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In This Issue

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COMPUTER SCIENCES, SOCIAL SCIENCES

Geography and population density in online social networks

In online communities and other social networks, David Liben-Nowell *et al*. report that any two members can usually find a connection with only a few degrees of separation, partly because individuals tend to optimize friendships geographically.

Short chains in social networks, based on geography.

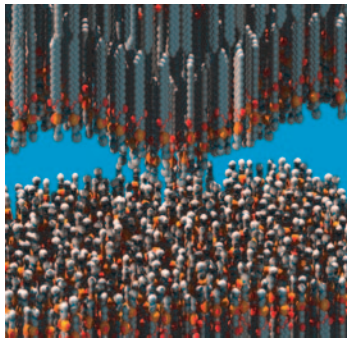
Sociological experiments have shown that social networks are often "navigable small worlds," in which any person, given only meager information about an arbitrary target person's geographic location and occupation, can likely transmit a message to the target through a short chain of intermediate friends. Liben-Nowell *et al*. explored the role of geography alone in routing within a large, online social network. The researchers used data from ≈500,000 members of the LiveJournal online community, who made available their state and city of residence, as well as a list of other LiveJournal friends. Message-forwarding simulations based on these data showed that a routing strategy based solely on geography could successfully find short chains in the network. The researchers proposed a model relating geography and social-network friendship that accounts for variances in population density and showed that short connections can be made in every network exhibiting their friendship/geography relationship. — R.N.

"Geographic routing in social networks" by David Liben-Nowell, Jasmine Novak, Ravi Kumar, Prabhakar Raghavan, and Andrew Tomkins (see pages 11623–11628)

PHYSICS

Characterization of a single floating lipid bilayer

Jean Daillant *et al.* characterized a single lipid bilayer floating near a second bilayer supported on a silicon substrate, facilitating the comparison of experimental measurements with theoretical predictions. Lipid bilayers are increasingly being used in biophysical studies as a controlled, idealized model system of cell membranes. Most measurements of the structure and fluctuations of bilayers come from experiments with vesicles or multilayer stacks. The authors first determined the bilayer structure by examining its electron density profile, corresponding molecular dimensions, and variations across the bilayer gel–liquid transition. The scattering was compared with that of a two-dimensional theoretical membrane, from which the authors could then deduce the main physical parameters governing the bilayer height fluctuations. Such fluctuations include wall attraction, surface tension, and bending modulus change at the bilayer gel-to-fluid transition. According to the authors, this reconstruction is consistent with the picture of a nearly free bilayer floating a few nanometers above a fixed layer. — R.N.



Single lipid bilayer floating above second bilayer.

"Structure and fluctuations of a single floating lipid bilayer" by J. Daillant, E. Bellet-Amalric, A. Braslau, T. Charitat, G. Fragneto, F. Graner, S. Mora, F. Rieutord, and B. Stidder (see pages 11639–11644)

ECOLOGY, GEOLOGY

Asynchronous sloth extinctions on American continents vs. islands

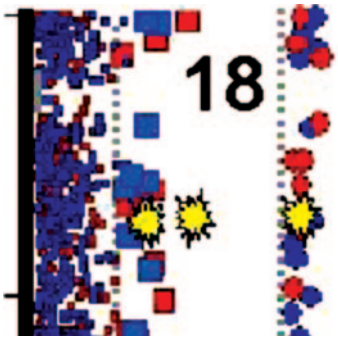
Based on radiocarbon dating of fossil bones, David Steadman *et al*. report that human arrival appears to correlate with mass sloth extinctions in the Americas. During the late Quaternary period, many large mammals became extinct throughout the western hemisphere, including 90% of the genera of the xenarthran suborder Phyllophaga (sloths). If human effects such as predation were responsible for these losses, the last appearance dates for sloths in the Americas should coincide with human arrival. Alternatively, if climate change were responsible, the youngest radiocarbon dates should fall within the last glacial–interglacial transition (9,000–15,000 years ago). On the American continents, however, human arrival coincided with climate change, thus obscuring the cause–effect relationship. Steadman *et al*. radiocarbon-dated fossil bones of West Indian island sloths and compared these with existing dates of sloth bones or dung from the continental Americas. The last appearance dates for extinct sloths were found to be 11,000 years B.P. in North America, 10,500 years B.P. in South America, and 4,400 years B.P. on West Indian islands. The island dates do not correspond with climate changes but rather appear to correlate with human migration into these lands, the authors say. — R.N.

Carbon-dated fossil bones of extinct sloth from Haiti.

"Asynchronous extinction of late Quaternary sloths on continents and islands" by David W. Steadman, Paul S. Martin, Ross D. E. MacPhee, A. J. T. Jull, H. Gregory McDonald, Charles A. Woods, Manuel Iturralde-Vinent, and Gregory W. L. Hodgins (see pages 11763–11768)

MEDICAL SCIENCES

Mining the genome for addiction genes



Chromosome 18 distribution of abuser/control SNPs.

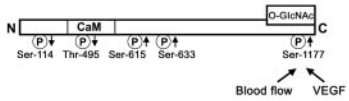
Using association genome scanning, Qing-Rong Liu *et al.* identified multiple genetic loci believed to be involved in drug addiction. Unlike traditional gene identification methods for complex disorders, association genome scanning does not require the participation of family members and allows pooling of multiple samples. These attributes may help preserve confidentiality and reduce costs. To determine the efficacy of this method in identifying potential drug addiction genes, Liu *et al.* used 10k SNP microarrays to analyze pooled DNA samples from polysubstance abusers (addicts who abuse multiple drugs) and control subjects. The authors identified 38 candidate genetic loci displaying robust allele frequency differences between abusers and controls, including an alcohol/acetaldehyde dehydrogenase gene cluster and genes involved in metabolism, cell signaling, gene regulation, development, and cell adhesion. Because many of the genetic loci were comparable to linkage and association results from other methods, this study may validate association genome scanning as a reliable and cost-effective strategy to identify the genetic underpinnings of complex disorders. — M.M.

"Pooled association genome scanning: Validation and use to identify addiction vulnerability loci in two samples" by Qing-Rong Liu, Tomas Drgon, Donna Walther, Catherine Johnson, Oxanna Poleskaya, Judith Hess, and George R. Uhl (see pages 11864–11869)

MEDICAL SCIENCES

Mechanism of erectile dysfunction in diabetes

Biljana Musicki *et al.* demonstrate that the glycosylation of endothelial nitric oxide synthase (eNOS) by the monosaccharide *O*-GlcNAc inhibits proper erectile function in rats with type 1 diabetes. The phosphorylation of eNOS at Ser-1177 is an important step in the promotion of tumescence. The enzyme's activity is regulated by extracellular stimuli including electrical stimulation, shear stress, and VEGF signaling. Previous research has shown that hyperglycemia-induced *O*-GlcNAc modification inhibits eNOS activity in blood vessels, but the physiologic relevance of this modification in diabetic vascular tissues is unclear. Musicki *et al.* induced diabetes in rats and examined the penile tissues of the animals. Increased levels of eNOS-linked *O*-GlcNAc were detected, and significant decreases in the levels of both Ser-1177-phosphorylated eNOS and phosphorylated Akt, the upstream mediator of eNOS phosphorylation, were observed. Although electrical stimulation increased blood flow in penile tissue of control and diabetic rats, an increase in activated eNOS in diabetic rats was not seen. VEGF administration and shear stress were similarly ineffective in the diabetic animals, with rates of full erectile status decreased by 40%, magnitude of erectile response decreased by 30%, and tumescence rise time decreased by 70%. — F.A.



Model of eNOS phosphorylation sites and proposed *O*-GlcNAc site.

"Inactivation of phosphorylated endothelial nitric oxide synthase (Ser-1177) by O-GlcNAc in diabetes-associated erectile dysfunction" by Biljana Musicki, Melissa F. Kramer, Robyn E. Becker, and Arthur L. Burnett (see pages 11870–11875)