Situations that meet these conditions can readily be contrived in laboratory microcosms (*2*), but whether they also hold—as a general explanation for the bulk of diversity—in natural communities at modest spatial scales remains to be proven. Well-documented instances of precise local adaptation are of great interest from many points of view, but they are not a refutation of the neutral model.

Third, growth, reproduction, and dispersal vary among sites. Although true, this is beside the point. Neutral theories of diversity assert the equivalence of species, not of sites.

Regarding the comments by Enquist *et al.* on null models, explanations of distribution and diversity fall into three categories. Random models attribute the patterns to the effect of chance alone; neutral models to chance and history; and functional models to chance, history, and selection. Either a random or a neutral model might supply the appropriate null hypothesis for a particular functional interpretation, but it is important to distinguish between them. Neutral models readily lead to highly nonrandom outcomes, such as the distribution of abundance among species (*3*) or the correlation of species distributions with environmental factors (*4*). Random models are not based on dynamic processes such as local dispersal, do not give rise to realistic ecological patterns, and are of limited utility in evaluating functional interpretations.

The neutral theory is one of diversity; it is not a theory of processes such as ecological succession, just as the neutral theory of population genetics is not a theory of adaptation. Within its restricted realm, however, it is very successful, and its impressive ability to explain patterns that have puzzled ecologists for a century has not yet been challenged. This ability might merely reflect some unexpected statistical anomaly, as Enquist *et al.* suggest, but it also raises the exciting possibility of a conceptual unification of community ecology with population genetics, to form a general theory of variation and diversity extending from single-nucleotide polymorphism to plant community structure. This goal seems well worth striving toward.

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References and Notes

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## CORRECTIONS AND CLARIFICATIONS

**NEWS OF THE WEEK:** "Leukemia protein spurs gene silencing," by J. Marx (8 Feb., p. 943). The name of researcher Jean-Pierre Issa, mentioned on p. 945, second column, was misspelled. Furthermore, his correct affiliation is with the University of Texas at MD Anderson Cancer Center in Houston.

**NEWS OF THE WEEK:** "Pulsars solve mystery of missing gas" by G. Schilling (19 Oct., p. 497). The paper by P. C. Freire *et al.* discussed in this article was erroneously stated to have been published in the 10 October 2001 issue of *Astrophysical Journal Letters*. The paper was published in the 20 August 2001 issue of the journal (vol. 557, pp. L105–108).