

and a fishery sample should not differ significantly in their genetic composition if both originated from the same stock: *this* was actually the most robust ( $P = 0.0026$ ) result in our study. As Mariani suggests, the proportion of mislabeled Chilean sea bass in our sample could be as low as 6% (the proportion with haplotypes known from uncertified stocks), but it might also be higher given that (1) 15% of the haplotypes in the retail sample were not found in a much larger sample from the certified stock (Shaw *et al.* 2004), (2) haplotype B was unexpectedly common in the retail sample, and (3) haplotypes C and D were entirely absent from the retail sample (plus the additional information that three fish were not even Chilean sea bass, even though they were labeled as such). If mislabeling was really not a problem, then a very modest sample of 36 fish should not have detected any evidence of it, particularly fish that were not even Chilean sea bass.

The seafood industry clearly has an interest in increasing consumer confidence in their products. Although it is unclear to us whether governments should monitor food labels that they have had no hand in developing, Mariani's assertion – that it is unrealistic for non-government certification agencies to effectively monitor the use of their own wildlife eco-labels – seems somewhat specious, given that most seafood testing requires very simple and inexpensive methods. Following our earlier study (Marko *et al.* 2004), we have advised several high-school teachers on similar projects working with very limited funds (one of the most prominent seafood-labeling studies in recent years was initiated by two high-school students). Regular publication of commissioned tests completed entirely (ie from sample acquisition to data analysis and interpretation) by qualified independent entities seems like an obvious and essential component for the success of any wildlife eco-label.

Because some well-known eco-

labels are controlled by national governments (eg Energy Star, US Department of Agriculture Organic), government oversight of seafood eco-labeling may happen, but probably only with additional pressure from consumers. Indeed, the US Food and Drug Administration is currently creating a DNA database for fish and will begin comparison of those data to those in the Fish Barcode of Life ([www.fishbol.org](http://www.fishbol.org)). In the meantime, we hope that any attention that our study generates can be channeled toward greater public awareness of the problem (and consequences) of seafood mislabeling, as well as the enormous challenges facing any program working toward the goal of complete traceability (Dickhoff *et al.* 2007; Miller and Mariani 2010; Stiles *et al.* 2011).

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## Multi-dimensional space use: the final frontier

### Peer-reviewed letter

Because many animals fly, climb, swim, or dig throughout volumes of air, water, and soil, space use is most appropriately characterized within three spatial dimensions:  $x$ ,  $y$ , and  $z$ . The  $x$  and  $y$  dimensions are typically planar coordinates (eg latitude and longitude, or Universal Transverse Mercator northing and easting), whereas  $z$  can represent altitude (eg flying or arboreal species), depth (eg aquatic or fossorial species), or elevation (WebFigure 1a). Yet quantification of multi-dimensional space use has relied almost entirely on univariate examination of the  $z$  dimension, independent of use in the  $x$ ,  $y$  dimensions (WebFigure 1b), or has simply ignored the  $z$  dimension (WebFigure 1c). Such approaches overlook potential heterogeneity in vertical space use within an animal's home range and disregard interactions between surface and above- or below-surface resources affecting space-use choices. For decades, statisticians have refined methods appropriate for quantifying trivariate probability distributions (Epanechnikov 1969), with a few models initially developed to estimate three-dimensional (3D) space use of small semi-arboreal mammals (eg Meserve 1977). Surprisingly, these analytical tools have rarely been applied by members of the ecological community and have received only limited recent attention (Bailleul *et al.* 2010). As such models are expanded to incorporate other dimensions (eg time; Keating and Cherry 2009), we wish to emphasize the theoretical and applied importance of these models, along with technological advances in data-collection tools, for examining multi-dimensional aspects of space use.

Consider one of the most fundamental constructs in ecology: Hutchinson's concept of a niche hypervolume corresponding to potential or realized resource use within multivariate resource “space” (Hutchinson 1957). The most critical general resource dimension may

be physical space; for example, overlap between species – in all other resource dimensions – can occur if there is spatial differentiation of the “realized” niches (Cunha and Vieira 2004). Yet if resource use and resource overlap among animals are not considered in all three spatial dimensions simultaneously, then characterization of the spatial aspect of resource use will be inadequate (WebFigure 1d). Spatial differentiation among species is often achieved through differential use of vertical space (eg MacArthur 1958), in combination with inherent differentiation among available resources (such as food and nest sites) along the vertical dimension. Therefore, quantification of 3D space use can improve our understanding of resource use and spatial overlap or differentiation by species. For instance, consider the seminal work by MacArthur (1958); resource partitioning among ecologically similar species could be placed in a 3D context, with volumes of space assigned a probability of occupancy for each species based on resource attributes and ecological constraints (ie competitors; WebFigure 1d).

Probabilistic estimation of 3D space use will also be invaluable for addressing numerous conservation and societal issues, including some involving human health and safety. For example, bird strikes with aircraft cost worldwide civil aviation >US\$1.2 billion annually (Allan 2002). Currently we are investigating approaches for predicting 3D space use by birds to assess associated aviation risks, which will provide information to wildlife managers on how to reduce the likelihood of strikes. Similar quantification of organisms’ 3D space use could be integrated into wind farm planning efforts to mitigate associated bird, bat, and insect mortality. Likewise, knowing the spatial distributions of target and non-target marine organisms could be used to optimize timing and location of harvest to reduce fisheries bycatch.

An important practical limitation in implementing these ideas is the “curse of dimensionality”; overall data

requirements necessary for appropriate inference increase by at least one order of magnitude for each additional dimension of interest (Silverman 1986). However, current technology for tracking animals allows today’s researchers to collect large amounts of data accurately and to pursue these fundamental ecological and applied questions for many species. During the past decade, there has been an explosion of technological advancements, dramatically improving the ability to assess multi-dimensional space use, examine mechanisms driving resource-use patterns, and understand the causes of observed use (Cooke *et al.* 2004), including reduced size and cost, and increased availability of Global Positioning System transmitters; increased locational accuracy from acoustic and other tags (eg Melnychuk and Christensen 2009); and advanced integration of sensors recording vertical space use (eg Moll *et al.* 2007). Furthermore, remote sensing technologies (eg light detection and ranging [LiDAR]) that characterize above-ground structure with more accuracy and precision will assist in quantifying habitat use in 3D space. However, although modern technology may be of enormous benefit in many situations, simple field observations (eg MacArthur 1958) can often still provide the necessary data for development of models summarizing multi-dimensional space use.

We are approaching the next frontier in advancing our understanding of multi-dimensional space use. This understanding is critical for better assessing theoretical and applied questions that have long been of importance to ecologists. The appropriate data-gathering technologies are now available. What remains is the challenge of integrating and applying them to answer those questions.

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## Is assisted colonization feasible? Lessons from past introductions

Assisted colonization – or the translocation of species to previously unoccupied ranges predicted to be favorable for persistence under future climate scenarios (hereafter AC) – has been proposed for addressing

extinction risk of climate-imperiled species, and is hotly debated because of associated uncertainties, such as the risk of translocated species becoming invasive (eg Loss *et al.* 2011; Thomas 2011). Here, we focus on factors limiting its applicability and potential risks for target species overlooked by both AC advocates and opponents (Hewitt *et al.* 2011).

Deliberate introductions of alien species have similarities with AC; through a comparative framework, examining the former may help to identify some of the latter's constraints and predict its success, despite inherent differences between traits of introduced alien and imperiled species (Blackburn and Jeschke 2009). A large proportion of deliberate introductions of alien species failed across taxa and regions, with establishment success depending in part on species-specific traits, biotic and abiotic conditions of the recipient region, and complex interactions between them (eg Blackburn *et al.* 2009). Regarding AC of climate-imperiled species, abiotic conditions of source and recipient areas should match future – not present – conditions. Current models of the climate–biosphere interface remain overly simplistic, however, thereby undermining the credibility of projections (McMahon *et al.* 2011) and complicating the selection of appropriate recipient areas. Although substantial progress in modeling could soon be made, which would improve our predictive ability (McMahon *et al.* 2011), AC is proposed as a method of last resort to prevent the extinction of climate-imperiled species. Consequently, what would be the establishment likelihood for species translocated decades before recipient regions are predicted to be climatically suitable (surely much lower than that resulting from alien species' introductions matching native to non-native conditions)?

In addition, propagule size and number are key determinants of establishment success of alien species (Simberloff 2009); the more individ-

uals per introduction and the more introductions altogether, the more likely those introduced species are to become established. Indeed, much uncertainty exists about propagule pressure thresholds to guarantee successful alien establishments, given the magnitude of variance among species and introduction events (Simberloff 2009). Variance was also pronounced when reviewing the success of reintroduction of species within portions of their former range, although Griffith *et al.* (1989) found that successful programs released, on average, more animals than unsuccessful ones (160 as compared with 54, respectively). Taking this into account, is it advisable to translocate a sufficient number of wild-caught animals, as recommended by Hewitt *et al.* (2011), to ensure successful AC, given that highly imperiled species often have global population sizes of only a few hundred individuals? Paradoxically, AC could increase extinction risk of remnant native populations for the sake of obtaining large enough propagule sizes.

Clearly such problems would not be affiliated with organisms from which seeds or gametes could be stored or frozen until suitable AC sites could be found (Vitt *et al.* 2010). There is, however, an additional challenge related to genetics. Surprisingly, alien species introductions were apparently not compromised by the expected low genetic variability of small founder populations (Simberloff 2009); introduced alien species commonly have large native populations and widespread distributions (Blackburn and Jeschke 2009), thus ensuring genetic variability. By way of comparison, imperiled species often exhibit restricted ranges, depleted population sizes, and low genetic variability, likely symptomatic of their inability to keep pace evolutionarily with severe anthropogenic threats (Kinnison and Hairston 2007). Indeed, reintroduction success of endangered species is half that of more common

species (Griffith *et al.* 1989). Therefore, the diminished genetic potential of imperiled species to face new selective forces in recipient areas might seriously compromise AC success.

In a changing world driven by anthropogenic forces, we feel that controversial actions such as AC must be seriously considered. However, potential risks affecting the viability of AC and target species should be further debated and incorporated into decision-making frameworks (Loss *et al.* 2011) before action is taken.

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