

Molecules to models: the future role of genetic data in population viability analysis

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Project Objectives

Population viability is a function of environmental, demographic and genetic factors and can be quantitatively assessed using population viability analysis (PVA). Population viability analyses are practical tools to evaluate management options associated with factors such as habitat fragmentation and climate changes. Typically, PVA have done a poor job of integrating genetic and demographic processes and have been primarily demographic models. Yet, evolutionary processes such as adaptive potential will become increasingly more important in determining viability as threats due to climate change increase.

Fortunately, individual-based models (IBM) provide an opportunity for integrating detailed genetic and demographic processes (Frank *et al.* 2011). Additionally, the genomics era will continue to increase the ease with which large amounts of genetic data are attainable from non-model species (Steiner *et al.* 2013) creating a timely need to assess the inclusion of genetic processes in PVA.

The objectives of this working group were to:

- (i) review and synthesize the current use of PVA and consideration of genetic processes in threatened and endangered species recovery plans
- (ii) broadly assess the current role of genetics in population viability models
- (iii) examine the future possibilities and potential pitfalls of integrating genetic and demographic processes in population viability analyses
- (iv) provide practical guidelines for conservation professionals on when and how genetic data is important to include in models

Methods

We created a standardized questionnaire based on a review of US endangered species recovery plans (Hoekstra *et al.* 2002) and the role of PVA in particular (Morris *et al.* 2002). We reviewed over 300 recovery plans from three regions: 108 Australian plans, 111 European plans, and 100 US plans.

We addressed the remaining objectives in a review manuscript. We conducted a literature review to determine the current role of genetics in PVA. The team developed a conceptual model that describes how to use individual-based models (IBM) with individual genotype tracking and dynamic genotype-phenotype mapping to model population level effects. We used HexSim (<http://www.hexsim.net>), a highly flexible IBM, to simulate a hypothetical case study to model the interacting effects of inbreeding depression, outbreeding depression, local adaptation, and genetic rescue in small populations. Finally, we synthesized the major ways in which genomics will facilitate the estimation of genetic parameters for inclusion in PVA.

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Major Findings

Australian and European recovery plans very seldom used quantitative models (PVA) to assess population viability (4% of plans each; Figure 1). While 38% of US plans included PVA, only 3% included genetic factors in the PVA. However, a majority of Australian (56%) and US (63%) plans consider genetic factors a risk to population persistence, yet relatively few plans actually include any type of genetic data (12% Australian plans; 46% US plans; Figure 1). Fortunately, this paucity of data seems to be recognized as 46% of Australian plans assign tasks to collect genetic data (Figure 1). European plans generally considered genetic aspects of viability less often, with 33% of plans considering genetics a risk factor, only 11% of plans including genetic data, and even fewer plans assigning tasks to collect genetic data (Figure 1).

More generally, few studies have integrated ecological and evolutionary processes to evaluate the effects of environmental perturbations or management actions on the probability of population persistence. Our hypothetical model demonstrated the importance of considering multiple interacting genetic and demographic processes. In this case, a management action – translocation of individuals from a large to a small population – increased the probability of persistence (POP) through both demographic and genetic rescue. However, interactions between multiple genetic and demographic processes likely combined to produce extinction vortices that, when outbreeding depression was strong, nearly overwhelmed the benefit derived from translocations (Figure 2). The interactions apparent in these results reinforce the need for PVA models that couple together both demographic and genetic processes. Importantly, model outcomes can be used to determine what information is central to decision-making – in the case our hypothetical model, it is the strength of outbreeding depression likely to occur due to translocations.

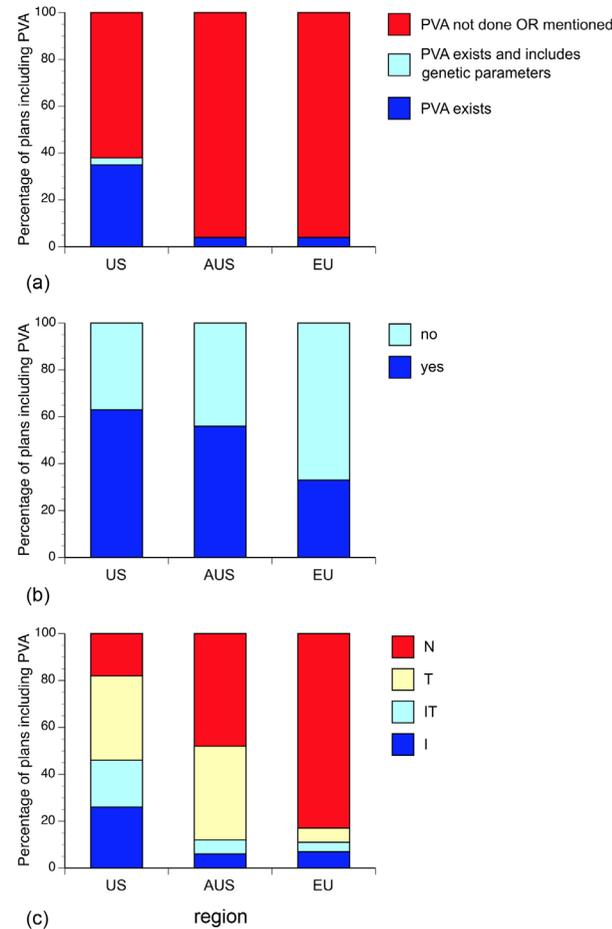


Figure 1: The results from a global review of threatened and endangered species recovery plans. **(a)** Over 300 plans (100 from each region) from the United States (US), Australia (AUS), and Europe (EU) were assessed to determine the use of population viability analysis and if genetic processes were included in PVA. **(b)** We determined whether genetic factors were considered a risk to viability (yes/no). **(c)** We then determined if any genetic data had been included in the plan (I), if tasks had been assigned to collect genetic data (T), or if genetic data was not to be collected or not mentioned (N).

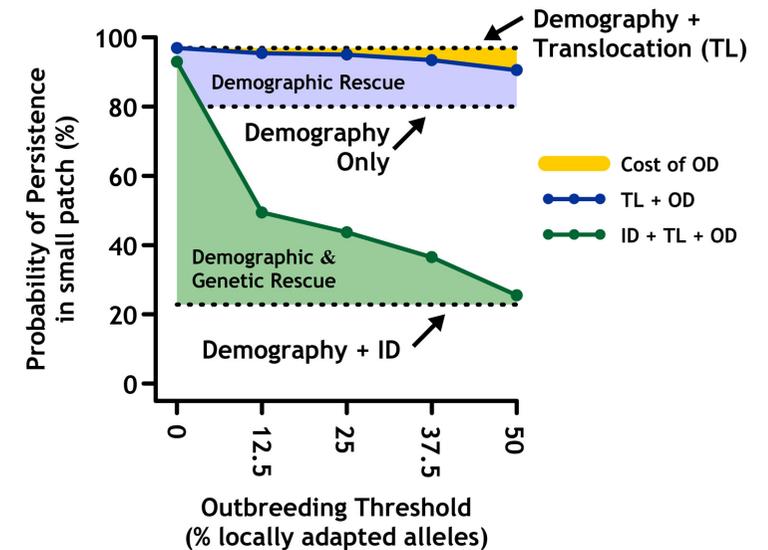


Figure 2: Results from a heuristic Eco-Evo PVA of the effects of translocations on population persistence of a population in small patch loosely based on the bristlebird example (see text). The average probability of persistence based on 5000 replicates of each scenario. Outbreeding depression and translocations were always included in a scenario together; scenarios with an outbreeding threshold ≥ 0 include translocations. ID = inbreeding depression, OD = outbreeding depression.

How will this affect Australian ecosystem science and management?

We highlighted gaps in the use of quantitative tools and consideration of genetic aspects of population viability in species recovery planning in Australia. The inclusion of evolutionary processes in population projections will be necessary to adequately model population dynamics, and may provide more realistic and optimistic outlooks for species than PVAs that model the effects of global warming and other threats in the absence of eco-evolutionary change. The reality of limited funding for conservation requires prioritizing when adding genetic processes to PVAs. Genetic processes should ideally be included in PVAs for all sexual species and for populations with small effective population sizes that are to be maintained over many generations. We recommend the focus remain on PVAs as decision-support tools for evaluating relative differences among scenarios such as competing management options, for sensitivity analyses to compare the relative importance of data inputs and processes, and for informing research agendas.

Key papers or products

Pierson J.C., Beissinger S., Bragg J., Coates D., Frankham D., Oostermeijer G., Sunnucks P., N Schumaker N., M Trotter, A Young. (in review) Eco-Evo PVAs: Incorporating Eco-Evolutionary Processes into Population Viability Models

Manuscripts under preparation

Do Threatened and Endangered Species Recovery Plans consider both genetic and demographics aspects of population viability?

A methods paper describing how to couple demography and genetics in a PVA

References

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- Hoekstra J.M., Clark J.A., Fagan W.F., Dee Boersma P. (2002) A comprehensive review of Endangered Species Act recovery plans. *Ecological Applications* 12: 630-640.
- Morris W.F., Bloch P.L., Hudgens B.R., Moyle L.C., Stinchcombe J.R. (2002) Population viability analysis in endangered species recovery plans: past use and future recommendations. *Ecological Applications* 12: 708-712
- Steiner, C.C., Putnam, A.S., Hoeck, P.E.A. & Ryder, O.A. (2013) Conservation genomics of threatened animal species. *Annual Review of Animal Biosciences* 1: 261-81