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channels as well as more stagnant ones, consistent with macroscopic observations. — MSL
J. Non-Newtonian Fluid Mech. **143**, 59 (2007).

CLIMATE SCIENCE

Melting Faster

Observations of the extent of Arctic sea ice in September—at the end of the melt season, when ice coverage is at its annual minimum—have shown a large decline over the past several decades, consistent with current qualitative understanding of natural variability and the effects of a warming climate. Nearly all climate models predict that September Arctic sea ice extent will continue to decline through the 21st century, largely in



response to rising concentrations of atmospheric greenhouse gases. How well do observations and models agree, though? To answer that question, Stroeve *et al.* compared the output of the more than a dozen models participating in the Intergovernmental Panel on Climate Change Fourth Assessment Report that calculated sea ice. They found that nearly all of the models overestimated annual minimum Arctic sea ice area, in many

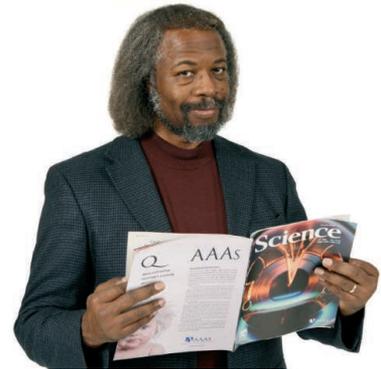
cases by large amounts. These findings have two important implications: first, that the effect of rising greenhouse gases may have been more important than has been believed; and second, that future loss of Arctic sea ice may be more rapid and extensive than predicted. — HJS
Geophys. Res. Lett. **34**, L09501 (2007).

VIROLOGY

Shifting Landscapes

Influenza epidemics are thought to emerge as a result of escape from host immunity as the viral genome mutates along a trajectory of antigenic drift. However, a puzzle for influenza epidemiologists is the limited diversity of observed antigenic types. Recker *et al.* present a model in which successive antigenic types emerge independently of the mode or tempo of mutation in a cyclical manner. The model is consistent with data from hemagglutination inhibition assays of H3N2. The authors suggest that rather than virus mutation driving the epidemiology of influenza, the changing landscape of host population immunity governs whether and when epidemics emerge. Much of the epidemiology of influenza, such as the re-emergence of an antigenic type, is probably missed in routine clinical data based on detection of symptoms. For instance, data from poultry workers chronically exposed to avian influenza suggest that they enjoy a significant degree of cross-protection against the lethal effects of H5N1. This shift in perspective could have important implications for the way we monitor influenza virus for epidemic prediction and vaccine design. — CA
Proc. Natl. Acad. Sci. U.S.A. **104**, 7711 (2007).

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Jim Gates is a theoretical physicist and professor at the University of Maryland. He's also a member of AAAS.

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<< Who You Are Versus Where You Are

The ability to identify essential components by network analysis may provide one means of ranking targets for disrupting specific cellular processes. Yu *et al.* have assessed the relative importance of being a hub (that is, being a highly connected node) in comparison to being a bottleneck, a node that serves as a conduit for nonredundant paths through the network. These attributes do overlap, but they were able to find all four types of nodes in large-scale protein-protein interaction maps: hub-bottleneck, nonhub-bottleneck, hub-nonbottleneck, and nonhub-nonbottleneck. For instance, in signaling networks, hub-bottlenecks and nonhub-bottlenecks were likely to be encoded by essential genes, whereas hub-nonbottlenecks were not. Thus, being a bottleneck may be a better indicator of necessity than the degree of connectedness. A refinement of the nonhub-bottleneck nodes was achieved by dividing them into those that participate in permanent interactions, such as those that hold multisubunit complexes together, versus those that mediate transient protein-protein interactions. Not surprisingly, permanent nodes were more likely to be encoded by an essential gene than were the transients. Furthermore, the authors suggest that nonhub-bottlenecks are key to pathway crosstalk. Cak1p, which is encoded by an essential gene in yeast and is a cyclin-dependent protein kinase-activating kinase, is offered as an example of a nonhub-bottleneck that is the critical link between two signaling pathways: regulation of the cell cycle and sporulation. — NRG
PLoS Comp. Biol. **3**, e59 (2007).