Representing Ocean Eddies in Climate Models

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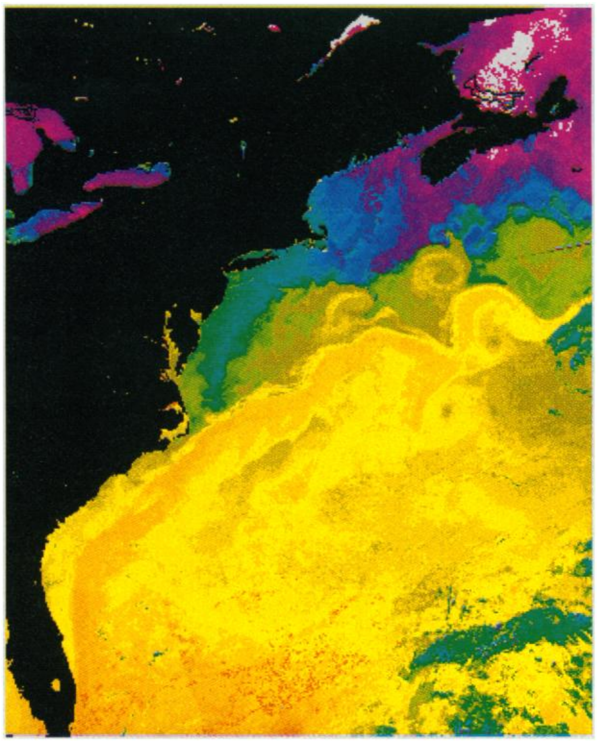
Numerical models of the Earth's atmosphere and oceans are used to simulate the behavior of the climate system, to assess likely impacts of greenhouse warming, and recently, to predict some aspects of climate fluctuations on time scales up to a year (*1*). Typically, the ocean is represented by a large number of grid boxes some hundreds of kilometers wide and tens to hundreds of meters deep. The equations of motion are marched forward in time for each grid box, in steps whose length must be decreased if the grid length is decreased. As a result, cutting grid length in half in every direction increases computational cost by an order of magnitude. Developing models that are fast enough, even on massively parallel computers, to run long climate simulations with smaller grid size is thus widely regarded as one of the grand challenges for scientific computing. But there is an even greater challenge to increasing the fidelity of climate models: improving the representation of the aggregate effect of processes that occur at scales smaller than the model grid size. In this issue, Danabasoglu, McWilliams, and Gent (*2*) report a striking example of such efforts helping to solve several endemic problems in a global ocean model.

No matter how small the model grid, there are always turbulent motions and physical processes occurring at still smaller scales. These smaller scale processes are influenced by the larger scale motions and, in turn, have a bulk effect on the large scales. The term "parameterization" refers to the representation of these bulk effects of the subgrid scales in terms of large-scale variables and a few parameters. An example is molecular diffusion of heat or dissolved substances (such as salt) through an unstirred fluid. Representing this in terms of the gradient of temperature or salinity and a molecular diffusivity coefficient is vastly more useful than calculating each of the molecular collisions individually (the small scales) to find the net effect on the large-scale variables, temperature and salt concentration.

In modeling the oceans and atmosphere, one must also account for diffusion of heat and salt or other substances (known as "tracers" in oceanography) except that the relevant small-scale motions are eddies and turbulence. In addition to heat transport by currents at large scales, such as the Gulf Stream, ocean eddies can (on average) also transport heat because eddy flow across the large-scale temperature gradient tends to mix warmer and colder water. The ring-like structures to either side of the Gulf Stream (see figure) are examples of what are termed "mesoscale" eddies. For grid sizes typical of most present-day ocean climate models, these features are not resolved and therefore must be included in the parameterized scales. Parameterization of eddy transports, based on physical concepts of what governs eddy creation and motion, has previously been examined in oceanographic contexts (*3*) and has a long history in atmospheric sciences (*4*). The parameterization of eddy heat and tracer transport presented by Danabasoglu *et al.* (*2*) is arguably the most successful ever to be used in a global ocean model. They implemented an updated version of a parameterization developed by Gent and McWilliams (*5*) into a standard global ocean model and demonstrate dramatic improvements in the ocean thermal structure, north-south mass and heat transports, and circulation in several regions.



Sea surface temperature in the western North Atlantic. Orange and yellow indicate warm water; purple, blue, and green show cold water. The Gulf Stream leaves the coast at Cape Hatteras, meanders, and small eddies form. Although the eddies are constantly changing, they have an average effect on the ocean climatology. [Image courtesy of T. Lee, Massachusetts Institute of Technology; data courtesy of R. Evans, University of Miami]

The appeal of the improved parameterization derives not only from its success but also from the simple and plausible physical picture upon which it is based. Two key ingredients enter: the dynamics of eddy creation, and the effect of the eddies on the distribution of temperature, salinity, and other tracers like radiocarbon. Eddies arise because they can draw on the potential energy that is available where surfaces of constant density (isopycnal surfaces) slope steeply. This occurs where currents are strong, like in the Gulf Stream.

The creation of eddies depletes the energy source; hence, the slope of the isopycnals is reduced. The crucial ingredient of the Gent-McWilliams parameterization is that isopycnals are flattened without changing the density of individual water parcels, whereas conventional parameterizations, such as horizontal diffusion, lead to strong departure from this behavior.

Once created, the eddies are believed to slide along isopycnal surfaces, and their net effect on the large-scale distributions of temperature and tracers is to mix them within the isopycnals. Isopycnal mixing had been implemented into an ocean model before (*6*), but the dynamical part linked to the creation of the eddies had been left out. This led to such significant numerical problems that the isopycnal mixing assumption had to be severely compromised. The parameterization of Danabasoglu *et al.* can be interpreted (*7*) as producing an eddy transport velocity that is added to the large-scale velocity carrying the tracers. This identification helps ensure many desirable properties of the scheme, such as overall conservation of heat and tracers.

This more sophisticated parameterization may have solved one of the most vexing problems in the coarse-resolution modeling of the North Atlantic circulation, that of weak north-south mass transport, and hence, weak heat transport (*2*, *8*). The traditional assumption of horizontal, as op-

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posed to isopycnal, eddy mixing led to spurious upwelling from the abyss into the top kilometer of the ocean, inshore of the Gulf Stream, in virtually all North Atlantic models (*8*). As a consequence, the modeled southward flow of deep water near the western boundary was too weak. This problem appeared even when a numerical ocean model was fitted to observed temperature and salinity distributions with data assimilation (*9*), a statistically optimal way of combining a model and observations. In the Antarctic Circumpolar Current (a region dominated by eddy activity), circulation changes attributable to the new parameterization result in better placement of regions where surface waters sink into the deep ocean. Although one cannot expect a parameterization to fix all problems associated with large grid size—for instance, narrow currents like the Gulf Stream cannot be accurately represented—the list of improvements outlined by Danabasoglu *et al.* (*2*) is noteworthy for a single change to a model.

Parameterizations, sometimes disparaged as a necessary evil, are unavoidable for many climate processes. For instance, even a billionfold increase in computational power would not allow global atmospheric models to resolve cloud scales. However, in the case of mesoscale eddies in the ocean, small–grid-size models are becoming available (*10*) that resolve at least some portion of the mesoscale eddies explicitly. Why then is the Danabasoglu *et al.* work so exciting?

One answer is that smaller grids merely shift the problem to smaller scales and aspects of the new parameterization may also be useful for smaller eddies. A second answer is that a good parameterization is often more useful for understanding large-scale processes than is a simulation of small-scale details, as in the example of molecular diffusion. When diagnosing results in an eddy-resolving model, it can be helpful to contrast explicit eddy transports to parameterized estimates. But the most persuasive answer is that a good parameterization enables experimenters to work with models of various levels of complexity and computational requirements. Even when computational advances eventually make eddy-resolving models practical for routine multidecadal climate runs, models with parameterized eddies will remain very much in use. They will be used for examining still longer time scales, for the huge task of assimilating observations into the models, and for understanding the results of more costly models. The task of understanding phenomena once they have been simulated is a thought-intensive task that is facilitated by building a hierarchy of simpler models in which the phenomenon can be more easily examined. For example, McWilliams and Gent (*11*) examine the effect of their parameterization on the Gulf Stream in a model far simpler than the one considered here. The project that led to the results reported in this issue (*2*) thus epitomizes an approach to climate modeling that is complementary to brute force numerical simulation.

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Architectural Transcription Factors

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In textbooks, eukaryotic transcription factors bind to a specific DNA sequence and stimulate transcription by directly interacting with the basal transcriptional machinery. Different parts of the protein usually recognize DNA and activate transcription, such that removal of the activation domain prevents transcriptional stimulation. In spite of the strength of this paradigm, a growing number of DNA binding proteins are being characterized that stimulate transcription from specific genes, yet lack distinct transcriptional activation domains. A large family of these transcription factors function primarily through their control of DNA conformation. These proteins are architectural; they provide a correct framework for the rest of the transcriptional machinery to operate. A dramatic example of this phenomenon is described in this week's issue by Bazett-Jones *et al.* (*1*) in which a dimer of the transcription factor specific for the large ribosomal RNA genes, UBF, is shown to wrap more than 180 base pairs of promoter DNA into a distinct structural unit. UBF appears to position two dispersed regulatory elements into the optimal spatial arrangement for transcriptional enhancement.

UBF represents a family of transcription factors that contains a common DNA binding motif. Although this high mobility group (HMG) domain was originally described within the abundant nonhistone proteins HMG 1 and 2 (*2*), specific HMG domain proteins have now been defined that control lymphoid transcription, mating type switching, and sex determination (*3*). The HMG domain consists of an L-shaped arrangement of three α helices, with two independent DNA binding surfaces on the outside of the L at right angles to each other (*4*). A single HMG domain may cover 20 base pairs at a specific binding site and can potentially distort the DNA molelcule through as much as 130° (*3*). Proteins with a single HMG domain associate with specific DNA sites relatively weakly, probably because of the energy required to direct the distortion of inflexible DNA. However, other proteins often contain several HMG domains, which form more stable complexes with DNA.

The UBF protein contains five HMG domains flanked by an amino-terminal dimerization motif and an acidic carboxyl-terminal tail. Any adjacent pair of HMG domains will bind to DNA; however, the selectivity of binding is conferred by the three domains closest to the amino terminus (*5*, *6*). Each UBF dimer contains 10 HMG domains, a binding site that potentially includes up to 200 base pairs of DNA. This extended region contains a site of DNA distortion every two turns of the double helix as a consequence of the binding of an HMG domain. Because these sites occur on the same face of the helix, DNA is bent into a superhelical turn around the contiguous HMG domains. Deoxyribonuclease I digestion of UBF-DNA complexes reveals a 10– to 11–base pair periodicity of cleavage that is reminiscent of the restricted

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