

biologically suspect measure might well make one parameter seem less important than another. Thomas *et al.* measured isolation simply as the distance to the nearest suitable habitat patch. A better measure would reflect the total number of individuals likely to immigrate to this site from existing local populations anywhere in the system, and such a definition might further emphasize the importance of isolation [2]. Second, the relative importance of size, isolation and quality will depend on the specifics of the

system. Size will have a larger effect in a system where patch size is heterogeneous compared with a system where all patches are approximately the same size. Third, the importance of habitat quality will probably vary with geographical location. The effect of habitat quality is generally assumed to be accentuated in populations near the edge of the species range. Nevertheless, habitat quality can usefully be thought of as a third parameter in metapopulation dynamics. Its inclusion can add realism to

metapopulation modeling, which is vital for the conservation of our rarest species.

1 Thomas, J.A. *et al.* (2001) The quality and isolation of habitat patches both determine where butterflies persist in fragmented landscapes. *Proc. R. Soc. London B Biol. Sci.* 268, 1791–1796

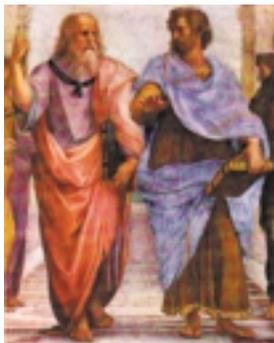
2 Moilanen, A. and Nieminen, M. Simple connectivity measures in spatial ecology. *Ecology* (in press)

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The rise of the Aristotelean worms

Most developmental research focuses on a few model organisms, among which the nematode *Caenorhabditis elegans* is particularly prominent. Until recently, *C. elegans* was viewed as the ultimate deterministic organism, because there is a virtual absence of variation in cell number (eutely). However, Azevedo *et al.* [1] in their 'Demise of the Platonic worm', previously showed that the 'platonic ideal' of a worm, where each individual faithfully represents the essentialist idea of the species, does not hold true for all nematodes. The authors reported that, in the epidermis, the variance in cell number between individuals of a species increased with the mean cell number in that species.



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In a new article [2], Azevedo and Leroi report that the variability in some supposedly eutelic taxa is not unusually low, and that the relationship between cell number variation and mean cell number generally follows a power law with an exponent of 2 across a wide range of multicellular taxa. They use stochastic branching processes to model the way in which variation builds up in a lineage and convincingly argue that the relationship between cell variability and cell number must be maintained by selection. In another new article, Delattre and Félix [3] report

variability in vulval cell lineages in several strains of *C. elegans* and of its close relative *Oscheius* sp. CEW1, and demonstrate that this variability is affected by several loci. Thus, lineage variability can even evolve over short evolutionary timescales.

These studies are important for several reasons. First, they provide a solution to the paradox that the *C. elegans* nematode model displays no developmental variation, whereas there is variation in development among nematode species. The current results no longer exclude a standard neo-darwinian scenario where the gradual divergence of a developmentally polymorphic population can lead to species differences. Second, these studies dispel the notion that *C. elegans* can serve as the platonic model for all nematodes. Finally, these studies provide a framework for unraveling the genetic mechanisms underlying developmental stochasticity. It is perhaps ironic that animals known for their invariance should provide materials for a better understanding of the developmental basis of phenotypic variability. This would really please Aristotle. In his view, knowledge comes from understanding and classifying variation in the empirical world.

1 Azevedo, R.B.R. *et al.* (2000) The demise of the platonic worm. *Nematology* 2, 71–79

2 Azevedo R.B.R. and Leroi, A. (2001) A power law for cells. *Proc. Natl. Acad. Sci. U. S. A.* 98, 5699–5704

3 Delattre, M. and Félix, M-A. (2001) Polymorphism and evolution of vulval precursor cell lineages within two nematode genera, *Caenorhabditis* and *Oscheius*. *Curr. Biol.* 11, 631–643

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Searching for Pax in hydromedusa

Pax6 is a perplexing gene with a fundamental role in eye development in a wide range of bilaterian animals. The puzzling thing is that the eyes of all of these animals are entirely different: the compound eyes of flies, eyespots of flatworms, and lens eyes of vertebrates cannot be considered homologous in the usual sense. Yet *Pax6* is expressed in the early development of all of them, and the functional domains are so highly conserved that mouse *Pax6* can induce eye formation in *Drosophila* – and not only in the usual place. Expression of *Pax6* (either the fly gene or its mouse homolog) can turn on eye formation throughout a *Drosophila* embryo, resulting in flies with eyes on their wings, legs or antennae. Homeotic mutants such as these, where a whole structure is induced to develop in a novel location, have played a key role in the hypothesis that body plans in animals arose by discreet (and potentially very rapid) evolutionary processes, rather than by the slow plodding of classic darwinian gradualism. But how can the puzzle of homologous gene expression (*Pax6*) in nonhomologous structures (metazoan eyes) with a common function (vision) be resolved? One approach is to work out what *Pax6* was doing in the ancestor of all animals that now use it as a regulator of eye development.

Cnidarians could hold the key piece of this puzzle. One of the most basal groups in the animal kingdom, Cnidaria includes creatures with a range of eye types from simple eyespots to complex lens eyes. Earlier studies of sea nettles, hydra and corals identified cnidarian Pax-family genes (including *PaxA*, *PaxB* and *PaxCAM*), but found no clear homologs of *Pax6*. But these cnidarians either have no eyes or just simple eyespots, hence this new study

by Sun *et al.* [1], which reports on a search for *Pax6* in a cnidarian with 'true' lens eyes, the hydromedusa *Cladonema californicum*. But still no *Pax6*. Neither did the authors find *PaxA*, which has been identified previously in hydra and sea nettles. However, they did identify *PaxB* in *Cladonema*, and characterized the paired domains that allow the gene product to bind to DNA as a transcription factor. Although the consensus sequences of these Pax domains are very similar to their mammalian counterparts, the hydromedusa Pax-B

sequence is degenerate, in that it can bind with a broader range of target sequences. The authors suggest that this broad binding efficiency could represent an ancestral form capable of carrying out a range of functions.

The study concludes that the ancestral Pax had broad DNA-binding affinity, like the cnidarian Pax-B, and was capable of a range of functions, including involvement in eye-development. The ancestral Pax gave rise to a gene family with more specialized binding properties, including *Pax6*, co-opted into

eye development in bilaterians. However, failure to find *Pax6* in cnidarians is not proof of its nonexistence. The hunt for the ancestral *Pax6*, and the baseline metazoan body-patterning toolkit, continues.

- 1 Sun, H. *et al.* (2001) Isolation of *Cladonema Pax-B* genes and studies of the DNA-binding properties of cnidarian Pax paired domains. *Biol. Evol.* 18, 1905–1918

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In Brief

Impact of grizzly bear hunting in Canada

The Environmental Investigation Agency (EIA), a USA- and UK-based international conservation organization (<http://www.eia-international.org>), is focusing efforts on the hunting of grizzly bears in British Columbia (BC), Canada. The controversy over this hunting centers around the methods used to set hunting quotas. Some scientists charge that the estimates of population size, which are based on a habitat capability model as opposed to direct population counts, are fundamentally flawed and tend to produce unrealistically high population estimates that, in turn, lead to intolerably high hunting quotas. Although hunting of grizzlies was suspended in February 2001 after a critical review by the Canadian Wildlife Service, it resumed following a change of Government in May 2001. The annual kills have been as high as 363 in 1996 and as low as 236 in 1993. The significance of these kills obviously depends on how large the baseline population is, which is why so much attention is focused on the scientific approaches used to estimate the size and trend of the Canadian grizzly population.

It might seem that hunting of grizzlies in BC is a 'local issue', but the BC population has much greater significance. The grizzly populations in Alberta, Yukon, Idaho, Washington and Montana are unlikely to be viable without a strong core population in BC. The North American grizzly once had a range that extended from Alaska into Mexico, and as far east as the Hudson Bay. Although the Alaskan population of grizzlies remains large (30 000 – 40 000), further shrinkage of its range would pose a real threat to those numbers. Against this risk is the economic

value of hunting for grizzlies, which provides Can\$3 000 000 each year to BC in the form of hunting licenses and hunting-related activities (guides, hunting outfitters, lodging, etc.). The next step in this controversy is likely to be a scientific review of hunting impacts, and appeals to international and non-Canadian organizations to pressure BC to reconsider its hunting policy. *PK*

Climate science and policy struggle to keep up with each other

Because predicting the magnitude and impact of climate change remains an uncertain science, policy makers do not have an easy time choosing a course of action. The dilemma is well illustrated by a recent report by Andronova and Schlesinger in the 16 October 2001 issue of *Journal of Geophysical Research*. This concludes that there is a >50% chance that the magnitude of climate warming lies outside the 1.5–4.5°C envelope widely embraced as 'consensus science' by the International Panel on Climate Change. Obviously, if average temperatures increase by >4.5°C, some countries will be in for extremely difficult times. However, if temperatures rise by <1.5°C, the risks will be substantially muted.

The interplay of science and policy in the climate arena is a fascinating testing ground for different approaches to linking science with policy, when the science is well developed yet still includes substantial uncertainty. The three major approaches to fostering this link are complex decision theoretic models, scenario analyses (e.g. reductions of decision-theoretic models) and case studies. In an interesting move to inform policy debates that are coming before the US Congress regarding CO₂ emissions

(and the extent to which emissions should be reduced through government policy), several environmental organizations are adopting a case-history approach. For example, the Defenders of Wildlife and the National Resource Defense Council are examining probable impacts of climate change on coldwater fisheries, some of which might already be suffering from global warming. The idea is that stories of climate impacts that are already evident or likely to be seen soon might be more compelling than are the abstract discussions of confidence intervals and uncertainty. Although academics have emphasized decision theory in such matters, the power of scenarios and storytelling should not be underestimated. *PK*

Fisheries Agency accused of 'arbitrary' science

A US federal judge reversed an earlier decision by the National Marine Fisheries Service (NMFS) to list Oregon Coast coho salmon as threatened under the US Endangered Species Act (ESA). The reason for this was a logical inconsistency in the way that NMFS had applied the ESA to these salmon: although hatchery coho are genetically indistinguishable from wild coastal coho, and hence considered part of the same evolutionary unit, only the wild populations had been listed. Because the ESA does not allow for listing of populations at a taxonomic level lower than a distinct population segment, both the wild and the hatchery populations would need to be listed (<http://www.forests.org/archive/america/costdown.htm>). Although this might seem like an arcane legal point, the ruling has spawned a flurry of dialog and analysis that might clarify some fundamental issues that fisheries biologists have tended to sweep under the rug.