

Notes for September 21, 2016

Sam Fleischer

Last Modified: September 21, 2016

1 Overview of the PBG Core Course

1. Fall

- Sebastian Schreiber: Single Species Ecology
- Graham Coop: Population Genetics
- Artyom Kopp: Genomics

2. Winter

- Gary (???): Species Interactions
- Sharon Lawler: Community Ecology
- Santiago Ramirez: Behavior and Evolution

3. Spring

- Michael Turelli: Macroevolution
- Brian Moore and Annie (???): Phylogenetics

The main goal of Sebastian's part is to understand the distribution of a population abundance in time. We will start with the most simplistic view: homogeneous populations. In this case, every individual is identical, the population is well-mixed, and there is no change in the environment.

Then we will explore:

1. Temporal Heterogeneity: The environment changes over time, for example, fluctuations due to precipitation or temperature. Real-life examples are:
 - Rate of development of moths is dependent on temp
 - Number of seeds produces is dependent on precipitation
 - This can cause evolution of life history to try to "hedge bets" against uncertainty
2. Individual Heterogeneity: The individuals are potentially distinct, for example, separated in to age classes (egg → hatchling → turtle), sex classes, size classes
3. Spatial Heterogeneity: The population is not necessarily well mixed, for example, one beaker is warmer than another and there is some mixing between the two. There are three paradigms of spatial models:
 - Metapopulation (Ilkka Hanski)
 - Ideal Free Distribution (Milinski)
 - Sourcing dynamics (counterpart to Ideal Free Distributions)

2 Homogeneous Populations

Denote N as the population density ($N \in \mathbb{R} > 0$). N is a function of time, $N = N(t)$, and denote $G = G(N)$ as the growth rate of the population of density N .

$$G(N) = \underbrace{B(N)}_{\text{births}} + \underbrace{I(N)}_{\text{immigration}} - \underbrace{D(N)}_{\text{deaths}} - \underbrace{E(N)}_{\text{emigration}}$$

Usually, $B(N) = Nb(n)$, $D(N) = Nd(N)$, and $E(N) = Ne(N)$, where b , d , and e are the per-capita birth, death, and emigration rates, respectively.

There are two types of models:

1. Differential Equation Models (instantaneous change)

$$\frac{dN}{dt} = G(N)$$

2. Difference Equation Models (discrete time, time-delay)

$$N_{t+1} - N_t = G(N_t)$$

A population is defined to be **closed** if $I(N) = E(N) \equiv 0$. Otherwise it is **open**. On shorter timescales, populations tend to be closed, while on longer timescales, since immigration/emigration events are not impossible, populations tend to be open. Examples of closed populations include

- forcibly closed populations in a flask in a lab
- non-swimming/non-flying populations on islands
- high-altitude-only populations on sky-islands (isolated mountain-tops)
- water-dwellers in an isolated lake

The most simple density-independent model of a closed population is to assume $b(N) = b$ and $d(N) = d$ are constants. Then, defining $r := b - d$, we see

$$\dot{N} = rN$$

Given initial condition $N(0) = N_0$, this has the solution

$$N(t) = N_0 e^{rt}$$

This is an incredibly nice model because if we define $x := \log N$, then $\dot{x} = \frac{\dot{N}}{N} = r$, which implies $x(t) = x_0 + rt$ where $x_0 = \log N_0$. This is a linear model, and so we can very easily use linear regression to match log-density data.

Supposing we have data points y_t for $t = 0, 1, \dots, k$, then we can form a predictive function y :

$$y(t) = x_0 + rt + \text{"error"}$$

NOTE: here we are assuming the error is normally distributed with mean 0 and fixed variance. In this model, the values x_0 and r are thus the “most likely” values to produce the observed data.