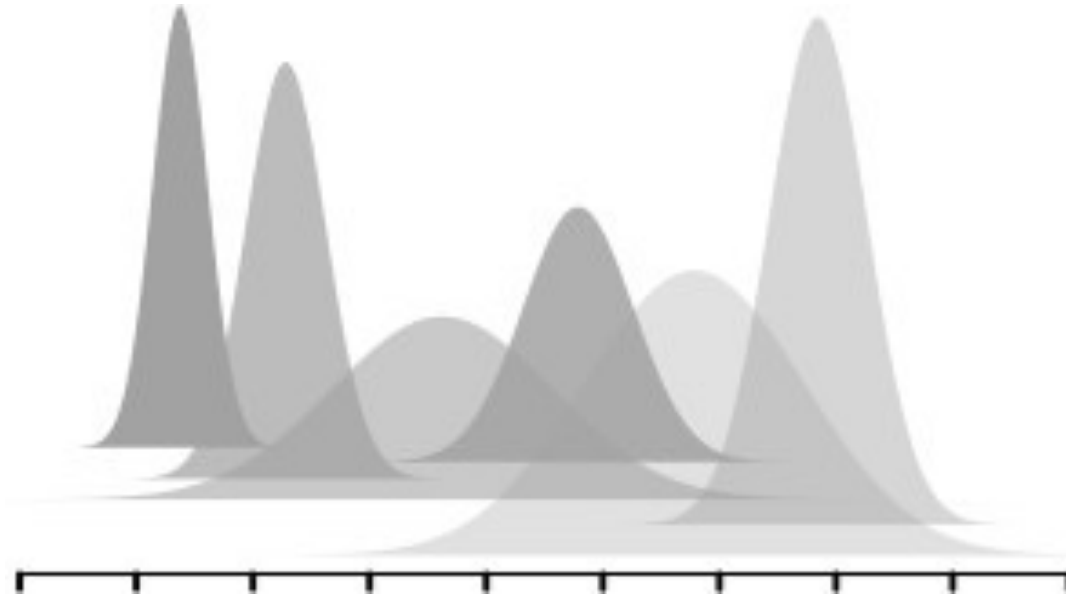


3.2 Models and data in ecology case studies, Part 2



Jelena H. Pantel

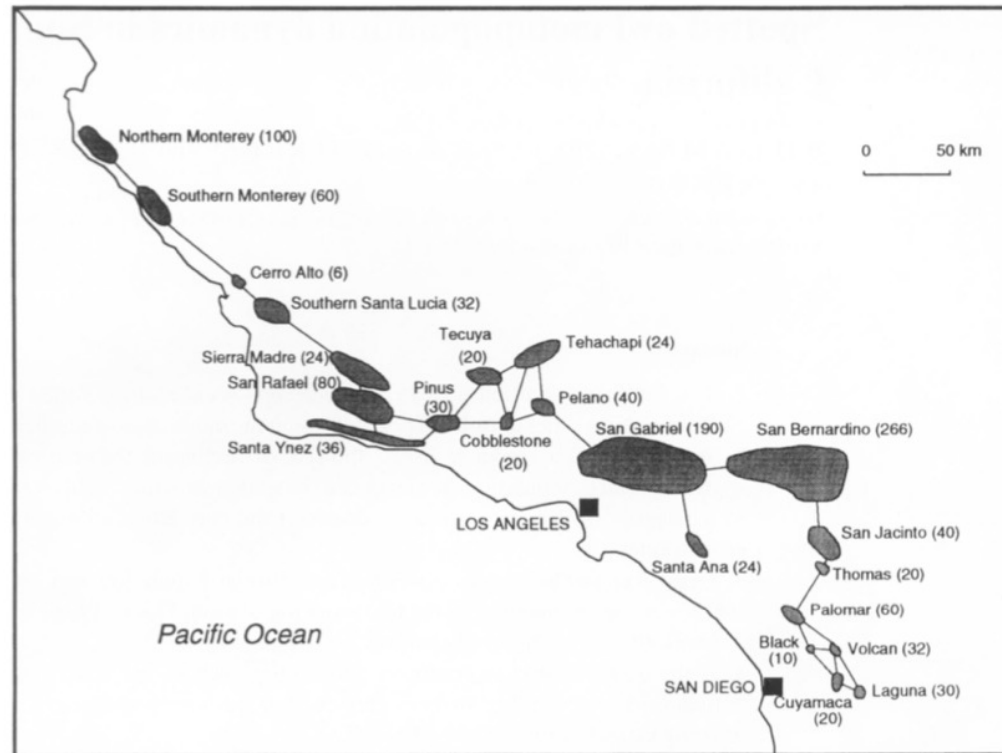
Faculty of Biology

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Model

‘Survivorship was estimated from capture-recapture data for owls’



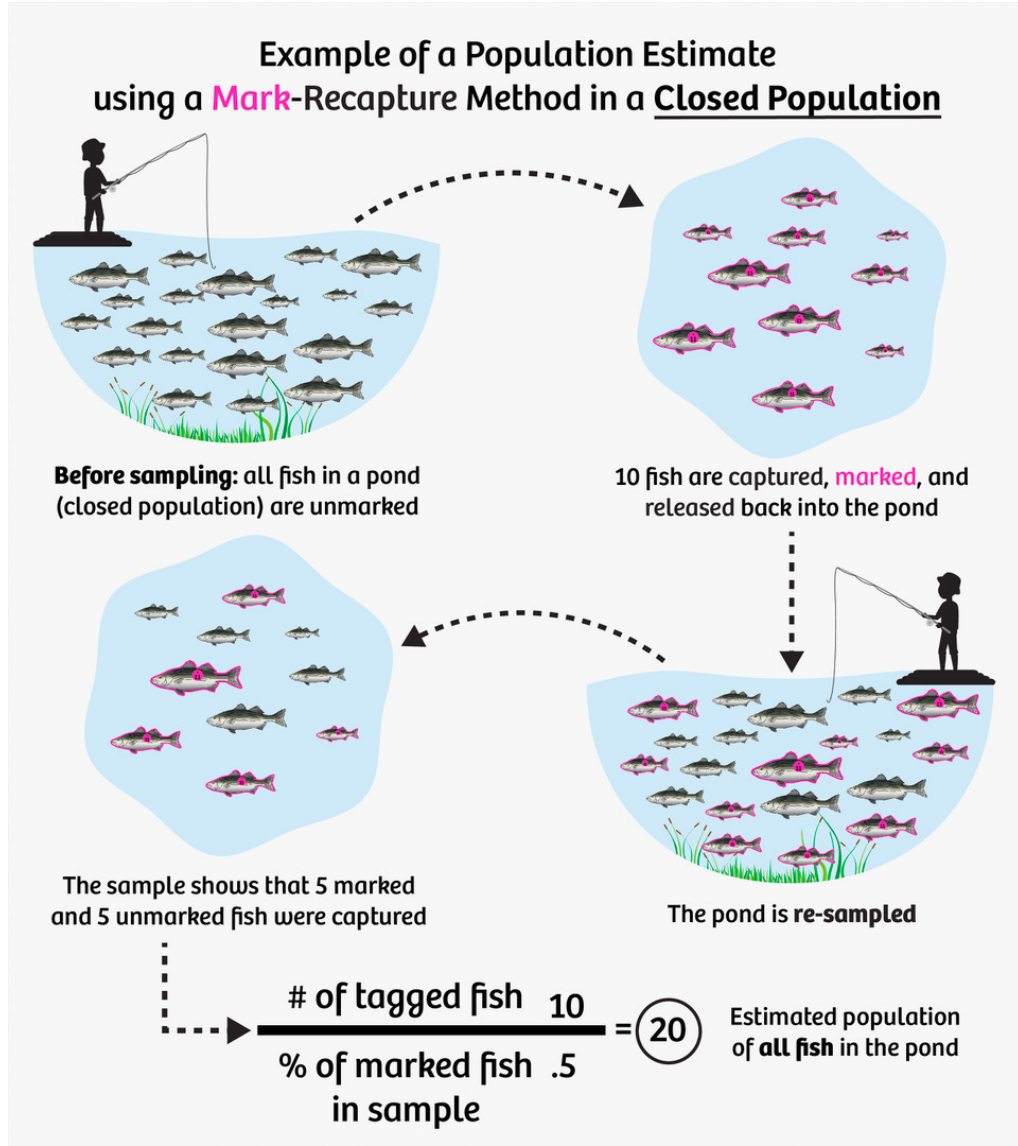
$$\begin{bmatrix} N_1 \\ N_2 \end{bmatrix}_{t+1} = \begin{bmatrix} F_1 & F_2 \\ P_{1 \rightarrow 2} & P_{2 \rightarrow 2} \end{bmatrix} \cdot \begin{bmatrix} N_1 \\ N_2 \end{bmatrix}_t$$

$$N_i(t+1) = N_i(t)R_i(t) - \sum_{j=1}^n m_{ij}N_i + \sum_{i=1}^n m_{ji}N_j$$

Model

$$\begin{bmatrix} N_1 \\ N_2 \end{bmatrix}_{t+1} = \begin{bmatrix} F_1 & F_2 \\ P_{1 \rightarrow 2} & P_{2 \rightarrow 2} \end{bmatrix} \cdot \begin{bmatrix} N_1 \\ N_2 \end{bmatrix}_t$$

‘Survivorship was estimated from capture-recapture data for owls’



Lincoln-Peterson Index:

$$N = \frac{M \cdot S}{R}$$

N = population size estimate

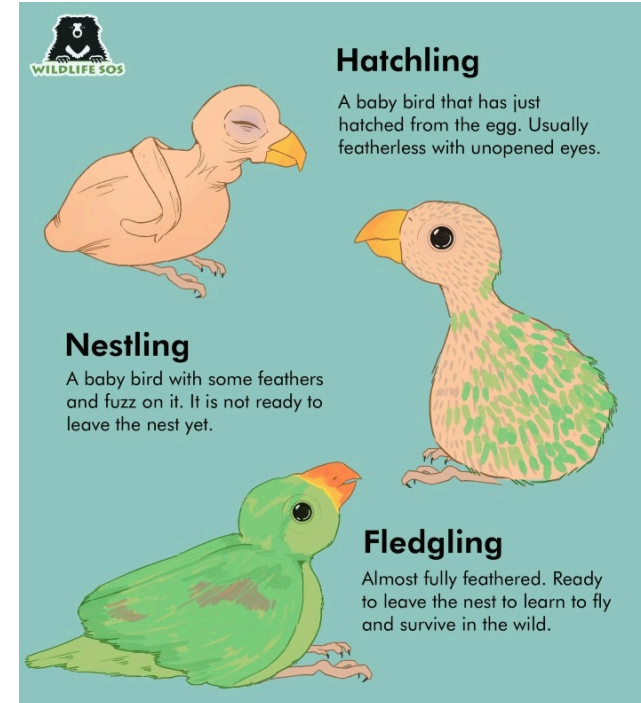
M = marked individuals released

S = size of second sample

R = marked animals recaptured

(I am not 100% sure how this was used to get survivorship estimate. Most likely repeating the survey over multiple years)

‘Fecundity was computed by dividing the number of fledged young by the number of pairs checked for fledgling’

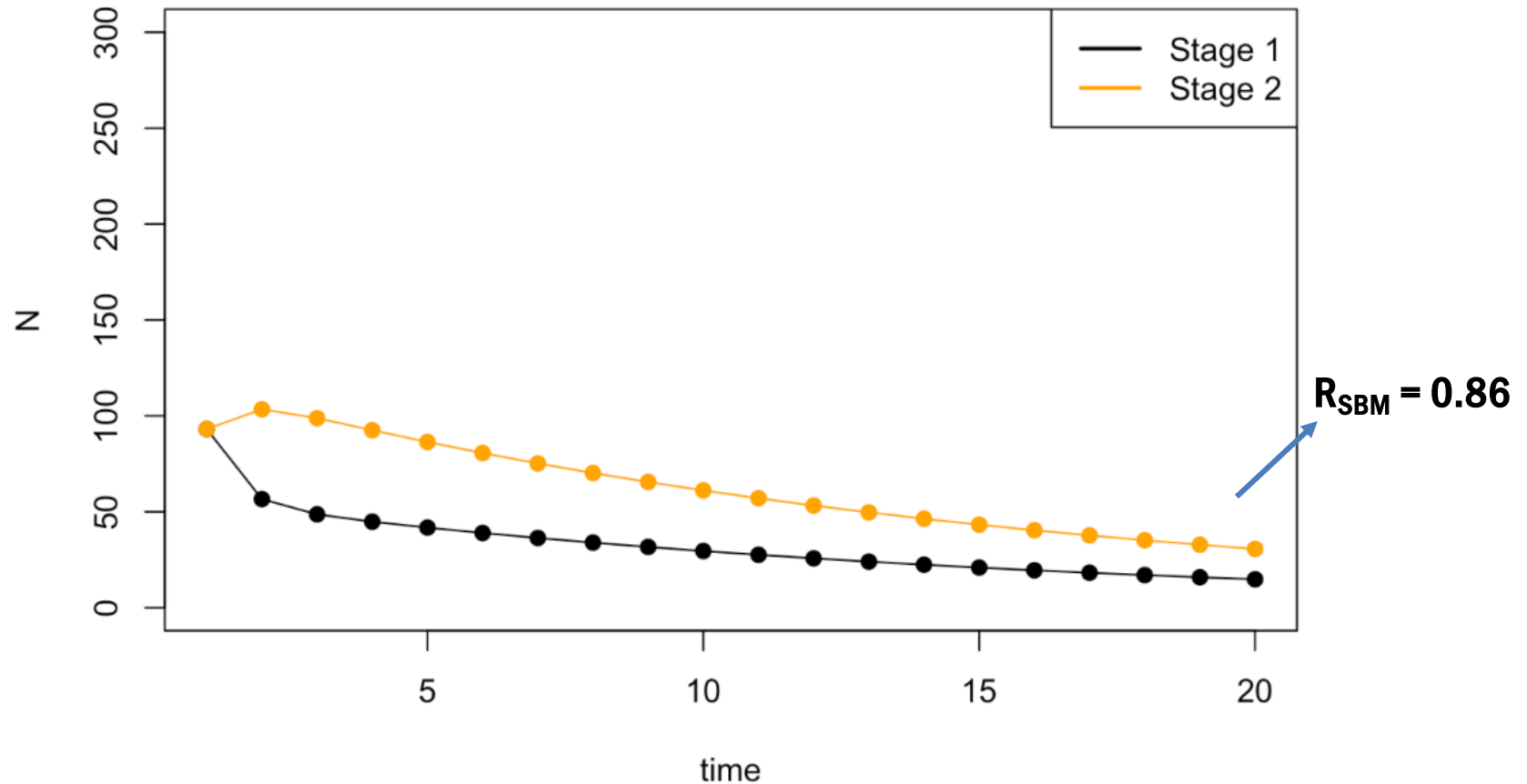


Model

$$\begin{bmatrix} N_1 \\ N_2 \end{bmatrix}_{t+1} = \begin{bmatrix} F_1 & F_2 \\ P_{1 \rightarrow 2} & P_{2 \rightarrow 2} \end{bmatrix} \cdot \begin{bmatrix} N_1 \\ N_2 \end{bmatrix}_t$$

‘The finite annual rate of population increase was estimated using a two-stage Leslie projection matrix’

```
##           [,1] [,2]  
## [1,] 0.304 0.304  
## [2,] 0.344 0.767
```



Model

$$N_i(t+1) = N_i(t)R_i(t) - \sum_{j=1}^n m_{ij}N_i + \sum_{i=1}^n m_{ji}N_j$$

$R_{SBM} = 0.86$

Number of populations ($n = 22$)

Proportion of individuals immigrating (dispersing) from population j to population i

Proportion of individuals immigrating (dispersing) from population i to population j

“The empirical observations of population change, as well as estimates of vital rates indicated that the population we modelled was declining.”

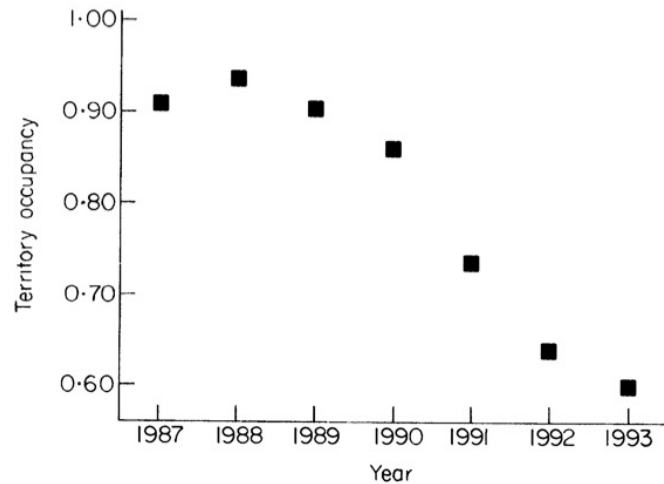
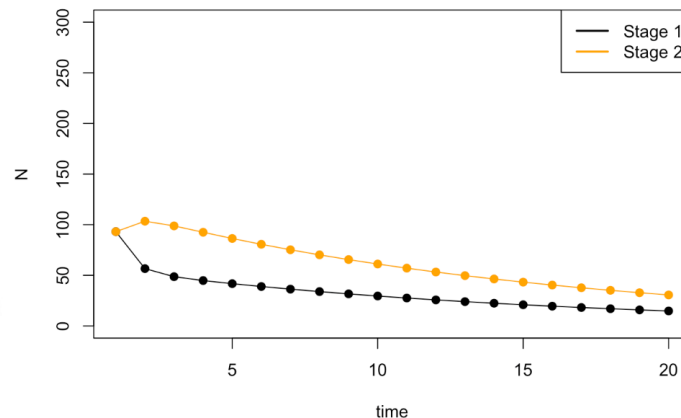


Fig. 3. Territory occupancy in the San Bernardino Mountains population.

“Since the cause of this decline was unknown to us, we modelled the dynamics of this population under two different hypotheses...”



1) Deterministic decline – fixed population growth rate $R_{SBM} = 0.86$

2) Environmental fluctuations – population growth rate is temporarily negative but can recover if environmental conditions improve

Model

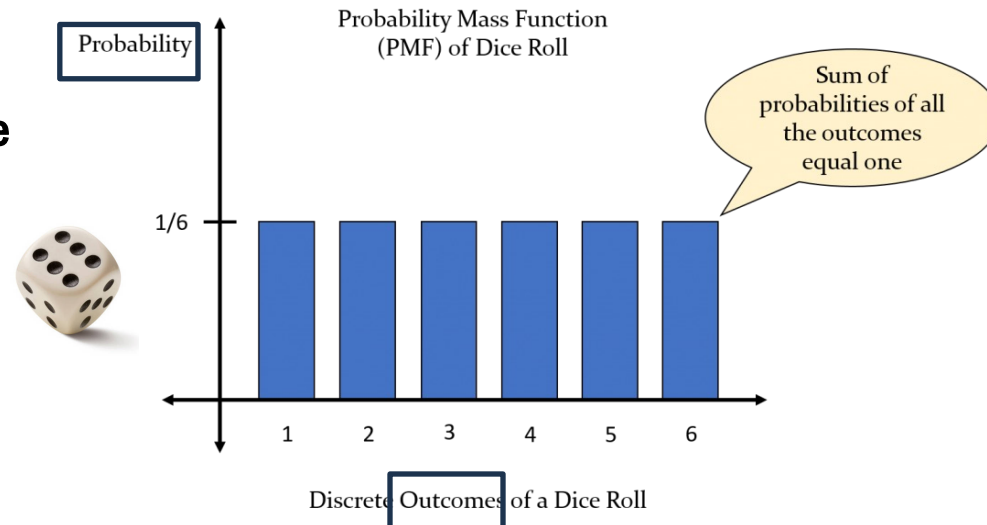
$$N_i(t+1) = N_i(t)R_i(t) - \sum_{j=1}^n m_{ij}N_i + \sum_{i=1}^n m_{ji}N_j$$

$R_i(t) \rightarrow \text{Lognormal}(\mu, \sigma)$

2) Environmental fluctuations – population growth rate is temporarily negative but can recover if environmental conditions improve

“At each time step, the growth rates $R_i(t)$ were selected from a multivariate lognormal distribution defined by the mean and standard deviation of the growth rate of each population and by the matrix of correlations among growth rate”

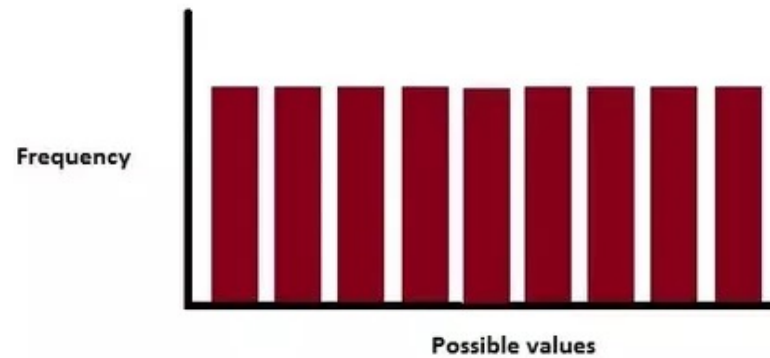
What is this? A probability distribution – a distribution of possible outcomes and their associated probabilities



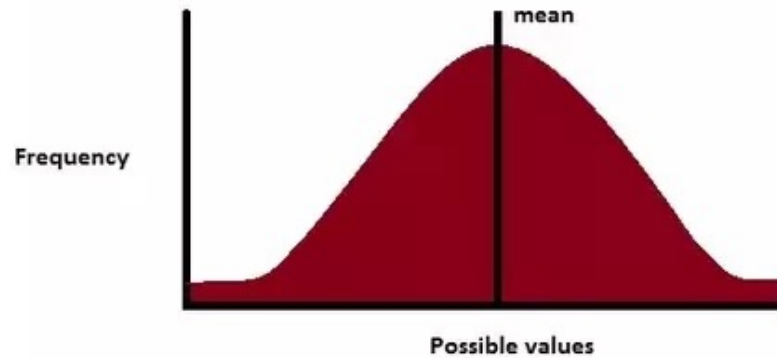
Probability distribution

a distribution of possible outcomes and their associated probabilities

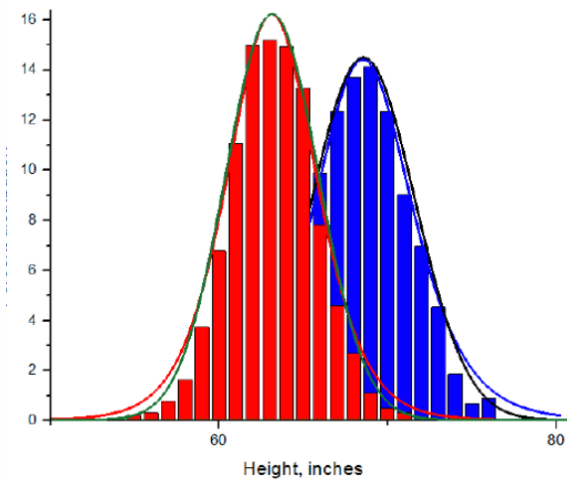
UNIFORM DISTRIBUTION



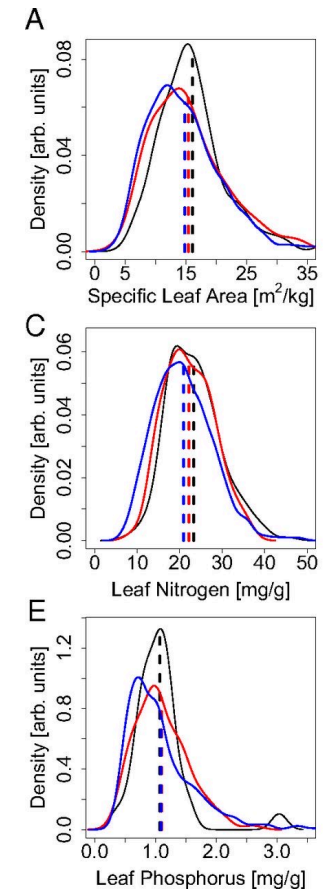
NORMAL DISTRIBUTION



Human height (women, men)

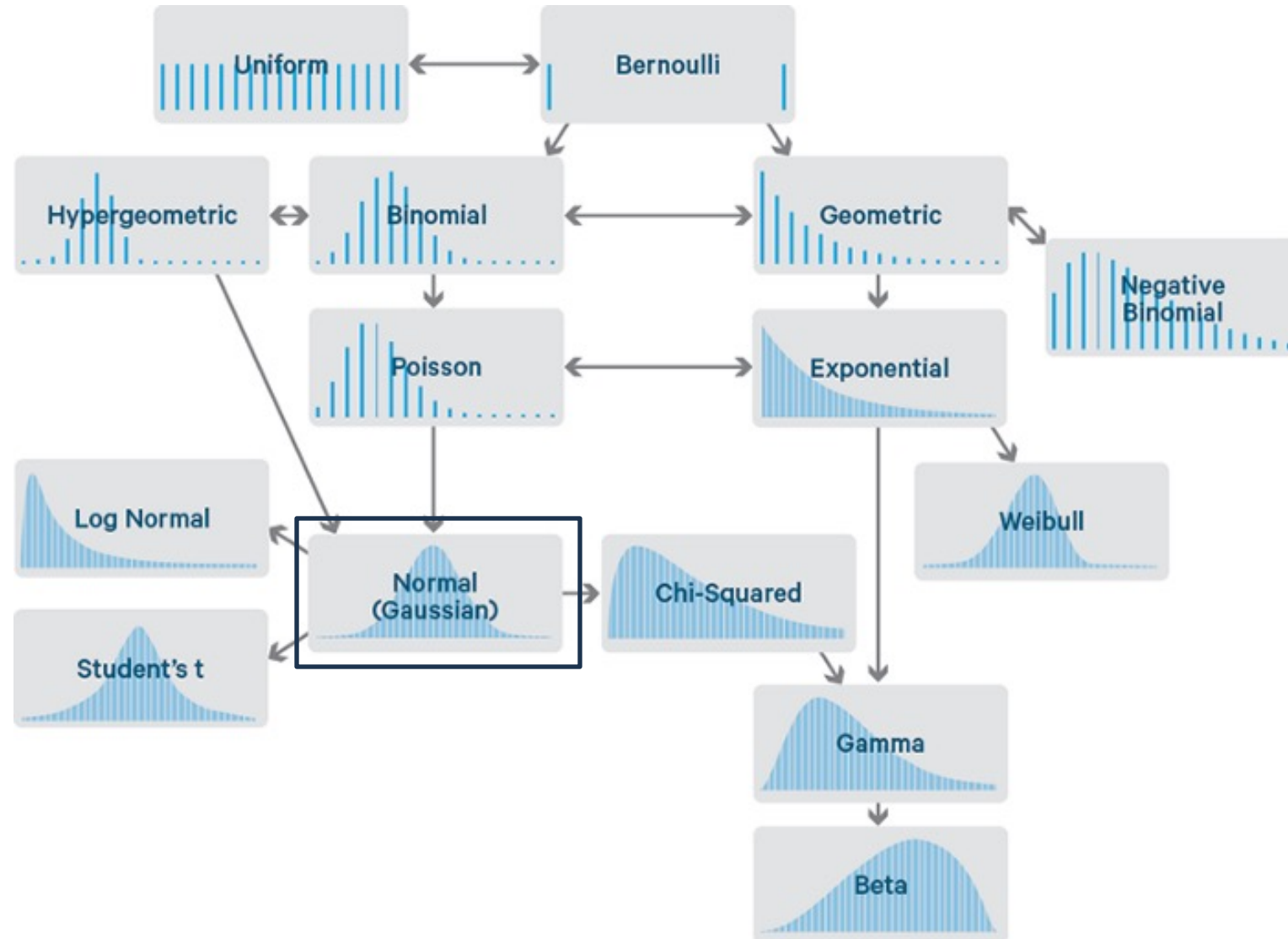


Plant traits (global database)



Probability distribution

a distribution of possible outcomes and their associated probabilities



Model

$$N_i(t+1) = N_i(t)R_i(t) - \sum_{j=1}^n m_{ij}N_i + \sum_{i=1}^n m_{ji}N_j$$

$R_i(t) \rightarrow \text{Lognormal}(\mu, \sigma)$

“At each time step, the growth rates $R_i(t)$ were selected from a multivariate lognormal distribution defined by the mean and standard deviation of the growth population and by the matrix of correlations among growth rate”

What is this? A probability distribution – a distribution of possible outcomes and their associated probabilities

Results

PARAMETER ESTIMATION

Estimates of vital rates and annual rate of population change

Survivorship estimates were 0.344 (95% CI = 0.249–0.453) and 0.767 (95% CI = 0.728–0.802) for first year birds and owls greater than 1 year old, respectively. All ages greater than one year, sexes and time (years) categories were combined because either no significant differences in survivorship and recapture probabilities existed between the groups, or the data would not support these models at this time. We estimated fecundity to be 0.304 female offspring per territorial female over the study period.

The Leslie matrix analysis indicated that the SBM spotted owl population had an annual finite rate of increase of 0.860. The results of the stochastic simulations with an age-structured single-population model (Ferson & Akçakaya 1990) showed that the variation observed in survivorships and fecundities translated to a standard deviation of 0.11 for the finite rate of increase.

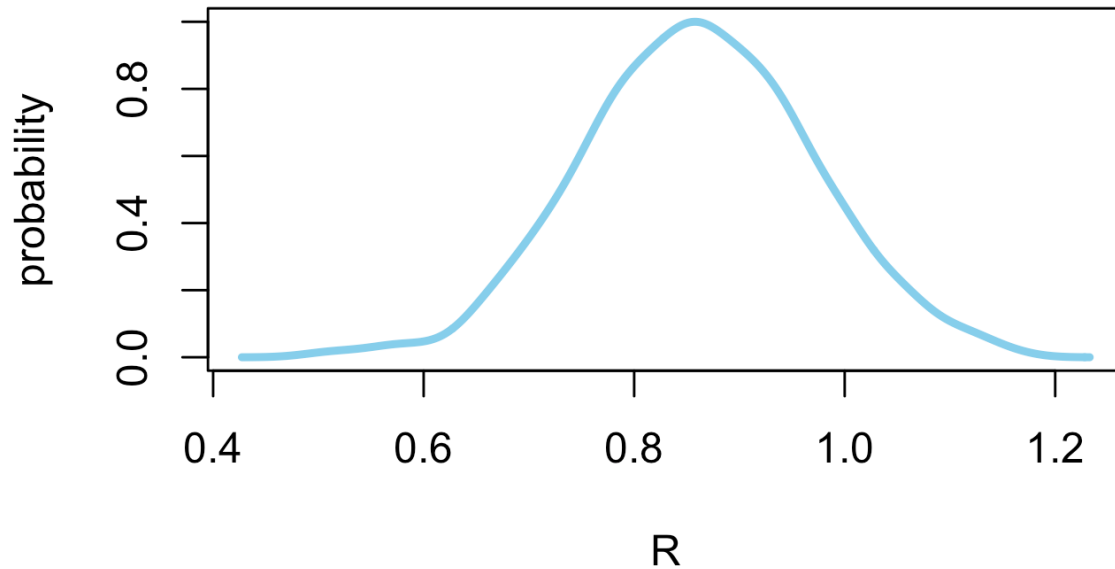
Model

$R_i(t) \rightarrow \text{Lognormal}(\mu, \sigma)$

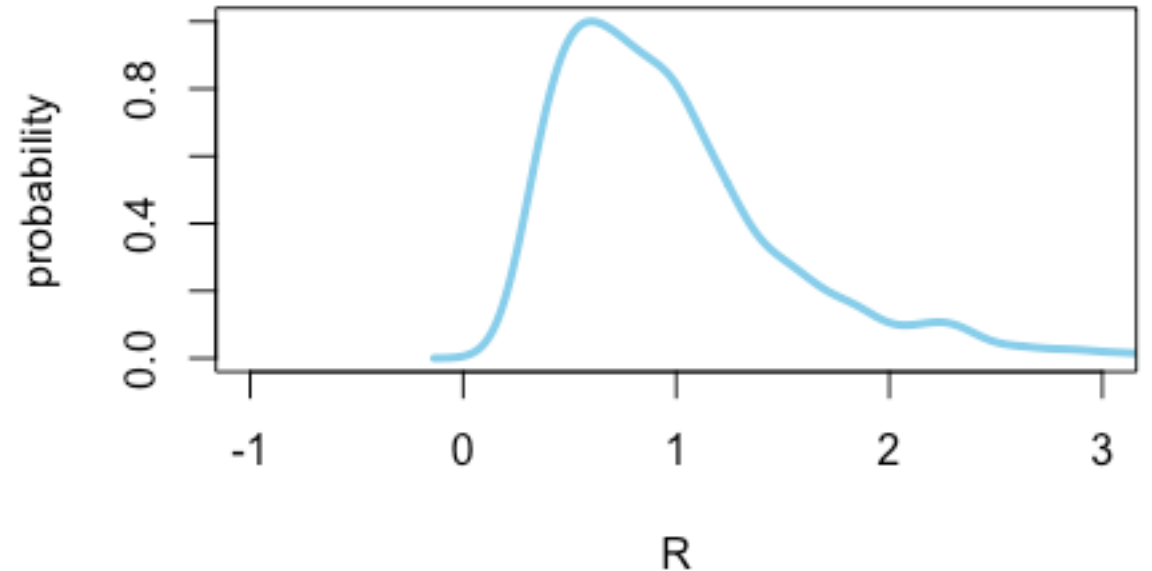
$$N_i(t+1) = N_i(t)R_i(t) - \sum_{j=1}^n m_{ij}N_i + \sum_{i=1}^n m_{ji}N_j$$

“At each time step, the growth rates $R_i(t)$ were selected from a *multivariate lognormal distribution* defined by the mean and standard deviation of the growth rate of each population and by the matrix of correlations among growth rate”

Normal: $\mu = 0.86, \sigma = 0.11$



Lognormal: $\mu = 0.86, \sigma = 0.11$



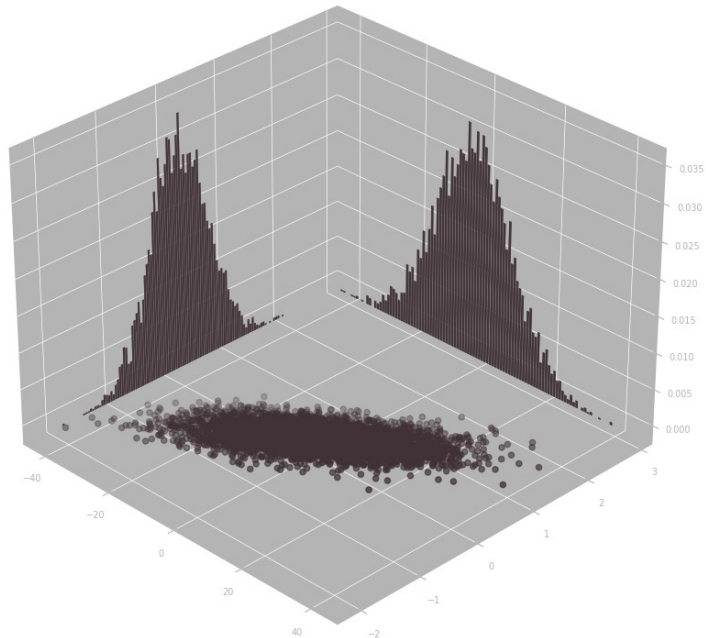
Model

$R_i(t) \rightarrow \text{Lognormal}(\mu, \sigma)$

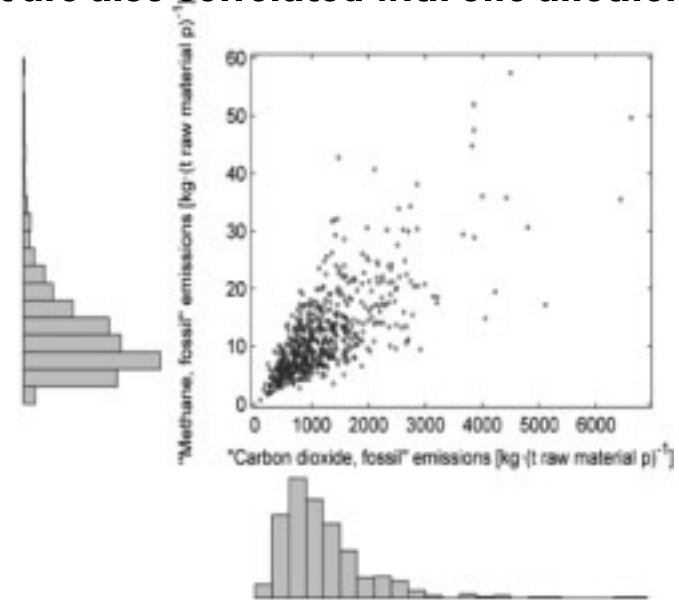
$$N_i(t+1) = N_i(t)R_i(t) - \sum_{j=1}^n m_{ij}N_i + \sum_{i=1}^n m_{ji}N_j$$

“At each time step, the growth rates $R_i(t)$ were selected from a **multivariate lognormal distribution** defined by the mean and standard deviation of the growth rate of each population and by the matrix of correlations among growth rate”

Multivariate normal – 2 normal distributions that are also correlated with one another



Multivariate lognormal – 2 lognormal distributions that are also correlated with one another



Model

$$N_i(t+1) = N_i(t)R_i(t) - \sum_{j=1}^n m_{ij}N_i + \sum_{i=1}^n m_{ji}N_j$$

$R_i(t) \rightarrow \text{Lognormal}(\mu, \sigma)$

Why use a different value every year from this distribution for R?
To represent random (stochastic) variation in the environment each year.

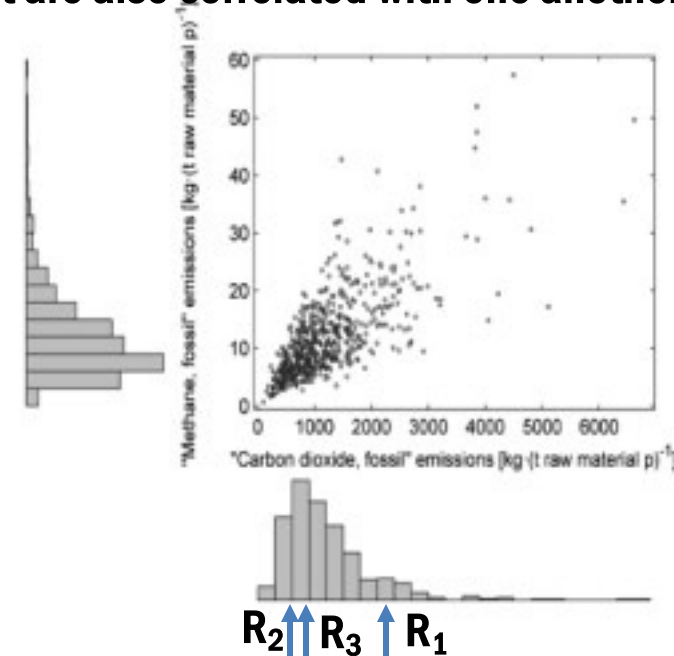
“At each time step, the growth rates $R_i(t)$ were selected from a **multivariate lognormal distribution** defined by the mean and standard deviation of the growth rate of each population and by the matrix of correlations among growth rate”

growth rates. These random variables were used to represent environmental stochasticity. In addition, demographic stochasticity was modelled by sampling the number of dispersers from a binomial distribution, and by decomposing the growth rate into components of survivorship and fecundity and sampling the number of survivors from a binomial and the number of young from a Poisson distribution (see Akçakaya & Ferson 1992; Akçakaya 1991; Lamberson 1992). The above equation shows that the dynamics of each population was modelled with a scalar (unstructured) model. The available data that we used to par-

Multivariate lognormal – 2 lognormal distributions that are also correlated with one another

μ_{ij}

$$\begin{bmatrix} F_1 & F_2 \\ P_{1 \rightarrow 2} & P_{2 \rightarrow 2} \end{bmatrix}$$



Model

$$N_i(t + 1) = N_i(t)R_i(t) - \sum_{j=1}^I$$

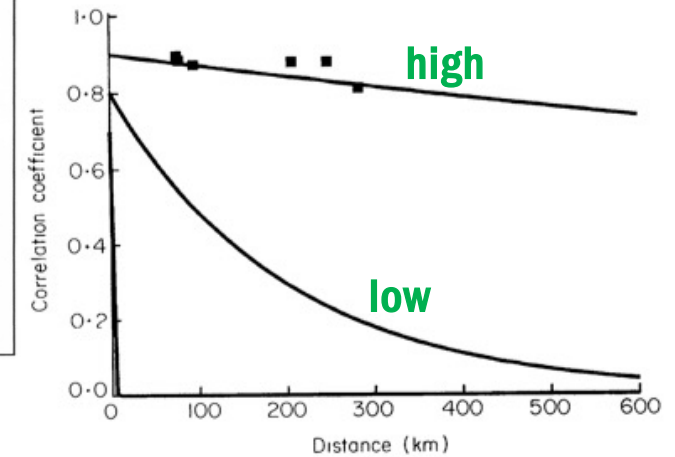
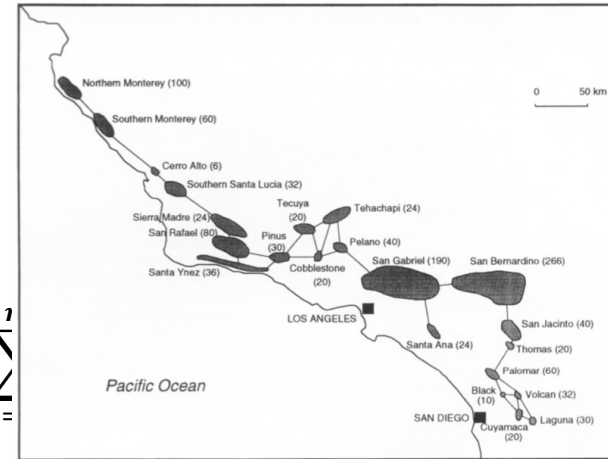
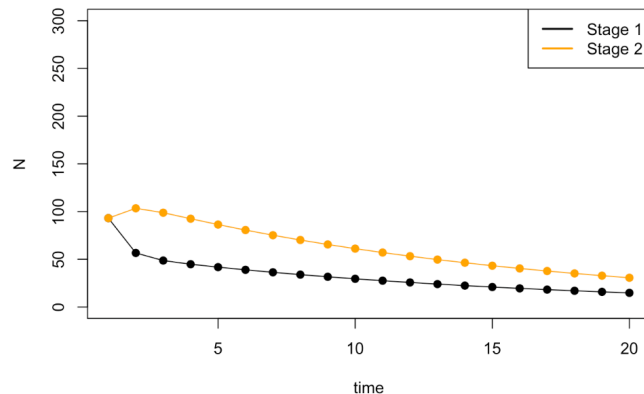


Fig. 2. Functions used to assign correlation among growth rates of populations as a function of the distance between them. Squares are the observed correlations among rainfall patterns from Table 2.

“The empirical observations of population change, as well as estimates of vital rates indicated that the population we modelled was declining. Since the cause of this decline was unknown to us, we modelled the dynamics of this population under two different hypotheses...”

Deterministic decline – fixed population growth rate $R_{SBM} = 0.86$

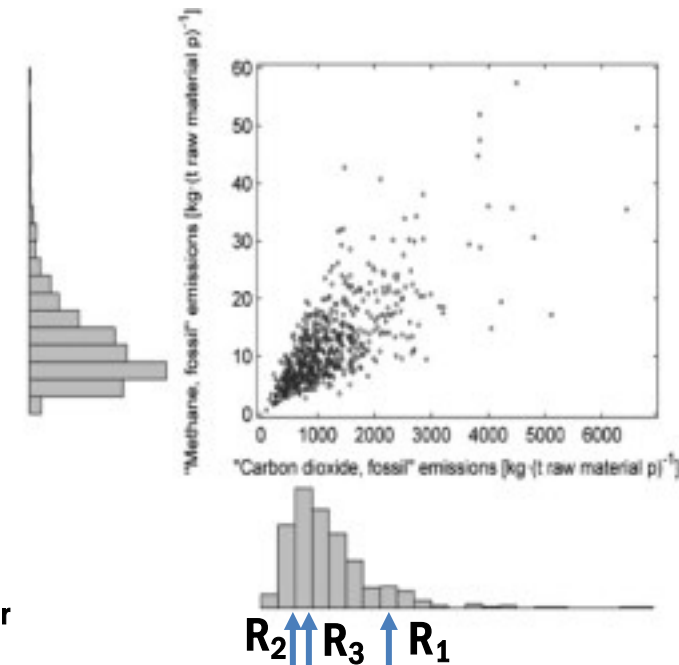


Environmental fluctuations – population growth rate is temporarily negative but can recover if environmental conditions improve

Three levels of correlation among sites:

- (1) no correlation in R among 22 sites
- (2) Correlation related to distance between sites - low
- (3) Correlation related to distance between sites - high

Sites with low R years might ‘bring down’ R at other sites, increasing metapopulation extinction risk



Key results

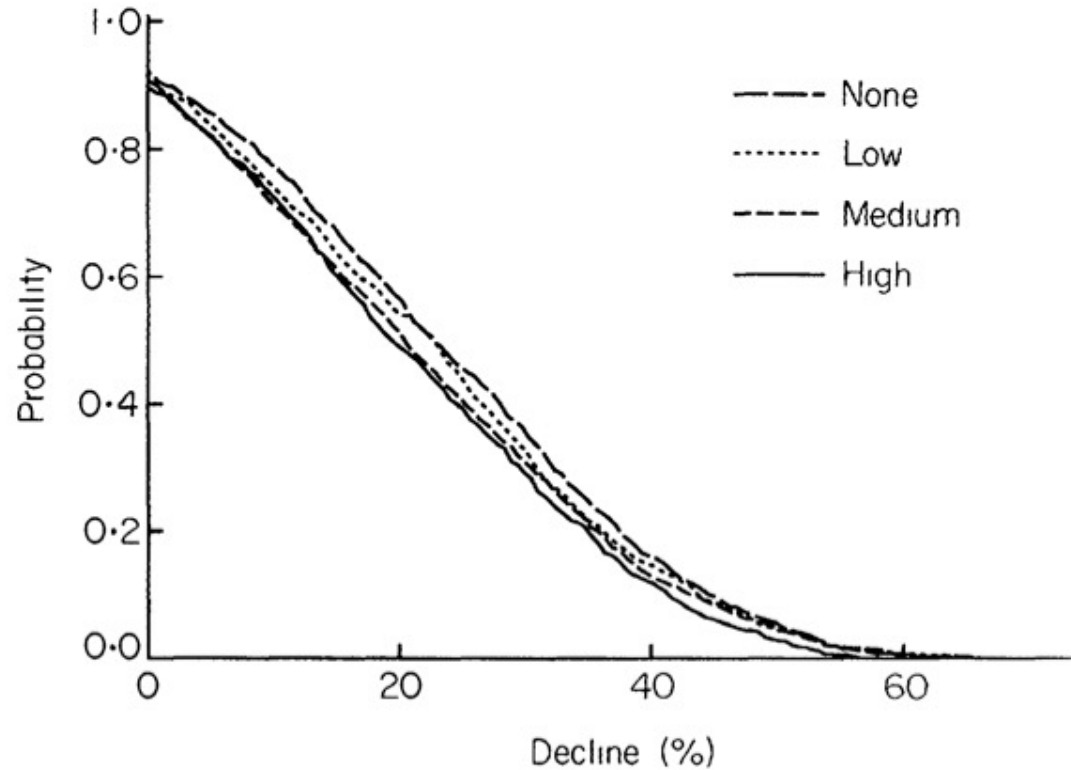


Fig. 8. Effect of dispersal on risk of decline in 20 years under the environmental fluctuations hypothesis and assumption of uncorrelated fluctuations.

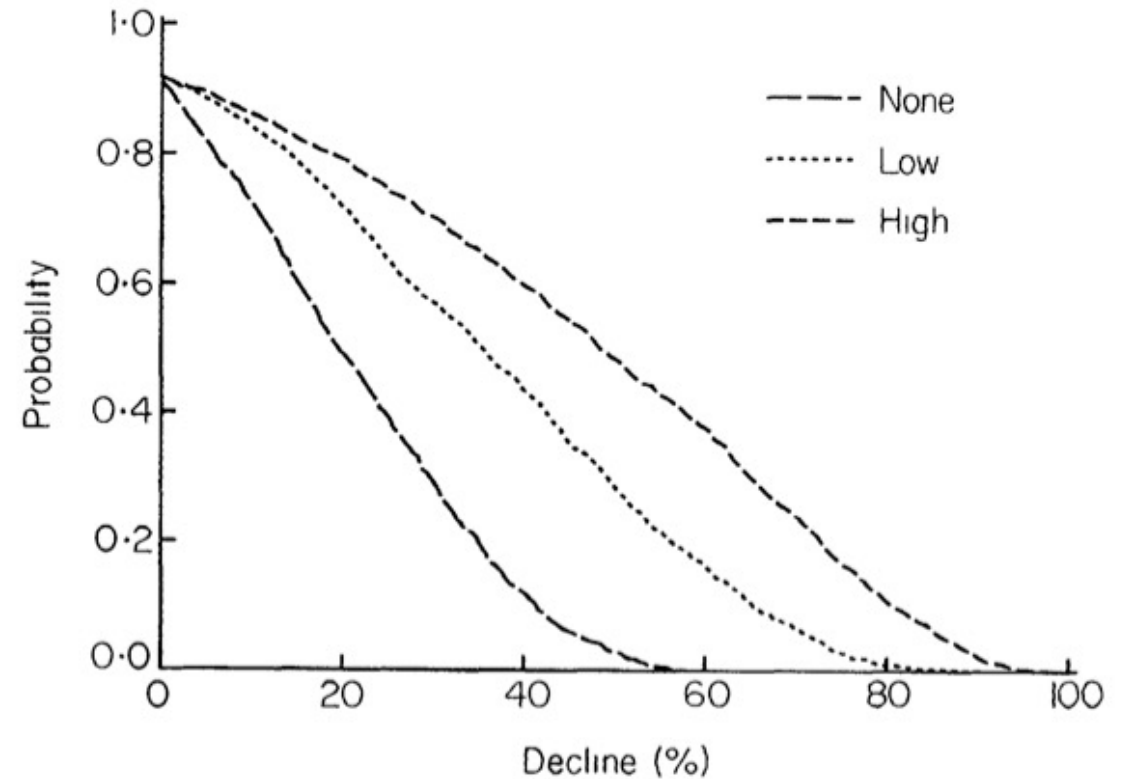


Fig. 9. Effect of correlation among population growth rates on risk of decline in 20 years under the environmental fluctuations hypothesis and assumption of high dispersal.