Finite conservation funds mean triage is unavoidable

Madeleine C. Bottrill[1], Liana N. Joseph[1], Josie Carwardine[1], Michael Bode[1], Carly Cook[1], Edward T. Game[1], Hedley Grantham[1], Salit Kark[1,2], Simon Linke[1], Eve McDonald-Madden[1], Robert L. Pressey[3], Susan Walker[4], Kerrie A. Wilson[1] and Hugh P. Possingham[1]

[1] The University of Queensland, The Applied Environmental Decision Analysis Centre, The Ecology Centre, Brisbane, QLD 4072, Australia
[2] The Biodiversity Research Group, Department of Evolution, Systematics and Ecology, The Institute of Life Sciences, The Hebrew University of Jerusalem, Jerusalem 91904, Israel
[3] Australian Research Council Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, QLD 4811, Australia
[4] Landcare Research, Private Bag 1930, Dunedin 9054, New Zealand

We welcome the interest generated by our recent article [1] on the use of triage principles for allocation of conservation resources in three letters featured in this issue of *Trends in Ecology and Evolution* [2–4] and appreciate the opportunity to respond to the issues raised. Jachowski and Kesler [3] and Parr and colleagues [4] from the Alliance for Zero Extinction (AZE) argue against the use of conservation triage. We consider that these authors have confused two issues: the allocation of resources currently available for conservation and decisions on how much society should spend on conservation. The first issue involves wise allocation of funds assisted by approaches such as triage and cost-efficient optimization. The second is an issue of societal values and political willingness. Conservationists fight on both fronts, but the issues should not be confused.

Continuous threats to biodiversity and inadequate funding make it inevitable that conservation managers apply triage in decision making. Current levels of funding are several orders of magnitude below what is needed to return rates of extinction to natural levels [5]. Under existing constraints to funding and capacity, conservation managers are faced with a resource allocation problem: which actions to take to maximize the achievement of their conservation goals given a fixed budget. If managers ignore the cost of management as well as (or along with) socioeconomic [6] and technical uncertainties of success, or attempt to manage everything simultaneously, they will not maximize conservation outcomes. In practice, all conservation managers and agencies allocate limited budgets to specific actions in the knowledge that there will be habitats and species that receive no, or less, investment and that these might degrade or become extinct owing to the choices made.

Species prioritization, as discussed by Jachowski and Kesler [3] and Parr and colleagues [4], was not the essential message of our paper. We argued that triage is not about abandoning difficult-to-save species, but rather about prioritizing actions given finite resources. Triage might employ other benefit-functions and objectives, such as phylogenetic diversity (as suggested by Faith [2]) or ecosystem services; our point is simply that triage provides a rational approach to allocating a given budget amongst management actions to achieve a stated goal. With a goal of maximizing species persistence, AZE have already applied triage in their process of selecting priority sites and species, albeit a triage approach that is not explicit about the opportunity costs of focusing efforts on only the most threatened. Furthermore, their efforts will not secure every species with 100% certainty in perpetuity. We do not argue that threatened species are necessarily expensive to save, only that the costs and uncertainties of their attempted salvation need to be considered. As an example of this approach, the Department of Conservation in New Zealand has developed a cost-efficiency framework for threatened species conservation based on triage principles, meaning that recovery of more species could be funded at a level of higher success [7].

Far from 'sanctioning extinction in the name of efficiency' [3], a conservation triage approach admits the possibility of extinction, both explicitly and transparently. Only when the consequences of inadequate funding are apparent can there be a realistic debate about the budget required to achieve our goals. By taking a triage approach in allocating funding for actions to save threatened Australian bird species, McCarthy and colleagues demonstrated that increasing current budgets by three times could decrease the future number of extinct species to one [8]. Thus, being explicit about potential consequences (i.e. extinctions) of inadequate funding can elicit more resources from governments and donors than fostering the 'we can save everything' delusion. By denying the realities of a constrained budget, we can lead policy makers to believe that current resources are sufficient to implement management actions needed to reduce extinction to zero. We too see possible opportunities for increased conservation funding from carbon markets [4] and other sources. However, while conservation weathers the present global recession [9], we foresee that prioritization will become ever more vital.

References

1 Bottrill, M. *et al.* (2008) Is conservation triage just smart decision-making? *Trends Ecol. Evol.* 23, 649–654
2 Faith, D.P. (2009) Phylogenetic triage, efficiency and risk aversion. *Trend Ecol. Evol.* 24, 182

Corresponding author: Bottrill, M.C. (m.bottrill@uq.edu.au).

3 Jachowski, D. and Kesler, D. (2009) Allowing extinction: Are we ready to let species go? *Trends Ecol. Evol.* 24, 180

4 Parr, M.J. *et al.* (2009) Why we should aim for zero extinction. *Trend. Ecol. Evol.* 24, 181

5 Balmford, A. *et al.* (2003) Global variation in terrestrial conservation costs, conservation benefits, and unmet conservation needs. *Proc. Natl. Acad. Sci. U. S. A.* 100, 1046–1050

6 McBride, M.F. *et al.* (2007) Incorporating the effects of socioeconomic uncertainty into priority setting for conservation investment. *Conserv. Biol.* 21, 1463–1474

7 Joseph, L.N. *et al.* (2008) Optimal allocation of resources among threatened species: a project prioritization protocol. *Conserv. Biol.* 23, 328–338

8 McCarthy, M.A. *et al.* (2008) Optimal investment in conservation of species. *J. Appl. Ecol.* 45, 1428–1435

9 Pergams, O.R.W. *et al.* (2004) Linkage of Conservation Activity to Trends in the U.S. Economy. *Conserv. Biol.* 18, 1617–1623
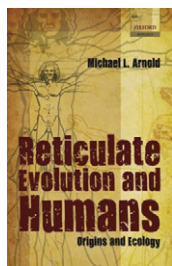
Book Review

Deconstructing the tree of life

Reticulate Evolution and Humans: Origins and Ecology by Michael L. Arnold, Oxford University Press, 2008, £59.95 hbk (222 pages) ISBN 978-0-19-953958-1

Davide Pisani

Department of Biology, The National University of Ireland, Maynooth, Kildare, Ireland

It has long been accepted that life evolved following a tree-like pattern, and the tree representing the evolutionary history of all life forms is generally known as the 'tree of life' [1]. The use of trees in biology can be backtraced to pre-darwinian times [2], and most of the current analytical tools used in evolutionary biology are, to some extent, tree dependent (e.g. [3]). Yet, evidence is accumulating that trees are often inadequate to model organismal evolution (e.g. [1]). Network-like patterns resulting from horizontal gene transfers (HGT) have long been known to affect microbial evolution [1]. More surprisingly, it is now becoming clear that, despite the fact that the metazoan germline cells are sequestered within the gonads, and thus protected from possible contacts with foreign DNA, HGT also had a role in animal evolution [4].

Reticulations, for example HGTs and hybrid speciations (i.e. the origin of novel evolutionary lineages through the crossing of individuals belonging to divergent populations and species), cannot be modelled using trees. This is because, in a tree, a lineage (e.g. a species) can split into two (or more) descending ones, but two (or more) lineages cannot merge to form a descending hybrid species. Accordingly, the discovery that reticulate evolution is common resulted in the tree of life being put on trial, and led to the suggestion that it should be replaced by a 'network of life,' in which lineages can split and merge [1]. Arnold's book *Reticulate Evolution and Humans* is a compilation of examples illustrating the extent to which network-like evolutionary processes have impacted our existence, from the origin of our species, to that of its most beloved companion, the dog, and that of diseases that makes our lives miserable, like AIDS. The book represents one of the most recent additions to the growing literature on the network of life hypothesis and, from this point of view, is not particularly innovative. However, Arnold's effort is laudable and

certainly not redundant. Indeed, most previous work on the network of life focussed on microbial evolution and HGT (e.g. [1]), whereas *Reticulate Evolution and Humans* principally focusses on complex eukaryotes (including animals) and the processes of introgression (i.e. gene flow between distinct populations or species) and hybrid speciation.

In *Reticulate Evolution and Humans*, Arnold describes many examples of reticulate evolution, involving life forms as varied as animals, plants and viruses. In this way, he provides a large number of case studies, such as that of the *Citrus* genus, which includes the grapefruit, mandarin, lemon, lime, pummelo, citron, sweet orange and sour orange, and which is shown to include only hybrid species, that are probably unfamiliar to the general public. When taken collectively, these examples represent a powerful argument supporting the network of life hypothesis.

Reticulate Evolution and Humans is informative and, I think, important. However, it is not flawless. For example, the Introduction is inadequate, as explanations of key concepts such as HGT, introgression and hybridisation have been relegated to the Glossary. Similarly, the Epilogue (in the absence of a conclusion chapter) seems too superficial. More importantly, Arnold seems a little uncritical when accepting phylogenetic incongruence as evidence of reticulate evolution. Phylogenies derived from alternative markers might disagree for a variety of reasons, such as long-branch attraction, compositional biases, more general model misspecification issues (e.g. the use of a poorly fitting substitution matrix), stochastic errors and hidden paralogy [5]. Although many of the case studies presented by the author are likely to represent real reticulations (e.g. [6]), I would have liked Arnold to have dedicated more of the discussion to exploring alternative explanations that could account equally well for the observed incongruence. For example, when discussing the origin of the human pathogen *Giardia lamblia*, Arnold concludes that the incongruence among alternative phylogenies for this

---

Corresponding author: Pisani, D. (davide.pisani@nuim.ie).