Metapopulations and Population Genetics

BIOL/BOT 160 – Ecology Delivered by Dr. Uricchio Prepared by Drs. Shaffer & Uricchio

Office hour

- Wednesday 9/20 in DH 547/548, 9am-11am
- Email me today if you'd like to come but you can't make it, I may be able to meet in the afternoon depending on your schedule
- If not we can correspond by email
- Also available immediately after class today

Learning objectives

- Students should be able to
 - Calculate R_0 from life tables, explain the relevance of exponential growth and logisite growth models to population ecology, and calculate future population sizes in exponential models (review)
 - Predict extinction probabilities for metapopulations using a simple model, and explain the relevance of habitat suitability, migration, and population variation to dynamics of metapopulations
 - Analyze simple genetic data to make predictions about phenotype prevalence in populations using the concept of Hardy-Weinberg equilibrium

Review of growth models

$$\frac{dN}{dt} = rN$$

Exponential

$$\frac{dN}{dt} = rN\left(\frac{K-N}{K}\right)$$
 Logistic

So far we have assumed

Populations are closed (no immigration or emigration)

 Individuals are all the same within a population (no genetic variation)

Closed populations

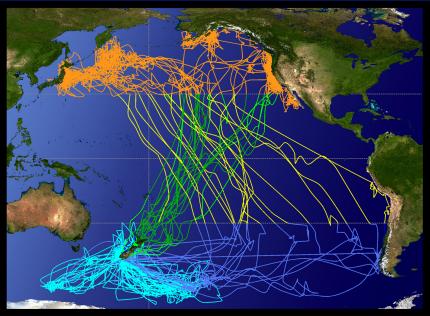
- Exponential & logistic models rely on changes in the per capita births and deaths
- Recall that r = [B]irths [D]eaths, but we were ignoring immigration and emigration

$$dN = [B + I] - [D + E]$$

Populations are more dynamic

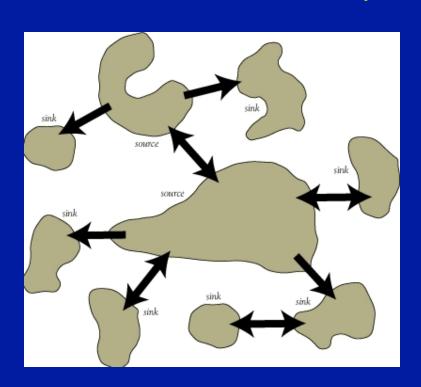
- Closed populations are convenient for modeling
- Not usually biologically relevant





Metapopulations

- What is a metapopulation?
 - Population of populations
 - Based on multiple 'distinct' populations

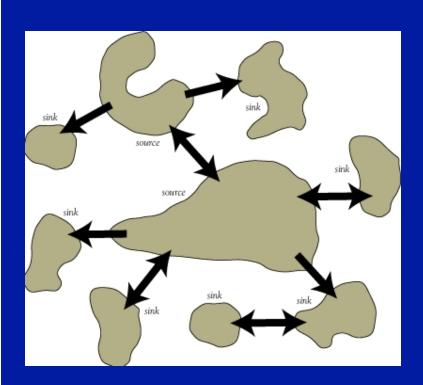


Populations separated by fragmentation of habitat

Potential mixing between populations

Metapopulations

- Dynamics of metapopulations
 - Depends on number of populations
 - Amount of occupied or unoccupied habitat



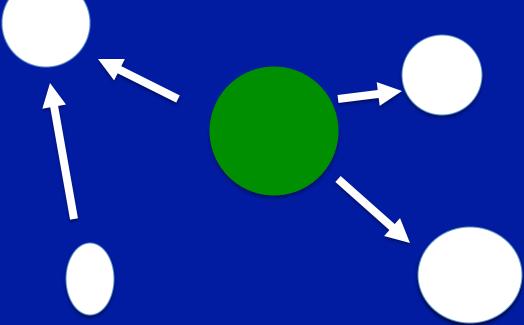
Distance between habitats

Size of habitats

Quality of habitats

Metapopulation Dynamics

Based local persistence and/or extinction



Local populations can go extinct then recolonize

Habitat suitability can change

Simple Model of Persistence

$$P_x = 1 - (p_e)^x$$

From Gotelli 2008

 P_x = probability of population persistence

 $p_e = probability of extinction (0 to 1)$

x = numbers of populations

Example 1

 $p_e = 0.7$ and we have 1 populations

 $P_1 = 1 - (0.7)^1 = 0.30$ low chance our population will persist to the following year

Simple Model of Persistence

$$P_x = 1 - (p_e)^x$$

From Gotelli 2008

Example 2

 $p_e = 0.7$ and we have 10 populations

 $P_{10} = 1 - (0.7)^{10} = 0.97$ high chance that at least one of our populations will persist

What does this mean:

The more populations we have, the lower the risk of regional extinction

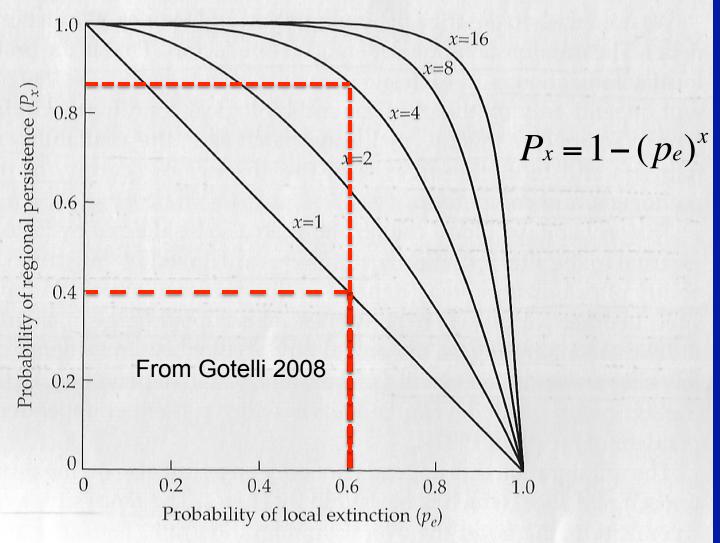
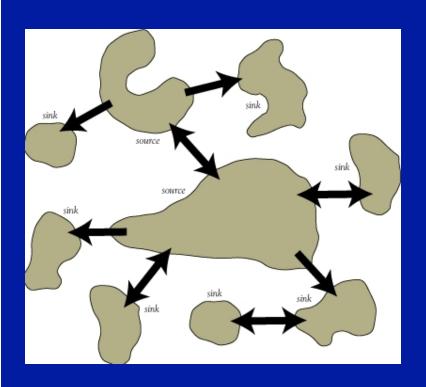


Figure 4.1 The relationship between the probability of regional persistence (P_x) , the probability of local extinction (p_e) , and the number of populations (x). Note that as the number of populations is increased, the probability of regional persistence is substantially higher, for a given probability of local extinction.

Sources and sinks

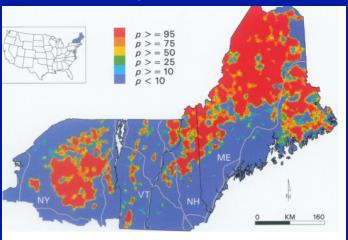
- Source population(s)
 - Typically large, robust habitat
 - Source dynamics are often density-dependent



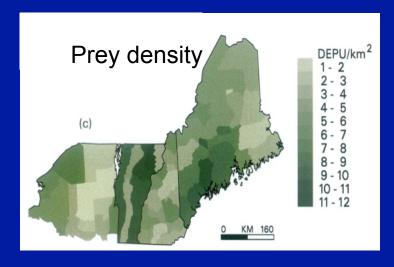
- Sink population(s)
 - Variable size
 - Population growth poor
 - Declining unless fed

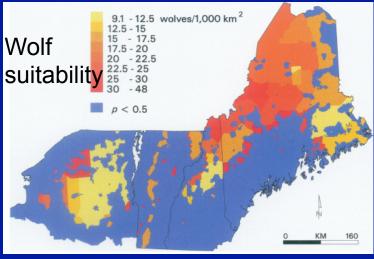
Example – hypothetical wolf reintroduction in Northeast

Habitat suitability



- Different areas may support distinct wolf populations
- Large, well connected habitats may support large source population
- Could overflow to less suitable areas





Genetic variation within populations

- Mutations arise randomly within populations and can cause variation in phenotypes
- Contributes to maintaining heterozygosity (genetic differences)

Why is this important to maintain?

 Mutations can drive EVOLUTION, defined as 'Change in gene frequency in a population over time'

Types of Variation

Discrete

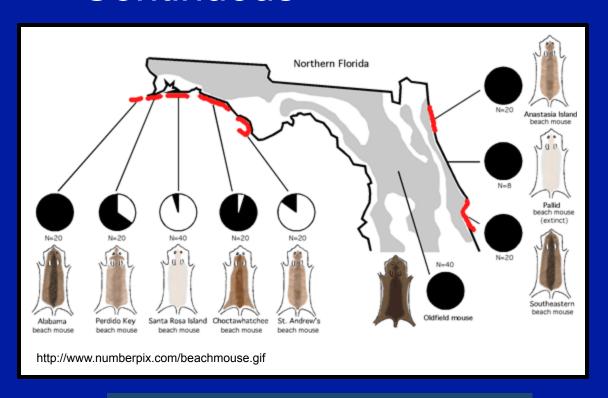


E.g. Variation in color

Types of Variation

E.g. Variation in height

Continuous





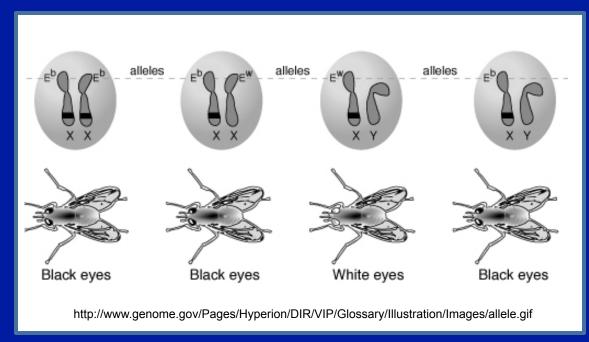
E.g. Variation in color

Genotype vs Phenotype

- Genotype hereditary information (i.e. alleles and gene sequences)
- Phenotype expression of the hereditary information

Genotype

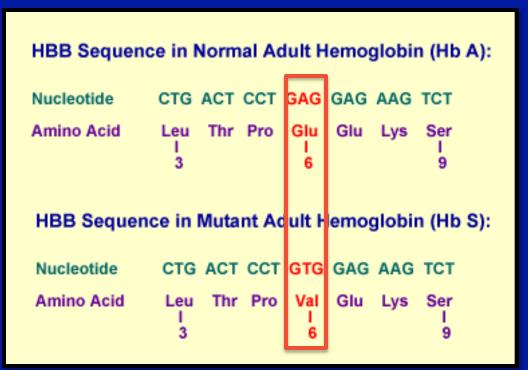
Phenotype



Source of variation

- Mutation –
 inheritable
 change in
 genotype
 - SNPs (Single Nucleotide Polymorphism)

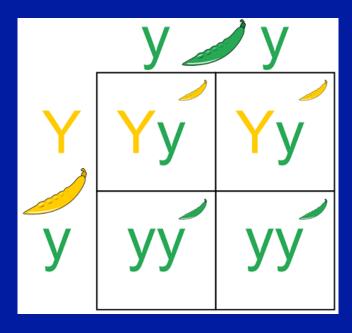




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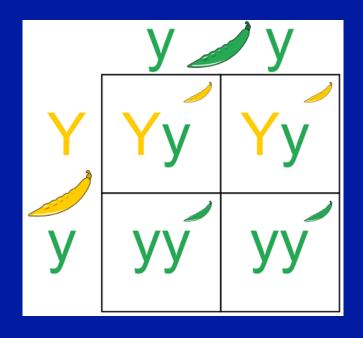
How to model population variation?

Punnett square (known parent genotypes)

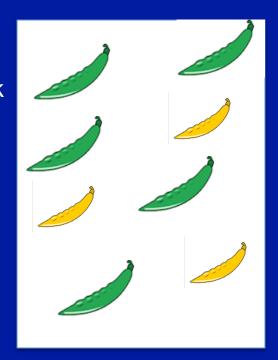


How to model population variation?

Punnett square (known parent genotypes)



Suppose instead we pick a random parent from the population



Hardy-Weinberg equilibrium principles will tell us how to model the rate of occurrence of genotypes and phenotypes in the population

Predicting phenotypes & genotypes in populations: Hardy Weinberg Equilibrium





http://plainview.files.wordpress.com/2009/02/coin-flip.jpg

Probability of A & B = $P_A * P_B$

2nd Coin





1st Coin





НН	HT



P _H *P _H =0.5*0.5	0.25
$P_H^*P_T + P_T^*P_H = 0.5*0.5 + 0.5*0.5$	0.50
$P_{T}^{*}P_{T} = 0.5^{*}0.5$	0.25

Probability of heads $P_H = 0.5$ Probability of tails $P_T = 0.5$ **2nd Coin**





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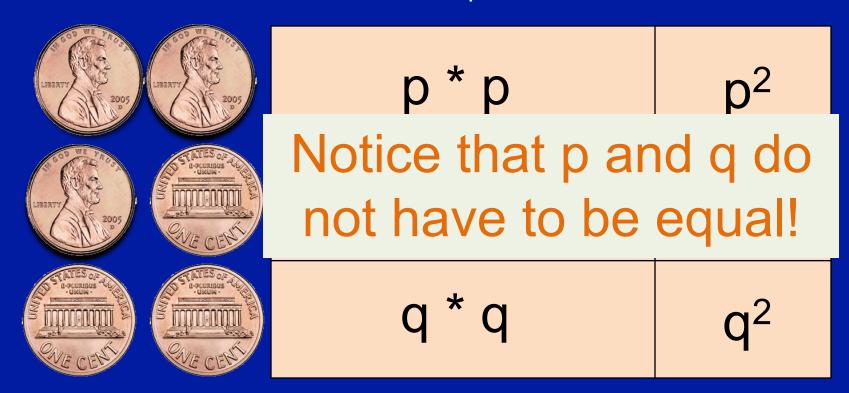


НН	НТ
TH	TT

LET Probability of heads $P_H = p$ Probability of tails $P_T = q$

LIBERTY 2005	p * p	p ²
LIBERTY 2005	2* p * q	2pq
PRIESOF B-PURIOUS CARROLL CONTROLL CONTROL CONTROL CONTROLL CONTROL CONTR	q * q	q ²

LET Probability of heads $P_H = p$ Probability of tails $P_T = q$



LET Probability of heads $P_H = p$ Probability of tails $P_T = q$



 $p^2 + 2pq + q^2 = p^2 + 2p(1-p) + (1-p)^2 = 1$



q * q

 a^2

Main assumptions of HWE

- No new mutations
- Random mating
- No linkage
- No natural selection

Note: Hardy-Weinberg Equilibrium represents what happens by chance alone!

Can be used to determine if something other than chance occurred

Hardy Weinberg application

- Suppose you are looking at one loci with two alleles (Blue and Brown eyes) in a population.
- Let p = brown eyes = 0.8
- q = blue eyes = 0.2 remember 1-p = q
- What would be the expected probability of getting a heterozygote?

$$2pq=2*0.8*0.2=0.32$$

 If the population size was 1000, how many should be heterozygotes if only chance was operating?

$$0.32 * 1000 = 320$$

- Let's assume that p and q express incomplete dominance and that p = red and q = white
- Given the following data, solve for p (number of red alleles divided by total number of alleles).

	Frequency	P alleles per flower	# of p alleles
	25	2	50
	200	1	200
Processing	75	0	0

Given the following dat Remember that

	Frequency of flowers	P alleles pe flower		ere are 2
	25		Z	r flower 5U
	200		1	200
Program of the Control of the Contro	75		0	0
2*300	=600			250

alleles

600

Given the following data, solve for p.

$$p = \frac{250}{600} = 0.417$$

Is this population at HWE?

	Frequency of flowers	P alleles per flower	# of p alleles	Expected flower frequency
	25	2	50	=300*p ² =300(0.417) ² =52.1
	200	1	200	=300*2pq =300(0.417)(0.583) =145.9
Parties of the Control of the Contro	75	0	0	=300*q ² =300*(0.583) ² =102

This population is not exactly in HWE

Think-pair-share

Fred	quency of wers	P alleles per flower		Expected flower frequency
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Suppose we observe a population out of Hardy-Weinberg Equilibrium

- What hypotheses might we have to explain this difference between our expectations and our observations?
- Are any of these hypotheses relevant to predicting population sizes or population persistence?



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