1   Appendix S1: Statistical Methods for Modeling Demographic Rates of Black-backed

2   Woodpeckers

3

4   **Detection Probability**

5   We modeled detection probability as a function of whether woodpecker i had an active

6   transmitter during timestep t:

7    $$d_{it} = \text{logit}^{-1}(\alpha_0 + \alpha_1 \tau_{it})$$

8   where $\tau_{it} = 1$ if woodpecker i has an active transmitter during timestep t, 0 otherwise, and α_0 and

9   α_1 are regression coefficients. We assumed normal ($\mu = 0$, $\sigma^2 = 1{,}000$) prior distributions on the

10   parameters α_0 and α_1. Because we do not know exactly how long transmitters lasted if we failed

11   to observe woodpeckers, we assumed adult transmitters were active for 5 time steps (5 months)

12   and juvenile transmitters were active for 7 time steps (14 weeks), unless we observed otherwise

13   (e.g., observed a woodpecker with an inactive transmitter prior to the assumed fail time or

14   observed a woodpecker with an active transmitter beyond the assumed fail time). If transmitters

15   were active beyond the assumed fail time, we assumed the transmitter failed the time step

16   immediately following the last observation with an active transmitter.

17   **Adult Survival Probability**

18   We modeled monthly adult survival probability as a function of sex, season, habitat, and

19   number of years post-fire:

$$\varphi_{it}^{ad} = \text{logit}^{-1}\left(\beta_0^{ad} + \beta_1^{ad}\varsigma_i + \beta_2^{ad}\gamma_{it} + \beta_3^{ad}\omega_{it}^{ad} + \beta_4^{ad}x_{it}^{ad} + \beta_5^{ad}\eta_{it}^{ad}\left[\omega_{it}^{ad} + x_{it}^{ad} \right] \right) \qquad \text{(Eqn. 1)}$$

20   where $\varsigma_i = 1$ if adult woodpecker i is male, 0 if female, $\gamma_{it} = 1$ if the observation of adult

21   woodpecker i is made during the breeding season (April –September), 0 if made during the non-

22   breeding season, $\omega_{it}^{ad} = 1$ if adult woodpecker i is occupying habitat created by wildfire at the

23   end of time step t, 0 otherwise, $x_{it}^{\text{ad}} = 1$ if adult woodpecker i is occupying habitat created by

24   prescribed fire at the end of time step t, 0 otherwise, η_{it}^{ad} is the age (in years) of habitat created

25   by wildfire or prescribed fire adult woodpecker i occupied at the end of time step t

26    $\left(\eta_{it}^{\text{ad}} \in [0,1,2,3,4,5] \right)$, and $\beta_0^{\text{ad}},...,\beta_5^{\text{ad}}$ are regression coefficients. We assumed normal ($\mu = 0$, σ^2

27    $= 1{,}000$) prior distributions on the parameters $\beta_0^{\text{ad}},...,\beta_5^{\text{ad}}$. Note that the time since fire term

28   applies only to woodpeckers occupying habitat created by wildfire or prescribed fire, since

29    $\omega_{it}^{\text{ad}} + x_{it}^{\text{ad}} = 0$ if adult woodpecker i is occupying habitat created by MPB infestations at the end

30   of time step t.

31   **Juvenile Survival Probability**

32   We modeled juvenile bi-weekly survival probability as a function of habitat (wildfire,

33   MPB, and prescribed fire), the number of years post-fire, and the number of two-week time

34   intervals since fledging:

$$\varphi_{it}^{\text{juv}} = \text{logit}^{-1}\left(\beta_0^{\text{juv}} + \beta_1^{\text{juv}}\omega_{it}^{\text{juv}} + \beta_2^{\text{juv}}x_{it}^{\text{juv}} + \beta_3^{\text{juv}}\eta_{it}^{\text{juv}}\left[\omega_{it}^{\text{juv}} + x_{it}^{\text{juv}} \right] + \beta_4^{\text{juv}}\log[\delta_{it}] \right) \qquad \text{(Eqn. 2)}$$

35   where $\omega_{it}^{\text{juv}} = 1$ if juvenile i occupied habitat created by wildfire at the end of time step t, 0

36   otherwise, $x_{it}^{\text{juv}} = 1$ if juvenile i occupied habitat created by prescribed fire at the end of time step

37   t, 0 otherwise, η_{it}^{juv} is the age (in years) of habitat created by wildfire or prescribed fire juvenile i

38   occupied at the end of time step t $\left(\eta_{it}^{\text{juv}} \in [0,1,2,3,4,5] \right)$, δ_{it} is the number of time steps juvenile i

39   has been fledged from the nest at the end of time step t $\left(\delta_{it} \in [1,2,...,21] \right)$, and $\beta_0^{\text{juv}},...,\beta_4^{\text{juv}}$ are

40   regression coefficients. Modeling juvenile survival probability as a function of the $\log_e$ number

41   of time steps fledged allowed survival probability to change in a non-linear manner. We

42   assumed normal ($\mu = 0$, $\sigma^2 = 1{,}000$) prior distributions on the parameters $\beta_0^{\text{juv}},...,\beta_4^{\text{juv}}$.

43   We fit adult and juvenile MSMR models in WinBUGS [1] via the R2WinBUGS interface

44   [2]. We simulated posterior distributions of all regression coefficients from 3 Markov chains,

45   each of which ran for 5.5 million iterations and discarding the first 500,000 iterations as burn-in.

46   There was evidence of correlation within Markov chains so we kept every 50th iteration to reduce

47   correlation between successive draws. Estimates of posterior distributions are thus based on

48   100,000 draws from each Markov chain for a total of 300,000 random draws from the posterior

49   distribution of each regression coefficient. The Brooks-Gelman-Rubin convergence diagnostic

50   [3] indicated adequate convergence $\left(\hat{R} = 1 \right)$ for all regression coefficients.

51   **Daily Nest Survival Probability**

52   We assumed survival ($y_{it} = 1$) or failure ($y_{it} = 0$) of nest i during day t was a Bernoulli

53   random variable:

54    $$y_{it} \sim \text{Bernoulli}(\psi_{it})$$

55   where ψ_{it} is the probability nest i survives day t. We further modeled daily survival probability

56   as a function of habitat and time since fire:

$$\psi_{it} = \text{logit}^{-1}\left(\theta_0 + \theta_1 \omega_i^{\text{nest}} + \theta_2 x_i^{\text{nest}} + \theta_3 \eta_i^{\text{nest}} \left[\omega_i^{\text{nest}} + x_i^{\text{nest}} \right] \right) \tag{Eqn. 3}$$

57   where $\omega_i^{\text{nest}} = 1$ if nest i is located in habitat created by wildfire, 0 otherwise, $x_i^{\text{nest}} = 1$ if nest i is

58   located in habitat created by prescribed fire, 0 otherwise, η_i^{nest} is the age (in years) of habitat

59   created by wildfire or prescribed where nest i was located $\left(\eta_i^{\text{nest}} \in [0, 1, 2, 3, 4, 5] \right)$, and $\theta_0, \ldots, \theta_3$

60   are regression coefficients. We assumed normal ($\mu = 0$, $\sigma^2 = 1{,}000$) prior distributions on the

61   parameters $\theta_0, \ldots, \theta_3$.

62   We fit nest survival models in WinBUGS via the R2WinBUGS interface. We simulated

63   posterior distributions of all regression coefficients from 3 Markov chains, each of which ran for

64   550,000 iterations, with the first 50,000 iterations discarded as burn-in. There was evidence of

65   correlation within Markov chains so we kept every 5th iteration to reduce correlation between

66   successive draws. Estimates of posterior distributions are thus based on 100,000 draws from

67   each Markov chain for a total of 300,000 random draws from the posterior distribution of each

68   regression coefficient. The Brooks-Gelman-Rubin convergence diagnostic indicated adequate

69   convergence $\left(\hat{R} = 1 \right)$ for all regression coefficients.

70   **Expected Number of Young Fledged**

71   We modeled the number of young fledged (z_i) from successful nest i using a zero-

72   truncated Poisson model:

73                           $z_i \sim$ truncated Poisson(ρ_i)

74   where $k_i = \rho_i / \left(1 - e^{-\rho_i} \right)$ is the expected number of young fledged from nest i [4]. We modeled

75   the number of young fledged as a function of habitat:

$$\rho_i = \exp\left(\pi_0 + \pi_1 \omega_i^{\text{nest}} + \pi_2 x_i^{\text{nest}} \right)$$ (Eqn. 4)

76   where π_0, π_1, and π_2 are regression coefficients. We assumed normal ($\mu = 0$, $\sigma^2 = 1{,}000$) prior

77   distributions on the parameters π_0, π_1, and π_2.

78   A zero-truncated Poisson distribution is not among the distributions offered in the

79   WinBUGS package. We therefore wrote a Metropolis-Hastings algorithm to sample from the

80   posterior distributions of model parameters. We tuned the Metropolis-Hastings algorithm to

81   have an acceptance probability of approximately 20% [5]. We simulated posterior distributions

82   of all regression coefficients from 3 Markov chains, each of which ran for 5.1 million iterations

83   with the first 100,000 iterations discarded as burn-in. To minimize correlation within chains due

84   to the accept / reject step in the Metropolis-Hastings algorithm, we kept every 50th iteration.

85   Estimates of posterior distributions are thus based on 100,000 draws from each Markov chain for

86   a total of 300,000 random draws from the posterior distribution of each regression coefficient.

87   **Scaling Demographic Rates**

88   We calculated habitat specific fecundity (m_h) as a function of habitat specific nest success and

89   number of young fledged per successful nest:

90 $$m_h = \varepsilon_h(\kappa_h / 2)$$

91   where ε_h is habitat specific nest success, defined as the probability a nest in habitat h successfully

92   fledges young. We divided the expected number of young fledged per nest, κ_h, by 2 because we

93   assume a 50:50 fledgling sex ratio. We estimated habitat-specific growth rates by calculating the

94   dominant eigenvalue of projection matrix $\mathbf{A}_h$.

95   We calculated habitat specific fecundity, annual adult survival probability, and the

96   probability a juvenile survives to the adult stage class as a function of the regression coefficients

97   estimated from demographic analyses above and habitat-specific covariates. We calculated

98   habitat-specific annual female adult survival as:

99
$$P_h^{\text{ad}} = \text{logit}^{-1}\left(\hat{\beta}_0^{\text{ad}} + \hat{\beta}_2^{\text{ad}}\gamma + \hat{\beta}_3^{\text{ad}}I_{\text{wild}} + \hat{\beta}_4^{\text{ad}}I_{\text{Rx}} + \hat{\beta}_5^{\text{ad}}\eta\left[I_{\text{wild}} + I_{\text{Rx}}\right]\right)^6 \times$$
$$\text{logit}^{-1}\left(\hat{\beta}_0^{\text{ad}} + \hat{\beta}_3^{\text{ad}}I_{\text{wild}} + \hat{\beta}_4^{\text{ad}}I_{\text{Rx}} + \hat{\beta}_5^{\text{ad}}\eta\left[I_{\text{wild}} + I_{\text{Rx}}\right]\right)^6$$

100   where I_{wild} and I_{Rx} are indicator variables = 1 if habitat h is wildfire or prescribed fire,

101   respectively, 0 otherwise, and $\hat{\beta}_0^{\text{ad}},...,\hat{\beta}_5^{\text{ad}}$ represent random samples from the posterior

102   distributions of regression coefficients defined in Eqn. 1. Equations are raised to the 6th power

103   because adult survival probability was modeled on monthly time steps. Note the term $\hat{\beta}_2^{\text{ad}}$

104   represents the regression coefficient for season-specific adult survival probability, which is why

105 the term is excluded from the equation for 6 months. We calculated the habitat-specific

106 probability a juvenile will survive to an adult as:

107
$$P_h^{\text{juv}} = \prod_{j=1}^{21} \text{logit}^{-1}\left(\hat{\beta}_0^{\text{juv}} + \hat{\beta}_1^{\text{juv}} I_{\text{wild}} + \hat{\beta}_2^{\text{juv}} I_{\text{Rx}} + \hat{\beta}_3^{\text{juv}} \eta\left[I_{\text{wild}} + I_{\text{Rx}}\right] + \hat{\beta}_4^{\text{juv}} \log[j]\right)$$

108 where $\hat{\beta}_0^{\text{juv}},...,\hat{\beta}_4^{\text{juv}}$ represent random samples from the posterior distributions of regression

109 coefficients defined in Eqn. 2. Note that the estimate of the probability a juvenile survives to the

110 adult stage class incorporates a different survival probability for each time step fledged. By

111 multiplying this term over 21 time steps, we assume a fledge date of approximately 24 June and

112 that juveniles transition to the adult stage by approximately 1 April the following year. We

113 calculate habitat-specific nest success as:

114
$$\varepsilon_h = \text{logit}^{-1}\left(\hat{\theta}_0 + \hat{\theta}_1 I_{\text{wild}} + \hat{\theta}_2 I_{\text{Rx}} + \hat{\theta}_3 \eta\left[I_{\text{wild}} + I_{\text{Rx}}\right]\right)^{36}$$

115 where $\hat{\theta}_0,...,\hat{\theta}_3$ represent random samples from the posterior distributions of regression

116 coefficients defined in Eqn. 3. Our calculation of habitat-specific nest success assumes a 36 day

117 nesting period (incubation period = 13 days, nestling period = 23 days), which was based on

118 observed length of nesting periods and closely corresponds with the published literature [6], [7].

119 Our nesting period was three days longer than [6] because we assumed the nest was at risk of

120 failure the day the first egg was laid. Finally, we calculated the expected number of young

121 fledged in habitat h as:

122
$$k_h = \frac{\rho_h}{1 - e^{-\rho_h}},$$

123 where

124
$$\rho_h = \exp\left(\hat{\pi}_0 + \hat{\pi}_1 I_{\text{wild}} + \hat{\pi}_2 I_{\text{Rx}}\right)$$

125   and $\hat{\pi}_0, ..., \hat{\pi}_2$ represent random samples from the posterior distributions of regression

126   coefficients defined in Eqn. 4.

127   We estimated the posterior distribution of habitat specific fecundity, annual adult survival

128   probability, and the probability a juvenile survives to the adult stage class by repeatedly

129   sampling from the posterior distributions of component regression coefficients. This repeated

130   sampling allowed us to propagate uncertainty in estimated regression coefficients. We repeated

131   this process 300,000 times for each habitat-specific demographic rate. Finally, we estimated the

132   posterior distribution of habitat-specific growth rates by constructing 300,000 random projection

133   matrices for each habitat, with each cell element comprising a random draw from the posterior

134   distribution of habitat-specific adult survival, juvenile survival, and fecundity.

135   **Life-stage Simulation Analysis**

136   We calculated the proportion of variation in population growth rates explained by variation in

137   component demographic rates by first regressing estimates of population growth rates (the

138   dominant eigenvalue of $\mathbf{A}_h$) against the random values of adult survival, juvenile survival, nest

139   success, and expected number of female young fledged used to construct $\mathbf{A}_h$ (life-stage

140   simulation analysis [8]). We next calculated the coefficient of determination (r^2) from each

141   regression model to calculate the proportion of variation in λ explained by variation in each

142   component demographic rate (Fig. S3).

143   **References**

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