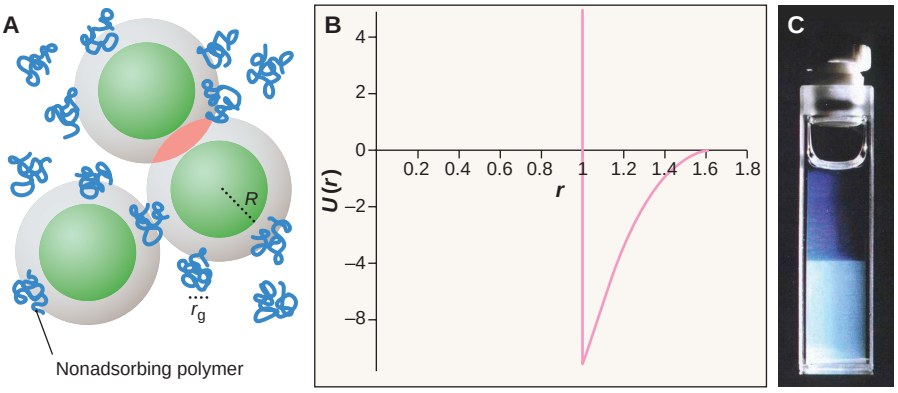


Colloidal coexistence. A schematic illustration of the origin of the polymer-induced depletion attraction between hard spheres. (**A**) The centers of mass of the polymer coils with radius of gyration (r_g) (blue) are excluded from a thin shell (white) surrounding each particle of radius R (green). There is no polymer in the lens-shaped region (red) between two nearby particles, leading to a net osmotic force pushing them together. (**B**) The depletion potential, $U(r)$, for a polymer that is ~60% the size of the colloids (with diameter $2R$ set to unity). (**C**) A colloid-polymer mixture showing coexisting colloidal liquid (lower) and colloidal vapor (upper) phases. Note the macroscopically sharp interface. Aarts *et al.* (*1*) obtained images of the interface in a similar system at near–single-particle resolution.

verified that attraction is necessary but not sufficient for vapor-liquid coexistence. An attraction of long enough range is needed—something like a quarter of the size of the particles or larger. Thus, by adding sufficiently large polymers to a suspension (Aarts *et al.* used polymers that were 60% the size of their particles), it is possible to create colloidal vapor-liquid coexistence—thermodynamically stable phases of dilute and dense disordered arrangements of diffusing particles, separated by an interface (see the figure, C).

The colloidal vapor-liquid interface has many of the properties one expects from its molecular analog. For example, Wijting *et al.* have demonstrated that the colloidal interface shows a curved meniscus next to a wall as a result of capillary rise (*8*). Now Aarts *et al.* have studied the capillary waves at this interface. To understand why their work is feasible and beautiful, we need to know that the surface tension scales as the inverse square of the particle diameter, d. Thus, colloids, with $d \approx 10$ nm to 1 μm, give very low values of surface tension indeed, from micronewtons per meter down to nanonewtons per meter (compare this with the surface tension of water at 70 mN/m). This made the task of Wijting *et al.* (*8*) rather difficult because capillary rise is proportional to surface tension. On the other hand, the low surface tensions in colloid-polymer mixtures mean that the capillary wave amplitude and velocity have values of ~0.1 to 1 μm and ~1 to 10 μm/s, respectively, in the system of Aarts *et al.* This made it possible for them to catch capillary waves "in the act" by real-time imaging using fluorescent particles and a confocal microscope.

Their observations confirmed various features expected of classical capillary waves, including a dramatic increase in amplitude near the critical point [see the bottom part of figure 1 in (*1*)] and certain predictions for the interfacial roughness and dynamics. The full power of this approach, however, emerges with the observation by Aarts *et al.* of capillary waves roughening up the surface of droplets, leading to their coalescence [figure 3C of (*1*)]. That capillary waves have this role has long been suspected; their small amplitudes and fast speeds in molecular systems, however, have hampered experimentation.

The longer term significance of the work of Aarts *et al.* lies in the possibilities it opens up. An optical microscope can resolve submicrometer features. By using somewhat larger particles, one could image capillary waves down to the single-particle level. In this case, the depletion attraction has strictly finite range, so we may expect that the decrease in surface tension with length scale observed in molecular systems (*6*) will not occur in the colloidal system. On the other hand, Wijting *et al.* have found evidence for wetting transitions in a similar system (*8*); high-resolution imaging should be a powerful technique for investigating these transitions in the future. In any case, Aarts *et al.* have demonstrated again the continued fecundity of Einstein's and Perrin's approach to "colloids as (big) atoms."

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ECOLOGY

Domains of Diversity

Stuart L. Pimm and James H. Brown

Leaving an English winter, Charles Darwin was soon writing gushing prose to his family about Brazil's biodiversity (*1*). He expected such variety because for centuries naturalists had returned from the tropics with unusual and colorful specimens. Yet, even today, pointed disagreements persist about why the tropics have more species than other latitudes. The many hypotheses (*2*–*4*) reflect three deeply different approaches. Two date back to the time of Wallace (*2*): One stresses ecological processes, such as a location's temperature and rainfall, the other historical factors, such as whether a region was covered in ice during recent glaciations. The third approach is a newcomer that explains species richness as a simple, statistical consequence of the observation that some species have large geographical ranges, whereas others have small ranges. This explanation echoes a classic debate about the patterns of communities (*5*, *6*). (By "pattern," ecologists mean such features as how many species a community houses, or how similar those species are morphologically.) Proponents and critics of all three approaches have recently exchanged salvos (*7*–*9*).

Most species live in the tropics and, in particular, within moist forests (see the figure). Why do warm, wet places generate diversity? "There are more niches," goes one argument, "as demonstrated by their being more species to fill them," goes its circular conclusion. Warm, wet places are proposed to be more productive and to support more individuals, which in turn permit more species to coexist (*10*). Unfortunately, tropical richness increases much faster than ex-

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pected with the increase in individuals (*11*).

Perhaps species are preserved longer or are born more frequently in the tropics (*9*). Wallace (*2*) suggested that the tropics avoided the devastation of periodic ice ages. Higher birthrates would fill the tropics with "young species"—those with many "siblings" in the same genus. The tropics, however, simply have more of every taxonomic level. More than half of all bird families are tropical.

Based on the excellent fossil record for marine bivalves, the tropics are *both* the primary source of diversity *and* the accumulator of species (*9*). Species appear in the tropics, then expand outwards. High latitudes are a "sink"—that is, places from which species disappear forever. Tropical oceans house enormous diversity today because it is here that the geographic ranges of old and mostly widespread species overlap with those of young and spatially restricted ones.

Proponents of the third approach ask us to imagine a child's pencil box wide enough for many pencils (*8*). Barely used pencils—analogous to species with large ranges—will span almost the entire length of the box. Other pencils will be worn to mere stubs—analogous to species with small ranges. The length of the box is *any* well-defined gradient. Now shake the box end-to-end to randomize the pencils. Pencils larger than half the box's length must encompass its middle. With enough long pencils, more pencils overlap at the middle than at the ends—producing the "mid-domain effect." Such unavoidable constraints generate the expected statistical distribution of numbers of species along the gradient against which to compare empirical patterns (*8*).

This model explains why South American bird diversity peaks equatorially (see the figure), but then so do the other approaches. Impressive victories lie elsewhere (*8*). Climatic predictions would have diversity along the narrow, north-south strip of moist forest in eastern Madagascar peaking at the end nearest to the equator. In fact, diversity peaks in the middle. Warm, wet lowland tropical forests should have more species than progressively higher, colder elevations. Diversity often peaks at mid-elevations (*8*).

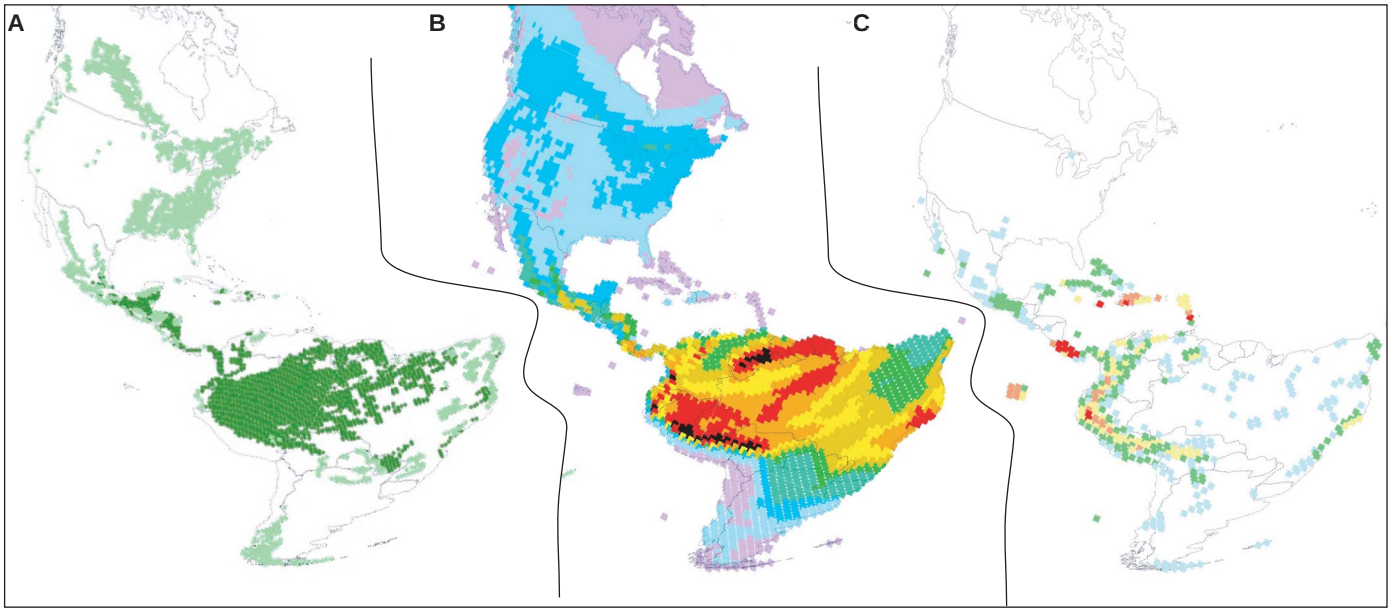
The births and deaths of species readily amend this basic model. New species disperse from where they originate. Even if origins are distributed uniformly [and are not tropically centered (*9*)], the middle will have more species (*12*). As with culture, provinces are (pejoratively!) provincial. Isolated, they receive fewer novelties, whereas centers accumulate them from all directions. We speculate that extinctions might also be greater at the periphery. Climate cooling eliminates small-ranged species in peripheral warm habitats, whereas warming eliminates small-ranged species in cold ones—just as global warming seems poised to do (*13*).

There are both statistical and conceptual issues with all explanations of diversity. Proving a hypothesis statistically sufficient or at least better than its alternatives is difficult. Historical explanations provide their most compelling predictions for the places of origin and extinction of fossil taxa. Their predictions for modern patterns of diversity are quite subtle and are not yet widely tested (*9*).

Some regressions of diversity against modern climatic factors yield statistical significances simply too good to be true. Data points apparently proliferate as maps of diversity and its predictors become more spatially resolved. Not all studies have resisted the temptation to treat interpolated observations from maps as statistically independent. Few studies have worried about the natural scale of species ranges—the "pencil lengths"—or of the sparse specimen collections that generated them. Few studies ask if the statistical model predicts diversity on a different continent.

There are also methodological difficulties in applying mid-domain models (*7*, *8*). More fundamentally, critics object to assertions that geometric constraints must apply (*7*). They do, but that is not the point. The validity of one hypothesis does not deny the validity of its alternatives. The patterns of biodiversity that we observe are likely to have multiple causes.

Like beauty, what constitutes a more fundamental explanation often lies in the eye of the beholder. The mid-domain models are



Figuring out biodiversity. (**A**) Areas of tropical moist forest (dark green) and temperate broadleaf forest (light green) in North and South America (*15*). (**B**) Numbers of passerine bird species per 1° latitude/longitude grid, and (**C**) numbers of passerine bird species with ranges of <100,000 km^2 (*14*). (B) Scale: 10 equal divisions of 33 species (1 to 33, 34 to 67, etc., up to 333), from light purple, light blue, darker blue, light green, darker green, buff, yellow, orange, red, black. (C) Colors indicate number of species: blue, 1; green, 2 to 5; yellow, 6 to 10; orange, 11 to 15; and red, 15 to 36. Map projection is Albers equal area.

silent about what determines a species' range. For example, ~5% of South America's passerine birds have ranges larger than half that continent's area (*14*). That fact contributes to the high numbers in the continent's middle (see the figure) and the success of mid-domain models in predicting that pattern. These species are mostly forest dwellers, and the continent's center has a lot of forest. So, argue the critics, it is really forest cover that determines the pattern.

Defining the domain requires care. In North America, the continent's center has relatively few species (see the figure). Colwell *et al.* (*8*), recognizing the importance of habitats, consider three broad habitats. Triumphantly, for the inverted "V"-shaped domain that is North American broadleaf forest (see the figure), forest species peak at the middle—the tip of the "V" (New England)—not at the southern terminus (Georgia). Critics will likely howl that this is selecting the domain to obtain the right result. Comparable results are obtained for the other two North American habitats: grasslands and western forests (*8*).

Mid-domain models are perhaps most interesting when rejected (*8*). Fill the box only with the shortest pencils and shaking will generate a near-uniform distribution from end to end. By analogy, small-ranged species can be anywhere. For example, one species of American passerine bird (see the figure) occupies the continent's southern tip and another, almost equidistant from the equator, lives in Michigan—but small-ranged species are most certainly not uniformly distributed. Some areas have large numbers of them (see the figure). One might suppose that small-ranged species would be concentrated where most species are found, because the more species there are, the more speciation would bud off new ones. If so, the paucity of small-ranged species from the central Amazon is even more puzzling.

Darwin was able to visit one of the world's greatest concentrations of small-ranged species on his way back to England. "This is where species are born," he wrote of the Galapagos Islands with profound consequences (*1*). Today, those concentrations are where species are dying (*14*). Predicting diversity patterns is not only an intellectual problem, but an urgent practical one as well.

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STRUCTURAL BIOLOGY

The p75 NGF Receptor Exposed

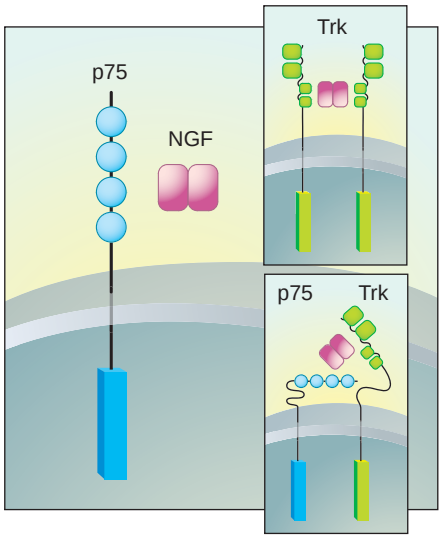
Niccoló Zampieri and Moses V. Chao

Among growth factors, the NGF (nerve growth factor) family of neurotrophins has always behaved in unorthodox ways. First, the neurotrophins bind to two completely different cell surface receptors—the Trk tyrosine kinase receptors (TrkA, TrkB, and TrkC) and the shared p75 receptor (see the figure) (*1*). These ligand-receptor interactions produce a dazzling array of effects, lasting from milliseconds to days, that influence neuronal cell plasticity and survival. Second, each receptor forms myriad interactions with other plasma membrane receptors. The Trk receptors interact with ion channels, such as TRPC3, the TRPV1 capsaicin receptor, and a voltage-sensitive sodium channel (*2*). In contrast, p75 associates with the leucine-rich repeat proteins Nogo receptor and LINGO, which are involved in axonal regeneration (*3*), and sortilin, a trafficking receptor that brings the precursor form of NGF (proNGF) together with p75 (*4*). In addition, Trk and p75 mutually form complexes that contribute to high-affinity binding of neurotrophins. In contrast to the Trk receptors, which display a more selective preference for their ligands, p75 binds to all neurotrophins including brain-derived neurotrophic factor (BDNF), NT-3, and NT-4.

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The three-dimensional structure of NGF bound to p75, described by He and Garcia on page 870 of this issue (*5*), provides an unexpected view of a neurotrophin-receptor complex. The crystal structure of NGF in a complex with the extracellular domain of p75 at 2.4 Å resolution reveals a 2:1 NGF:p75 stoichiometry (see the figure). This result is surprising for a number of reasons. Neurotrophins exist as biologically active dimers, and so it would be expected that the ligand dimer would bind to a dimeric receptor. This is certainly the case for TrkA: The immunoglobulin domains of two TrkA receptors form a complex with the NGF dimer (*6*). After affinity cross-linking by ligand, p75 dimers are easily detected. However, the new crystal structure reveals that, in the case of NGF, only one p75 molecule contacts the NGF dimer.



Models of NGF-receptor interactions. The NGF dimer binds to a monomeric form of p75 (*5*) but to a dimeric form of the TrkA receptor (*6*). (These studies used the mature 118–amino acid form of NGF, rather than the precursor proNGF, with the four CRDs of p75.) Heterodimers of p75 and Trk are possible, but the receptors would need to be in opposite orientations to accommodate the NGF dimer.

As the founding member of the TNF (tumor necrosis factor)/Fas receptor family, p75 possesses four extracellular cys-

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