suggests that this type of analysis may also be useful in understanding similar corporate, government, or social networks, where one cannot so easily intervene. — LBR

Sci. Signal. **3**, ra79 (2010).

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