

# INDIVIDUAL-BASED INTEGRAL PROJECTION MODELS: THE ROLE OF SIZE-STRUCTURE ON EXTINCTION RISK AND ESTABLISHMENT SUCCESS

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## INTRODUCTION

Computations of extinction probabilities or likelihoods of establishment success lie on opposing sides of a theoretician's coin and are used to address questions in conservation biology, restoration ecology, biological invasions and population genetics. Risks of extinction or establishment failure stem from populations consisting of a finite number of individuals each of which faces a non-zero risk of mortality on any given day. These risks are shaped, in part, by the size and composition of a population in which individuals may differ in age, size, geographical location, or other important characteristics influencing demography. When population structure is finite-dimensional (i.e. a finite number of age classes, stages, geographical locations), multi-type branching processes serve as the stochastic counterpart of matrix models [Harris, 1963, Athreya and Ney, 2004, Caswell, 2001]. These models allow one to examine how extinction risk or establishment success depend on the population size and its distribution across a finite number of states (e.g. ages, size classes, patches).

When collecting demographic data, one commonly makes continuous measurements (e.g. mass, length) about individuals. Consequently, since their introduction in the early 2000s, there has been a surge of interest in integral projection models (IPMs) that account for continuous population structure [Easterling et al., 2000, Ellner and Rees, 2006, Rees and Ellner, 2009, Childs et al., 2004, Ramula et al., 2009, Jongejans et al., 2011, Ellner and Schreiber, In press]. As IPMs correspond to infinite-dimensional matrix models which are numerically approximated by finite-dimensional matrix models, many of the standard demographic concepts and methods for matrix models (e.g. stable state distributions, reproductive values, life table response experiments) extend to IPMs [Metcalf et al., 2013, Rees et al., 2014, Merow et al., 2014].

Here, we describe individual-based counterparts of IPMs by making use of the theory of continuous-state branching processes introduced by Harris [1963]. We present an analytical method, differing from Harris, for computing extinction probabilities for these individual-based IPMs. These methods are easily implemented numerically and circumvent running individual-based simulations to examine how extinction probabilities depend on continuous or discrete population structure. To illustrate the implementation of these methods, we introduce and analyze an individual-based IPM of the endangered alpine plant *Dracocephalum austriacum*, which corresponds to a stochastic counterpart of the IPM developed by Nicole et al. [2011].

## THE GENERAL MODELS AND METHODS

**The Individual Based IPM.** We consider an individual-based model where the set of all possible individual states (e.g. age, size, etc.) lies in a compact metric space  $X$ . For example, for the standard size-structured IPM,  $X = [a, b]$  corresponds to the range of sizes measured in the field. For models with a mixture of age and size structure,  $X$  could be given by  $\{1, \dots, T\} \times [a, b]$  where  $T$  corresponds to the maximal age of an individual.

As we consider finite populations, the state of the population at any point of the time is characterized by the different sizes  $(x_1, x_2, \dots, x_k)$  of individuals within the population and how many individuals there are of each these sizes  $(n_1, n_2, \dots, n_k)$ . Specifically, if there  $n_1$  individuals of size  $x_1$ ,  $n_2$  individuals of size  $x_2$ , ...,  $n_k$  individuals of size  $x_k$ , then the state of the population is given by  $(n_1, n_2, \dots, n_k; x_1, x_2, \dots, x_k)$ . Following Harris [1963], the set of all possible population states is

$$\mathcal{S} = \{(\mathbf{n}, \mathbf{x}) = (n_1, \dots, n_k, x_1, \dots, x_k) : k, n_i \in \mathbb{N}, x_i \in X\} \cup \{0\}$$

where  $\mathbb{N} = \{1, 2, 3, \dots\}$  denotes the natural numbers and 0 is the extinction state corresponding to no individuals in the population.

Let  $\mathbf{s}_t = (\mathbf{n}, \mathbf{x}) \in \mathcal{S}$  be the population state at time  $t$ . The dynamics of  $\mathbf{s}_t$  are determined by a set of probabilistic rules that determine the contribution of each individual in the population to the population in next time step  $t+1$ . These "contributions" may correspond to an individual surviving and changing state (e.g. growing in size), or having offspring. Consistent with standard branching process theory, each individual in the population updates independent of all other individuals. The update rule for an individual of size  $x$  is given by a probability measure  $m(x, d\mathbf{s})$  on the state space  $\mathcal{S}$ . Specially, the probability an individual in state  $x$  contributes  $\mathbf{s}$  individuals to the population in the next time step where  $\mathbf{s}$  lies in a subset  $A \subset \mathcal{S}$  equals

$$\mathbb{P}[\mathbf{s}_1 \in A | \mathbf{s}_0 = (1, x)] = \int_A m(x, d\mathbf{s})$$

where the left hand side reads "the probability the population state lies  $A$  at time  $t = 1$  after initially having only one individual in state  $x$ ."

If the population state is currently  $\mathbf{s}_t = (n_1, \dots, n_k, x_1, \dots, x_k)$ , then the state  $\mathbf{s}_{t+1}$  is determined as follows:

- (1) for each of the  $n_1$  individuals in state  $x_1$ , randomly and independently choose the number of replacement individuals from distribution  $m(x_1, d\mathbf{s})$ .
- (2) repeat step 1. for the types  $x_2, \dots, x_k$ .
- (3) determine the new population state by identifying the states of all individuals and counting the total number of individuals in each of these states.

This iterative algorithm can be used to create individual based simulations of the individual based IPM. As with any branching process, stochastic realizations of this process, with probability one, either go to extinction in finite time, or the population size grows without bound.

**Probability generating functionals and extinction probabilities.** As with multiple-type branching processes, we can characterize the probabilistic state of the system using probability

generating functionals  $\Psi$  (pgfs). Our approach differs from Harris [1963] who used moment generating functionals instead. Unlike mgfs, the pgfs allow us to compute how extinction probabilities change in time as well as compute asymptotic extinction probabilities.

To define the pgf  $\Psi$ , we introduce the following notation: given a continuous function  $h : X \rightarrow \mathbb{R}$  and  $\mathbf{s} \in \mathcal{S}$ , let

$$h^{\mathbf{s}} = \begin{cases} \prod_{i=1}^k h(x_i)^{n_i} & \text{if } \mathbf{s} = (n_1, \dots, n_k, x_1, \dots, x_k) \\ 1 & \text{if } \mathbf{s} = 0. \end{cases}$$

We define the pgf by

$$(*) \quad \Psi(h)(x) = \int h^{\mathbf{s}} m(x, d\mathbf{s}).$$

In words,  $\Psi(h)(x)$  corresponds to the expected value of  $h^{\mathbf{s}}$  due to the contributions of individuals in the next time step from an individual in state  $x$ . This requires integrating over all possible populations states in the next time step.

The utility of  $\Psi$  for computing extinction probabilities follows from two facts. The first fact stems immediately from the definition: if  $h_0$  is the zero function (i.e.  $h_0(x) = 0$  for all  $x$ ), then

$$\Psi(h_0)(x) = \int 1 m(d\mathbf{s}, x) = \mathbb{P}[\mathbf{s}_1 = 0 | \mathbf{s}_0 = (1, x)]$$

is the probability the population goes extinct in one time step given that initially it consisted of one individual in state  $x$ . For the second fact, we define

$$\Psi^t(h) = \underbrace{\Psi(\Psi(\dots \Psi(h) \dots))}_{t \text{ times}}$$

to be the  $t$ -fold composition of  $\Psi$  with itself. We claim that

$$(**) \quad \Psi^t(h_0)(x) = \mathbb{P}[\mathbf{s}_t = 0 | \mathbf{s}_0 = (1, x)] =: E_t(x)$$

is the probability of extinction by time  $t$  given that the population initially consisted of one individual in state  $x$ . To see why this fact is true, we argue by induction. The first fact proves that the statement holds for  $t = 1$ . Now suppose the assertion holds for  $t$ , we will show it holds for  $t + 1$ . On the event that  $\mathbf{s}_1 = (n_1, \dots, n_k, x_1, \dots, x_k)$  is the population state at time 1, extinction occurs by time  $t + 1$  only if each of the lineages of the  $n_1 + \dots + n_k$  individuals go extinct in the next  $t$  time steps. As the fates of these lineages are independent of one another, it follows that

$$\begin{aligned} \mathbb{P}[s_{t+1} = 0 | \mathbf{s}_0 = (1, x), \mathbf{s}_1 = (n_1, \dots, n_k, x_1, \dots, x_k)] &= \prod_{i=1}^k \mathbb{P}[\mathbf{s}_t = 0 | \mathbf{s}_0 = (1, x_i)]^{n_i} \\ &= \prod_{i=1}^k (\Psi^t(h_0)(x_i))^{n_i} = \Psi^t(h_0)^{\mathbf{s}_1} \end{aligned}$$

where the second equality follows from our inductive hypothesis. By the law of total probability

$$\mathbb{P}[s_{t+1} = 0 | \mathbf{s}_0 = (1, x)] = \int [\Psi^t(h_0)]^{\mathbf{s}} m(d\mathbf{s}, x)$$

which, by definition, equals  $\Psi^{t+1}(0)(x)$  as claimed.

Hence, equation (\*\*) can be used to compute extinction probabilities iteratively. Furthermore, as individuals update independent of one another, the probability of the population going extinct by time  $t$  for any initial condition  $\mathbf{s} = (n_1, \dots, n_k, x_1, \dots, x_k)$  equals

$$\mathbb{P}[\mathbf{s}_t = 0 | \mathbf{s}_0 = \mathbf{s}] = E_t^{\mathbf{s}}.$$

These analytic expressions allow us to efficiently compute extinction probabilities by constructing a numerical approximation of the pgf and iterating it with an initial condition of a zero vector which corresponds to the numerical approximation of the zero function.

As  $E_0(x) \leq E_1(x) \leq E_2(x) \dots$  for any  $x \in X$  and  $E_t(x) \leq 1$  for all  $t$ , there is a well defined limit corresponding to the probability of eventual extinction:

$$E_{\infty}(x) := \lim_{t \rightarrow \infty} E_t(x).$$

Using moment generating functionals and under suitable technical hypotheses, Harris showed that  $E_{\infty}(x) < 1$  for all  $x$  if the dominant eigenvalue of the mean-field IPM is greater than one, and  $E_{\infty}(x) = 1$  for all  $x$  otherwise.

#### AN ILLUSTRATION WITH AN ENDANGERED PLANT SPECIES

To illustrate how these general methods can be applied to a data set, we develop an individual-based IPM based for the endangered alpine plant *Dracocephalum austriacum*. This model will correspond to an individual-based counterpart of the IPM developed by Nicole et al. [2011]. The Austrian Dragonhead (*D. austriacum* L., *Lamiaceae*) is a long-lived perennial plant that is listed as Vulnerable by the World Conservation Union [Nicole et al., 2011]. We use data collected by Nicole et al. [2011] in 2001-2002 to build the IPM.

If  $N_t(x)$  denotes the density of individuals of size  $x$  in year  $t$ , then Nicole et al. [2011] used an IPM of the form

$$N_{t+1}(x) = \int_a^b s(y)G(y, x) + e(x)p(y)f(y)N_t(y) dy$$

where  $s(y)$  is the probability of surviving to the next year for individuals of size  $y$ ,  $G(y, x)dy$  is the infinitesimal probability that a surviving individual of size  $y$  is size  $x$  in the next year,  $p(y)$  is the probability an individual of an individual size  $y$  flowers,  $f(y)$  is the mean number of germinating offspring produced by an individual of size  $y$ , and  $e(x)$  is the infinitesimal probability of an offspring is of size  $x$  at the time of the annual census.

Consistent with citetnicole-etal-11, we used generalized linear models (GLMs) to select functional forms for each of the demographic kernels. Computation were performed using the GLM package for R [R Core Team, 2015]. Specifically, we used logistic regression (i.e. a GLM with the binomial family) for determining  $s(y)$  and  $p(y)$ , a GLM with the Poisson family for modelling  $f(y)$ , and modeled the  $e(y)$  using a normal distribution whose mean and variance were determined by the empirical distribution of germinants. For the growth kernel, linear regression determined the expected size of an individual in the next year and the actual size was assumed to be normally distributed about this mean. For more information, see citetnicole-etal-11 and online supplement kernels.R. Figure 1 shows the data and fits for  $s(y)$ ,  $G(y, x)$ ,  $p(x)$  and  $f(x)$ .

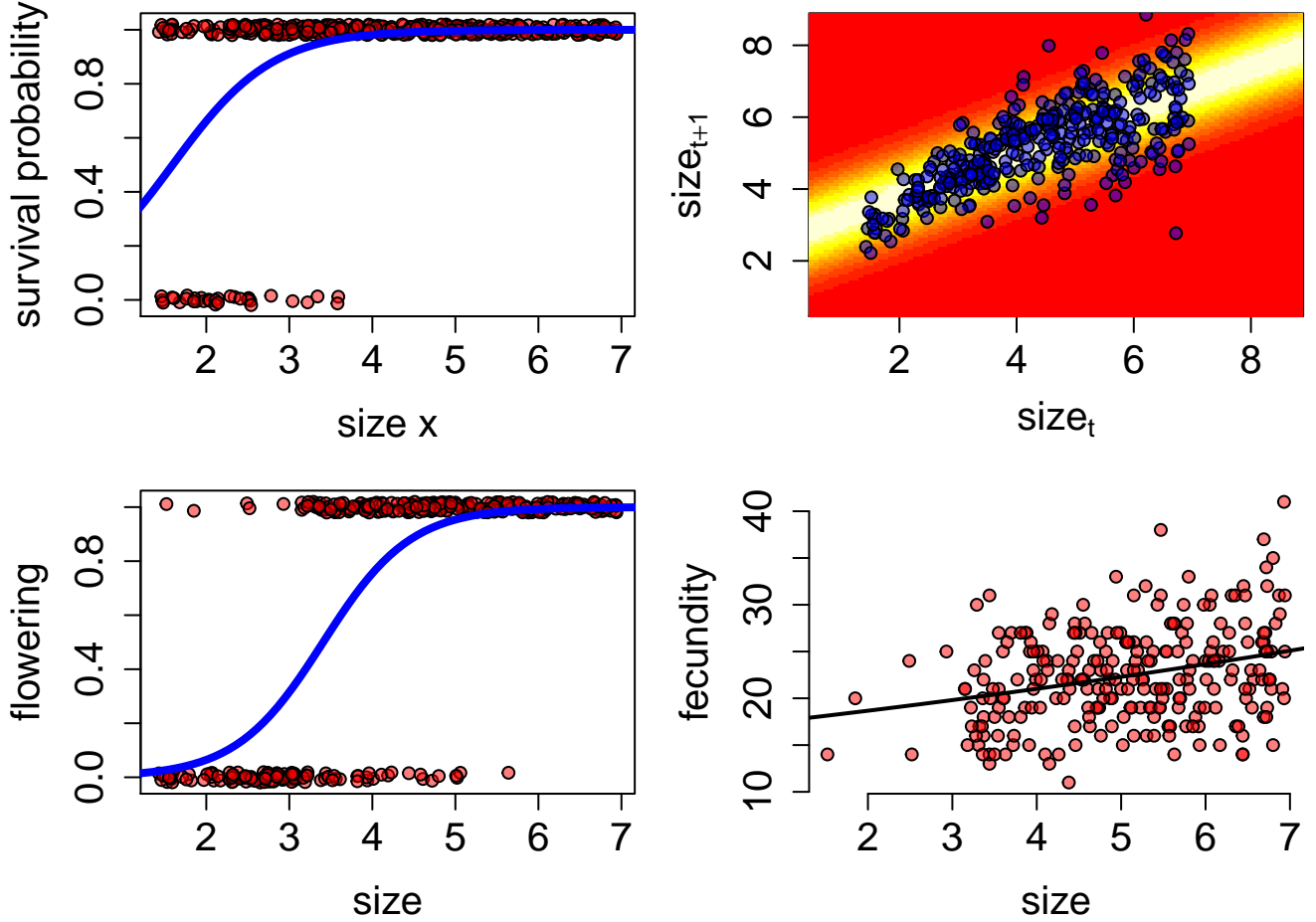


FIGURE 1. The demographic kernels and the corresponding data.

The kernels  $s(x)$ ,  $G(y, x)$ ,  $p(x)$  and  $e(x)$  provide us with all the information that the individual-based IPMs requires for probabilistic updating individuals for survival, growth, flowering or not, and size at first census. The fecundity kernel  $f(y)$ , however, only specifies the mean number of offspring produced, but for an individual-based IPM, we need the distribution of the number of offspring produced by an individual. Fortunately, when using GLMs for the fecundity data, this extra information comes for free. For example, the fecundity data was modeled using a Poisson family for the GLM. In which case, the mean number  $f(x)$  of offspring also specifies the distribution. More general, one might use multi-parameter distributions such as a zero inflated Poisson or a negative binomial in which case parameters beyond the mean are needed to specify the distribution of offspring number.

**Deriving the pgf  $\Psi$ .** To define  $\Psi$ , we observe that the contributions of an individual of size  $x$  to the population in the next time step involves the sum of two independent random variables: the

contribution due to survival and growth and the contribution due to reproduction. We will identify the pgfs,  $\Psi_g$  and  $\Psi_f$ , for each of these processes separately. Then, we make use of a fundamental property of pgfs:

!The pgf for a sum of independent random variables is the product of the pgfs of these random variables.

to get that

$$\Psi = \Psi_g \times \Psi_f.$$

When the random variables are identically, distributed, we have the following generalization of this fundamental property of pgfs:

!The pgf for a sum of  $N$  independent, identically distributed random variables  $X_i$  is the composition of the pgf for  $N$  with the pgf for the  $X_i$ .

For the pgf  $\Psi_g$  for survival and growth,  $\Psi_g(h)(x)$  corresponds to integrating  $h^{\mathbf{s}}$  over all possible contributions  $\mathbf{s}$  from an individual of size  $x$  surviving and growing. These contributions are of two types:  $\mathbf{s} = \emptyset$  when the individual dies, and  $\mathbf{s} = (1, y)$  when the individual survives and grows to size  $y$ . The first event occurs with probability  $1 - s(x)$  and the infinitesimal probability of the second event is  $s(x)G(y, x)dy$ . As  $h^{\mathbf{s}} = 1$  when  $\mathbf{s} = \emptyset$  and  $h^{\mathbf{s}} = h(y)$  when  $\mathbf{s} = (1, y)$ , integrating over all possible contributions due to survival and growth yields

$$\Psi_g(h)(x) = (1 - s(x)) \times 1 + s(x) \int h(y)G(y, x)dy.$$

For the pgf  $\Psi_f$  corresponding to contributions due to fecundity,  $\Psi_f(h)(x)$  is given by integrating  $h^{\mathbf{s}}$  over all possible states  $\mathbf{s}$  corresponding to the offspring produced by an individual of size  $x$ . To write this down, we apply the second fundamental property of pgfs twice. We begin by conditioning on the event that an individual of size  $x$  flowers. On this event, the individual produces a Poisson number  $N$  of offspring with mean  $f(x)$ . The size of each of these offspring is drawn interdependently from the common offspring distribution  $e(y)dy$ . Hence, the contribution of a flowering individual of size  $x$  is the sum of  $N$  independent random variables with distribution  $e(y)dy$ . By the second fundamental property of pgfs, we need to take the composition of the pgf for  $N$ , namely  $\phi(x, \cdot)$ , with the pgf for a single offspring, namely

$$\Psi_e(h)(x) = \int h(y)e(y)dy.$$

Thus, we get the pgf associated with a flowering individual is

$$\Psi_{flower}(h)(x) = \phi(x, \int h(y)e(y)dy)$$

To get the pgf for flowering and non-flowering contributions to fecundity, we observe that fecundity contributions of an individual of size  $x$  is given by the "sum" of a Bernoulli number of flowering individuals where the probability of success is  $p(x)$ . Namely, we need to compose the pgf of a Bernoulli, which is  $\theta(s) = 1 - p(x) + p(x)s$  where  $s$  is the dummy variable, with the pgf of a flowering individual. This composition yields

$$\Psi_f(h)(x) = \theta(\Psi_{flower}(h)(x)) = 1 - p(x) + p(x)\phi(x, \int h(y)e(y)dy)$$

Putting together the two pieces, we get the desired pgf  $\Psi$ :

$$\Psi(h)(x) = \left( (1 - s(x)) \times 1 + s(x) \int h(y)G(y, x)dy \right) \phi(x, \int h(y)e(y)dy).$$

We note that this argument works did not rely on the form of the offspring pgf  $\phi$ . Hence, we can use the same expression for alternative offspring distributions as illustrate later.

**Numerically Implementing and Using the pgf  $\Psi$ .** To create this probability generating functional numerically, we discretize the size interval  $[\alpha, \beta]$  using  $n$  equal sized intervals of width  $dx = (\beta - \alpha)/n$ . To use the midpoint rule to approximate the integrals, we created a vector  $xs$  corresponding to the midpoints of these intervals. Using this vector we discretized the survival function as a vector  $s.vec = s(xs)$ , the growth kernel as a matrix using the outer product  $g.mat = outer(xs, xs, g)$ , the probability of flowering function as a vector  $p.vec = p(xs)$ , the fecundity function as a vector  $f.vec = f(xs)$ , and the offspring size distribution as a vector  $e.vec = e(xs)$ .

For the previously described methods to work, it is critical that column sums for growth and the sum of offspring size distribution vector equal one i.e. the columns are probability vectors. For most IPMs, this will not occur automatically due to individuals being evicted from the size interval  $[\alpha, \beta]$ . There are a variety of ways to handle this issue (Ref). As the offspring size vectors nearly summed to one, we simply re-normalized it so that it summed to one. For the growth matrix, we treated eviction as mortality to be consistent with the model developed by Nicoles et al. To do this, we took one minus the column sums and subtracted them from the survival vector and then normalized the column sums so that they added to one. When taking the product of survival and growth, the mean-field IPM is unaffected by this change.

Using these discretized demographic components and the pgf  $\phi$  for fecundity, we get the discretized pgf  $\Psi$  is given by

$$\Psi_{discrete}(h) = s.vec \circ (g.mat^T h) + 1 - s.vec \circ (1 - p.vec + p.vec \circ phi(xs, e.vec^T h))$$

where  $h$  corresponds to a discretized function i.e. a vector of length  $n$ ,  $^T$  denotes the transpose of a matrix or vector, and  $\circ$  denotes element by element multiplication.

Figure 2 illustrates how extinction probabilities  $E_t(x)$  vary with size over a 100 year time frame. Intuitively, this figure illustrates that the probability of extinction decreases with the size of individual initially founding the population, and extinction probabilities increase over time. Furthermore, this figure illustrates that  $E_t(x)$  are approaching limiting extinction probabilities  $E_\infty(x)$  which are less than one. This stems from the fact that the dominant eigenvalue of the mean-field IPM is greater than one. To estimate this asymptotic probability of extinction one can iterate  $\Psi$  until a tolerance condition is met e.g.  $|E_{t+1}(x) - E_t(x)| \leq \epsilon$  for all  $x$ .

To scale things up to an entire population, recall that for a population initially in state  $s_0$ , the extinction probability at time  $t$  is  $E_t^{s_0}$ . For example, Figure illustrates how the extinction probabilities over time vary for a population with initially 100 individuals of the smallest size  $\alpha$  versus a population with 5 or 6 individuals of the largest size  $\beta$ . This figure suggests that, from the extinction risk perspective, about 5 or 6 large individuals are equivalent to 100 small individuals. These types of comparisons may be particularly useful when trying to assess whether planting germinates or adults are more effective for establishment success.

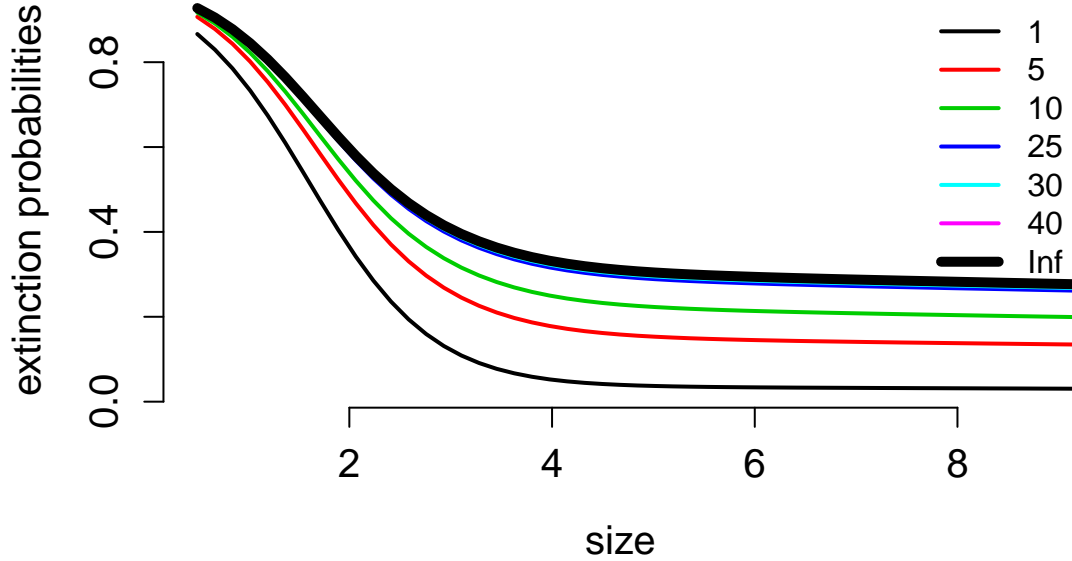


FIGURE 2. Extinction probabilities for a population consisting of a single individual of size  $x$ . Different curves correspond to extinction in different number of years.

Alternatively, we can use the data from 2001 to see how extinction risk over different time frames depends on the size and composition of the population. Specifically, in Figure 3, we computed extinction risk over 5 and 50 year periods for 100 random samples (per sample size) of 2001 size distribution. Expectedly, we see that log extinction risk decreases, on average, linearly with the sample size and is, on average, greater for the 50 year period than the 5 year period. However, for smaller sample sizes, there is overlap in the distributions of extinction times for 5 and 50 year time frames. This overlap stems from samples of mostly large individuals being more likely to persist at least 50 years than samples of mostly small individuals persisting at least 5 years. Interestingly, variation in the extinction times across samples is consistently greater over the 5 year period than the 50 year period.

#### RECOMMENDATIONS, EXTENSIONS, AND FUTURE CHALLENGES

To implement the methods presented here, there are two main steps. First, one needs to identify the main demographic processes of the population, the order in which these processes occur relative to the censuses used for data collection, and develop the statistical models for each of the demographic processes. Rees et al. [2014] and Merow et al. [2014] provide excellent reviews on the philosophical and methodological issues associated with this step for mean-field IPMs. One like



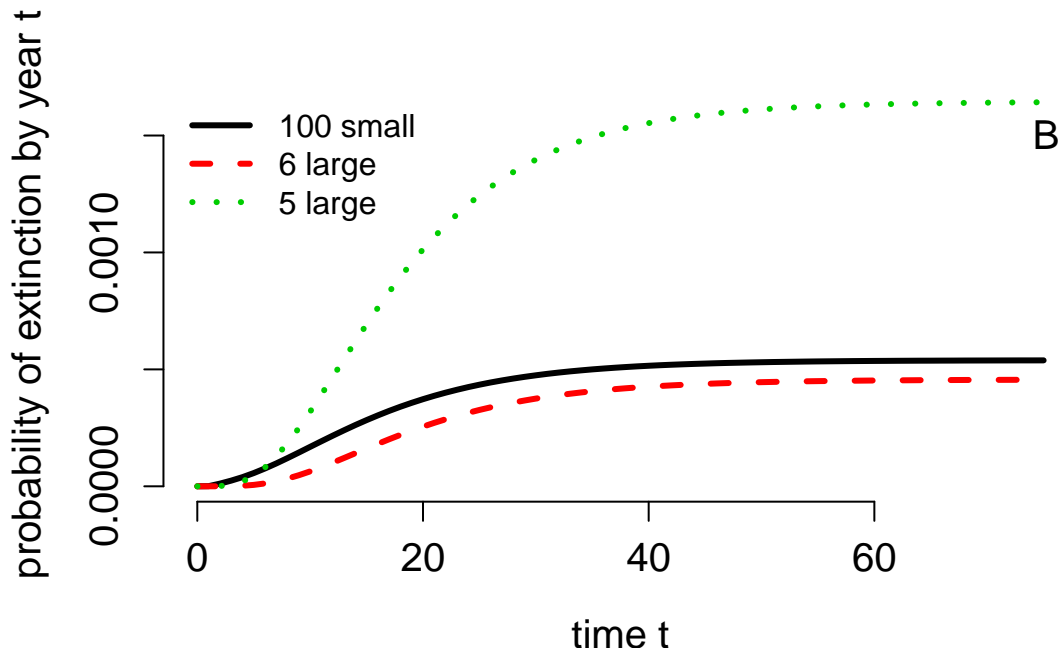


FIGURE 3. Extinction probabilities as a function of time for populations of different sizes and compositions.

these mean-field IPMs, individual-based IPMs require complete distributional information associated with fecundity. As with other areas of stochastic demography, the shapes, not just the means, of these distribution can have significant effects on the likelihood of extinction. Hence, it is best to examine several options (e.g. Poisson, negative Binomial, zero-inflated distributions) to identify which distribution does a better job of describing the fecundity data. As in all areas of modeling, if there is significant uncertainty about what is the “best” model to use for the demographic analysis, then perform the analyses with each of the alternatives to identify the sensitivity of predictions of extinction risk to these distributional alternatives.

The second step, the focus of this paper, involves constructing the probability generating functional  $\Psi$ . For the uninitiated, this step can be quite intimidating. However, there are three basic principles that simplify this construction. First, while this pgf  $\Psi$  takes functions to functions, one should focus on writing down  $\Psi(h)(x)$  which involves understanding the contributions of a single individual of size  $x$  to the next census. Second, one can often break up these contributions into a sum of independent contributions, find the pgfs associated with these simpler contributions, and then use the two fundamental properties of pgfs (see *Deriving the pgf  $\Psi$* ) to “stitch” together these simpler contributions to construct  $\Psi$ . Third, the distributions used to describe the number of offspring produced by an individual typically involve random variables (e.g. Poisson, negative

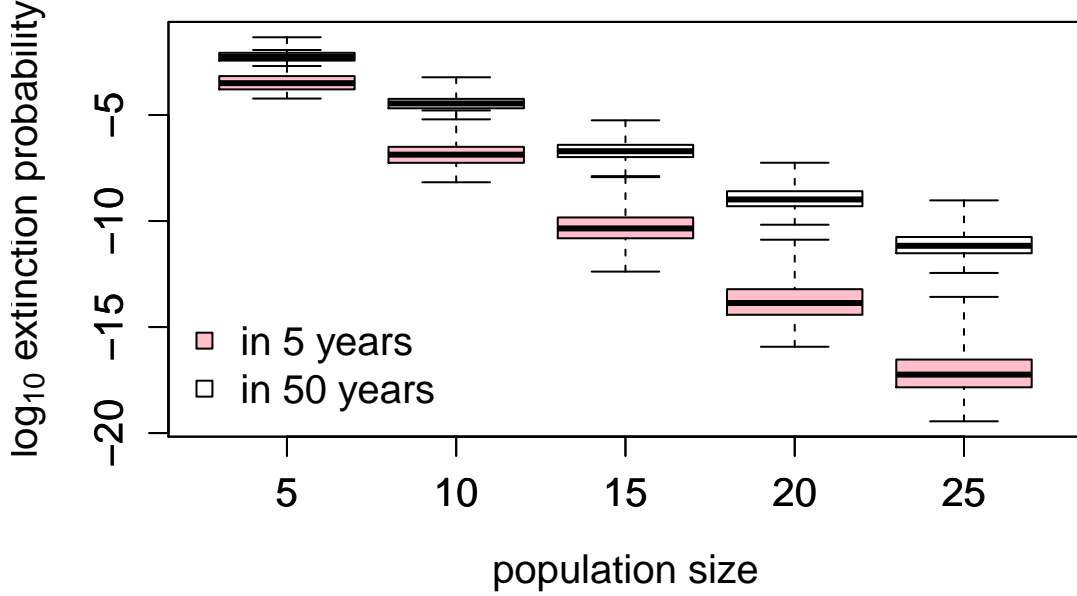


FIGURE 4. Extinction probabilities for populations of different sizes sampled for the 2001 size distribution data. For each population size  $N$ , extinction probabilities by year 5 and year 50 were calculated for 500 samples of size  $N$ .

binomial) for which their associated pgf is well-known and can be found easily e.g. Wikipedia. When in doubt, find a collaborator that you trust to put the pieces together correctly.

For the individual-based models considered here, we assumed the environment was constant. However, IPMs have and continue to be used to study the effects of fluctuating environmental conditions on population demography and life history evolution [childs-etal-04](#), [dahlgren-ehrlen-11](#), [rees-ellner-09](#). The methods described here easily extended to fluctuating environments. Specifically, if  $\Psi_t$  is the pgf of individual-based IPM associated with year  $t$ , then the probability of extinction for a population initially in state  $\mathbf{s}$  is

$$\Psi_0(\Psi_1(\dots \Psi_t(h_0)))^{\mathbf{s}}$$

where  $h_0$  as before is the zero function. Notice that the composition here is in the reverse order of what one does when iterating the mean-field IPM model forward in time. While we know of no formal proof, in the case of a stationary environment and under suitable technical assumptions, we conjecture the following limit theorem holds: the asymptotic extinction probabilities are strictly less than one if and only if the stochastic growth rate (aka dominant Lyapunov exponent) of the mean-field IPM is positive. For multi-type branching processes, this result was proven by [@tanny-81](#).

Despite this simple extension to temporally variable environments, many future challenges remain. From the computational perspective, finding the efficient methods to deal with multi-dimensional states variables (e.g. size and location, or multi-dimensional traits) is likely to be challenging, as it is for mean-field IPMs. While the analytical methods presented here cover multi-dimensional state variables, their numerical implementation involves approximating multi-dimensional integrals which can be computationally expensive. From the analytical perspective, accounting for temporal correlations in individual growth or reproductive rates (e.g. individuals that grew larger than expected in one year being more likely to grow larger than expected in the next year) or correlations among individuals are particularly important problems as strong correlations likely have large effects on extinction risk. Finally, and perhaps most importantly, the manners in which size-structured demography may shape extinction risk for real-world population remains to be understood. One might hope that by applying these methods to the many data sets for which IPMs have been developed, as well as future data sets, might provide a computationally efficient means to explore how size-structure for populations differing in their evolutionary history and environmental context influences their vulnerability to extinction.

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