ED Peer Review '07

Population-level Ecological Risk Assessment to Support Pesticide Registration (SP2 MYP): Incorporating Simple Population Models into the Risk Assessment Process and Extending Their Complexity to include Greater Realism

Jason Grear, Glen Thursby, Jill Awkerman (Gulf Ecology Division), Matt Etterson (Mid-Continent Ecology Division), Sandy Raimondo (Gulf Ecology Division), Rick Bennett (Mid-Continent Ecology Division), Ruth Gutjahr-Gobell, Diane Nacci, Anne Kuhn, Denise Champlin

gency Problem

e development of regulatory guidelines and criteria to protect wildlife requires scientifically valid approaches for assessing risks to populations of these species from chemical stressors. This broad agency need is reflected in the specific problems faced ndividual Program Offices. For instance, the Office of Water (OW) requires criteria protective of populations of aquatic species and aquatic-dependent wildlife. The Office of Solid Waste and Emergency Response (OSWER) recognizes the need to blish consistency in wildlife risk assessment approaches employed in remedial investigations of hazardous waste sites. Further, the Office of Pesticides Programs (OPP) within EPA's Office of Pollution Prevention and Toxic Substances (OPPTS) is ling the way in expanding ecological risk assessments to provide probabilistic expressions of risk to fish and wildlife populations.

Research Goals

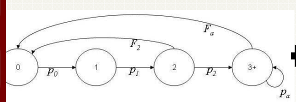
Long Term Goal 2 of the Safe Pesticides/Safe Products MYP is *"To create the scientific foundation for probabilistic risk assessment methods to protect natural populations of birds, fish and other wildlife."* The NHEERL Wildlife Research Strategy (US EPA 2005) conveys a conceptual model for achieving this goal. Consistent with that model, AED research has focused on methods and data requirements for:

- incorporating population-level endpoints into the Office of Pesticide Programs (OPP) risk assessment process;
- incorporating stochasticity (variation) into demographic models to produce probabilistic projections of population responses to stressors; and
- addressing complex population processes such as compensatory mechanisms (e.g., density dependence, adaptation) and spatial dynamics in projections of population responses to individual and multiple stressors.

These efforts are being integrated with NHEERL-level efforts to address sampling error issues associated with model parameters harvested from the literature and to provide guidance on when model complexities are necessary and feasible given available data from the literature and the chemical registration process.

Approach

initial step to address this agency problem was to elucidate specific technical challenges to the integration of ple population modeling approaches into OPP's risk assessment process. This was accomplished through elopment and demonstration of a population-level risk assessment using standard toxicity test data for the test anism *Americamysis bahia*. Based on previous work at AED (e.g., Kuhn et al. 2001), we developed a life cycle del and its matrix equivalent:



$$\mathbf{A} = \begin{Bmatrix} 0 & 0 & 1.6599 & 2.1117 \\ 0.9485 & 0 & 0 & 0 \\ 0 & 0.9584 & 0 & 0 \\ 0 & 0 & 0.8702 & 0.8478 \end{Bmatrix}$$

re 1. Life cycle graph and matrix model parameters for A. bahia. The projection interval is one week. tages are neonates, juveniles, sexually mature individuals, and fully reproducing adults

Figure 2. Mean matrix showing estimated fecundities (top row) and survival probabilities.

parameterized a stochastic version of the mean model shown in Figure 2 using Kendall's (1998) maximum likelihood estimators of vital rate means and variances in control treatment from past toxicity studies conducted at AED (Table 1). These data, along with dose-response data on chemical toxicity provided by OPP for a specific chemical, became the basis for hastic projections of risk (using parameter substitution). The risk threshold was defined as the probability (first passage) of a 5% decline from initial population size. Results were essed in terms of projected risk given specific chemical dose levels (Figure 3).

1. Mean vital rates used in construction of the mean matrix (and their estimated variances). Maternity rates (*m*) e used in birth-flow computation of matrix model fecundities (*F*). The first three survival rates (*s*) are used irectly in the model as survival probabilities (*p*). p_a involves assumptions about constant survival rate to an ssumed lifespan of 13 weeks. Survival rates are computed using Kendall's (1998) maximum likelihood methods.

Param.	$\bar{X}$	$\hat{\sigma}^2$	Description
m_2	1.366	0.6799	Juvenile females produced per interval per stage 2 female.
m_a	2.346	0.8607	Juvenile females produced per interval per stage 3 and above female.
s_0	0.9485	0.002	Survival from day 0 to day 7.
s_1	0.9584	9e-04	Survival from day 7 to day 14.
s_2	0.8702	0.005	Survival from day 14 to day 21.
s_3	0.8494	2e-04	Survival from day 21 to day 28.

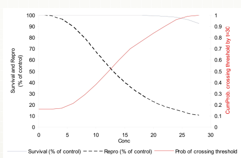


Figure 3. Example output from stochastic mysid population model showing dose responses for a specific chemical and population-level risk projections at increasing concentrations.

esults and Conclusions

- Provided a detailed demonstration to program office risk assessors
- Current population models designed to address OPP needs require parameters that may be technically incompatible with current toxicity data standards
- Parameter uncertainty is large, both for point estimates and the variances needed for probabilistic models

mpacts and Outcomes

- acilitated discussion of specific technical needs and inconsistencies between model parameters and standard toxicity data
- Models written in R and Matlab and translated to Excel for preliminary exploration by taff scientists
- Demonstrated data requirements and sample size issues for parameterizing models
- lluminated the role of stochasticity and other ecological complexities in population modeling
- Provided specific population models for exploratory test runs by OPP risk assessors

Future Directions

- Continue to address technical issues regarding compatibility of model constraints with toxicity data
- Examine importance of parameter distribution assumptions and error partitioning to risk assessment uncertainty
- Provide additional narrative guidance for model interpretation
- Test, refine, and document models for incorporation into OPP risk assessment

Approach

OPP needs simple "problem formulation" screening tools for predicting possible chemical effects on wildlife population fitness in agricultural landscapes. In a collaboration with GED and MED, AED is combining published data with theory-based life history assumptions to elucidate general patterns of demographic sensitivity in birds of these environments. To facilitate this work, Grear and Elderd (submitted) describe the fitness estimation bias associated with common assumptions regarding survivorship.

- We used the following Weibull function to construct theoretical life histories ranging from Type I (low early mortality) to Type III (high early mortality) surviviorship strategies.

$$l_x = \exp[-(ax)^b]$$

- Next, we used full (i.e., Leslie) and partial life cycle (PLC) representations of these synthetic life histories. The PLC uses a weighted average to collapse survival into a constant rate (i.e. Type II).
- Figure 4 shows that, when the "true" survivorship is Type II (i.e., $b = 1$ in the Weibull function), the simpler PLC is adequate. For species where constant survival is less likely, bias is potentially large.
- Grear and Elderd use Jensen's Inequality to describe the mathematical basis of this outcome:

$$f(E[X]) \geq E[f(X)]$$

Jensen's Inequality states that the difference between the function of an expectation (e.g., the averaged survival curve) and the expectation of a function (the geometrically projected survival rates) is related to the concavity of the function, which in our study is captured by the survivorship shape parameter (*b*).

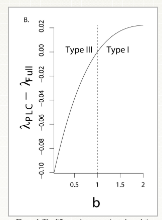


Figure 4. The difference between estimated population growth rates (λ) for the PLC and the full-matrix approaches plotted against the shape parameter (*b*) of the underlying synthetic life histories. The dashed vertical line corresponds to a Type-II life history.

Results and Conclusions

- Assumptions about lack of age-dependence in survival impact the direction and magnitude of growth rate estimation bias in ways that are predictable from the size of the shape parameter in survivorship curves (via Jensen's inequality)
- This shape parameter can sometimes be surmised from life history theory (e.g., Type III survival strategy)

Impacts and Outcomes

- Assumptions derived from life history theory can lead to cost savings for ecological risk assessment
- Our work helps risk assessors to identify the consequences of cost-saving assumptions about survival and determine when such assumptions are defensible in screening level analyses
- Such knowledge allows more efficient allocation of effort or recognition of uncertainty in cases where these screening level assumptions are not justifiable

Future Directions

- Incorporate life history assumptions to address information gaps in screening level assessment of chemical impacts on bird populations and provide guidance to their interpretation
- Apply findings to screening-level applications through collaboration with WED (spatial population models) and MED (models of toxicity effects on nest success)
- Provide technical guidance to OPP for specific screening-level applications

Approach

We are developing "spatially implicit" methods for incorporating spatial patterns and dynamics into risk assessment methodology. These methods require less data than do spatial explicit or individual-based methods, so discovering their effectiveness and data requirements is important. Our work in this area currently focuses on spatial population dynamics of *Peromyscus leucopus* (Grear and Burns 2007, Burns and Grear *submitted)*, but we are also developing spatial models for regional population dynamics of the common loon.

The basic structure for our spatial matrix models is an extension of vector permutation methods described by Hunter and Caswell (2005), where each B-subblock is patch or region-specific demography and each M sub-block represents migratory linkage between the demographic blocks:

$$\mathbb{B} = \begin{Bmatrix} \mathbf{B}_a & & \\ & \mathbf{B}_b & \\ & & \mathbf{B}_c \end{Bmatrix} \qquad \mathbb{M} = \begin{Bmatrix} \mathbf{M}_1 & & \\ & \mathbf{M}_2 & \\ & & \mathbf{M}_3 \end{Bmatrix}$$

We parameterized this model using mark-recapture data from trapping grids in three southern New England habitat mosaics.

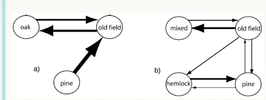


Figure 5. Graphical depiction of habitat-dependent movement probabilities conditional on survival in two habitat mosaic landscapes. Line thickness depicts size of the maximum likelihood estimate from the best mark-recapture model (based on AICc). Estimates range from 0.04 to 0.272 (probability of movement at the end of a six-week projection interval).

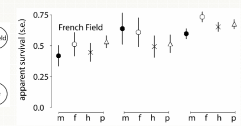


Figure 6. Stage-specific survival rates for the four habitats in Figure 5b (six-week interval).

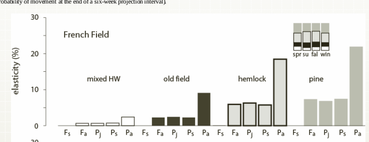


Figure 7. Elasticities (i.e., proportional sensitivities) of landscape-level population fitness to perturbations of individual habitat-specific rates of survival and reproduction. Impairment of adult survival in pine forest would be predicted to have a large effect at the landscape level (from Grear and Burns 2007).

Results and Conclusions

The importance of a specific habitat type to population fitness appears to depend on that habitat's context within the landscape. The interconnectedness of habitats linked by migration has great relevance for predicting how localized impairments (e.g., pesticide applications) will impact landscape level population dynamics. However, empirical evidence for this expectation is elusive due to the complexities of estimating movement and modeling spatial population dynamics. Our study applies recent developments in mark-recapture analysis and spatial matrix modeling to address this problem. In a second manuscript (Burns and Grear, submitted), we test predictions of these models in a landscape level manipulative experiment.

Impacts and Outcomes

The methods developed here are being generalized to predict landscape-level effects of other spatially discrete stressors (e.g., regional or local pollution effects). This study demonstrates the methods, data requirements and challenges likely to be faced as OPP incorporates spatial realism into its decision-making.

Future Directions

- Extend the computational tools developed in this analysis to spatial modeling of chemical risk to the common loon
- Exploit our expertise with the white-footed mouse to encourage and facilitate disease vector ecology research on links between ecosystem services and human health

Approach

We are using both citizen-collected and original population count data to examine methods for addressing effects of stochasticity on parameter estimation and probabilistic population modeling for wildlife risk assessment activities by OPP.

We are also studying stochasticity in demographic models, but we begin with count-based models (i.e., without demographic structure) because the theory is better developed for these simpler models. We focus on the diffusion and stochastic-logistic models of Dennis et al. (1991) and Dennis and Taper (1994). Application of diffusion-based approaches was recently described in Holmes (2004).

Grear et al. (2006) estimated stochastic population growth rates for the common loon using citizen-collected annual count data. More recently, we used the stochastic-logistic model to test for density dependence (Figure 8), but deviated from Dennis and Taper (1994) by using information-theoretic inference methods.

Table 2. AIC results for random walk, diffusion, density dependent and lagged density dependent models of common loon annual count data.

Model	Log Likl.	Δ AIC$_c$	AIC$_c$ wgt
σ^2	11.71	6.35	0.04
a, σ^2	12.04	8.92	0.01
a, b_1, σ^2	11.99	13.3	0
a, b_1, b_2, σ^2	22.64	0	0.95

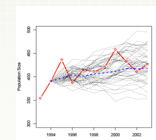


Figure 8. Simulation projections of a stochastic-logistic model (Dennis and Taper 1994) estimated from annual loon surveys in New Hampshire (manuscript in prep).

We are applying this stochastic modeling framework to controlled laboratory studies of mysid population dynamics in multiple independent populations (see poster by Nacci et al., this session). We are exploring information-theoretic approaches for modeling genetic and stress effects on these populations using linear models for each of the stochastic-logistic parameters, but the potential for inflated Type II error rates needs to be explicitly addressed before this analysis can be fully developed.

Results and Conclusions

Population growth rates estimated using simple diffusion models for the common loon compared favorably to independent estimates made from professional monitoring studies of loon productivity (see posters by Grear et al. and Kuhn et al., this session). The stochastic-logistic model, to which we added a one-year time lag, was better than the diffusion model based on AIC (Table 2). However, Type II error rates in AIC-based inference are not well understood for this kind of analysis. Nonetheless, we argue in a new manuscript on loon population demography (in prep.) that our analysis should lead to more targeted studies of density-dependence in common loon population dynamics, and that such density dependence may have critical influence on estimation of risk to common loons from anthropogenic stressors.

Impacts and Outcomes

Exponential models that lump potential density-driven dynamics into the stochastic term have the potential to overestimate extinction risk, so parsing out the effects of density dependence is sometimes important in ecological risk assessment. This work demonstrates application to development of population models that will ultimately be used by OPP to conduct chemical risk assessment.

Future Directions

- Continue to develop and investigate methods for incorporating diffusion-based methods into stochastic modeling approaches for population-level risk assessment by OPP
- Test the predictions from these stochastic models in experimental systems
- Use experimental data described in Nacci et al. poster to examine issues associated with multiple time series and error rates in parameter estimation, possibly through extramural collaboration.

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EPA Atlantic Ecology Division Narragansett, Rhode Island

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