Management of Toxic Chemicals Based on the Estimate of Population Extinction Risk.

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Abstract

Environmental threats, such as habitat size reduction or environmental pollution, may not cause immediate extinction of a population but shorten the expected time to extinction. We develop a method to estimate the mean time to extinction for a density-dependent population with environmental fluctuation, and compare the impacts of different risk factors. The relative importance of different risk factors is evaluated by the decrease in the mean extinction time. We study a formula for the reduction in habitat size that enhances extinction risk by the same magnitude as a given decrease in survivorship caused by toxic chemical exposure. We also study an estimate of the parameters from time series data. By Monte Carlo sampling, we can remove the bias very effectively and determine the confidence interval. We propose to use "risk equivalent" in ecological risk management of toxic chemicals.

1. Introduction

Nakanishi (1995) proposed that the risk of extinction of animals and plants might be used as the basis for quantifying ecological risk. The extinction of species, race, or any taxonomic unit is an unrecoverable and deprives future human generations of the

opportunity to enjoy its potential use. Even if most species are of no direct economical value, their loss serves as a good measure of ecological risk because it is correlated with the magnitude of the general threat to the ecosystem. Hence extinction risk is a good candidate of a measure upon which quantitative risk management can be based.

Suppose that a fraction of the habitat of a population is demolished. This may not cause immediate extinction, but it depresses the population size to a lower level than before, resulting in a shorter mean time to extinction (Fig. 1). Similarly, the mean time to extinction should be shorten if the population is exposed to a toxic chemical in a low concentration that reduces the survivorship or fertility. We developed a method to compare different risk factors by using a common currency of mean extinction time (Hakoyama and Iwasa 2000a, b; Hakoyama et al., 2000; Iwasa et al., 2000). For this purpose we need to consider a population model that incorporates density-dependent population regulation and environmental fluctuations (see also Middleton and Nisbet 1997; Saether et al. 1998).

Population size

Fig. 1   Extinctio   Time
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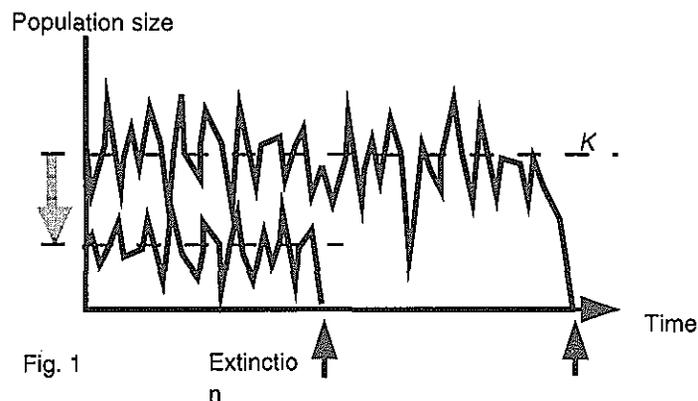
Many models in conservation biology handle the situation in which the population shows a clear negative trend, and the expected time to extinction is relatively short. In such a case, a useful method of risk estimate is available, which is based on a density-independent population model considering fluctuating population growth rate (Lande and Orzack 1988; Dennis et al. 1991). However this is not suitable for density-dependent populations, which would go extinct only after a long period of fluctuation around the equilibrium.

In this chapter, we present a method to evaluate the extinction risk of a density-dependent population and discuss the relative impact of the decrease in habitat size and the decrease in survivorship. This gives a basis of the next chapter by Mayuko Nakamaru who evaluated the ecological risk of DDT to a herring gull population.

2. Canonical Model

As a simple standard model of population dynamics, we choose a model that includes the minimum number of factors needed to consider the extinction risk of a

density-dependent population. Let X be the population size at time t. The dynamics are expressed in terms of the following stochastic differential equation:

$$\frac{dX}{dt} = rX\left(1 - \frac{X}{K}\right) + \sigma_e \xi_e(t) \circ X + \xi_d(t) \bullet \sqrt{X}, \qquad (r, K \text{ and } \sigma_e > 0), \qquad (1)$$

where r is the intrinsic rate of population growth, K is carrying capacity, $\xi_e(t)$ and $\xi_d(t)$ are independent white noises for environmental and demographic stochasticities, and σ_e is the intensity of the environmental fluctuation. We call Eq. (1) "canonical model." We here assume Stratonovich-calculus in the environmental fluctuation (denoted by a small open circle) and Ito-calculus in the demographic stochasticity (denoted by a solid circle). This choice is made for the convenience of parameter fitting to time series data (see Hakoyama and Iwasa 2000a for detail).

For a long-term sustainable population, the small size of initial population causes a relatively high extinction rate in the first several generations. Once the population survives through the initial critical period and reaches the carrying capacity, the population may stay around it for a long time before extinction. Thereaftrer, the extinction time follows an exponential distribution, and we can treat extinction events as if they occur at random (Quinn and Hastings 1987). The extinction risk can then be characterized by a single quantity -- mean time to extinction, which can be calculated as

$$T = \frac{2}{\sigma_e^2} \int\limits_0^{x_0} \int\limits_x^{\infty} e^{-R(y-x)} \left(\frac{y+D}{x+D}\right)^{R(K+D)+1} \frac{dy}{(y+D)y} dx, \qquad (2)$$

where $R \equiv \dfrac{2r}{\sigma_e^2 K}$ and $D \equiv \dfrac{1}{\sigma_e^2}$ (Hakoyama and Iwasa, 200a). We use the average extinction time starting from the carrying capacity $x_0 = K$ in the following analysis (see Lande 1993; Lande et al. 1995).

3. Comparison of different risk factors

Effect of reduction in habitat size

When the habitat area is reduced, carrying capacity K becomes smaller and the average extinction time T becomes shorter. The way it depends is

$$\log T = \frac{2r}{\sigma_e^2} \log K + [\text{terms independent of } K], \qquad (3)$$

(Ludwig 1976; Lande 1993; note the difference in the expression of proportionality coefficient caused by their choice of Ito-calculus). The mean extinction time is a power function of the carrying capacity $T \propto K^{2r/\sigma_e^2}$. The dependence of the mean extinction time on carrying capacity varies with the environmental fluctuation. When the environmental fluctuation is small, the average time to extinction T increases very quickly with carrying capacity K. In contrast when environmental fluctuation is large, it increases with K slowly.

Effect of decrease in survivorship

Consider a population exposed to toxic chemical substances in the environment. Let α be the magnitude of the subsequent reduction in survivorship per generation. Population dynamics have an additional negative term for the loss:

$$\frac{dX}{dt} = rX\left(1 - \frac{X}{K}\right) + \sigma_e \xi_e(t) \circ X + \xi_d(t) \bullet \sqrt{X} - \alpha X,$$

$$= \tilde{r}X\left(1 - \frac{X}{\tilde{K}}\right) + \sigma_e \xi_e(t) \circ X + \xi_d(t) \bullet \sqrt{X}, \qquad (4)$$

where $\tilde{r} = r - \alpha$, $\tilde{K} = K - K\dfrac{\alpha}{r}$. The decrease in survivorship by α per generation makes both r and K smaller in the canonical model Eq. (1), and its impact on the mean extinction time can be evaluated by using Eq. (2). The same is applicable to the risks caused by pathogens, genetic deterioration, or any process that decreases the survivorship or fertility.

Comparing different risk factors

Figure 2a shows the relationship between the decrease in the survivorship per generation α and the mean extinction time T. This was calculated for severalcarrying capacities K indicated by different curves. Two other parameters (intrinsic rate of population growth r and environmental noise σ_e^2) are the estimates for the crucian carp in Lake Biwa, Japan, from fishery records (Hakoyama and Iwasa 2000a). Around Lake Biwa, there are many lakelets and small populations of crucian carp that may have similar r and σ_e^2, but different K. The estimate of mean extinction time shown here is the extinction risk of crucian carp populations in these lakelets. Mean extinction time decreases quickly with α and $\log T$ declines with α almost linearly. The decrease in logarithmic mean extinction time is larger for a large population ($K = 10^5$) than a small population ($K = 10^2$). This implies that the decrease in the survival rate per generation α are very effective in threatening large populations that are otherwise quite stable.

Figure 2b illustrate the decrease in the mean extinction time and the habitat loss. A value on the horizontal axis of 50 implies that half of the area is demolished without

changing the condition in the remaining part of the habitat. Mean extinction time decreases with habitat area, initially at a slow rate and then rapidly decrease to zero between 90% loss and 100% loss. Note that the curves corresponding to different K are parallel to each other, implying that the decrease in a fixed fraction of habitat area causes the same decrease in log T, irrespective of the total population size K.
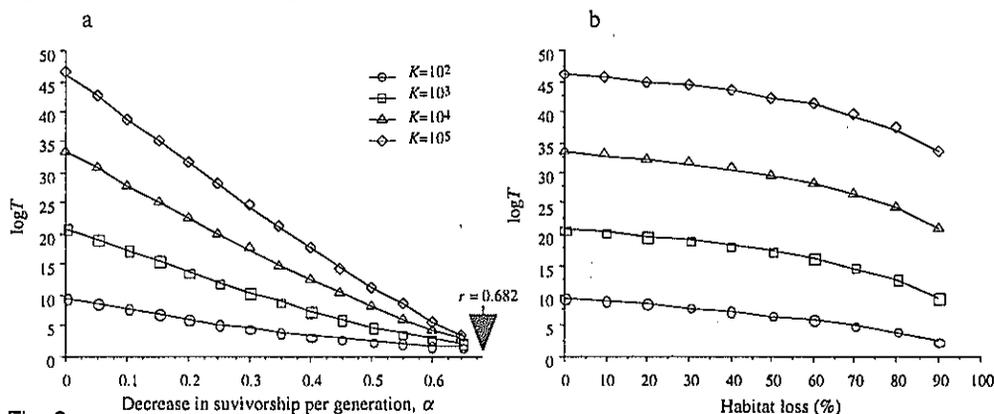
Fig. 2

With a small carrying capacity $K = 10^2$, 25 % decrease in survivorship per generation is needed to cause the risk equivalent to 50 % habitat loss. In contrast with a large carrying capacity $K = 10^5$, 5 % decrease in survivorship per generation ($\alpha = 0.05$) is equivalent to about 50 % habitat loss. In general, the magnitude of the reduction in habitat size in terms of the decrease in the logarithm of carrying capacity $\Delta \log K$ is approximately proportional to the decrease in the survivorship per generation α.

$$\Delta \log K = \left(\frac{\sigma_e^2}{2r} \log T \right) \frac{\alpha}{r}, \qquad (5)$$

where T is the mean extinction time (Hakoyama et al., 2000b). The proportionality coefficient increases with carrying capacity K because it increases $\log T$ if the other two parameters are fixed. This implies that the relative importance of the decrease in the habitat area compared to the decrease in survivorship is high for unstable and endangered population (with a small $\log T$); but is low in stable populations (a large $\log T$).

To relate the decrease in survivorship α and concentration of toxic chemicals z, we need to use a nonlinear relationship between them as summarized by Tanaka (1997).

4. Parameter Estimation from a Time Series

To apply the model to field populations, we need to estimate three parameters. Hakoyama and Iwasa (2000a) studied the estimate of unknown parameters from a time series of population size $\{X(t)\}$.

For density-dependent populations, the population size fluctuates around the carrying capacity for a long time before going extinct. We may consider quasi-equilibrium probability distribution of population size controlled by logistic growth and environmental stochasticity. If the demographic stochasticity is much smaller than environmental stochasticity, as is the case if the population size is moderately large, carrying capacity K is equal to the expectation of population size:

$$K = \mathrm{E}[X(t)], \tag{6}$$

in which the expectation can be replaced by the average over the years. Equation (6) implies that the carrying capacity can be estimated simply from the average population size. This is possible even if the magnitude of fluctuation in the population size caused by environmental stochasticity is large.

The environmental stochasticity can be estimated from the magnitude of population fluctuation, as the variance of the population size increases with the environmental stochasticity σ_e^2. If the intrinsic growth rate r is known from separate sources, we can estimate the carrying capacity by the average population size from Eq. (6), and then the environmental variance σ_e^2 by the observed variance of the population fluctuation. If a reliable estimate of intrinsic rate of population growth r is not available, we can still estimate r from only a time series of population size. If r is larger, autocovariance drops faster, i.e. the population fluctuates more quickly over time. Hakoyama and Iwasa (2000a) developed the approximate maximum likelihood (or the AML) estimate (see also Iwasa et al., 2000).

Mean and percentiles of estimators

To know the reliability of the estimation method, Hakoyama and Iwasa (2000a) carried out Monte Carlo analyses. We generated a number of independent Monte Carlo time series data using the model with a single set of parameters, and then calculated the AML-estimate of the three parameters $\left(\hat{r}, \hat{K}, \hat{\sigma}_e \right)$ for each time series. The average of the estimator $\hat{r}$ was larger than the value used for generating these time series data r, implying a bias. The biases of $\hat{K}$ and $\hat{\sigma}_e$ were small. The distribution of mean extinction time $\hat{T}$ calculated from these parameters had also a systematic bias. Figure 3 illustrates the mean and the 2.5 and 97.5 percentiles of the AML-estimates for different length of time series data. Both bias and variance of estimates are large for short time series (e.g. the length is 10), and they do not disappear even for a very long time series (such as 1000 data points).

Bias-corrected estimation based on Monte Carlo sampling

We can remove the bias in estimate by Monte Carlo iterations (Hakoyama and Iwasa 2000a). The basic idea underlying the method is as follows: Suppose that we generate a
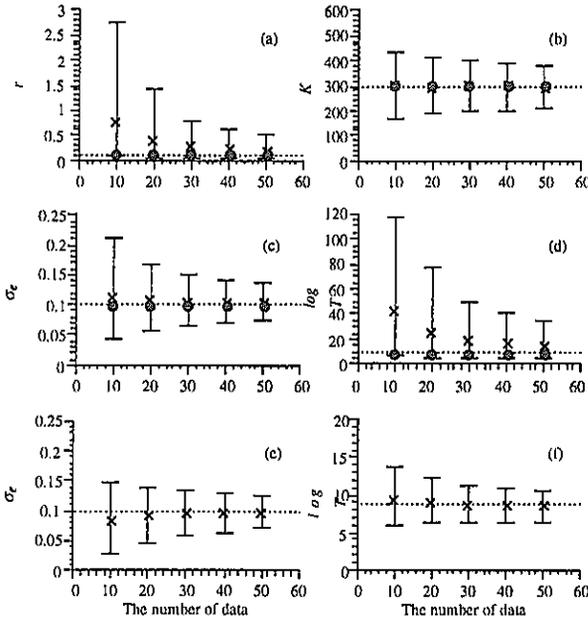
Fig. 3
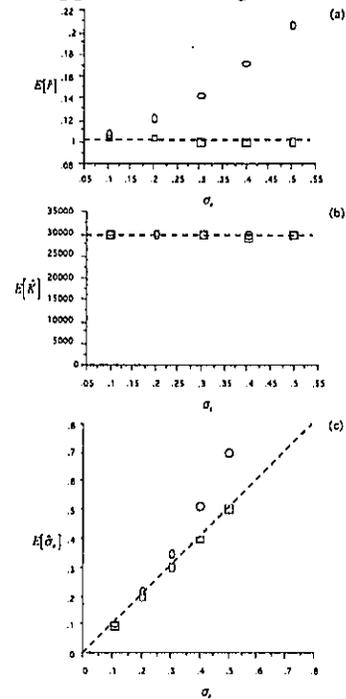
Fig. 4

number of independent Monte Carlo time series by a model with parameters $\left(r, K, \sigma_e^2\right)$, and then calculate the AML-estimates $\left(r^*, K^*, \sigma_e^*\right)$ for each. The averages of these values are different from $\left(r, K, \sigma_e^2\right)$, becauseof thebias. For example, the AML of r tends to overestimate the true value : $E\left[r^*\right] > r$Hence the AML-estimate calculated from an observed time series, denoted by $\left(r_{obs}, K_{obs}, \sigma_{e,obs}\right)$,, is likely to be systematically different from the true value. To remove this bias, we search for a value r_{bc}, which is smaller than the observed value r_{obs}, and the model using r_{bc} should generate the AML estimator that has the mean equal to r_{obs}. Since there are three parameters, we should search for a set of parameters $\left(r_{bc}, K_{bc}, \sigma_{e,bc}\right)$ so that the model with these values can generate the Monte Carlo time series with the AML having the averages equal to $\left(r_{obs}, K_{obs}, \sigma_{e,obs}\right)$. The bias corrected estimators $\left(r_{bc}, K_{bc}, \sigma_{e,bc}\right)$ can be obtained by iterative Monte Carlo calculation.

Figure 4 shows that the magnitude of bias in estimate of r increases with σ_e^2 from 0.1 to 0.5 ($r = 0.1$). These correspond to the cases in which the standard deviation of the population size (approximately equal to $\left(\sqrt{\sigma_e^2/2r}\right)K$) is larger than the mean, and the AML-estimate of r is much higher than the true value, showing a large bias. In contrast, the average of the bias corrected estimate based on Monte Carlo sampling with a mildly long time series (the length of time series is 50) are indicated by squares, which are close to the

true value indicated by a broken line. This demonstrates the effectiveness of bias correction procedures based on Monte Carlo sampling.

To evalulate the reliability of the estimate, we can obtain the confidence intervals of the estimates based on Monte Carlo methods (Hakoyama and Iwasa 200a; Iwasa et al. 2000).

Estimate of mean extinction time when r is known

In many cases, we have a relatively accurate estimate of intrinsic growth rate r based on biology of the species, but we need to estimate carrying capacity K and environmental noise σ_e^2 from a time series of population size.

Figures 3e and 3f illustrate the averages and percentiles of the AML-estimates when intrinsic population growth rate r is known. The variance of $\hat{\sigma}_e$ is smaller in Fig. 3e than in Fig. 3d when K is unknown. Note that the estimate of $\log \hat{T}$ is very accurate even for a short time series (e.g. the number of data points are as small as 10) if r is known. The knowledge of r greatly improves the estimate of parameters and the mean extinction time $\log T$, which is accurate even without Monte Carlo bias correction.

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