

New means to communicate population risk assessments among scientists and decision-makers

June 11 2013



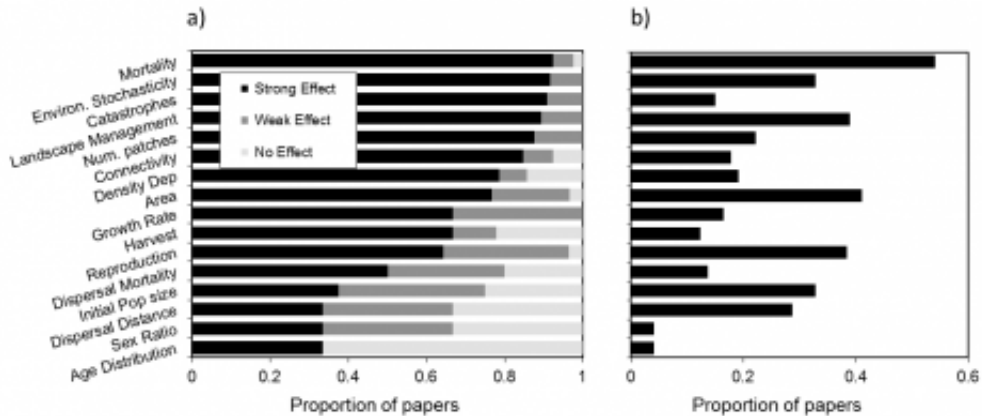
It's not a black swan, it's a black DAC. The DAC-PVA protocol tries to improve the Design, Application and Communication of Population Viability Analyses -- a central tool in conservation theory and practice. Credit: Guy Pe'er

Population viability analysis (PVA) is a method used by conservation scientists for a range of purposes – including advancing conservation

theory, planning, policy and management. PVAs are particularly important for assessing the risks of population extinction and for comparing alternative management options to protect species. The fact that so many PVAs are already available, for hundreds of species, offers an exciting opportunity for learning and especially for moving from single-species experience to multi-species knowledge. But this opportunity is often lost in translation: PVAs are usually complex, and many people find them hard to design, apply and communicate. Many PVA descriptions also lack sufficient structure, and are difficult to understand, assess, or even repeat.

In a review now published in the journal *Conservation Biology*, an international team of 11 researchers have shown that these drawbacks form a true barrier for the use of PVAs as a means of collective learning. As part of the EU project [SCALES](#), Guy Pe'er and colleagues suggest that there is a remedy to this problem: our capacity to learn from PVAs may be greatly improved by applying a common standard for Design, Application and Communication of PVAs - or, what they called the "DAC-PVA" protocol.

The aim of the DAC-PVA protocol is to enhance communication and repeatability of PVAs, strengthen their [credibility](#) and relevance for policy and management. It should further improve the capacity to generalize from PVA findings across studies. The protocol is further accompanied by an interactive [website](#), in order to enhance its usefulness.



An example of the gaps in collective learning: The proportion of PVA studies that found certain factors to have a strong effect on PVA results (left) does not match the proportion of PVA studies that addressed these factors (right). The authors hope that a standard protocol may aid in overcoming such mismatches. Published with courtesy of *Conservation Biology* journal. Credit: Guy Pe'er

Guy Pe'er: "There are many existing guidelines on how to design and implement reliable PVAs. There are also existing communication standards for documenting and communicating ecological models. But somehow, it seems that these two simply didn't manage to meet so far. This is sad because it means that many hundreds of existing PVAs, and many more that are likely to be developed and applied in the future, still do not effectively contribute to collective learning efforts or attempts to move from single-species results to supporting the [conservation](#) of biodiversity in its broader sense".

Klaus Henle: "PVAs are used very commonly nowadays. The [IUCN](#) suggests PVAs to be conducted for every species where enough data are available, and even offers guidelines on how to apply PVAs. Their use is particularly widespread for birds. We should strive to reach a point where, based on PVA knowledge, we could guess the conservation needs of species also without a PVA, for instance based on traits and ecological

requirements. But in the absence of standardized reporting, and a collective effort to learn when such guesses are likely to work or fail, we may never reach this goal".

The idea of the protocol and the website is therefore to create a common template, used by PVA developers, users and readers, that would enhance communication between all of them. Thereby, the authors hope to make PVAs more policy-relevant, and policy-makers more aware of the broad range of potential uses of PVAs for nature conservation.

More information: Pe'er, G., Y. G. Matsinos, K. Johst, K. W. Franz, C. Turlure, V. Radchuk, A. H. Malinowska, J. M. R. Curtis, I. Naujokaitis-Lewis, B. A. Wintle, and K. Henle. 2013. A protocol for better design, application and communication of population viability analyses. *Conservation Biology*, online first. [DOI: 10.1111/cobi.12076](https://doi.org/10.1111/cobi.12076)

Provided by Pensoft Publishers

Citation: New means to communicate population risk assessments among scientists and decision-makers (2013, June 11) retrieved 25 April 2024 from <https://phys.org/news/2013-06-population-scientists-decision-makers.html>

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