GEOPHYSICS

Fine-Scale Modeling of Global Plate Tectonics

Powerful numerical methods are enabling the creation of fine-grained models of Earth's dynamic geology.

Thorsten Becker

The tectonic motions on the surface of Earth and much of its geological activity can be explained as a part of mantle convection. Relatively rigid lithospheric plates form the top, cold boundary layer of the convecting mantle, and the potential energy released during the cooling of the planet is balanced by viscous dissipation during deformation of mantle rocks (1, 2). A theory of plate tectonics has to account for compositional and rock strength variations, both of which are affected by the dynamics of convective flow. Such behavior can lead to nonlinear feedback and result in heterogeneity, possibly down to sub-meter scale. On page 1033 of this issue, Stadler *et al*. (3) present a groundbreaking numerical model for plate tectonics that should help to resolve questions relating to how the strongly deforming and narrow plate boundaries form and evolve.

Stadler *et al*. use an adaptive mesh refinement (AMR) finite element method with variable resolution. Such techniques are widely used in fields such as engineering and physics, but have not been previously used for global mantle dynamics with such sophistication. What makes AMR valuable for studying the challenging continuum mechanics problems presented by plate tectonics lies in the details. Stadler *et al*. show how to best apply AMR methods on massively parallel supercomputers, in particular minimizing the additional overhead that arises from the mesh refinement stage of the solution process (see the figure). The newly afforded resolution allows the role of nonlinear rock creep laws for plate motions to be explored in detail. They focus on the important role of subduction zones where the oceanic slabs plunge back into the mantle, as reflected in the formation of steep trenches in the ocean floor and deep seismicity.
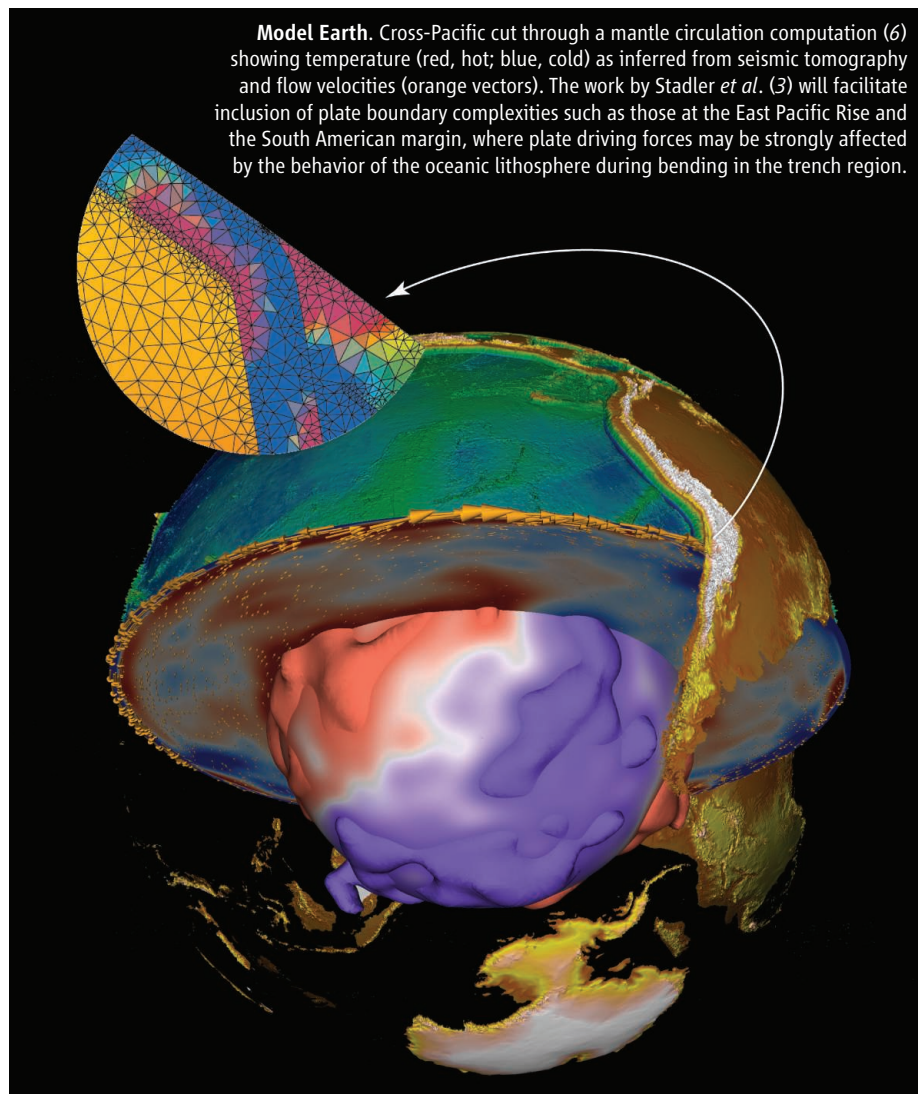
AMR allows inclusion of more realistic geometries for the subducting lithosphere alongside narrow plate boundaries, and on top of large lateral variations in strength in the mantle underneath the plates, such as those expected as a result of volatile release and melting below volcanic arcs.

The role of plate strength at subduction zones, where the lithosphere dives down into the mantle as slabs, is one example where previous models lead to opposite conclusions. Slabs appear to be the dominant control on plate speeds (4), but how slabs pull the plates and transmit deformation to the surface in detail is still unclear. On the basis of global, lower-resolution models, the asymmetry between fast moving oceanic and slow continental plates has been interpreted such that a one-sided slab pull is transmitted through a stiff slab (5). Alternatively, the mantle underneath oceanic plates may be weaker than beneath continents, which may explain plate motions and other aspects of plate tectonics with relatively weak slabs (6). How slabs pull the plates and move the trench that forms at sites of plate convergence with respect to the lower mantle appears to hinge on how the work done by bending the plate at the surface, and throughout the upper mantle, compares to the total viscous dissipation. If slab bending is important, then Earth's thermal evolution may be strongly controlled by the details of the temperature-dependent structure of the oceanic crust and lithosphere (7). Regional modeling can address slab dynamics and

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Model Earth. Cross-Pacific cut through a mantle circulation computation (6) showing temperature (red, hot; blue, cold) as inferred from seismic tomography and flow velocities (orange vectors). The work by Stadler *et al*. (3) will facilitate inclusion of plate boundary complexities such as those at the East Pacific Rise and the South American margin, where plate driving forces may be strongly affected by the behavior of the oceanic lithosphere during bending in the trench region.

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trench motions at high resolution but has also led to contrasting interpretations of the role of slab bending (*8, 9*). One reason for the disagreement between studies may be that large-scale flow effects and the lower mantle were not fully included in the regional models. The now more complete AMR models can test all of the important ingredients at both local and global scales. The initial results from Stadler *et al.* suggest relatively high viscous dissipation in a weak subduction margin, but a relatively small contribution of slab deformation to the total mantle dissipation budget.

In the AMR models, plate speeds can be explained well when only upper-mantle slabs are included as driving density anomalies. More surprisingly, Stadler *et al.* found that the model fit degrades when additional density anomalies in the lower mantle, as inferred from seismic tomography, are incorporated. Why the new computations show this behavior, which contrasts with findings from previous, lower-resolution models, is somewhat unclear. How slab strength

may have coupled to plate tectonic motions now and in the early Earth (*10*) remains to be fully explored. Evaluating the distribution of viscous dissipation and the slab force transmission from the faulted margin at the trench down into the deep mantle with further, high-resolution modeling should help to improve our understanding of the causes and consequences of reorganizations of plate motions and heat transport over geological time scales.

Models that can track dynamic properties of Earth's evolution are the next challenge for AMR methods. These could be used to tackle challenging problems such as the formation of plate boundaries during which strain localization processes may require locally very high resolution. There are some potential issues with applying AMR to dynamically evolving thermochemical convection problems that are related to nonlinear coupling between the equations governing mantle flow and temperature. However, if those are overcome and the method proves

to be robust and widely available, global computational geodynamics might never look back.

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IMMUNOLOGY

Prime, Boost, and Broaden

Robert W. Doms

A combined immunization approach represents a possible strategy for developing a "universal" flu vaccine.

The need to produce an effective seasonal flu vaccine every year, coupled with the recent H1N1 influenza virus pandemic, underscores the importance of developing a universal flu vaccine. However, a major obstacle is the ability of the virus to evade the immune system, accumulating mutations that allow it to avoid recognition by neutralizing antibodies. The continual evolution of such mutations results in an ever-changing variety of circulating virus strains that ultimately render a vaccine ineffective. Each year, components of the seasonal flu vaccine are altered in the hope of matching these to virus strains that will evolve and circulate in humans in the months to come (*1*). This results in vaccines with variable efficacy—as recently as the 2007/2008 flu season, the seasonal vaccine was a poor match for circulating strains and afforded little protection from infection. In addition to mutations, entirely new viral proteins can be introduced into human viruses from the large reservoir

of avian influenza strains. Thus, it is evident that a vaccine capable of eliciting antibodies that neutralize a much broader array of virus strains is needed. On page 1060 of this issue, Wei *et al.* (*2*) suggest that changing the way in which influenza virus vaccines are delivered, rather than the vaccine components themselves, may elicit antibodies that could confer protection from diverse viruses for years.

Immunization with the seasonal influenza virus vaccine evokes antibodies that bind to discrete sites in the globular head domain of the viral HA protein (see the figure). Influenza virus strains are grouped into subtypes that are numbered sequentially after the HA molecule they express (H1, H2, H3, etc.). The viral neuraminidase protein (the "N" in "H1N1") plays a negligible role in virus neutralization. In recent years, H1 and H3 virus strains have circulated in humans, with occasional localized outbreaks of H5 and H7 viruses from avian sources. The most commonly used seasonal vaccine contains representative, inactivated H1 and H3 viruses, which give rise to subtype-specific antibodies that neutralize H1 and H3 viruses. These are genetically similar
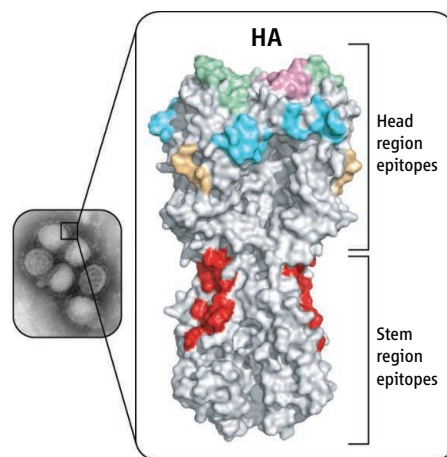
Antibody recognition. Most antibodies against influenza A virus (inset shows the 2009 H1N1 strain) bind to the highly variable part of the hemagglutinin (HA) glycoprotein at the surface of the virus particle (head region). In the H1 subtype, these antibodies recognize four major sites (Sa, Sb, Ca, and Cb are shown in green, pink, cyan, and yellow, respectively). The HA structure of the 2009 H1N1 virus is shown (PDB code 3LZG). Antibodies that neutralize multiple strains both within a virus subtype and from different subtypes bind to a highly conserved region (red) in the stem region of HA.

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