# Interactions between demography, genetics, and landscape connectivity increase extinction probability in a small population of large carnivores in a major metropolitan area

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Supplementary Materials: Appendix A, Tables S1-S6.

## Appendix A.

## Model structure details

We developed the model in R using multiple packages and self-authored code to implement the functions and processes executed within the model. The full R code for our model is available at https://github.com/PMahoney29/Puma_IBM. We used the R6 reference class system (package 'R6'), a light-weight object-oriented programming structure that operates within R and allows classes to be easily inherited across different R packages. The model was built with a nested class structure where an 'individual' class (mountain lions within the model) was nested within a 'population' class (all individuals within a single projection of the model) which was nested within a 'simulation' class (all populations projected during a given model run). The population and simulation classes were primarily containers for individuals and populations, respectively, and aided in data aggregation and model interpretation. Each class level contained class-specific methods for simulating demographic processes and for data aggregation.

### (i) Individual class

Every individual was characterized by 13 state variables within an individual class object: animal ID, sex, age (in months), mother's ID, father's ID, age class, age at transition to adult (sex-specific), reproductive status, survival status, birth month, mortality month, immigrant status, and genotype (54 loci). An individual's immigrant status indicated whether it was born in the

SMMs or immigrated from an external population (see below). All individuals in the starting and immigrant populations were assigned empirical genotypes, whereas genotypes for offspring produced within the model were derived through simple Mendelian genetics (i.e. 1 allele randomly inherited from each parent at each loci). We limited reproduction to adult males and to adult females without dependent offspring.

### (ii) Population class

During each monthly time step, the following procedures took place for all living individuals within the population: mortality assessment, increase of time/age increment, age class assessment, breeding status assessment, and reproduction assessment. All individuals (alive or dead) within a given population were retained as a complete list of individual class objects. Living individuals on this list were retained for future time steps. The model stored active litters as a list within the population class object that contained the ID of the mother and all dependent offspring. This active litter variable was used to classify reproductive status and breeding eligibility for adult females. Population size was stored as a list containing counts on a monthly basis by sex and age class combinations, and all ages and sexes combined. A final procedure during each time step updated all population-level statistics, including identifying population size and extinction status. The population was considered to be extinct only when no females remained in the population. The population persisted in the absence of males because it could be rescued by immigration of males. Genetic composition at the population level was aggregated on an annual basis to allow us to monitor trends in genetic diversity.

### (iii) Simulation Class

At the end of a simulation, the complete list of individuals was converted into a data frame and stored within the simulation object.  We queried these simulation objects to extract demographic and genetic results which were averaged across each population projection of a given simulation.

Table S1. Demographic parameters estimated from radiotelemetry data and field investigations of mortality and natal den sites for 33 mountain lions in the Santa Monica Mountains, southern California, 2002-2015.

| | Females | | Males | |
|---|---|---|---|---|
| | estimate ± SE | *n* | estimate ± SE | *n* |
| Adult survival[a] | 0.900 ± 0.09 | 5 | 0.833 ± 0.11 | 5 |
| Subadult survival[a] | 0.625 ± 0.17 | 10 | 0.444 ± 0.15 | 12 |
| Kitten survival[a,b] | 0.724 ± 0.12 | 9 | 0.724 ± 0.12 | 7 |
| Litter size | 2.88 ± 0.34 | 7 | NA | |
| Age of first reproduction | 25-33 months | 3 | 42 months | 1 |

[a] Annual estimate, [b] Males and females pooled due to small sample sizes

Table S2. Sensitivity and proportional sensitivity (elasticity) of density independent stochastic population growth ($\lambda s$) to 5% increases in age class and sex specific survival and litter size in individual-based population model for Santa Monica Mountain mountain lion population. Results based on 5000 projections of 25 years.

| Parameter | Sensitivity | Elasticity |
|---|---|---|
| Adult female survival | 0.90 | 0.25 |
| Subadult female survival | 0.48 | 0.09 |
| Kitten female survival | 0.34 | 0.08 |
| Adult male survival | 0.06 | 0.02 |
| Subadult male survival | 0.09 | 0.01 |
| Kitten male survival | 0.03 | 0.01 |
| Litter size | 0.09 | 0.08 |

Table S3. Demographic results predicted by individual-based population model for Santa Monica Mountain Mountain lions in Southern California with immigration of both sexes. Immigrants had an equal probability of being male or female. Values are mean (unless otherwise noted) estimates at year 50 based on 5000 population projections.

| | No immigration | | 1 immigrant/13 years | | 1 immigrant/4 years | | 1 immigrant/2 years | |
|---|---|---|---|---|---|---|---|---|
| | Estimate | 95% HPD* | Estimate | 95% HPD* | Estimate | 95% HPD* | Estimate | 95% HPD* |
| 2 males breeding | | | | | | | | |
| λ† | 1.01 | (0.91, 1.02) | 1.01 | (0.93, 1.02) | 1.01 | (0.96, 1.02) | 1.01 | (0.98, 1.02) |
| Extinction prob. | 0.220 | (0.208, 0.231) | 0.176 | (0.165, 0.186) | 0.102 | (0.092, 0.108) | 0.037 | (0.032, 0.043) |
| Extinction time | 30.79 | (12.08, 47.33) | 32.27 | (14.00, 49.67) | 32.11 | (12.58, 49.58) | 32.08 | (13.33, 49.58) |
| Adults (*n*) | 5.16 | (0, 8) | 5.49 | (0, 8) | 6.06 | (0, 8) | 6.63 | (3, 8) |
| $N_E$ | 3.95 | (0, 6) | 4.07 | (0, 6) | 4.10 | (0, 6) | 4.30 | (0, 6) |

* 95% highest posterior density credible intervals

† Median stochastic population growth rate

Table S4. Genetic results predicted by individual-based population model for Santa Monica Mountain Mountain lions, Southern California with immigration by both sexes. Immigrants had equal probability of being male or female. Values are mean estimates at year 50 based on 5000 population projections.

| | Starting population | | No immigration | | 1 migrant/13 years | | 1 migrant/4 years | | 1 migrant/2 years | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Estimate | SE | Estimate | SE | Estimate | SE | Estimate | SE | Estimate | SE |
| 2 males breeding | | | | | | | | | | |
| $H_e$ | 0.352 | 0.032 | 0.156 | 0.027 | 0.199 | 0.028 | 0.276 | 0.028 | 0.328 | 0.032 |
| $H_o$ | 0.388 | 0.040 | 0.178 | 0.032 | 0.224 | 0.033 | 0.311 | 0.033 | 0.366 | 0.040 |
| $N_A$ | 2.220 | 0.123 | 1.468 | 0.077 | 1.662 | 0.085 | 1.960 | 0.097 | 2.190 | 0.105 |
| Fis | 0.127 | 0.022 | 0.186 | 0.018 | 0.186 | 0.020 | 0.168 | 0.022 | 0.159 | 0.022 |
| Polymorphic (%) | 0.778 | --- | 0.429 | --- | 0.550 | --- | 0.715 | --- | 0.814 | --- |

Table S5. Annual demographic parameters used to simulate inbreeding depression in Santa Monica Mountain mountain lions. Values were obtained by reducing age class and sex-specific survival rates proportional to reductions documented in Florida panthers experiencing inbreeding depression relative to outbred panthers following genetic restoration (13, 19, 22).

| | Females | | Males | |
|---|---|---|---|---|
| | estimate | Proportional reduction | estimate | Proportional reduction |
| Adult survival | 0.825 | 0.92 | 0.769 | 0.92 |
| Subadult survival | 0.613 | 0.98 | 0.380 | 0.86 |
| Kitten survival | 0.340 | 0.47 | 0.340 | 0.47 |

Table S6. Demographic results predicted by individual-based population model for Santa Monica Mountain mountain lions, Southern California with inbreeding simulated by reducing age and sex-specific survival rates proportional to reductions documented in Florida panthers suffering inbreeding depression relative to outbred panthers following genetic restoration. Values are mean (unless otherwise noted) estimates at year 50 based on 5000 population projections with a maximum of 2 males breeding at any given time.

| | Estimate | 95% CI |
|---|---|---|
| $\lambda$* | 0.88 | (0.76, 0.98) |
| Extinction probability | 0.997 | (0.998 0.996) |
| Time to extinction* | 14.50 | (4.25, 30.25) |
| Adults (*n*) | <1 | (0, 0) |

* median value