

Lecture 19, 24 Oct 2006  
 CH6 Genetics, CH7 Populations

Conservation Biology  
 ECOL 406R/506R  
 University of Arizona  
 Fall 2006

Kevin Bonine  
 Kathy Gerst

## Conservation Genetics



PVA etc.

Lab this week:

7am 27-29 7pm October = ORPI, Pinacate, CEDO  
 (\$, food, see website for lab readings)

Housekeeping, 24 October 2006

### Upcoming Readings

today: [Text Ch.6 and 7](#), PVA, *Puma concolor*

Thurs 26 Oct: Guy McPherson (web for climate change reading)  
 Tues 31 Oct: Ed Moll (long web reading)  
 Thurs 02 Nov: Exam Two  
 Tues 07 Nov: Don Falk (web reading)  
 Thurs 09 Nov: Conservation Practices (Ch 10, Donlan EA 2005)

Short oral presentations :  
 24 Oct Cori and Robert  
 09 Nov Jon and Laura  
 14 Nov Dan and Lane  
 28 Nov Amanda and Fred

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## Global Climate Change Lecture Series

All lectures will take place at UA Centennial Hall.

All lectures begin at 7pm and are free to the public. Call 520.621.4090 for more information.

Tuesday, October 17  
 Global Climate Change: The Evidence  
 Malcolm Hughes, Professor of Dendrochronology  
<http://cos.arizona.edu/climate/>

Tuesday, October 24  
 Global Climate Change: What's Ahead  
 Jonathan Overpeck, Director of the Institute for the Study of Planet Earth and Professor of Geosciences

Tuesday, October 31  
 Global Climate Change: The Role of Living Things  
 Travis Huxman, Assistant Professor of Ecology and Evolutionary Biology

Tuesday, November 7  
 Global Climate Change: Ocean Impacts and Feedbacks  
 Julia Cole, Associate Professor of Geosciences

Tuesday, November 14  
 Global Climate Change: Disease and Society  
 Andrew Comrie, Dean of the Graduate College and Professor of Geography and Regional Development

Tuesday, November 21  
 Global Climate Change: Could Geoengineering Reverse It?  
 Roger Angel, Regents' Professor of Astronomy

Tuesday, November 28  
 Global Climate Change: Designing Policy Responses  
 Paul Portney, Dean of the Eller College of Management and Professor of Economics

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Cori and Robert

will speak for 10 minutes on xx



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## Applications of Genetics to Conservation Biology

- Molecular Taxonomy
- Populations, Gene Flow, Phylogeography
- Relatedness, Paternity, Individual ID



Dr. Melanie Culver  
 SNR, UA



## Molecular Taxonomy: Molecules versus Morphology

- **Cryptic species** (sibling species)
- Morphological variation without genetic variation

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Modern and museum puma samples collected, total of 315



## Molecular Methods Used

- Mitochondrial gene sequencing
  - 16SrRNA
  - NADH-5
  - ATPase8
- Nuclear microsatellite length determination
  - 10 domestic cat microsatellite loci

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Neutral Markers often studied.

Relevance to natural selection and adaptation?

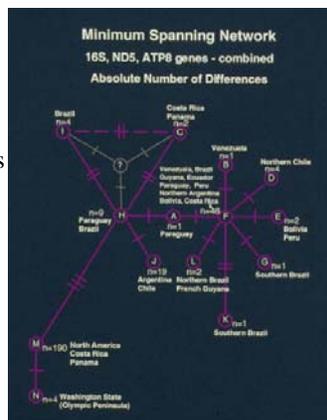
Ultimately, source of all variation is mutation.  
mutation rate =  $10^{-4} - 10^{-6}$

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## Mitochondrial DNA Haplotypes (in a geographical cline)



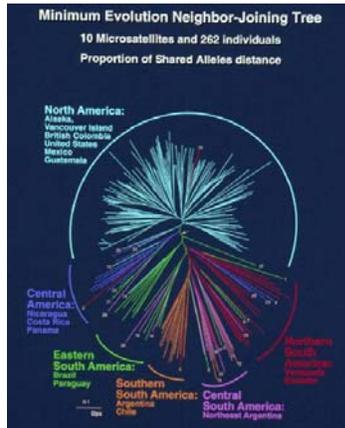
- Ancestral haplotypes
- 2 historical radiations
- NA is most recently founded population



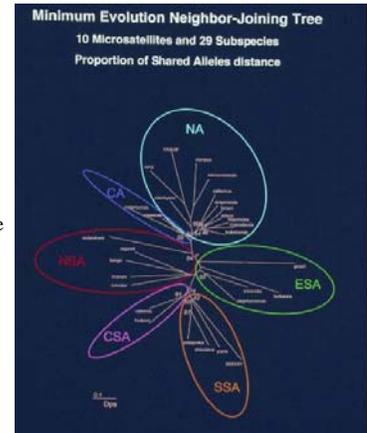
## Microsatellite Alleles at FCA008

Group	Subspecies	Tot no	Allele size																										
			126	128	130	132	134	136	138	140	142	144	146	148	150	152	154	156	158	160	162	164	166	168	170	172	174	176	
NA	m. baileyi	21																											
	m. arizonensis	19																											
	m. californicus	6																											
	m. baileyi	4																											
	m. californicus	23																											
	m. baileyi	4																											
	m. californicus	12																											
	m. baileyi	17																											
	m. arizonensis	35																											
	m. baileyi	12																											
	m. californicus	8																											
	m. baileyi	11																											
CA	m. californicus	13																											
	m. baileyi	2																											
	m. californicus	1																											
	m. baileyi	3																											
NSA	m. baileyi	5																											
	m. californicus	2																											
	m. baileyi	5																											
	m. californicus	1																											
CSA	m. californicus	10																											
	m. baileyi	7																											
SSA	m. baileyi	3																											
	m. californicus	4																											
	m. baileyi	8																											
	m. californicus	4																											

- 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:

$$H_i = \frac{1}{N_i} \sum_{j=1}^k \text{Heterozygotes}_{ij}$$

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 gene. The gene frequencies are used to calculate the expectations for heterozygosity in the average subpopulation  $H_s$  and the total population ( $H_t$ ). The expectation for the average subpopulation is given by:

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

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  $H_t = 2p - p^2$  where  $p$  is the frequency of the gene averaged over all individuals in the population without respect to the subpopulation they came from.  $H_s$  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 subpopulation.

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:

$$F_{IS} = \frac{H_i - H_s}{H_s}$$

When there are fewer heterozygous individuals than expected ( $H_i < H_s$ ),  $F_{IS}$  will be positive. When  $H_i > H_s$  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.  $F_{IS}$  is calculated in a similar manner:

$$F_{IT} = \frac{H_i - H_t}{H_t}$$

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:

$$F_{ST} = \frac{H_s - H_t}{H_t}$$

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 diffusion-metapopulation 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), Cheverie (1991a,b), Wade and McCauley (1988), and Whitlock and McCauley (1999).

Groom, Meffe, & Carroll 2006

Wright's  $F_{ST}$  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	-

( $F_{ST}$  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	-

- Summary:
- 6 groups identified using microsatellites
  - mtDNA haplotypes overlaid 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  $5 \times 10^{-9}$ /yr for microsatellite flanking regions, pumas are less than 230,000 years old

## Historical Inferences

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

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

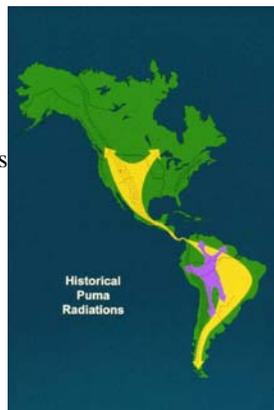
-Puma origin in Brazilian Highlands ~300,000 ya



2 Major historical radiations

-One locally distributed

-One broad ranging



## Puma Bottlenecks

- Subspecies-level
  - North America low overall genetic variation
- Population-level
  - Florida monomorphic at 8/10 microsatellite loci
  - Olympic Peninsula and Vancouver Island, monomorphic at 5/10 microsatellite loci

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## Puma Conclusions

- Pumas originated in Brazil approximately 300,000 years ago
- Possible extirpation and recolonization in North America (Pleistocene age?)
- Molecular data does not support 32 subdivisions, instead 6 groups
- Pumas are fairly panmictic within 6 groups

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## Conservation Implications

- Maintain habitat connectivity within 6 large groups
- Management should consider effects of bottlenecked populations
- Eastern cougar, Florida panther and Yuma puma management take into account revised subspecies

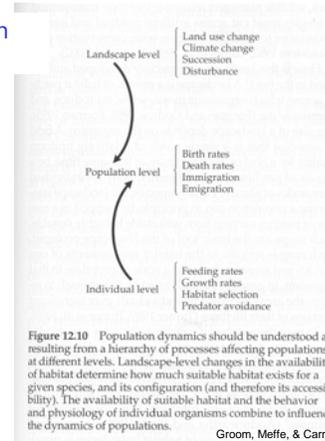
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# What is population viability analysis? (PVA)

Thanks to Margaret Evans, 2003

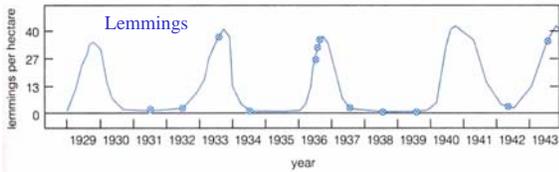
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## Population Dynamics



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populations are dynamic, not static

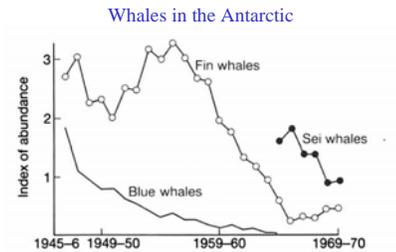


Cause of cyclic change in population not completely understood. Cycle length average 3.8 years Mass migration in response to high density with decreasing food supply, sometimes swimming involved.



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populations are dynamic, not static



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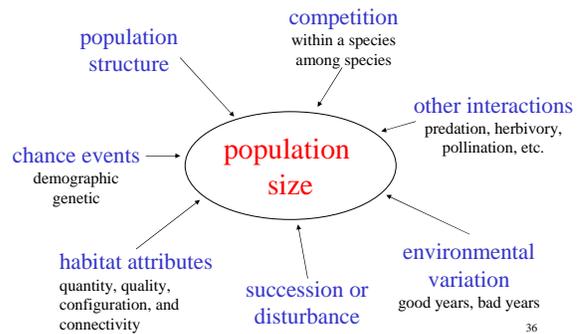
## Population sizes change over time

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



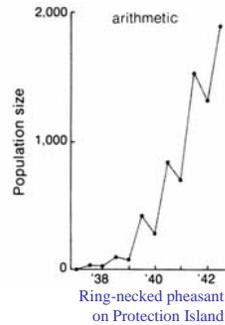
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# 1. Exponential growth

density-independent, deterministic

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

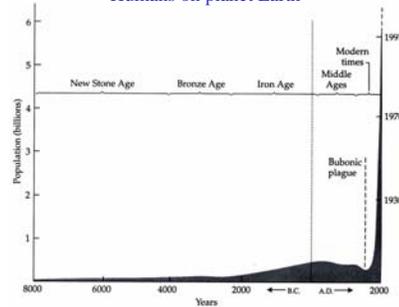
$$\frac{dN}{dt} = (b-d)N$$



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exponential growth: an unrealistic model?

## Humans on planet Earth



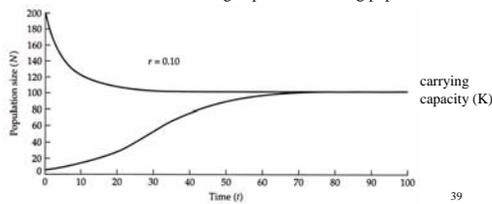
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# 2. Logistic growth

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

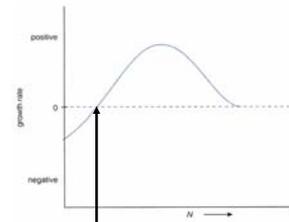


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Alternatively,

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).



How?

group defense against predators

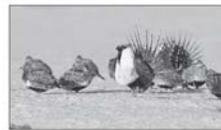


Figure 7.6 The sharp grouse (Centrocercus urophasianus), a gallinaceous bird of the western United States, goshawk for nesting on communal display and breeding grounds known as leks. If numbers are insufficient to provide lek formation, display and breeding may not take place.

## Allee effect

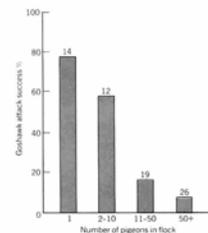


FIGURE 13.17 Success rate of goshawk attacking pigeons in flocks.

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

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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

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### 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.

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**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		Proportion surviving one year
		Dead	Alive	
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

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**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:  $n_x$  is the actual number of individual squirrels alive in each age interval;  $d_x$  is the number dying during the interval;  $l_x$  is the proportion of the original cohort alive at the beginning of the age interval;  $q_x$  is the mortality rate from interval  $x$  to  $x + 1$ ;  $e_x$  is the life expectancy of individuals in the age interval, and  $x$  is the age interval to which the value refers. Calculations of  $l_x$  do not include individuals first marked as adults.

AGE (YEARS)	FEMALES					MALES				
	$n_x$	$d_x$	$l_x$	$q_x$	$e_x$	$n_x$	$d_x$	$l_x$	$q_x$	$e_x$
0-1	337	207	1.000	0.61	1.33	349	227	1.000	0.65	1.07
1-2	252*	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	0.91
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 Moore 1984.  
 \*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  $\lambda$  to each matrix element describes how much  $\lambda$  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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### 3. Density-independent, deterministic, structured population growth

What else can structured population models tell us?

#### Elasticity

Elasticities quantify the proportional change (e.g., 1%) in the asymptotic growth rate that can be expected given a particular change (1%) in each life history transition.

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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	Forman et al. 1996, Menges 1990, Allendorf et al. 1997
Guiding management	Analyzing and synthesizing monitoring data	Menges and Gordon 1996, Gerber et al. 1999
	Identifying key life stages or demographic processes as management targets	Croone 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	Setting limits on the harvest or "take" from a population that are compatible with its continued existence	Nantel et al. 1996, Katziranson et al. 1998, Taffu 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, Orin 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 (Lande)	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	9	12
Maximum individual age	12	12	12	3	3
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	6.025	2.0	4	10.0	5.0
Female mortality in year 2	10.1	—	0	10	20
SD in female mortality, year 2	—	—	—	—	—

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