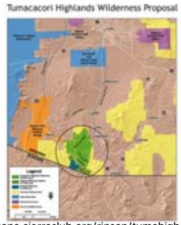
Lecture 18, 18 Oct 2007
Populations
Reserves

Conservation Biology
ECOL 406R/506R
University of Arizona
Fall 2007

Kevin Bonine
Cathy Hulshof



http://arizona.sierraclub.org/rincon/tumahigh.html
http://www.tumacacoriwild.org/default.php
http://www.icmj2.com/RecentNews/Tumacacori.htm
http://thomas.loc.gov/home/gpoxmlc110/h3287_ih.xml
http://uscode.house.gov/uscode-cgi/fastweb.exe?getdoc+uscview+t13t16+6792+0++%2716%20USC%2

Upcoming Readings
today: Ch 7, Ch 8
Tues 23 Oct: Debate- see website
Come to class with TWO WRITTEN Questions - on a piece of paper with your name and the date.
Thurs 25 Oct: SIA link on website

Thanks to Kathy Gerst
Q4 due 13 November

1

Conservation Biology Lab 406L/506L

Friday 19 Oct 1230 –> 1530
Meet 1230h S or W side BSE
(4th and Highland)

Hat, water, sunscreen, close-toed shoes

Readings on Course Website re:
Sewage Treatment Plant, Sweetwater Wetland

2

Debate 23 Oct 2007:
Should the Tumacacori Highlands be Wilderness?

Three groups – one will debate, another will evaluate, third will observe, then we rotate.

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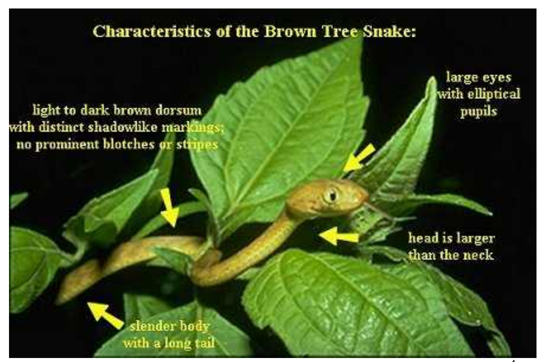
Debate 1 (20 Sept.)
Group A debate
Group B evaluate
Group C observe
Debate 2 (23 Oct.)
Group A observe
Group B debate
Group C evaluate
Debate 3 (15 Nov.)
Group A evaluate
Group B observe
Group C debate

Debate 1 (20 Sept.)
506 A assist
506 B assist
506 C observe
Debate 2 (23 Oct.)
506 A observe
506 B assist
506 C assist
Debate 3 (15 Nov.)
506 A assist
506 B observe
506 C assist

3

http://www.fort.usgs.gov/resources/education/bts/bts_home.asp



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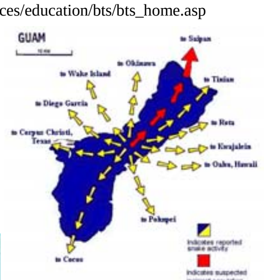
http://www.fort.usgs.gov/resources/education/bts/bts_home.asp



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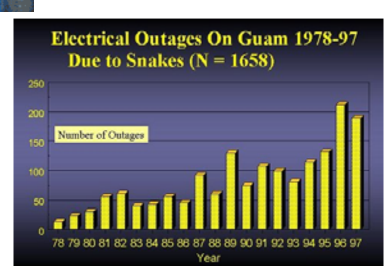
http://www.fort.usgs.gov/resources/education/bts/bts_home.asp



http://www.fort.usgs.gov/resources/education/bts/bts_home.asp

The hand of an infant with swelling, discoloration, and bleb formation.

Results of one night's captures by hand.

7

Applications of Genetics to Conservation Biology

Dr. Melanie Culver
SNR, UA

8

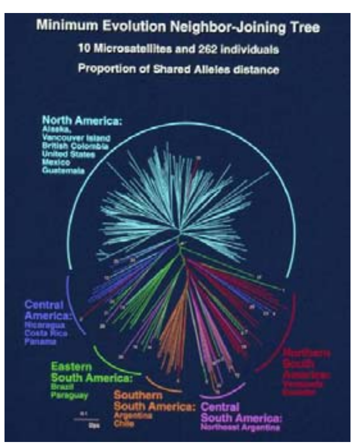
32 Puma subspecies, as of the early 1900s

Modern and museum puma samples collected, total of 315

-Geographic clustering of individuals

~Six groups identified

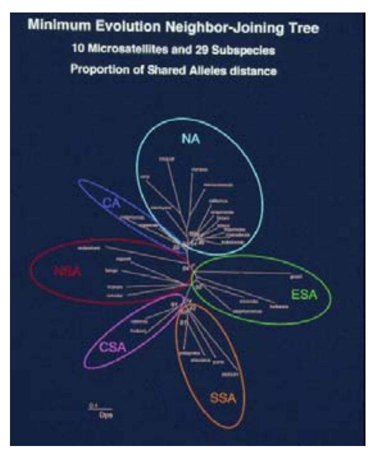
2 distance methods agree



-Subspecies associate into same 6 groups

-Statistical support from bootstrap values

-2 distance methods agree



BOX 11.3 Calculation of *F*-Statistics

Derrick W. Sugg, *University of Georgia, Savannah River Ecology Laboratory*

F_{IS}, F_{IT}, F_{ST}

Fixation indices, or *F*-Statistics, were developed by Sewall Wright (1922, 1965, 1969, 1978) as a means to describe how genetic diversity is partitioned in a population. By partitioning genetic diversity into different components one can determine the relative amounts residing within individuals, subpopulations, and the overall population. Because adaptive evolution requires genetic variation to proceed, it is important to understand how much of the total variation is available for selection acting on individuals. More recently, conservation biologists have shown renewed interest in fixation indices because they provide a means to determine how natural populations maintain genetic variation (beneficial for developing management strategies) and to determine levels of genetic variation in threatened or captive populations (beneficial for assessing the success of management strategies).

Typically when one calculates fixation indices it is for a structured population. The classical approach is to sample individuals from different subpopulations at fairly distinct geographic locations. Such a population is said to consist of three levels of structure: individuals (*I*), subpopulations (*S*), and the total population (*T*). One calculates the average individual heterozygosity by counting the number of heterozygous individuals in a subpopulation and dividing that sum by the total number of individuals in the subpopulation. This calculation is made for every subpopulation, and the average for all subpopulations is called the average individual heterozygosity:

$$\left(H_I = \frac{1}{k}\sum_{i=1}^{k}\frac{\#\,Heterozygotes_i}{N_i}\right)$$

where *k* is the number of subpopulations and N_i is the number of individuals in the *i*th subpopulation. At the same time one can use those individuals to determine the frequency of the genes. The gene frequencies are used to calculate the expectations for heterozygosity in the average subpopulation $\bar{H}_S$ and the total population (H_T). The expectation for the average subpopulation is

$$\bar{H}_S = \frac{2}{k}\sum_{i=1}^{k} p_i - p_i^2$$

where p_i is the frequency of the gene in the *i*th subpopulation. The expected number of heterozygous individuals for the entire population is given by, $H_T = 2(\bar{p} - \bar{p}^2)$ where $\bar{p}$ is the frequency of the gene averaged over all individuals in the population without respect to the subpopulation they came from. $\bar{H}_S$ predicts the frequency of heterozygous individuals in subpopulations had they mated at random and H_T predicts the same frequency if individuals are mating at random without respect to subpopulations.

These estimates of the observed and expected frequency of heterozygous individuals can be used to calculate the fixation indices, F_{IS}, F_{IT}, and F_{ST}. Values for F_{IS} determine whether or not subpopulations have fewer or more heterozygous individuals than expected. It is calculated from:

$$F_{IS} = \frac{\bar{H}_S - H_I}{\bar{H}_S}$$

When there are fewer heterozygous individuals than expected ($\bar{H}_S > H_I$), F_{IS} will be positive. When $\bar{H}_S < H_I$ then F_{IS} will be negative. Therefore, negative values for F_{IS} indicate an excess of heterozygous individuals in subpopulations and positive values indicate the opposite condition. F_{IT} is calculated in a similar manner:

$$F_{IT} = \frac{H_T - H_I}{H_T}$$

and the interpretation of positive and negative values are the same except that they apply to the total population instead of the subpopulations. Finally, the degree of genetic differentiation among subpopulations (how unique they are) is given by:

$$F_{ST} = \frac{H_T - \bar{H}_S}{H_T}$$

which is always greater than or equal to zero. High values for F_{ST} indicate that subpopulations have very different gene frequencies, and when $F_{ST} = 1$ then subpopulations are said to be "fixed" for different genes; each subpopulation has a unique gene for each locus.

Models by Wright make simplifying assumptions including equal reproductive contributions among breeding adults and a large number of subpopulation of equal and constant size contributing dispersers to the pool of migrants. More recently, Wright's models have been recast using different methodologies or by emphasizing the importance of different evolutionary forces. Readers interested in this subject area are encouraged to read additional literature in this area including Slatkin (1991), Crow and Aoki (1984), Chesser (1991a,b), Wade and McCauley (1988), and Whitlock and McCauley (1999).

Groom, Meffe, & Carroll 2006

Wright's Fst Estimates and Slatkin's Migration Estimates

mtDNA

	NA	CA	ESA	NSA	CSA	SSA
NA	-	0.1	0.1	0.02	0.03	0.1
CA	*0.784	-	8.3	0.5	1.6	1.6
ESA	*0.815	0.057	-	0.8	2.3	2.2
NSA	*0.958	*0.492	0.384	-	4.2	0.5
CSA	*0.935	0.233	*0.177	*0.107	-	1.3
SSA	*0.835	0.240	*0.186	*0.526	*0.281	-

(Fst near 0 = little divergence) (Migrants/generation)

microsatellites

	NA	CA	ESA	NSA	CSA	SSA
NA	-	4.0	4.4	8.0	2.2	0.9
CA	*0.110	-	2.3	3.5	3.5	1.2
ESA	*0.103	*0.179	-	15.7	4.8	1.0
NSA	*0.059	*0.126	*0.031	-	6.0	1.1
CSA	*0.186	*0.126	*0.094	*0.077	-	2.4
SSA	*0.367	*0.288	*0.330	*0.316	*0.172	-

mtDNA vs. nuclear microsatellites

- Mitochondrial
  - from maternal lineage
  - no recombination with paternal genes
  - evolves more quickly
- Microsatellites
  - nuclear DNA
  - short repeats of 2-4 base pairs (bps)

ACGACGACGACGACGACGACGACGACG

Summary:
-6 groups identified using microsatellites
-mtDNA haplotypes overlayed onto map, supports 6 groups
-Location of 2 ancestral haplotypes

Major restrictions to gene flow:
-Amazon River
-Rio Parana
-Rio Negro
-Andes?

Fossil Record versus Molecular Divergence Estimates

- Oldest fossils in North and South America date to 0.2-0.3 Mya
- From mtDNA mutation rate of 1.15%/My, divergence for extant puma lineages is 390,000 years ago
- From mutation rate of 5 x 10^{-9}/yr for microsatellite flanking regions, pumas are less than 230,000 years old

Historical Inferences

- Extant pumas originated in Brazillian Highlands (ancestral haplotypes)
- Fossil record suggests dispersal to NA soon after the common origin in Brazil
- 2 historical radiation events occurred

-Ancestor to puma crosses land-bridge ~2-3 Mya

-Puma origin in Brazilian Highlands ~300,000 ya

2 Major historical radiations

-One locally distributed

-One broad ranging

Populations
and
PVA
(population viability analysis)

Thanks to Margaret Evans

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Population Dynamics

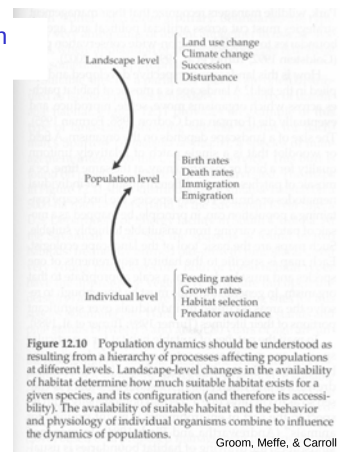

Figure 12.10 Population dynamics should be understood as resulting from a hierarchy of processes affecting populations at different levels. Landscape-level changes in the availability of habitat determine how much suitable habitat exists for a given species, and its configuration (and therefore its accessibility). The availability of suitable habitat and the behavior and physiology of individual organisms combine to influence the dynamics of populations.

Groom, Meffe, & Carroll 2006

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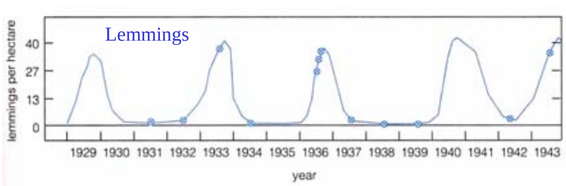
populations are dynamic, not static



Cause of cyclic change in population not completely understood. Cycle length average 3.8 years Mass migration in response to high density with decreasing food supply, sometimes swimming involved.

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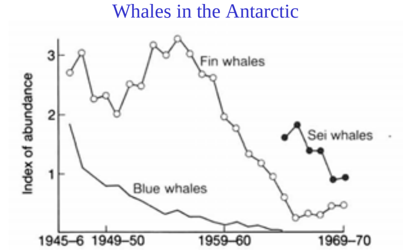
populations are dynamic, not static

Whales in the Antarctic



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Population sizes change over time

Why?
What causes change in population size?
What regulates population size?

If we can answer these questions, we might be able to make changes that increase populations of declining (endangered) species

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Many things affect population size

population size

- population structure
- competition: within a species, among species
- other interactions: predation, herbivory, pollination, etc.
- chance events: demographic, genetic
- habitat attributes: quantity, quality, configuration, and connectivity
- succession or disturbance
- environmental variation: good years, bad years

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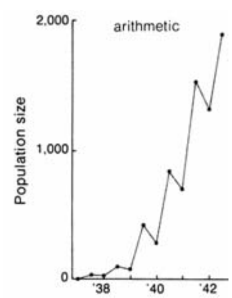
1. Exponential growth

density-independent, deterministic

In a closed population (no immigration or emigration), population growth is a function of birth and death rates

$$\frac{dN}{dt} = (b-d)N$$



Ring-necked pheasant on Protection Island

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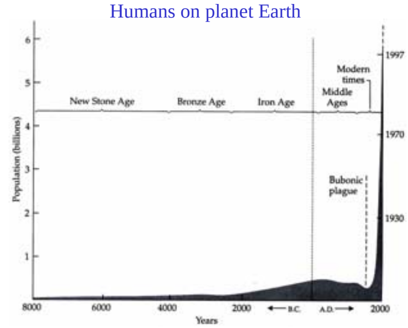
exponential growth: an unrealistic model?

Humans on planet Earth



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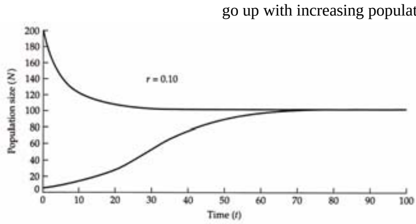
2. Logistic growth

density-dependent, deterministic

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

intraspecific competition stabilizes population size
birth rates go down and/or death rates go up with increasing population size



carrying capacity (K)

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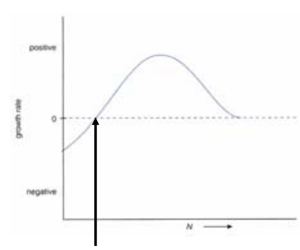
Alternatively,

The population growth rate may increase with population size (positive density-dependence)

Allee effect



minimum viable population size

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Allee effect

How?

In animals:

-group defense against predators
-group attack of prey
-mates difficult to find
-critical number to stimulate breeding behavior

In plants:

-pollinator limitation
-self-incompatibility
-inbreeding depression

37 Passenger Pigeon (adult male).

Allee effect

How?

group defense against predators

Figure 7.6
The sage grouse (*Centrocercus urophasianus*), a gallinaceous bird of the western United States, gathers for mating on communal display and breeding grounds known as leks. If numbers are insufficient to promote lek formation, displays and breeding may not take place.

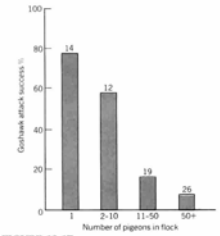

FIGURE 13.17
Success rate of goshawk attacking pigeons in flocks.
Attack by a trained goshawk rarely resulted in capture of a pigeon from a large flock, although most attacks on single pigeons were successful.

The two categories of models we have considered thus far assume that

- all individuals in a population have the same birth and death rates
  (no genetic, developmental, or physiological differences among individuals)

  under some circumstances, this might cause us to inaccurately predict population size

3. Structured population models

density-independent, deterministic

This is the type of model most often used in population viability analysis

What is meant by "structure"?

A population is **unstructured** if all individuals have the same rates of survival and fertility.
A population is **structured** if differences among individuals in **age**, developmental **stage**, or **size** cause them to have different survival or fertility rates.

TABLE 6.3 Survival data for red-cockaded woodpeckers in different reproductive stages, from Walters (1990)

Stage	Total number of bird-years	Fate at the end of a one-year interval: Dead	Fate at the end of a one-year interval: Alive	Proportion surviving one year
Fledglings	616	345	271	0.44
Solitary males	131	50	81	0.62
Helpers-at-the-nest	273	60	213	0.78
Breeding males	838	201	637	0.76
Floaters	29	11	18	0.62

Life Tables

Table 7.1 A Life Table for Belding's Ground Squirrel (*Spermophilus beldingi*). Life tables, properly constructed from appropriate data, provide important summaries of age-specific demographic characteristics of plant and animal populations: n is the actual number of individual squirrels alive in each age interval; d is the number dying during the interval; l is the proportion of the original cohort alive at the beginning of the age interval; q is the mortality rate from interval x to inteveral $x + 1$; e is the life expectancy of individuals in the age interval; and x is the age interval to which the value refers. Calculations of l do not include individuals first marked as adults.

AGE (YEARS)	FEMALES n_x	FEMALES d_x	FEMALES l_x	FEMALES q_x	FEMALES e_x	MALES n_x	MALES d_x	MALES l_x	MALES q_x	MALES e_x
0–1	337	207	1.000	0.61	1.33	349	227	1.000	0.65	1.07
1–2	252[a]	125	0.386	0.50	1.56	248[†]	140	0.350	0.56	1.12
2–3	127	60	0.197	0.47	1.60	108	74	0.152	0.69	0.93
3–4	67	32	0.106	0.48	1.59	34	23	0.048	0.68	0.89
4–5	35	16	0.054	0.46	1.59	11	9	0.015	0.82	0.68
5–6	19	10	0.029	0.53	1.50	2	0	0.003	1.00	0.50
6–7	9	4	0.014	0.44	1.61	0	—	—	—	—
7–8	5	1	0.008	0.20	1.50	—	—	—	—	—
8–9	4	3	0.006	0.75	0.75	—	—	—	—	—
9–10	1	1	0.002	1.00	0.50	—	—	—	—	—

Source: Sherman and Morton 1984.
[a]Includes 122 females first captured as yearlings.
[†]Includes 126 males first captured as yearlings.

3. Density-independent, deterministic, structured population growth

What else can structured population models tell us?

Sensitivity

The sensitivity of λ to each matrix element describes how much λ will be affected by a change in that transition probability

Would it be better to focus conservation efforts on improving the survival of hatchlings or large juveniles or adults???

(Lambda = population growth rate)

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When *lambda* is **greater** than 1 the population **increases** in size

When *lambda* is **less** than 1 the population **decreases** in size

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Van Dyke p. 178

“Four Horsemen of the Extinction Apocalypse:”

1. Genetic Stochasticity
2. Environmental Stochasticity
3. Demographic Stochasticity
4. Natural Catastrophes

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Population Viability Analysis

TABLE A *Potential Uses of PVA "Products"*

Category of use	Specific use	Sources for examples
Assessment of extinction risk	Assessing the extinction risk of a single population	Shaffer 1981, Shaffer and Samson 1985, Lande 1988
	Comparing relative risks of two or more populations	Forsman et al. 1996, Menges 1990, Allendorf et al. 1997
	Analyzing and synthesizing monitoring data	Menges and Gordon 1996, Gerber et al. 1999
Guiding management	Identifying key life stages or demographic processes as management targets	Crouse et al. 1987
	Determining how large a reserve needs to be to gain a desired level of protection from extinction	Shaffer 1981, Armbruster and Lande 1993
	Determining how many individuals to release to establish a new population	Bustamante 1996, Howells and Edwards-Jones 1997, Marshall and Edwards-Jones 1998, South et al. 2000
	Setting limits on the harvest or "take" from a population that are compatible with its continued existence	Nantel et al. 1996, Ratsirarson et al. 1996, Tufto et al. 1999, Caswell et al. 1998
	Deciding how many populations are needed to protect a species from regional or global extinction	Menges 1990, Lindenmayer and Possingham 1996

Groom, Meffe, & Carroll 2006

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Evolution of Population Viability Assessments for the Florida Panther: A Multiperspective Approach

David S. Maehr, Robert C. Lacy, E. Darrell Land, Oron L. Bass Jr., and Thomas S. Hoctor

IN: Population Viability Analysis. Steven R. Beissinger and Dale R. McCullough, eds. Univ. of Chicago Press, Chicago. xvi + 577 pps.

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-Panther Article on PVAs over time

-VORTEX
-data
-population size?
-source and sink?
-inbreeding problems?
-captive breeding?
-introgression?
-time scale?
-HABITAT LOSS

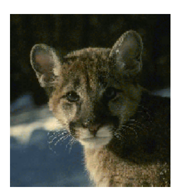

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Table 14.1 Comparison of VORTEX Model Inputs Provided Independently by the Five Authors and the Outputs Generated from These Simulations

Model Inputs and Output	Originator of Variable Estimates for the VORTEX Simulation				
	Population Ecologist (Lacy)	State Field Biologist (Land)	Federal Field Biologist (Bass)	University Landscape Ecologist (Hoctor)	University Conservation Biologist (Maehr)
Inputs					
Inbreeding depression?	Yes	No	No	No	No
Lethal equivalents	3.14	—	—	—	—
% due to recessive lethals	50	—	—	—	—
Reproduction correlated with survival?	Yes	No	No	No	No
Polygynous mating system?	Yes	Yes	Yes	Yes	Yes
Age 1st female reproduction	2	1	3	2	2
Age 1st male reproduction	4	3	2	3	3
Maximum individual age	12	12	12	9	12
Reproduction density dependent?	No	No	No	No	No
Sex ratio at birth	50:50	50:50	50:50	50:50	50:50
Maximum litter size	4	4	2	3	4
% females with litter/year	50	50	50	60	50
SD of above	20	5	10	10	5
% litter of size 1	32.5	17.5	50	20.0	10.0
% litter of size 2	40.0	50.0	50	50.0	50.0
% litter of size 3	20.0	30.0	—	30.0	30.0
% litter of size 4	7.5	2.5	—	0	10.0
Female mortality in year 1	26.5	20	0	20	20
SD in female mortality, year 1	6.625	2.0	4	10.0	5.0
Female mortality in year 2	10.1	—	0	10	20

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Table 14.1 (continued)

Model Inputs and Output	Originator of Variable Estimates for the VORTEX Simulation				
	Population Ecologist (Lacy)	State Field Biologist (Land)	Federal Field Biologist (Bass)	University Landscape Ecologist (Hoctor)	University Conservation Biologist (Maehr)
Male mortality in adults	21.7	20	66	20	20
SD in male mortality, adults	5.425	3.0	6	5.0	10
Number of catastrophe types	0	0	0	2	1
Probability for catastrophe 1	—	—	—	0.05	0.02
Probability for catastrophe 2	—	—	—	0.01	—
Reproduction rate for catastrophe 1[a]	—	—	—	0.50	.98
Reproduction rate for catastrophe 2[a]	—	—	—	0.50	—
Survival for catastrophe 1[a]	—	—	—	0.90	0.95
Survival for catastrophe 2[a]	—	—	—	0.50	—
% of adult males breeding	100	50	100	50	40
Starting population size	50	50	6	60	70
Habitat carrying capacity	50	60	8	70	85
SD of above	0	5	2	10	5
Change in habitat	Lost	0	0	Lost	0
# of years of habitat loss	25	0	0	20	0
% habitat change per year	−1.0	0	0	−1.5	0
Will panthers be removed?	No	No	No	Yes	No
At what annual interval?	—	—	—	1	—
For how many years?	—	—	—	10	—
# males removed/year	—	—	—	1	—
# females removed/year	—	—	—	1	—
Population augmentation?	Yes	Yes	Yes	No	No
If yes, at what interval?	20 years	10 years	10 years	—	—
For how many years?	100	100	100	—	—
# males added per event	0	0	1	—	—
# females added per event	6	1	2	—	—
Outputs					
Expected heterozygosity	0.692	0.597	0.659	0.537	0.635
Number of extant alleles	6.38	4.58	3.89	3.58	4.68
Probability of persistence to 100 years over 500 iterations	0.998	1.00	0.0880	.998	1.00
Mean final population	34.19	59.41	5.52	50.24	83.29
Median time to extinction	—	—	7.13 years	—	—

Note: SD = standard deviation.
[a]These values represent multipliers that reduce survival and reproduction due to catastrophe.

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Table 14.2 Comparison of Variables Used in the PVA Models

Model Inputs and Outputs	1989 Panther PVA	1992 Panther PVA Consensus	1992 Panther PVA Optimistic	1999 Consensus Simulation
Inputs				
Inbreeding depression?	Yes	Yes	No	Yes
Lethal equivalents	3.4	3.0	0	3.14
% due to recessive lethals	0	0	0	50
Reproduction correlated with survival?	Yes	Yes	No	No
Polygynous mating system?	Yes	Yes	Yes	Yes
Age 1st female reproduction	3	2	2	2
Age 1st male reproduction	3	2	2	4
Maximum individual age	15	12	12	12
Reproduction density dependent?	No	No	No	No
Sex ratio at birth	50:50	50:50	50:50	50:50
Maximum litter size	5	3	3	4
% females with litter/year	50	50	50	50
SD of above	1	0	0	10
% litter of size 1	10	25	25	17.5
% litter of size 2	20	50	50	50.0
% litter of size 3	40	25	25	30.0
% litter of size 4	20	—	—	2.5
% litter of size 5	10	—	—	—
Female mortality in year 1	50	50	20	20
SD in female mortality, year 1	5	0	0	6
Female mortality in year 2	30	20	20	20
SD in female mortality, year 2	3	0	0	3
Female mortality in year 3	25	—	—	—
SD in female mortality, year 3	3	—	—	—
Female mortality in adults	25	20	20	17
SD in female mortality, adults	3	0	0	3
Male mortality in year 1	50	50	50	20
SD in male mortality, year 1	5	0	0	6
Male mortality in year 2	30	20	20	30
SD in male mortality, year 2	3	0	0	5
Male mortality in year 3	25	—	—	30
SD in male mortality, year 3	3	—	—	5
Male mortality in adults	25	20	20	15
SD in male mortality, adults	3	0	0	5
Number of catastrophes	2	0	0	1
Probability for catastrophe 1	0.01	—	—	0.5
Probability for catastrophe 2	0.02	—	—	—
Reproduction rate for catastrophe 1	—	—	—	0.95
Reproduction rate for catastrophe 2	—	—	—	—
Survival for catastrophe 1	—	—	—	0.95
Survival for catastrophe 2	—	—	—	—
% of adult males breeding	100	50	50	50
Starting population size	45	50	50	60
Habitat carrying capacity	45	50	50	70
SD of above	1	0	0	5

(continued)

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Table 14.4 Effects of Increasing Carrying Capacity on Genetic Heterozygosity after 100 Years, Using the Consensus VORTEX Simulation

Carrying Capacity	Predicted Heterozygosity (%)[a]
70	72.2
100	80.6
150	84.1
200	86.5
250	87.5
300	89.6
400	90.7
500	92.4

[a]As percentage of initial value of H.

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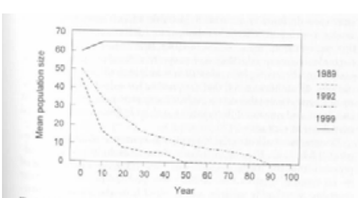

Fig. 14.3 Mean extant population sizes per ten-year intervals for Florida panther PVAs conducted in 1989 and 1992, and the consensus simulation from 1999.

~data

Evolution of PVA for the Florida Panther 301

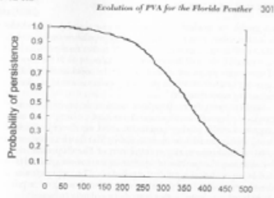

Fig. 14.4 Probability of persistence of the Florida panther based on the consensus simulation run for 500 years.

-time scale?

Comments on PVA

PVA requires lots of data, which takes time, work, and money, whereas managers want answers (predictions about extinction) now. Few species will get thorough PVA. When should PVA be used and what type of PVA (how complex)?

Predictions from PVA can only be as good as the data that go into the analysis. We can only have degrees of confidence in the predictions from PVA. Populations should not be managed to their "minimum viable population" size.

One of the greatest strengths of PVA is the ability to play "what if" games with the model. That is, what if management were to increase patch sizes or connectivity? What if adult survival were improved?

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Reserve Design Considerations

The Conservation of Habitat and Landscape

Multiple Use

Figure 10.10
"Zonation management" for wolves or other large, mobile predators. In a core protected area with low human densities and minimal human impacts, wolves receive complete protection. In a surrounding area (management area), wolf numbers are regulated and individual wolves that kill livestock or pets are destroyed. In surrounding areas of high human population densities and impacts, wolves are killed if they enter the area.
Based on a concept described by Mech (1995).

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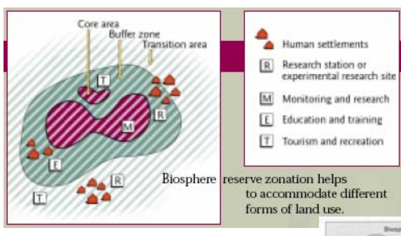
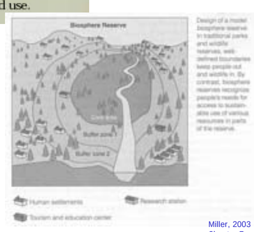
Van Dyke 2003



Biosphere reserve zonation helps to accommodate different forms of land use.



Biosphere reserves
(core, buffer, transition)
- Research and Monitoring
- Conservation
- Local Development

Miller, 2003
Chapter 7

Where?
Why?

Biodiversity Hot Spots

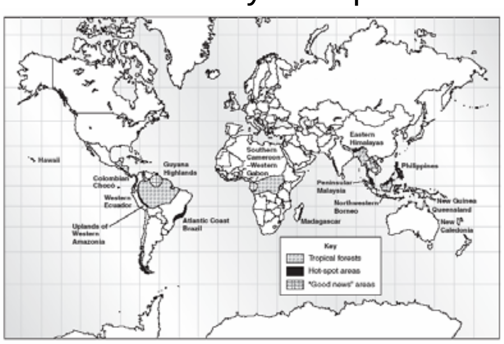


Figure 8.12
Examples of "hot spots" of biodiversity in the tropics. Concentrations of high biodiversity and endemism suggest priority areas for habitat conservation. "Good news" areas refer to regions where species loss due to deforestation is less than anticipated.
After Myers (1988).

Habitat Loss and Fragmentation

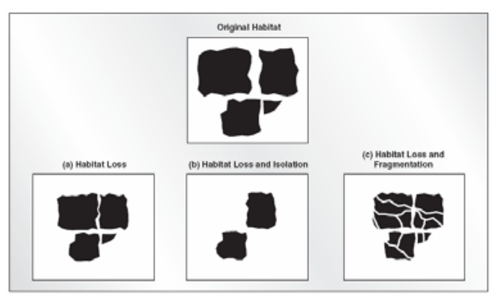


Figure 8.6
A conceptual illustration of habitat loss, isolation, and fragmentation. In (a), all patches are consistently smaller. In (b), habitat fragmentation is actually decreased because there are fewer patches, but habitat isolation increases. In (c), in addition to increasing patch separation, fragmentation decreases patch size.
Adapted from Fahrig (1997).

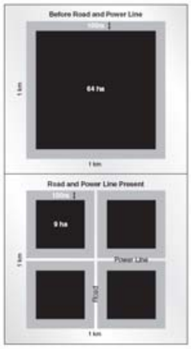


Figure 8.10
The effect of habitat loss on interior and edge species. Note that, in this scenario, when a road and power line intersect in the habitat, edge species experience a net habitat increase of 36 ha to 64 ha, whereas interior species lose 44% (28 ha of the original 64 ha) of previously available habitat.

Edge Effect

Generalists
vs.
Specialists

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Connectivity, Corridors, Habitat

-Scale Dependent
-Little Data
-Pros and Cons