Population Ecology

EEE330 · Lecture 1

Why populations rise and fall

The Florida panther case



Welcome

Course team

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Course page: everything, day by day

popecol.org/eee330 · OLAT only for uploading your worksheets and the lab report

Assessment

Final exam 50% · Rotifer lab report 30% · Participation 20%

Meeting times

Mornings 9:00–12:00: lectures · Afternoons 13:00–17:00: practicals and the rotifer experiment

Thursdays from 13:30, because of the BEEES seminar

Who are you — and what brought you to population ecology?

How we work with AI and other tools



AI-generated image

AI can be convincing even when it's wrong.

Your eye as an ecologist matters.

This course trains that eye.

You are free, and encouraged, to use AI and other tools, as long as you:

- understand what they produce;
- check it against the biology;
- take responsibility for what you hand in.

Where we are going

HS26 · 26 Nov–18 Dec

L1 Today: population ecology through the Florida panther case

Life histories & population structure

L2 Life histories, fitness, and demographic heterogeneity

L3 From biology to structured population models

Population growth & its drivers

L4 Population growth and structured dynamics

L5 Sensitivity, elasticity, and LTRE

Variation, feedback & harvest

L6 Variable environments, stochasticity, and small populations

L7 Density dependence, regulation, and biotic feedbacks

L8 Harvesting and management of exploited populations

Space, inference & management

L9 Dispersal and spatial population dynamics

L10 From observations to demographic parameters

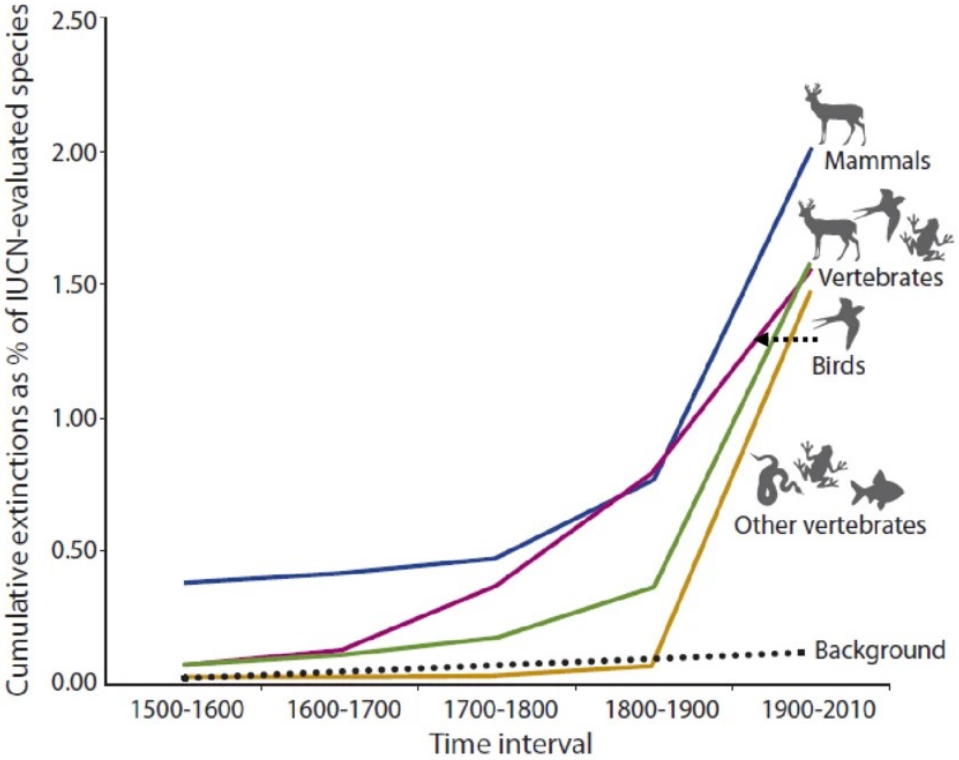
L11 Prediction, PVA, management, and synthesis

Our motto: the mathematics serves biological questions.



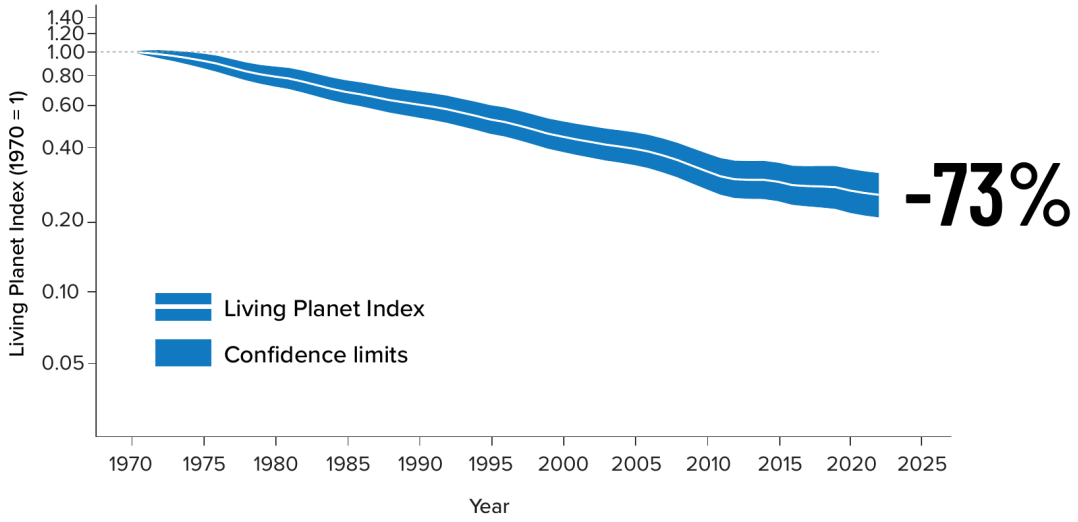
Extinction risk → population abundance

Recorded extinctions have accelerated



Ceballos et al. 2015, Science Advances, Fig. 1B

Population decline often precedes extinction



WWF 2026, Living Planet Report, Fig. 1.1

Extinction is an endpoint. Population abundance changes along the way.

Population ecology ≈ biodemography

Populations are where individual life histories become ecological and evolutionary dynamics.



The Florida Panther

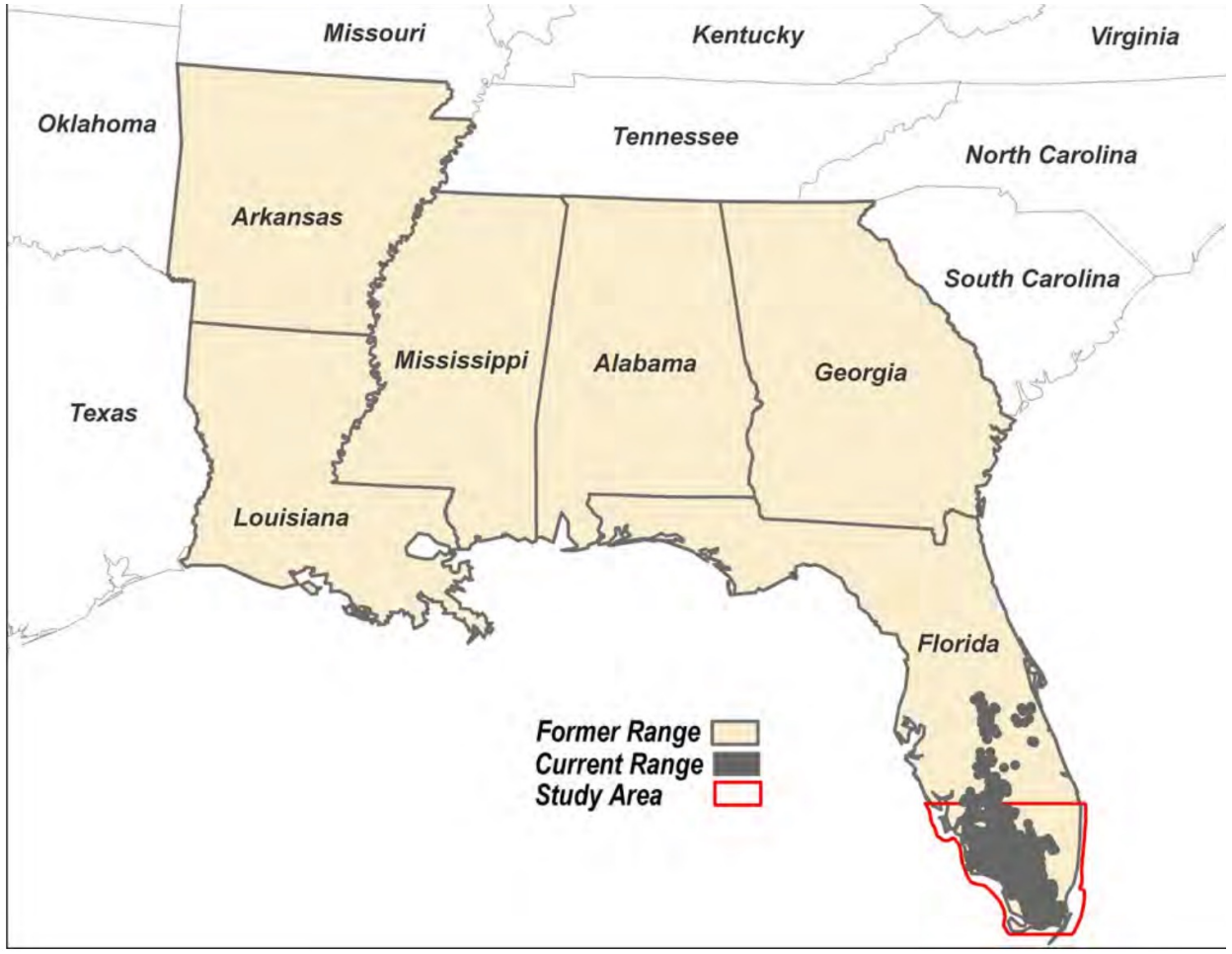
Case study

Puma concolor coryi

One population.
One controversial intervention.



From the southeastern US to South Florida



Swanson et al. 2008, FWRI Technical Report TR-13, Fig. 1

Historically widespread across the Southeast

1967 federally listed as endangered

1970s remnant confirmed in South Florida

1980s only a few dozen remained

range contraction → isolation → small population

A population in trouble



Kinked tail



Cowlick



Cryptorchidism

What processes could connect population isolation to these observations?

isolation + small N → related mating / drift → increased homozygosity → expression of deleterious alleles

Roelke et al. 1993; Barone et al. 1994; Mansfield & Land 2002



By the early 1990s, fewer than a few dozen panthers remained in one isolated population.

What should managers do?

Open discussion

What actions are possible? What information would you want before choosing?

There is no single ‘correct’ intervention to guess.

A controversial proposal

Introduce pumas from Texas?





Map: Swanson et al. 2008, Fig. 1

Potential benefits

restore gene flow

increase genetic diversity

reduce inbreeding depression

Potential concerns

outbreeding depression

loss of local adaptation

loss of Florida-panther genetic identity

the intervention itself carries risk

Would you do it?



1995: genetic restoration

8 female Texas pumas released into South Florida

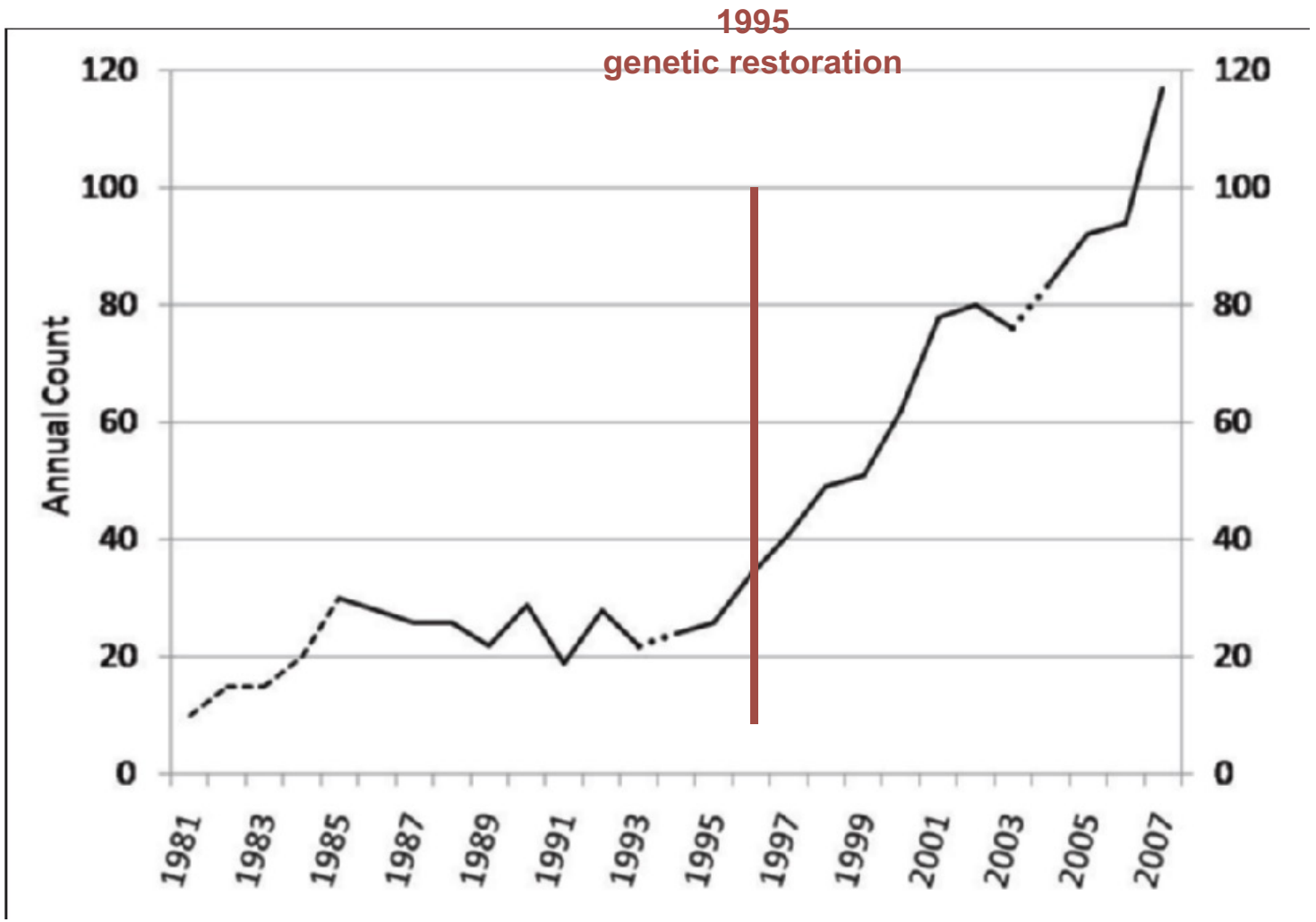
8
released

5
reproduced, producing admixed offspring

20+
known kittens

The Texas females later died or were removed.

The panthers after 1995



What can we conclude?

The recorded population increased strongly after the intervention.

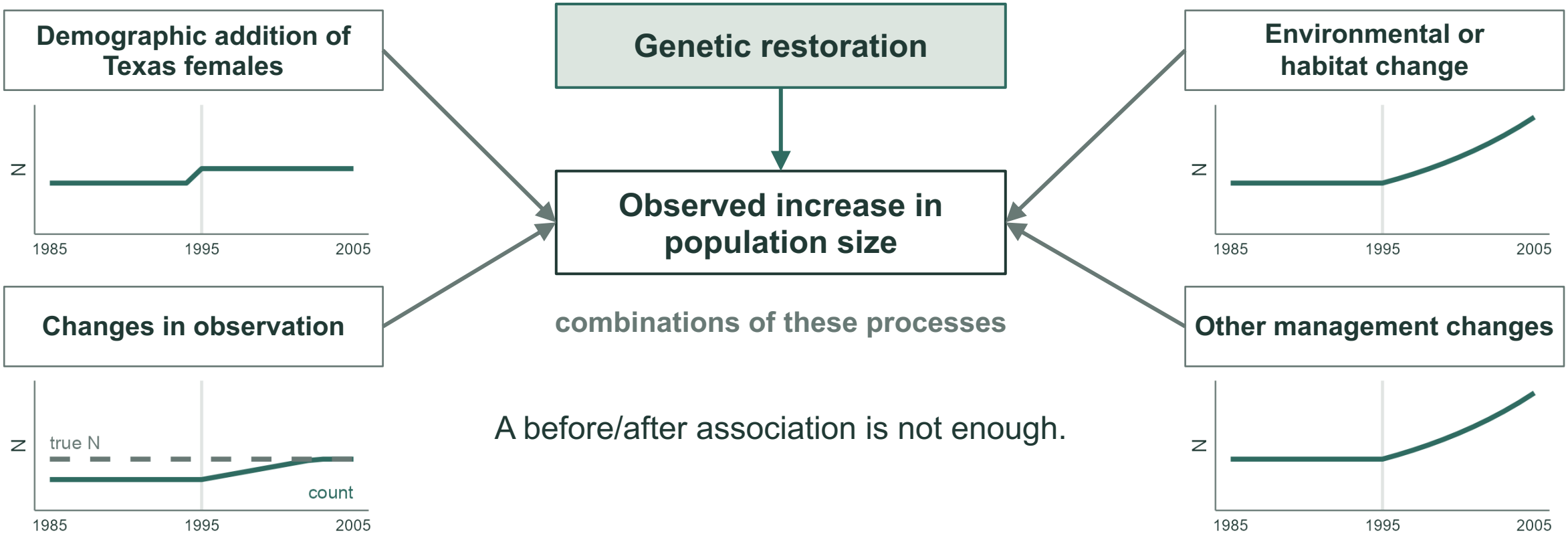
What can we not conclude?

A before/after trajectory alone does not identify cause.

Historical minimum counts are not a consistent series of unbiased abundance estimates.

McBride et al. 2008, Southeastern Naturalist, Fig. 3 · annual minimum counts, not unbiased abundance estimates

From increase to mechanism



A before/after association is not enough.

Illustrative count signatures; grey dashed line = true population size

If genetic restoration mattered, through what demographic mechanism?

Open the demographic black box

What processes change population size?

$$N_{t+1} = N_t + B + I - D - E$$

Additions

B births

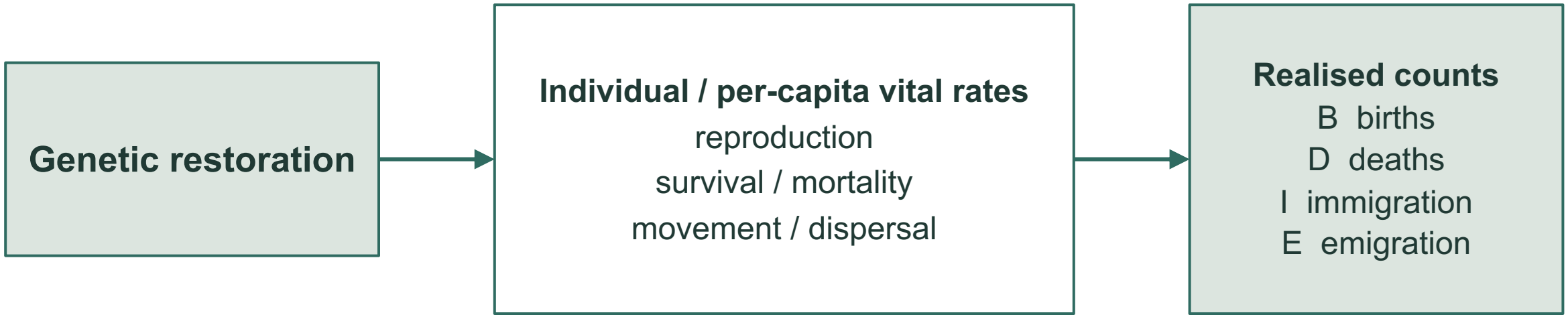
I immigration

Losses

D deaths

E emigration

From vital rates to BIDE

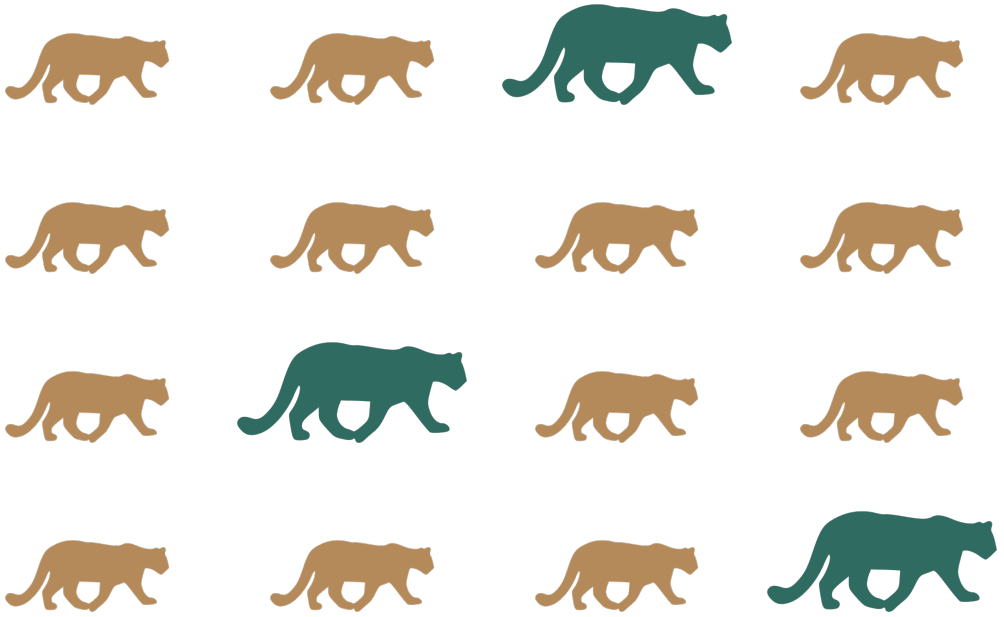


Do these rates vary among individuals? Through time? With population density?

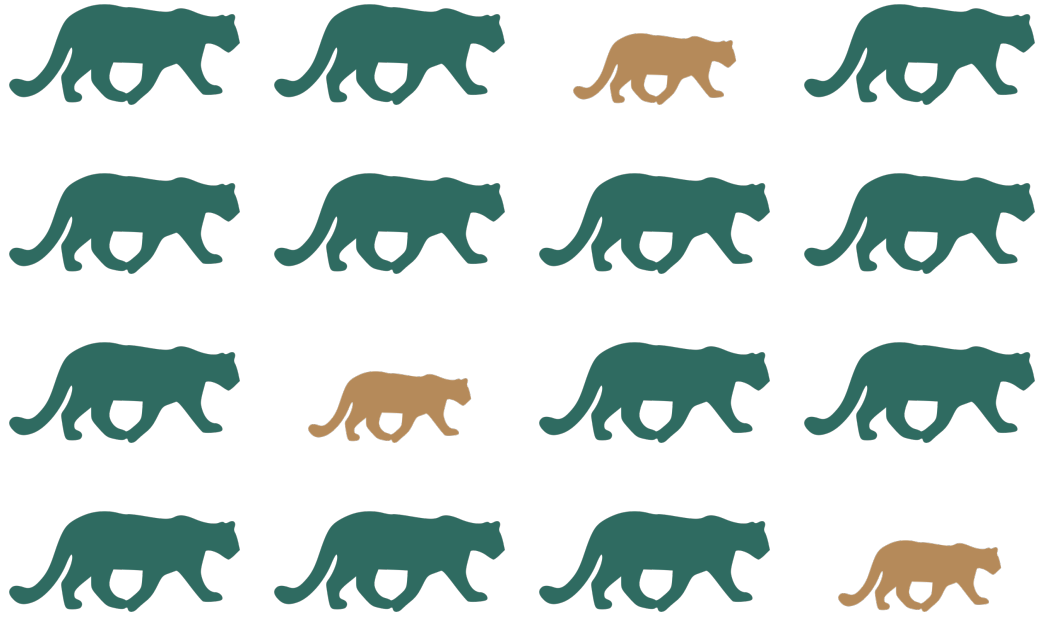
Individuals are not equivalent

Do these populations have the same future?

Population A: mostly subadults



Population B: mostly reproductive adults

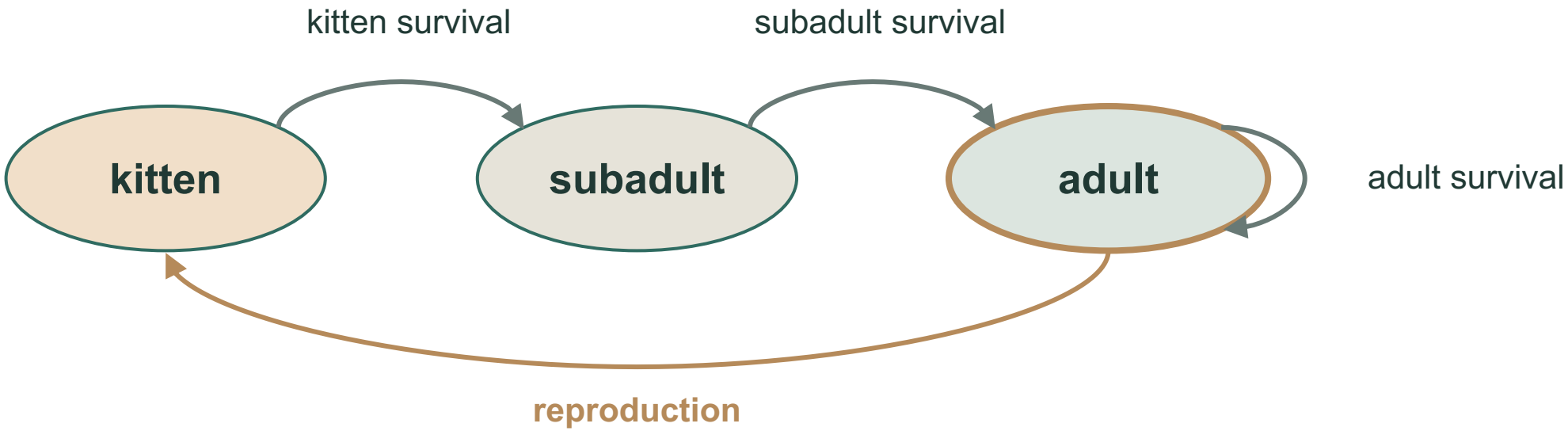


Same N. Different stage composition. Different demographic futures.

Rates that matter most

If we could improve one demographic rate, which would matter most?

Kitten survival? Subadult survival? Adult survival? Reproduction?



What would matter most if changed?
prospective sensitivity

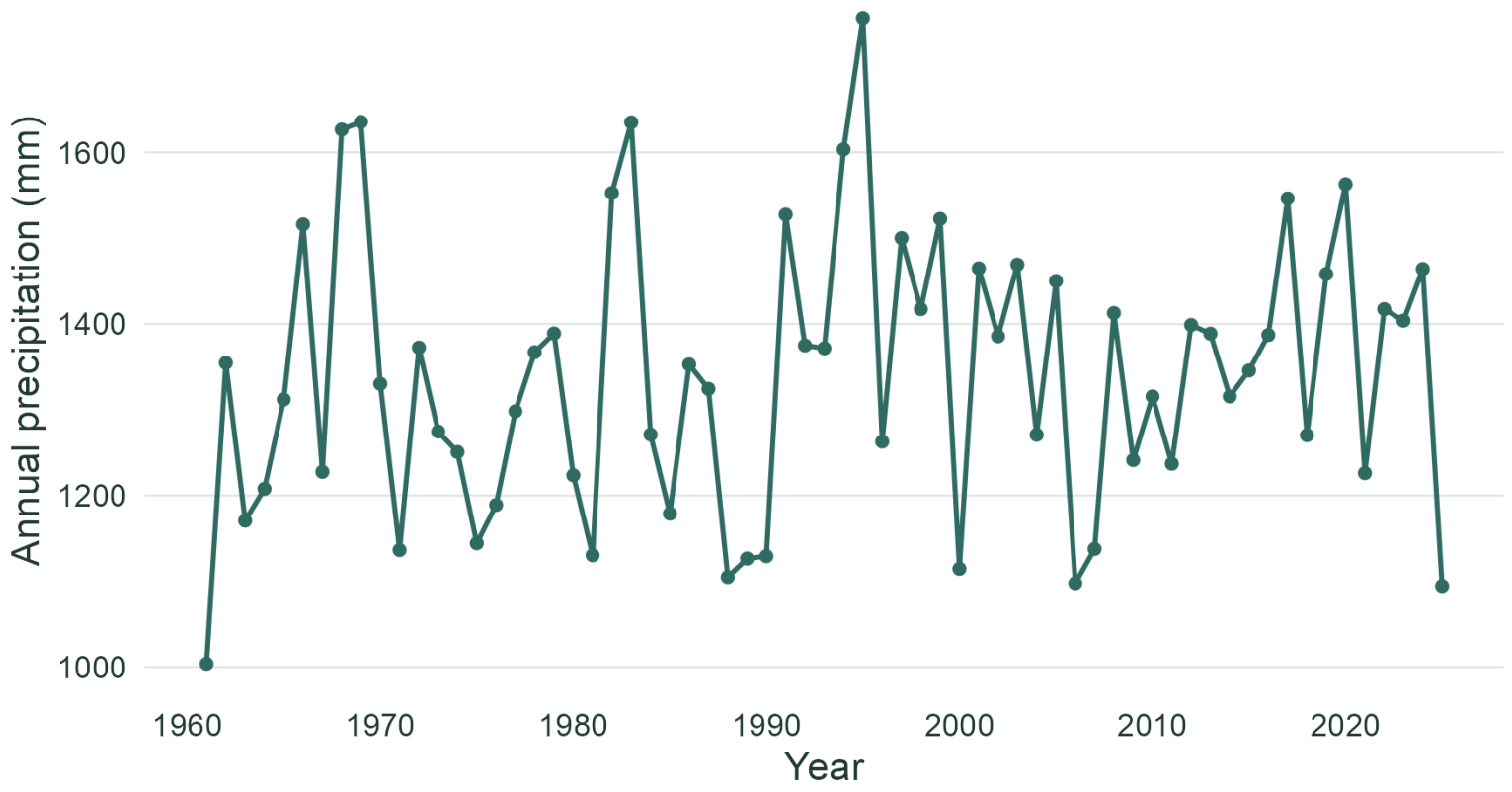
What actually contributed most?
retrospective contribution

Florida panther: improved kitten survival contributed most, followed by prime-adult survival.

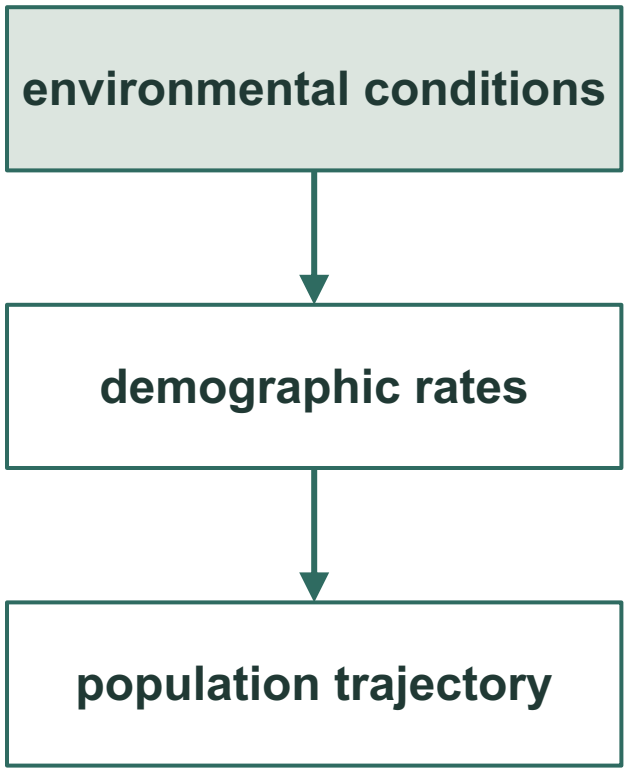
Qualitative result: Hostetler et al. 2013

The environment does not stand still

How do environmental variation and trends change a population's future?

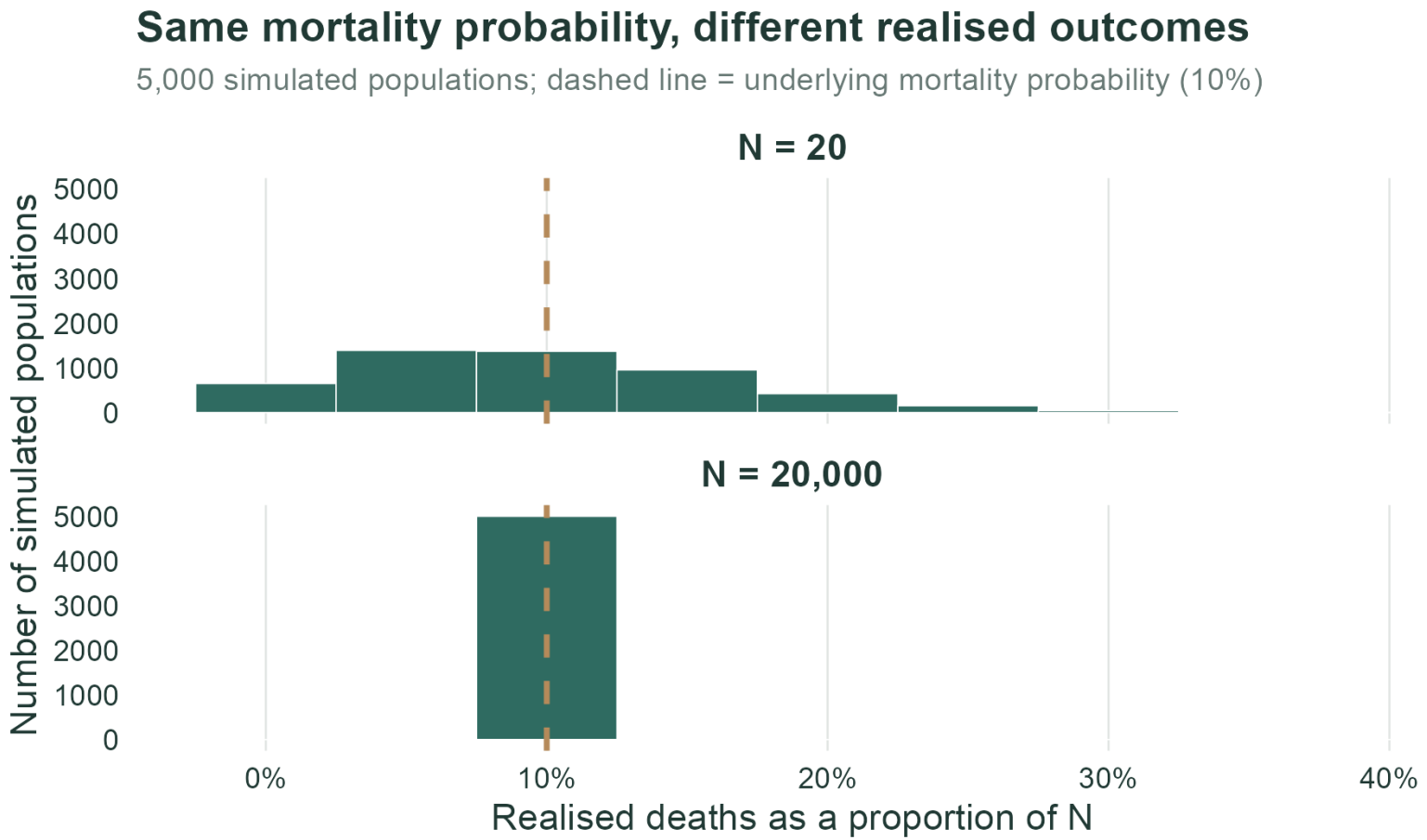


NOAA NCEI Climate at a Glance · Florida Climate Division 0805, Everglades and Southwest Coast



Small populations are different

Does chance matter equally in a population of 20 and a population of 20,000?



same probability

↓

different integer outcomes

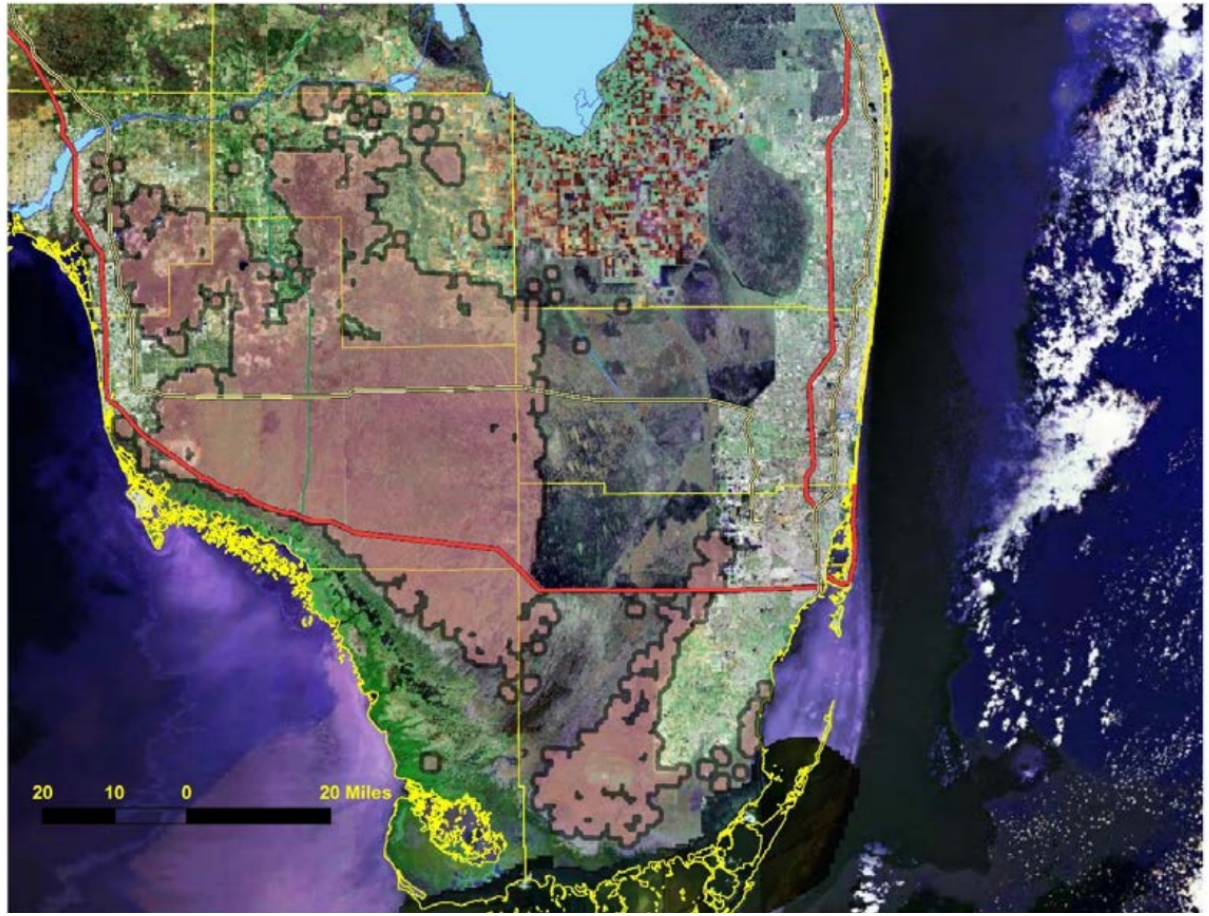
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larger proportional consequences at small N

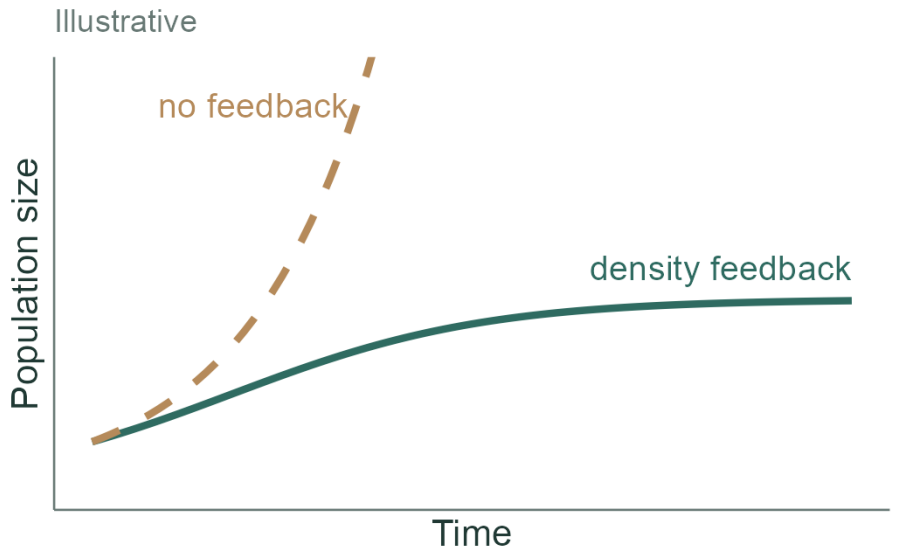
Simulated; not Florida-panther data

Limits to growth

What happens if the panther population keeps increasing?



Occupied range (rose shading): FWC 2016, after Frakes et al. 2015



More individuals → more competition for limited resources and space?

Population density can feed back on demographic rates.

Removing individuals

If habitat can support only so many panthers, what happens when individuals are removed or relocated?

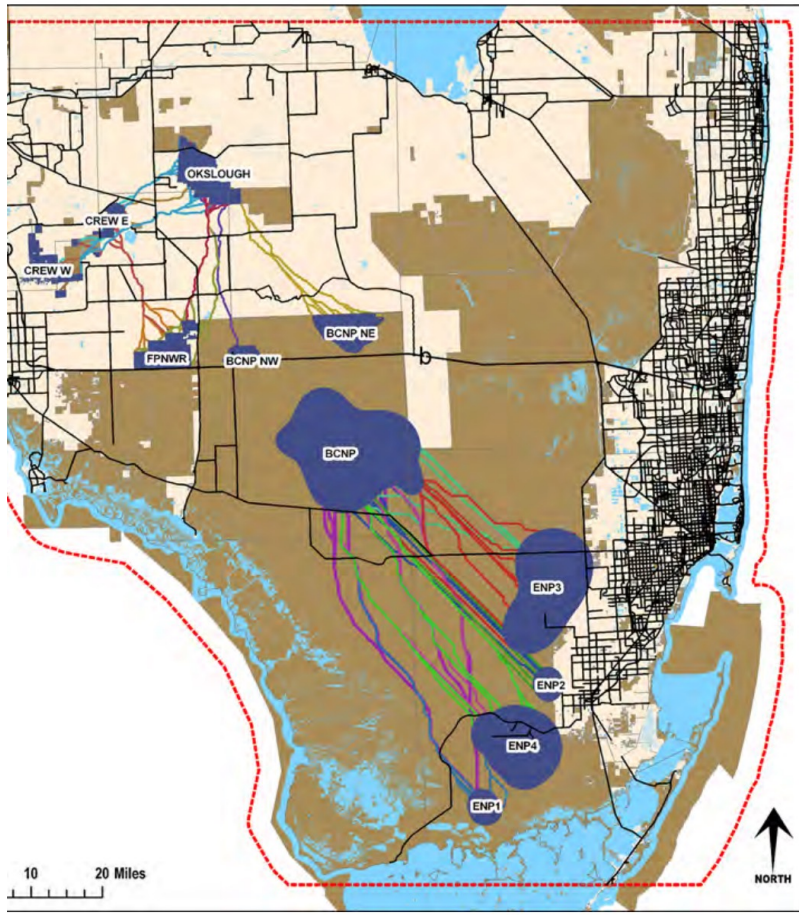


Which stages should be removed — and how many?

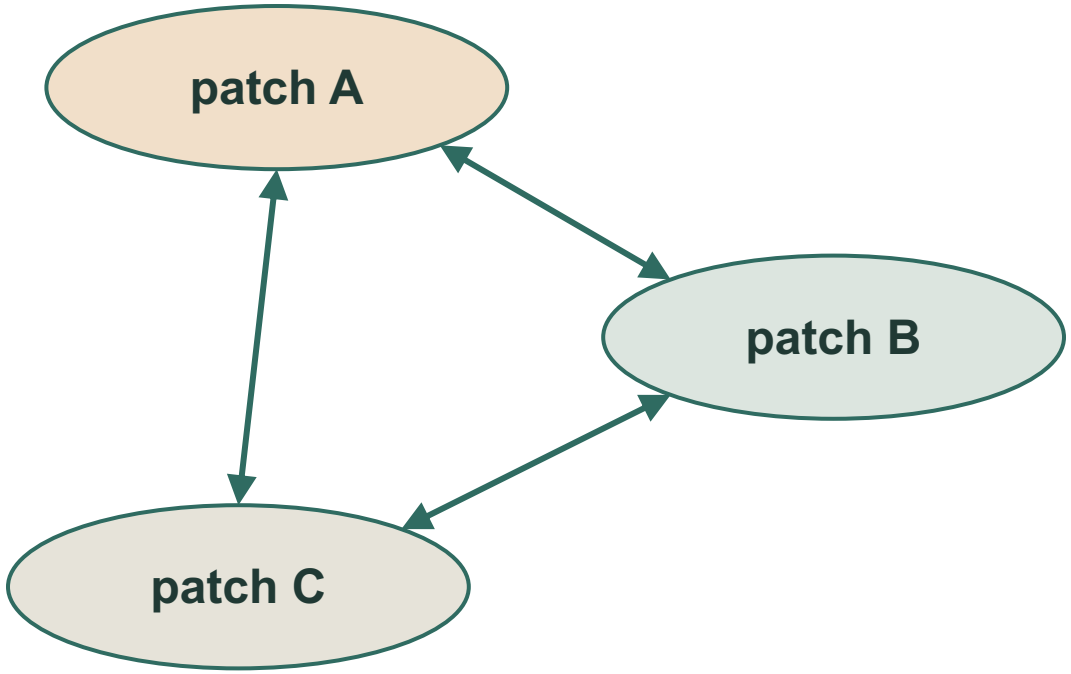
Hypothetical management scenario; not a recommendation for the current Florida-panther population.

Connected sub-populations

A population can consist of connected sub-populations.



Swanson et al. 2008, FWRI TR-13, Fig. 7

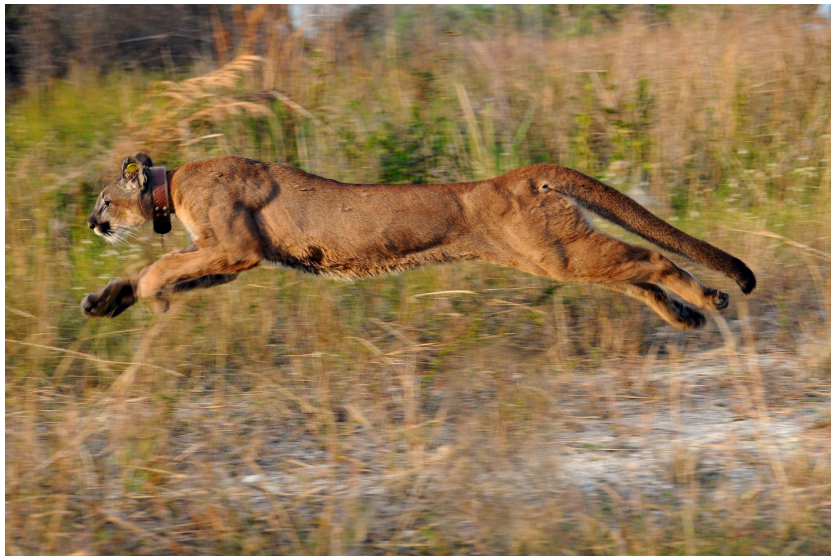


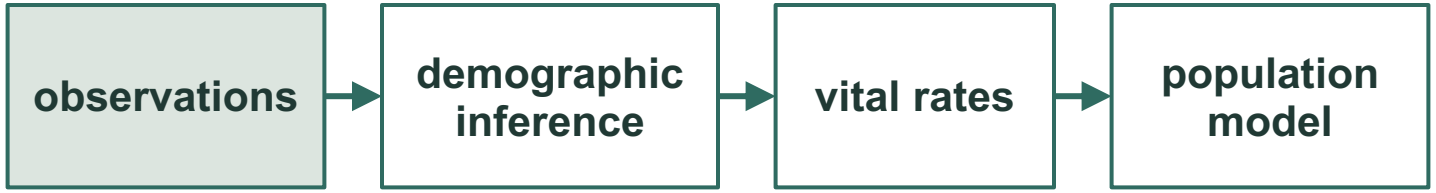
Dispersal links local sub-populations.

Connectivity can affect persistence.

Where vital rates come from

We have been talking about survival, reproduction and movement. How do we actually know them?





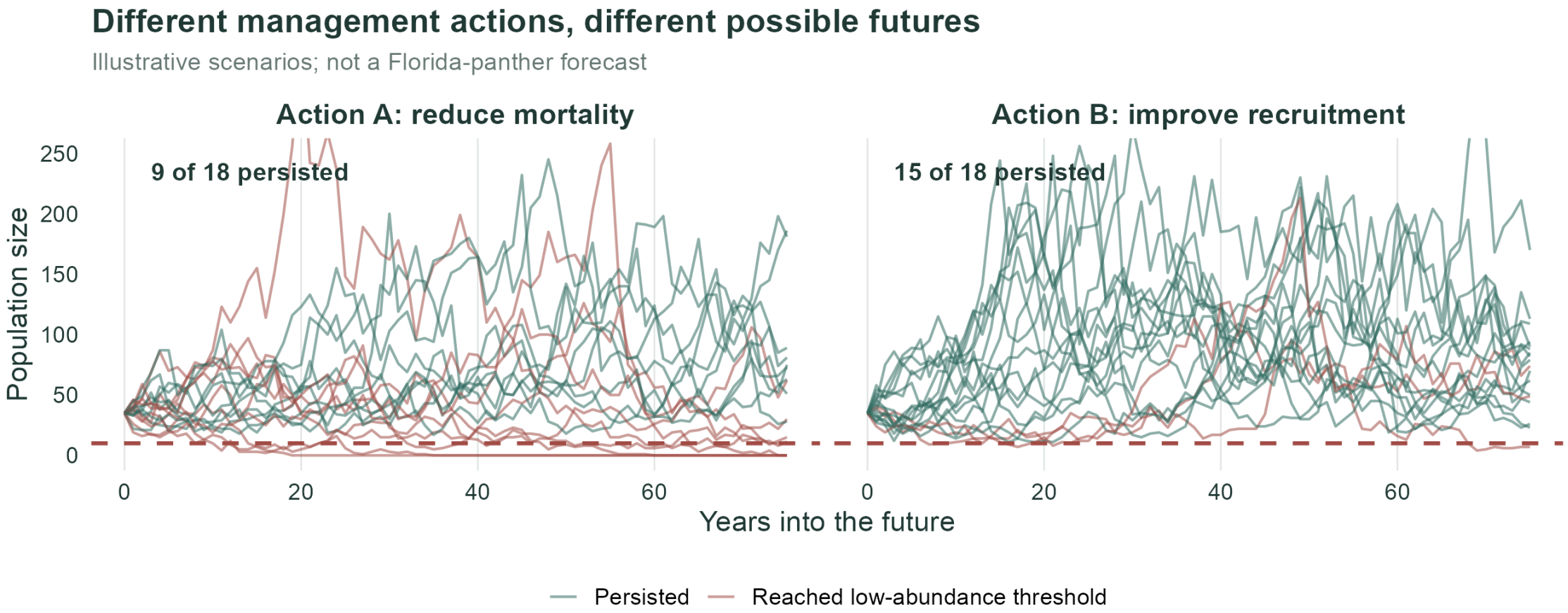
What we observe ≠ the underlying demographic state.

Detection and inference connect data to rates.

Persistence and management

What is the probability that this population persists for the next 50 or 100 years?

How would alternative management actions change that probability?



The questions so far

What did the panther case make us ask?

Life histories & population structure

Why do individuals differ?

Does age or stage structure matter?

L2–L3

Population growth & its drivers

What changes population size?

Which demographic rates matter most?

What actually caused the observed change?

L4–L5

Variation, feedback & harvest

How does the environment vary through time?

Why are small populations different?

Can the population grow indefinitely?

Which stages can be removed or relocated?

L6–L8

Space, inference & management

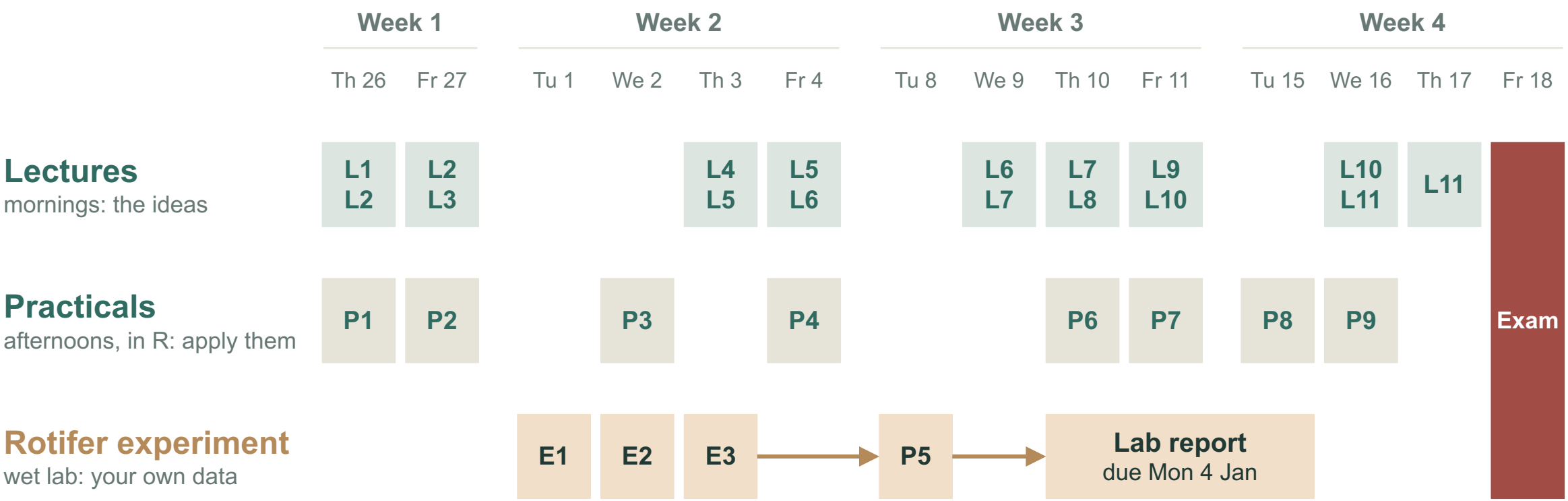
How do space and connectivity matter?

How do we estimate vital rates?

Will the population persist?

L9–L11

From Tuesday, you study your own population



The panther chain, at lab scale: measure survival, maturation and fecundity under copper (E1–E3), build the matrix and λ (P3, L4), compare populations with an LTRE (L5, P4), and bring it together in P5.

Exam 50% · Lab report 30% · Participation in practicals and class 20%

Further reading



Genetic Restoration of the Florida Panther

Warren E. Johnson,[1]† David P. Onorato,[2]† Melody E. Roelke,[3] E. Darrell Land,[2] Mark Cunningham,[2] Robert C. Belden,[4] Roy McBride,[5] Deborah Jansen,[6] Mark Lotz,[2] David Shindle,[7] JoGayle Howard,[8] David E. Wildt,[8] Linda M. Penfold,[9] Jeffrey A. Hostetler,[10] Madan K. Oli,[10] Stephen J. O'Brien[1]†

The rediscovery of remnant Florida panthers (*Puma concolor coryi*) in southern Florida swamplands prompted a program to protect and stabilize the population. In 1995, conservation managers translocated eight female pumas (*P. c. stanleyana*) from Texas to increase depleted genetic diversity, improve population numbers, and reverse indications of inbreeding depression. We have assessed the demographic, population-genetic, and biomedical consequences of this restoration experiment and show that panther numbers increased threefold, genetic heterozygosity doubled, survival and fitness measures improved, and inbreeding correlates declined significantly. Although these results are encouraging, continued habitat loss, persistent inbreeding, infectious agents, and possible habitat saturation pose new dilemmas. This intensive management program illustrates the challenges of maintaining populations of large predators worldwide.

Pumas (also called cougars, mountain lions, or panthers) are currently distributed throughout western North America and much of Central and South America (*1*). The endangered Florida panther (listed in 1967, table S1), the last surviving puma subspecies in eastern North America, is restricted to shrinking habitat between the urban centers of Miami and Naples (Fig. 1). By the early 1990s, the population of ~20 to 25 adults (*2*) showed reduced levels of molecular genetic variation relative to other puma populations (*3*–*5*), which is indicative of inbreeding (*4*, *6*). This may have led to defects, including poor sperm quality and low testosterone levels (*4*, *7*), poor fecundity and recruitment (*4*, *7*), cryptorchidism [where >80% of males born from 1990 to 1992 had one or no descended testes (*4*)], a high incidence of thoracic cowlicks and kinked tails (*4*), numerous atrial septal defects (*4*, *6*), and a high load of parasites and infectious disease pathogens (*4*, *8*–*10*).

In 1995, these cumulative observations, coupled with demographic models predicting a 95% likelihood of extinction within two decades, motivated the translocation of 8 wild-caught Texas (TX) female pumas into habitat occupied by at least 22 adult canonical (last-remaining, authentic) Florida panthers (CFPs) and 4 Everglades Florida panthers (EVGs) (Fig. 1A), because historically, gene flow occurred between Texas and Florida puma populations (*11*, *12*).

We compared data from 591 individuals sampled from 1978 to 2009 (table S2). Twenty-three informative (minimum allele frequency > 0.1) short tandem repeat (STR) loci were examined to reconstruct genetic heritage and parentage relationships, assess spatial and demographic patterns, distinguish CFP from other puma lineages, track morphological, biomedical, and life history traits as indices of fitness, and associate genetic heritage and heterozygosity with panther survival (*13*).

Pumas of diverse ancestry, time periods, and geographic origins, including wild-caught and captive animals in Florida, clustered into phylogenetic groups (Fig. 2). This analysis, combined with Bayesian population genetic results from STR genotypes that revealed nine distinct groups (fig. S1 and table S2), allowed us to explicitly infer the genetic heritage of each Florida panther (table S2, column 2; Figs. 1 and 2; and fig. S2) and to distinguish the two pre-1995 groups (CFP and EVG). Further, admixed Florida panthers (AdmFPs) were clearly identifiable, including first-generation (F_1) offspring of TX females bred by CFP or EVG males (CFPxTX-F_1 or EVGxTX-F_1) and panthers that were related to captive pumas of western U.S. origin who had escaped from enclosures on the Big Cypress Seminole Indian Reservation (SEM) from 1997 to 1999 (Figs. 1 and 2).

From 1986 to 1995, the minimum number of adult (>1.5 years old) panthers fluctuated from 24 to 32 (Fig. 3A), and genetic heritage remained relatively stable (85% CFP and 15% EVG; Fig. 1 and figs. S1 and S3). After their introduction, five of eight TX females bred (Fig. 1a) and produced 15 F_1 kittens with CFP, EVG, and at least five TX-backcross (TX-BC) offspring (figs. S3 and S4 and table S2). Twelve F_1 panthers produced offspring. From 1995 to 2008, 424 only as neonatal kittens). These largely AdmFP were responsible for colonizing former panther range and densities increased. For example, between 1995 and 2007, the number and density of panthers in the southern Big Cypress National Preserve (BCNP) (2174 km^2) increased eightfold from 3 (0.14/100 km^2) to 25 (1.15/100 km^2) (Fig. 1).

From 1996 to 2003, numbers (N) increased by 14%/year to at least 95 adults (Fig. 3A), 26.6 kittens were produced annually (fig. S2). The effective population size (N_e) rose from 16.4 in 1995 to 32.1 by 2007, and N_e/N was 0.314 (Fig. 1) (*13*). This paralleled an increase in average individual STR heterozygosity (to 25% from 18.4% in 1995; Fig. 3B) and a decrease in the average estimated age of adults from 6.6 to 4.2 years from 1997 to 2004. Population growth slowed and average age increased gradually after 2004 (Fig. 3C).

Admixed genetic ancestry was associated with increased survival of F_1, EVG-BC, and TX-BC kittens (<1 year old) relative to purebred CFP and CFP-backcross (CFP-BC) kittens (0.518 ± 0.130 versus 0.243 ± 0.074, $P = 0.020$) (Fig. 3D). F1 adults had significantly higher survival ($P = 0.002$) than other admixed or CFP groups (table S4), with a risk ratio (RR: relative instantaneous probability of mortality) of 0.118 (*13*). The survival of subadults and adults increased significantly with heterozygosity (RR for an increase of 0.1 = 0.643, $P = 0.011$). Interestingly, CFPs also experienced significantly higher mortality rates from intraspecific aggression than did AdmFPs (RR = 3.077, $P = 0.014$), and mortality rates from intraspecific aggression declined as heterozygosity increased (RR = 0.480, $P = 0.005$) (*13*).

Demographic differences among >1-year-old panthers from 2002 to 2004 (Fig. 3A) were evident when 23 out of 29 (23/29) (79%) CFPs

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*These authors contributed equally to this work.
†To whom correspondence should be addressed. E-mail

ONE PAPER

Johnson et al. (2010), *Science*

Fifteen years after the release: numbers, survival and defects.

Focus: Fig. 3A (counts by ancestry) and Fig. 3D (survival by ancestry); Table 1, last column (defects); the last paragraph, which lists what else changed after 1995.

Skip: the genetic markers, the pedigree and the tree (Fig. 2).

Keep in mind: genes were not the only thing that changed after 1995.

RESOURCES

Mills, Whiteley and Tourani (2025), Conservation of Wildlife Populations: the demographic modelling perspective used throughout EEE330.

Hostetler et al. (2013): demographic evidence for Florida panther genetic restoration (again in L5).

Pimm et al. (2006) and Creel (2006), Animal Conservation: genetic rescue or demographic rescue? A claim and its critique.

