

The heat is on: Rising temperatures alter when, how, and where
large terrestrial mammals move

Appendix B: Modeling

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1 Effects of temperature on movement rates

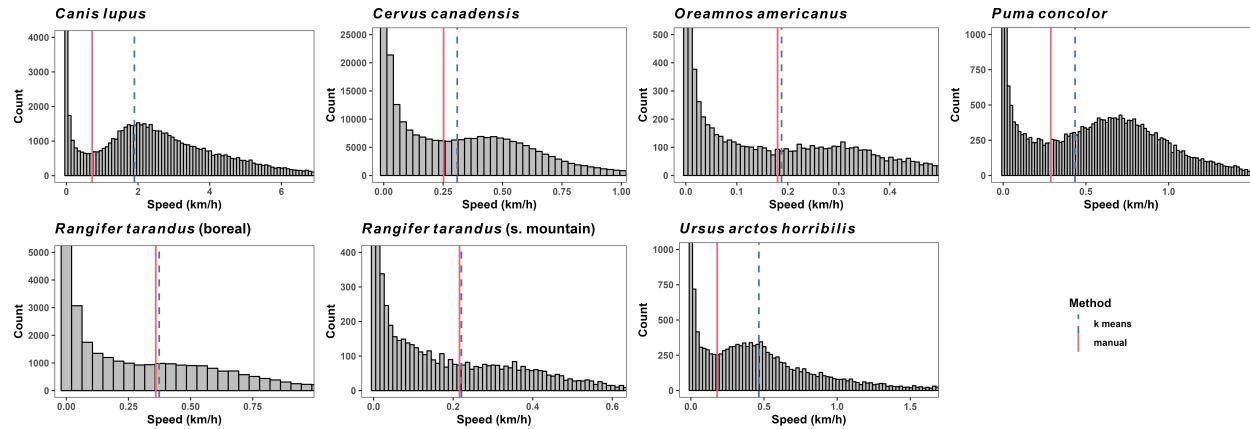


Figure B1: Histograms of each species' estimated speed. Continuous red lines indicate the values used to determine whether an animal was moving or not, which were determined visually using the inflection points of the histograms. Dashed blue lines indicate the minimum speed corresponding to a moving animal as determined by *k*-means algorithms with 2 clusters. For ease of readability, the x axes range from 0 to the 0.99 quantile, while the y axes range from 0 to one fortieth of the total number of estimates.

The two models for the probability of moving and speed when moving were fit using the code below:

```
m_moving <- bam(moving ~ # model estimating probability of moving
                    # random intercept for each animal
                    s(animal, bs = 're') +
                    # fixed intercept for each species
                    species +
                    # to account for changes in behavior within days
                    s(tod_pdt, by = species, k = 5, bs = 'cc') +
                    # to account for changes in behavior within years
                    s(doy, by = species, k = 5, bs = 'cc') +
                    # species-level effect of temperature
                    s(temp_c, by = species, k = 5, bs = 'tp') +
                    # to account for seasonal changes in day length
                    ti(doy, tod_pdt, by = species, k = 5, bs = c('cc', 'cc')) +
                    # to account for changes in day nocturnality with temperature
                    ti(temp_c, tod_pdt, by = species, k = 5, bs = c('tp', 'cc')) +
                    # to account for changes in fur coats seasonally
                    ti(temp_c, doy, by = species, k = 5, bs = c('tp', 'cc')) +
                    # larger sampling intervals underestimate movement speed
                    s(log(dt), k = 3) +
                    s(log(dt), species, k = 3, bs = 'fs'),
                    family = binomial(link = 'logit'),
                    data = d,
                    method = 'fREML', # fast REML
                    discrete = TRUE, # discretize the covariates for faster computation
                    knots = list(tod_pdt = c(0, 1), doy = c(0.5, 366.5)), #' for `bs = 'cc``
                    control = gam.control(trace = TRUE))
```

```

m_speed <- bam(speed_est ~ # model estimating speed when moving (i.e., speed > 0)
                 # random intercept for each animal
                 s(animal, bs = 're') +
                 # fixed intercept for each species
                 species +
                 # to account for changes in behavior within days
                 s(tod_pdt, by = species, k = 5, bs = 'cc') +
                 # to account for changes in behavior within years
                 s(doy, by = species, k = 5, bs = 'cc') +
                 # species-level effect of temperature
                 s(temp_c, by = species, k = 5, bs = 'tp') +
                 # to account for seasonal changes in day length
                 ti(doy, tod_pdt, by = species, k = 5, bs = c('cc', 'cc')) +
                 # to account for changes in day nocturnality with temperature
                 ti(temp_c, tod_pdt, by = species, k = 5, bs = c('tp', 'cc')) +
                 # to account for changes in fur coats seasonally
                 ti(temp_c, doy, by = species, k = 5, bs = c('tp', 'cc')) +
                 # larger sampling intervals underestimate movement speed
                 s(log(dt), k = 3) +
                 s(log(dt), species, k = 3, bs = 'fs'),
                 family = Gamma(link = 'log'), # can use Gamma because no zeros
                 data = d_2,
                 method = 'fREML', # fast REML
                 discrete = TRUE, # discretize the covariates for faster computation
                 knots = list(tod_pdt = c(0, 1), doy = c(0.5, 366.5)), #' for `bs = 'cc'` 
                 control = gam.control(trace = TRUE))

```

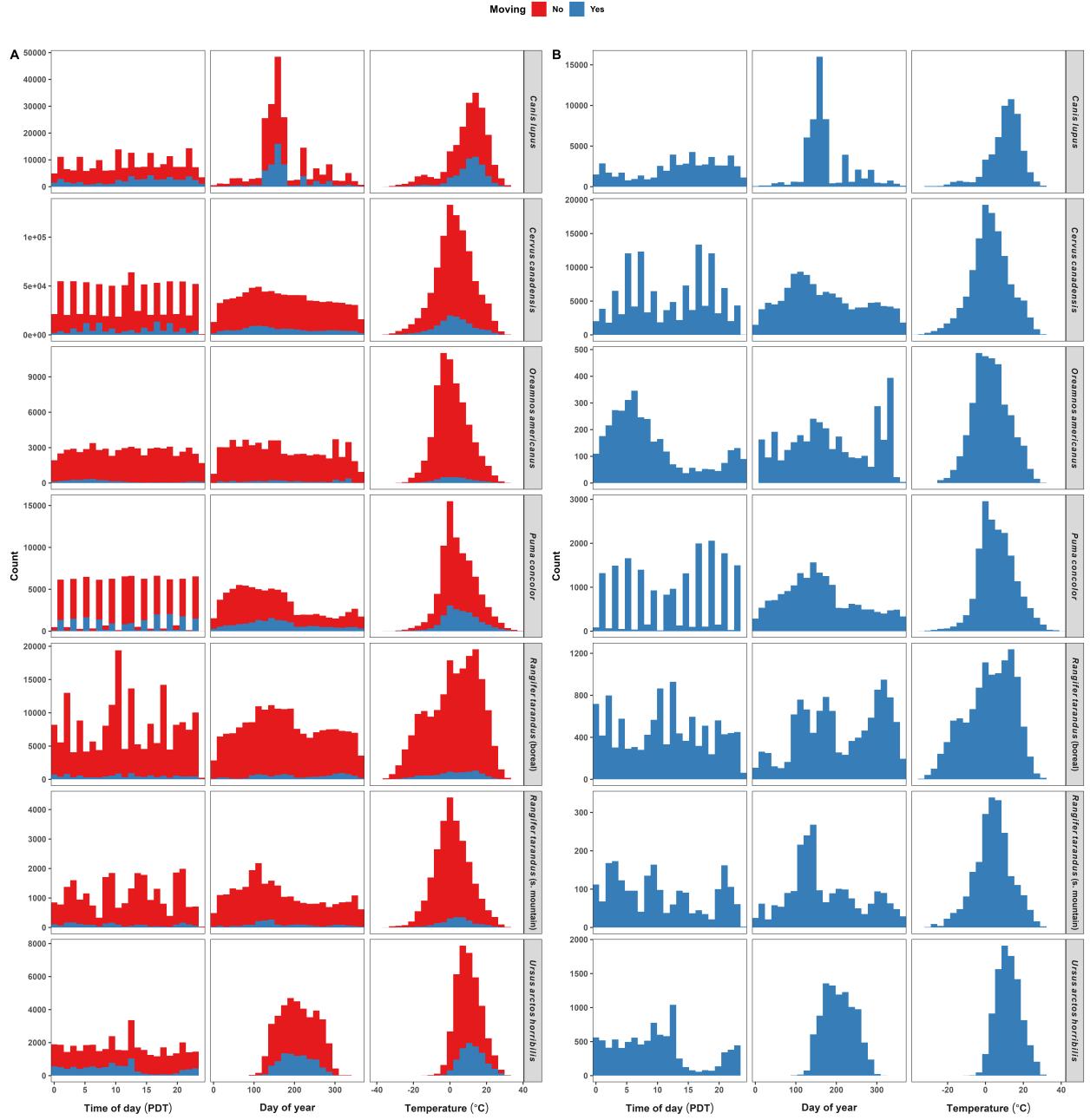


Figure B2: Histograms of the number of states (**A**) and speed estimates (**B**) over time of day (Pacific Daylight Time, PDT), day of year (Julian date), and air temperature.

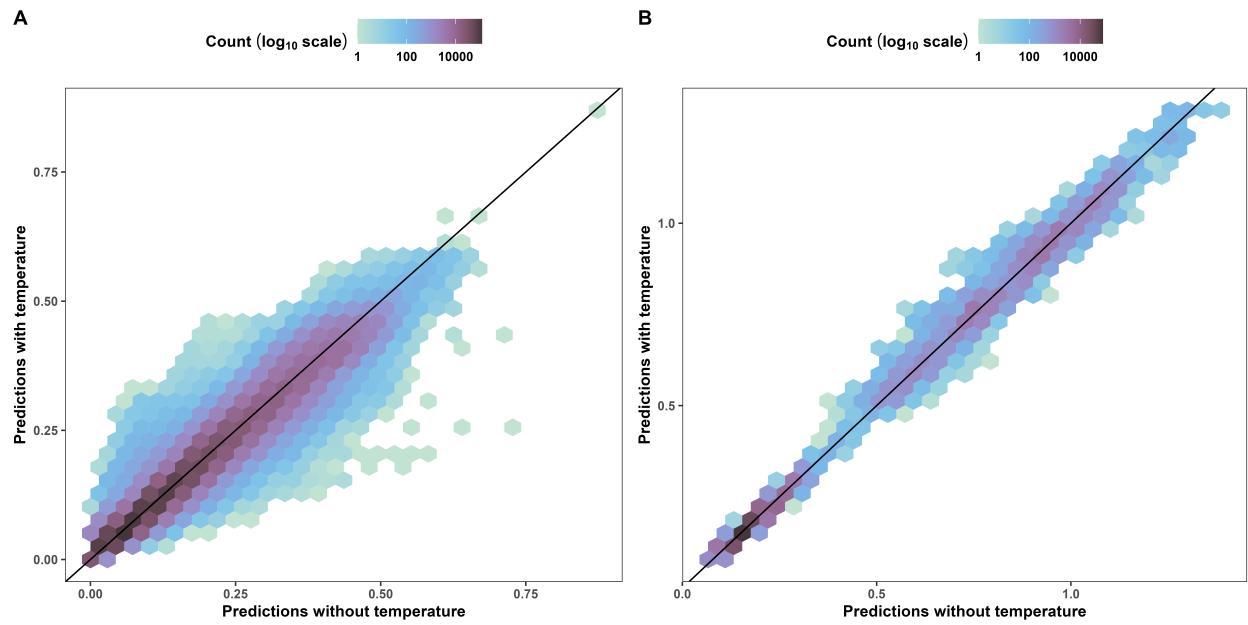


Figure B3: Hexplot of the fitted values from the HGAMs with and without including temperature for the probability of movement (**A**) and speed when moving (**B**).

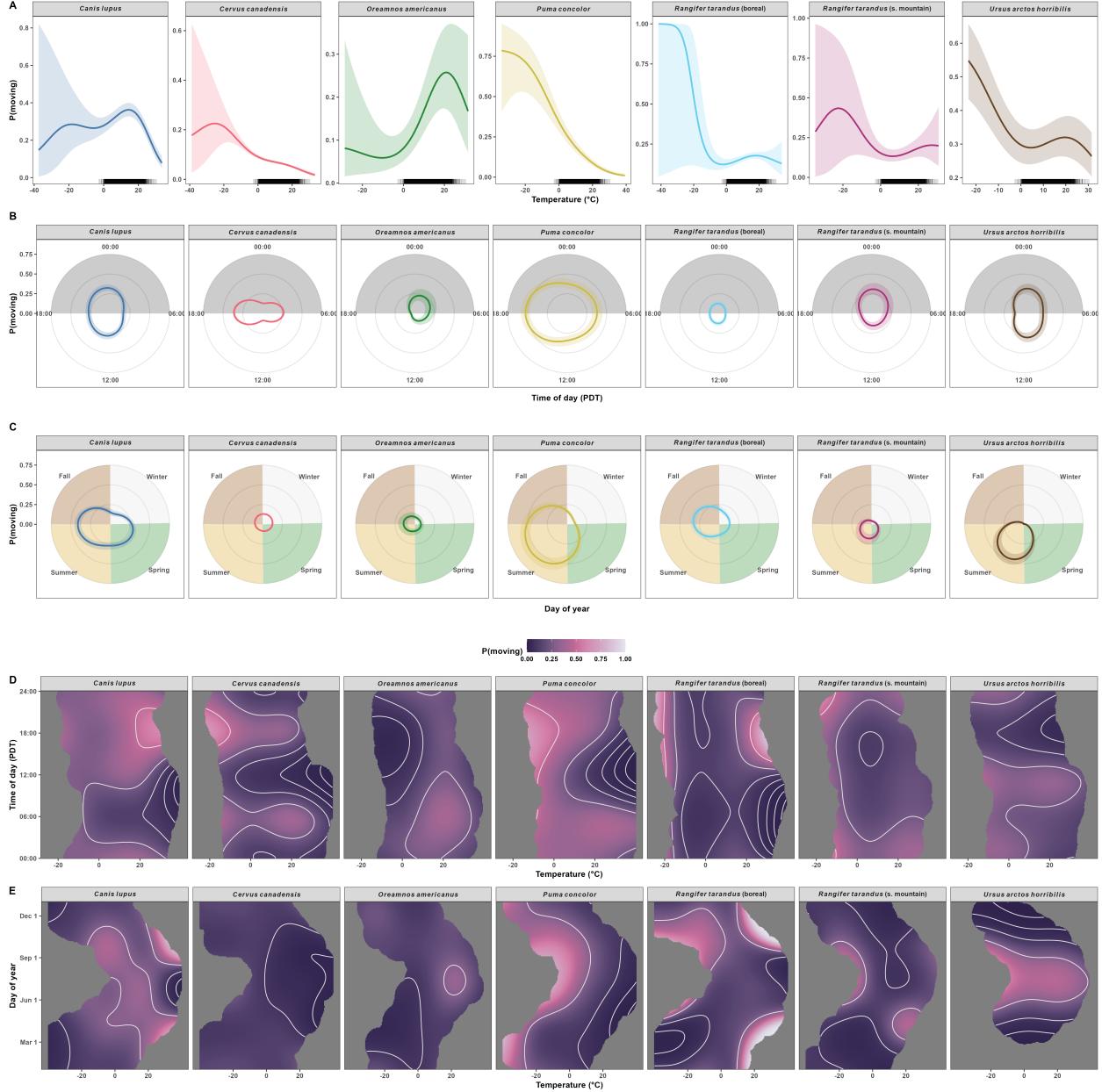


Figure B4: **A.** Estimated effects of temperature on each species' probability of moving on June 1st at 12:00, Pacific Daylight Time (PDT). The rug plot indicates each species' data on June 1st. **B.** Estimated effects of time of day on each species' probability of moving on June 1st at 0°C. The grey area indicates evening and night (hours between 18:00 and 6:00). **C.** Estimated effects of day of year on each species' probability of moving at 12:00 with a temperature of 0°C. The year is divided into the four seasons: winter (white), spring (green), summer (gold), and fall (brown). In panels A-C, ribbons indicate 95% Bayesian Credible Intervals, and the sampling rate was post-stratified to $\Delta t = 1$ hour for all species. **D.** Effects of time of day and temperature on species' probability of moving on June 1st at 12:00 PDT. Surfaces in panels D and E extend to 10% of the range away from each datum. **E.** Effects of day of year and temperature on species' probability of moving at 12:00 PDT.

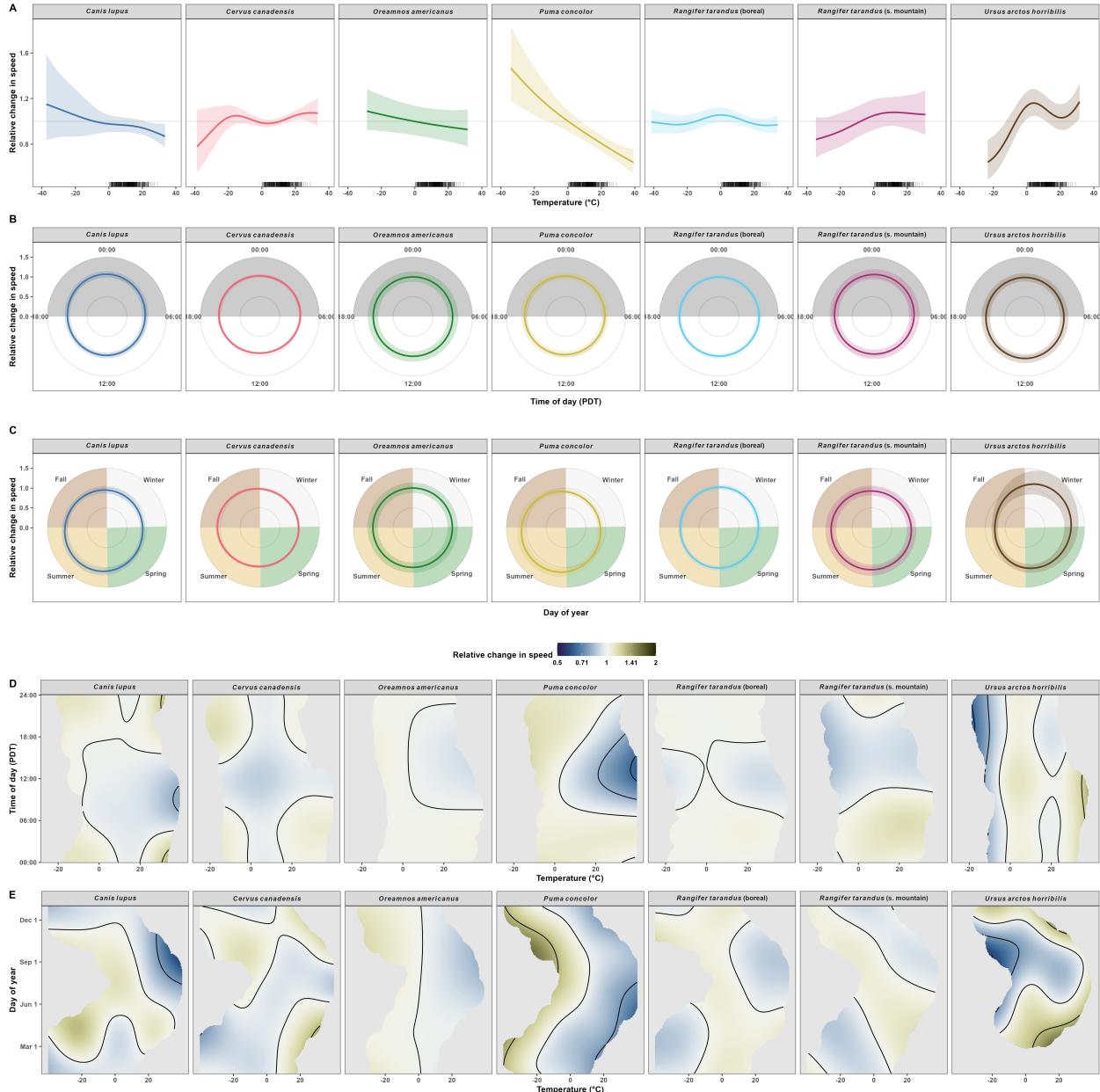


Figure B5: **A.** Estimated effects of temperature on each species' speed when moving on June 1st at 12:00, Pacific Daylight Time (PDT). The rug plot indicates each species' data points where an animal was moving on June 1st. **B.** Estimated effects of time of day on each species' speed when moving on June 1st at 0°C. The grey area indicates evening and night (hours between 18:00 and 6:00). **C.** Estimated effects of day of year on each species' speed when moving at 12:00 with a temperature of 0°C. The year is divided into the four seasons: winter (white), spring (green), summer (gold), and fall (brown). In panels A-C, ribbons indicate 95% Bayesian Credible Intervals, and the sampling rate was post-stratified to $\Delta t = 1$ hour for all species. **D.** Effects of time of day and temperature on species' speed when moving on June 1st. **E.** Effects of day of year and temperature on species' speed when moving, if the animal was moving at 12:00 PM PDT. Surfaces extend to 10% of the range away from each datum. The color bar is on the log₂ scale to help visualize patterns in doubling.

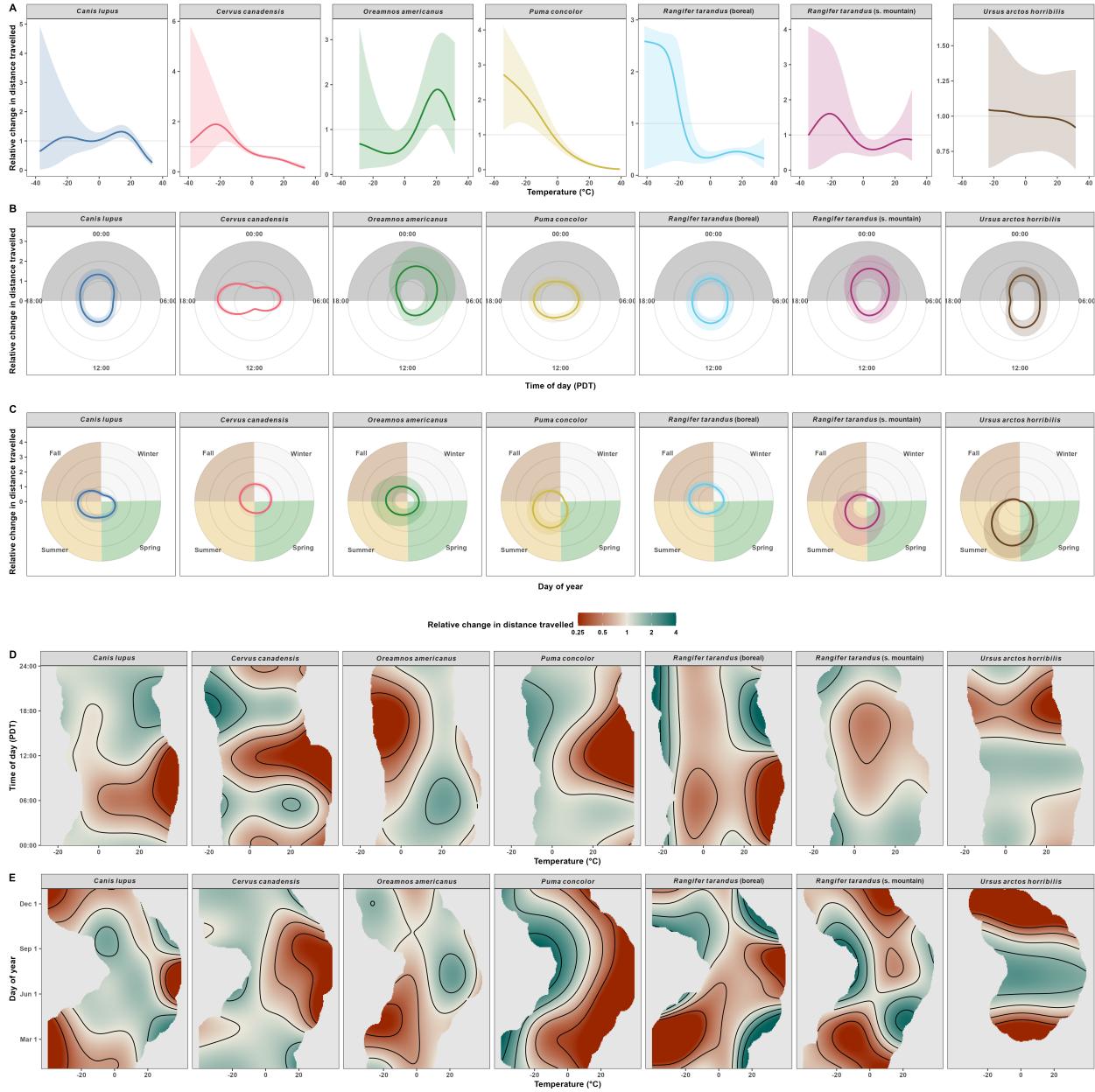


Figure B6: **A.** Estimated effects of temperature on each species' distance traveled on June 1st at 12:00, Pacific Daylight Time (PDT). The rug plot indicates each species' data points where an animal was moving on June 1st. **B.** Estimated effects of time of day on each species' distance traveled on June 1st at 0°C. The grey area indicates evening and night (hours between 18:00 and 6:00). **C.** Estimated effects of day of year on each species' distance traveled at 12:00 with a temperature of 0°C. The year is divided into the four seasons: winter (white), spring (green), summer (gold), and fall (brown). In panels A-C, ribbons indicate 95% Bayesian Credible Intervals, and the sampling rate was post-stratified to $\Delta t = 1$ hour for all species. **D.** Effects of time of day and temperature on species' distance traveled on June 1st at 12:00 PDT. **E.** Effects of day of year and temperature on species' distance traveled at 12:00 PDT. Surfaces extend to 10% of the range away from each datum. The color bar is on the \log_2 scale to help visualize patterns in doubling.

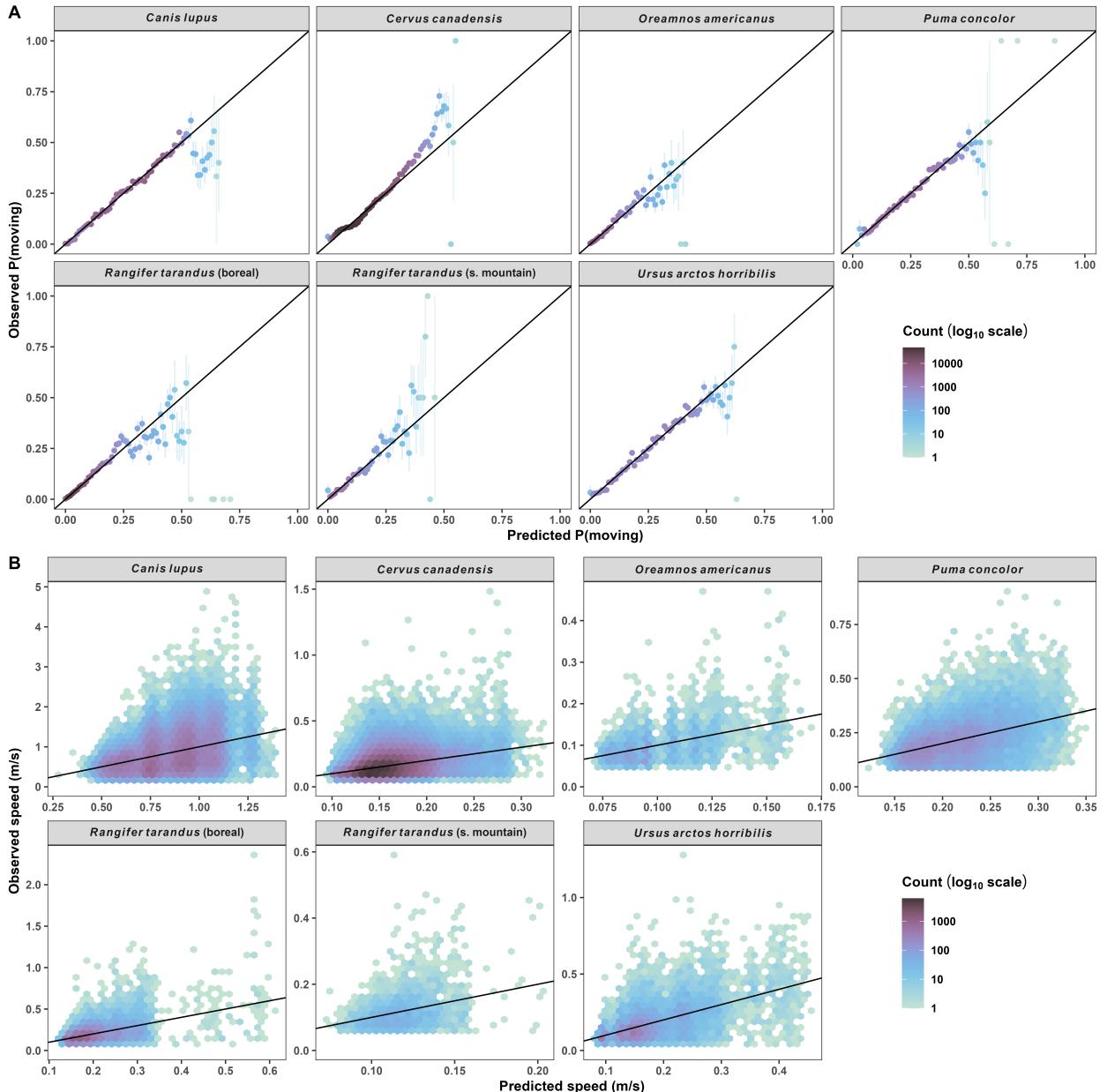


Figure B7: Relationships between the observed and predicted values for probability of movement (**A**) and speed given that an animal was moving (**B**). The color in panel **A** indicates the number of points used to calculate the estimate (on the \log_2 scale), while the grey lines in both panels indicate perfect prediction (i.e., the 1:1 line).

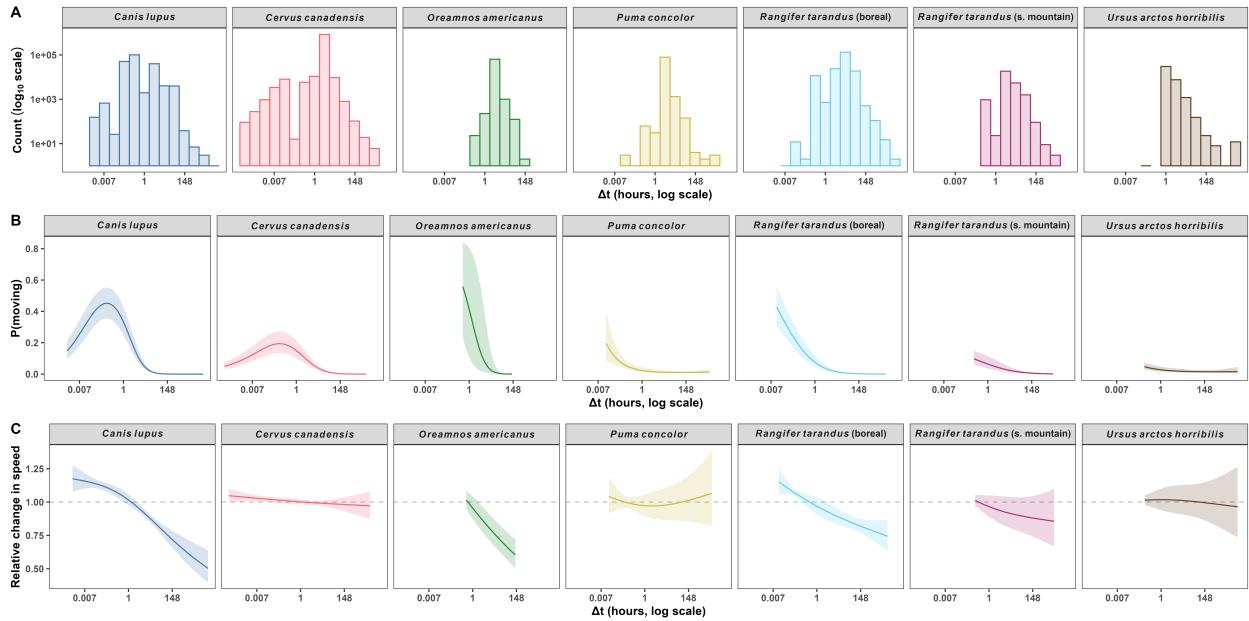


Figure B8: **A.** Histograms of sampling intervals between GPS locations. **B.** Species-level smooth effects of sampling interval on the estimated probability of the animal moving. **C.** Species-level estimated smooth effects of sampling interval on an animal's speed when moving. All x axes are on the natural logarithm scale.

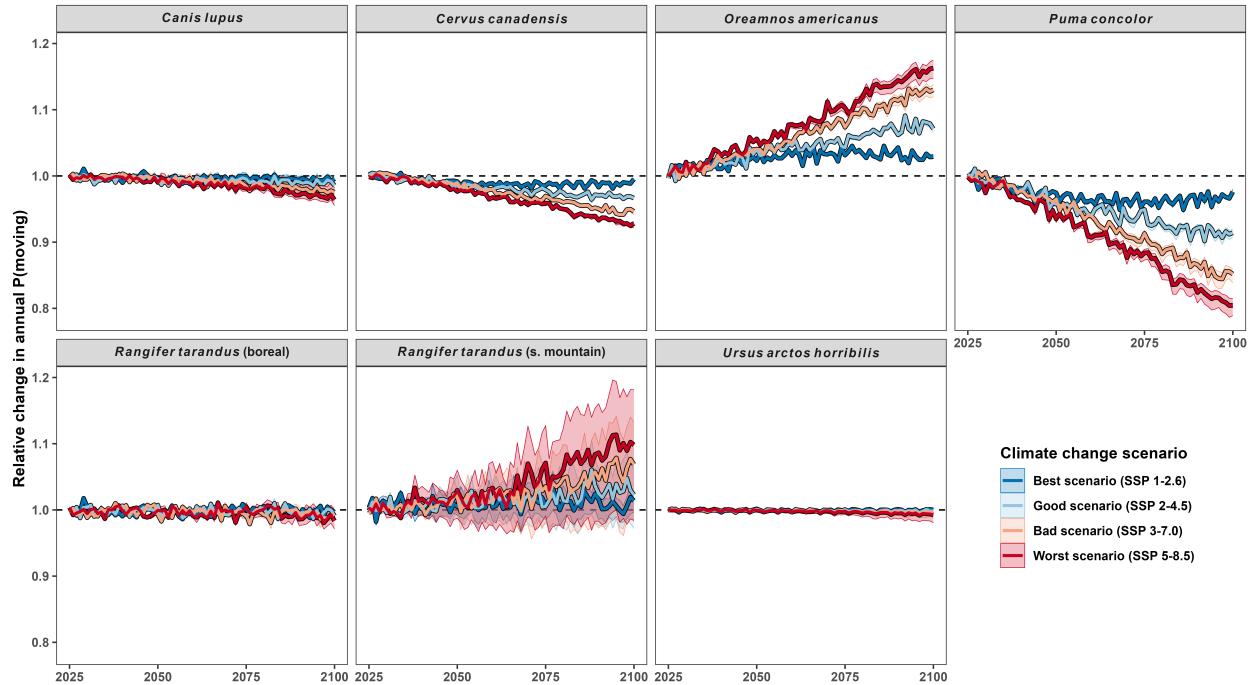


Figure B9: The direction and magnitude of changes in probability of moving due to climate change varies among species, but worse climate-change scenarios result in the greatest change. Lines indicate the median projected change in probability of moving due to changes in temperature changes in temperature within the area delimited by the 99.9% Autocorrelated Density Kernel Estimates of space use. Shaded areas indicate the range of predicted values between the 95th and 5th percentiles. Changes are relative to the predicted mean probabilities of moving in 2025 across the four Shared Socioeconomic Pathways (SSPs). If the intervals are fully above the dashed line, at least 90% of the estimated means increased, relative to the each pixel's average of the four climate scenarios in 2025. Similar conclusions can be drawn regarding a decrease if the ribbons are below the dashed line. The projections only account for changes in movement behaviour and ignore changes in physiology or movement costs.

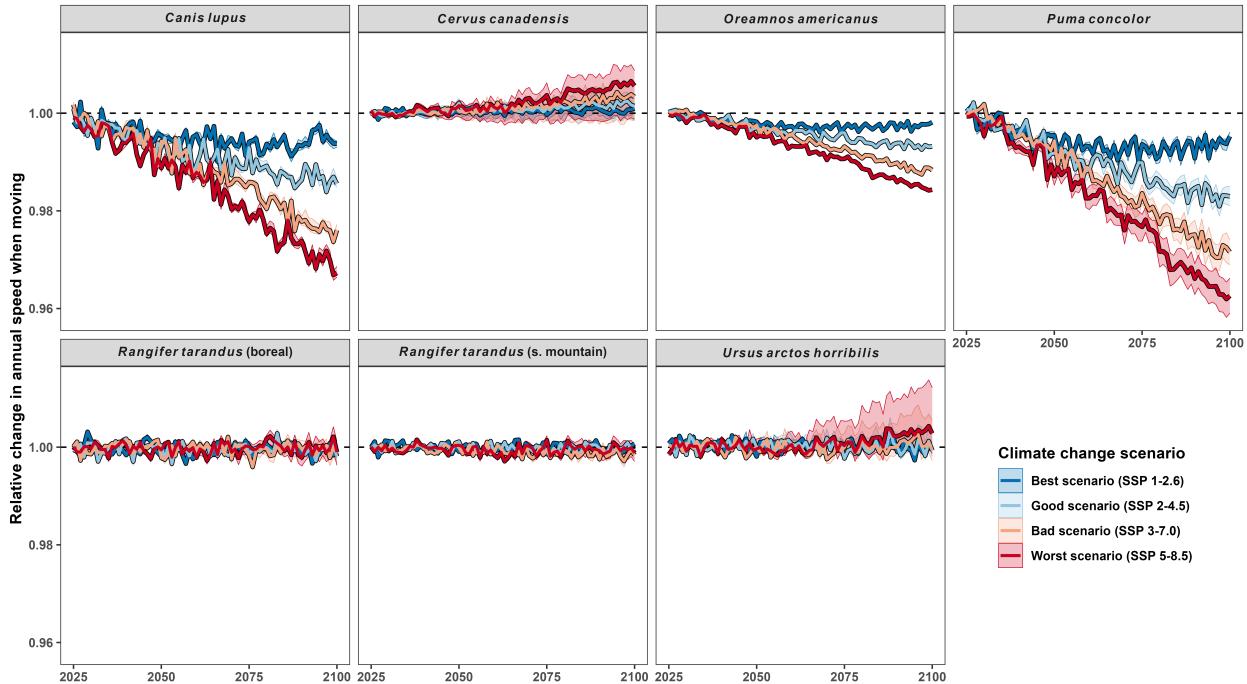


Figure B10: The direction and magnitude of changes in speed due to climate change varies among species, but worse climate-change scenarios result in the greatest change. Lines indicate the median projected change in speed due to changes in temperature within the area delimited by the 99.9% Autocorrelated Density Kernel Estimates of space use. Shaded areas indicate the range of predicted values between the 95th and 5th percentiles. Changes are relative to the predicted mean speeds in 2025 across the four Shared Socioeconomic Pathways (SSPs). If the intervals are fully above the dashed line, at least 90% of the estimated means increased, relative to the each pixel's average of the four climate scenarios in 2025. Similar conclusions can be drawn regarding a decrease if the ribbons are below the dashed line. The projections only account for changes in movement behaviour and ignore changes in physiology or movement costs.

2 Effects of temperature on habitat selection

Each species had a Hierarchical Resource Selection Function fit with the code below. See Aarts *et al.* (2008) for additional information on fitting Resource Selection Functions using Poisson models.

```
rsf <- bam(detected ~ # 1 for telemetry locations, 0 for quadrature points
            # species-level average resource preference
            s(forest_perc, k = 4, bs = 'cr') +
            s(elevation_m, k = 4, bs = 'cr') +
            s(dist_water_m, k = 4, bs = 'cr') +
            # animal-level deviations from the species-level average
            s(animal, bs = 're') +
            s(forest_perc, animal, k = 4, bs = 'fs', xt = list(bc = 'cr')) +
            s(elevation_m, animal, k = 4, bs = 'fs', xt = list(bc = 'cr')) +
            s(dist_water_m, animal, k = 4, bs = 'fs', xt = list(bc = 'cr')) +
            # changes in preference with temperature
            ti(forest_perc, temperature_C, k = 4, bs = 'cr') +
            ti(elevation_m, temperature_C, k = 4, bs = 'cr') +
            ti(dist_water_m, temperature_C, k = 4, bs = 'cr') +
            # include marginals of temperature to post-stratify over afterwards
            s(temperature_C, k = 4, bs = 'cr') +
            s(temperature_C, animal, k = 4, bs = 'fs', xt = list(bc = 'cr')),
            family = poisson(link = 'log'),
            data = d,
            weights = weight, # based on AKDE
            subset = species == sp, # subset to the species of interest
            method = 'fREML',
            discrete = TRUE)
```

Table B1: Number of animals (n) and proportion of animals (Proportion) used or excluded (Kept) when fitting the hierarchical resource selection function. The models only used animals that showed stationary range residency or two clear seasonal ranges within the tracking period. We excluded animals with insufficient data to estimate a range size and animals that migrated but did not establish clear ranges within the tracking period.

Species	Kept	n	Proportion
<i>Canis lupus</i>	no	5	0.128
<i>Canis lupus</i>	yes	34	0.872
<i>Cervus canadensis</i>	no	27	0.160
<i>Cervus canadensis</i>	yes	142	0.840
<i>Oreamnos americanus</i>	yes	11	1.000
<i>Puma concolor</i>	no	3	0.103
<i>Puma concolor</i>	yes	26	0.897
<i>Rangifer tarandus</i>	no	20	0.119
<i>Rangifer tarandus</i>	yes	148	0.881
<i>Ursus arctos horribilis</i>	yes	18	1.000
Total	no	55	0.127
Total	yes	379	0.873

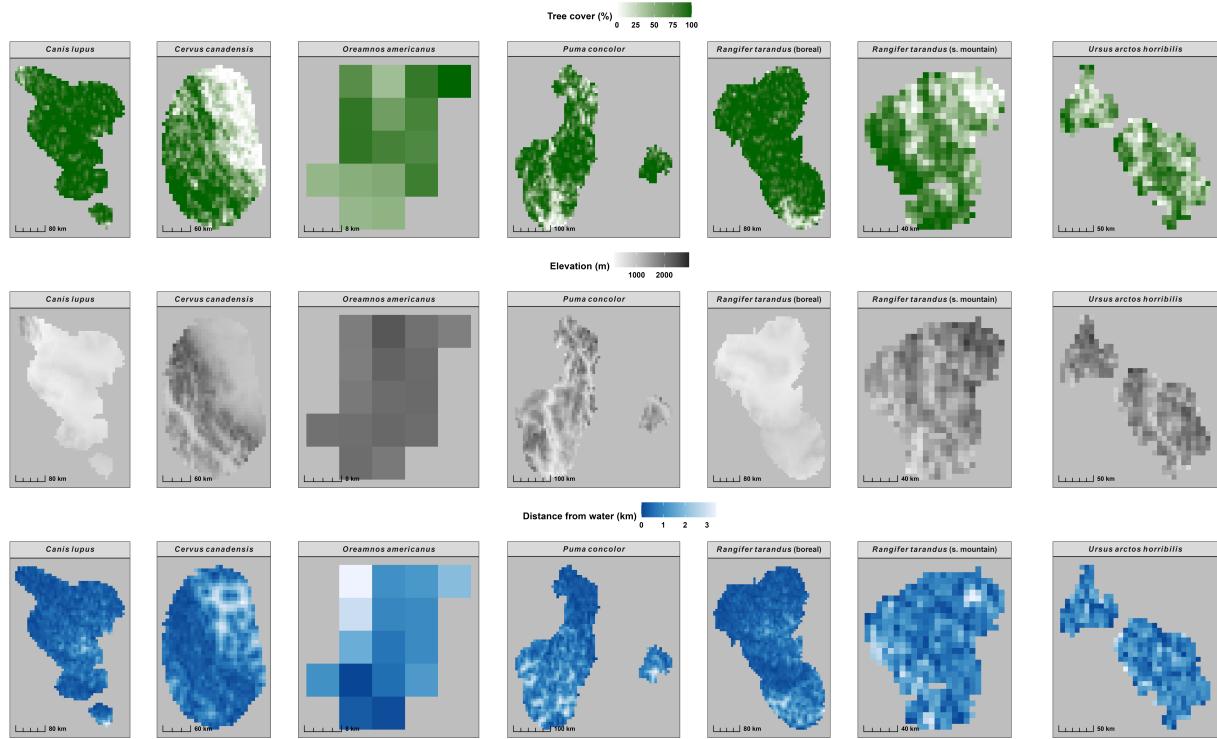


Figure B11: Resource rasters used for each species' hierarchical resource selection function.

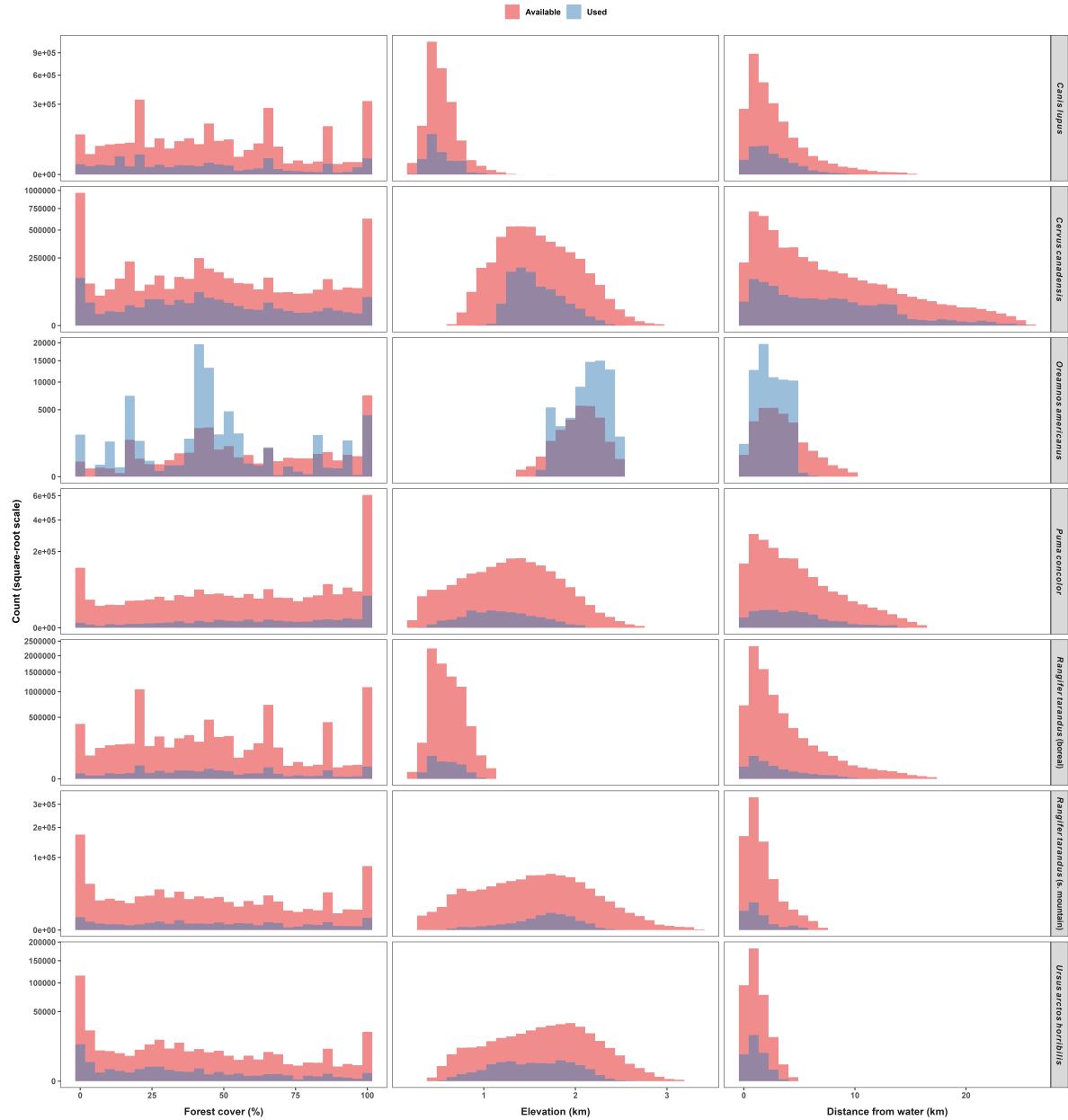


Figure B12: Histograms of available (red) and used (blue) resources. Each GPS fix counts as one observation. The y axis is on the square-root scale to help visualize values with low counts.

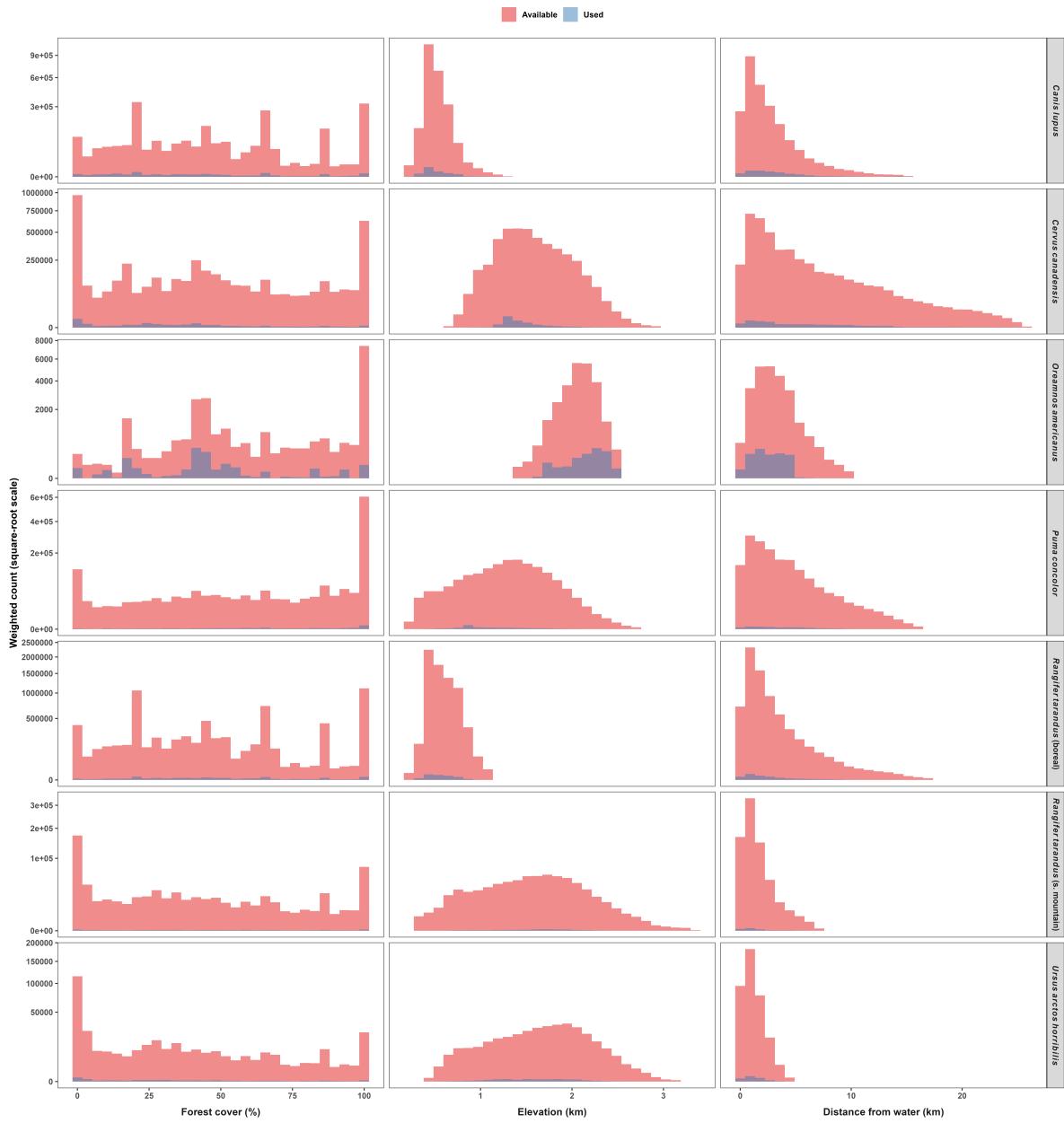


Figure B13: Histograms of available (red) and used (blue) resources. All GPS fixes are weighted according to their independence relative to the respective animals' range crossing time and Autocorrelated Kernel Density Estimate (i.e., the weights returned by AKDE weights multiplied by the number of home-range-crossing degrees of freedom). The y axis is on the square-root scale to help visualize values with low counts.

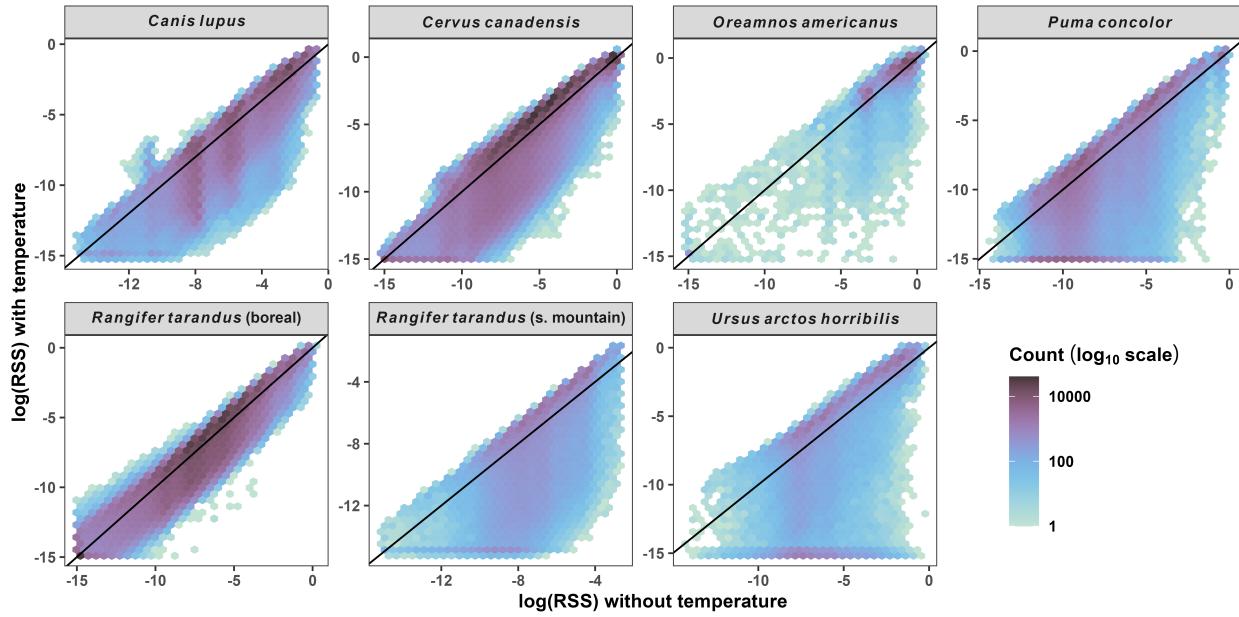


Figure B14: Hexplot of the fitted values from the HRSFs with and without including temperature. For ease of visibility, values < -20 (0.41%) were set to -20.

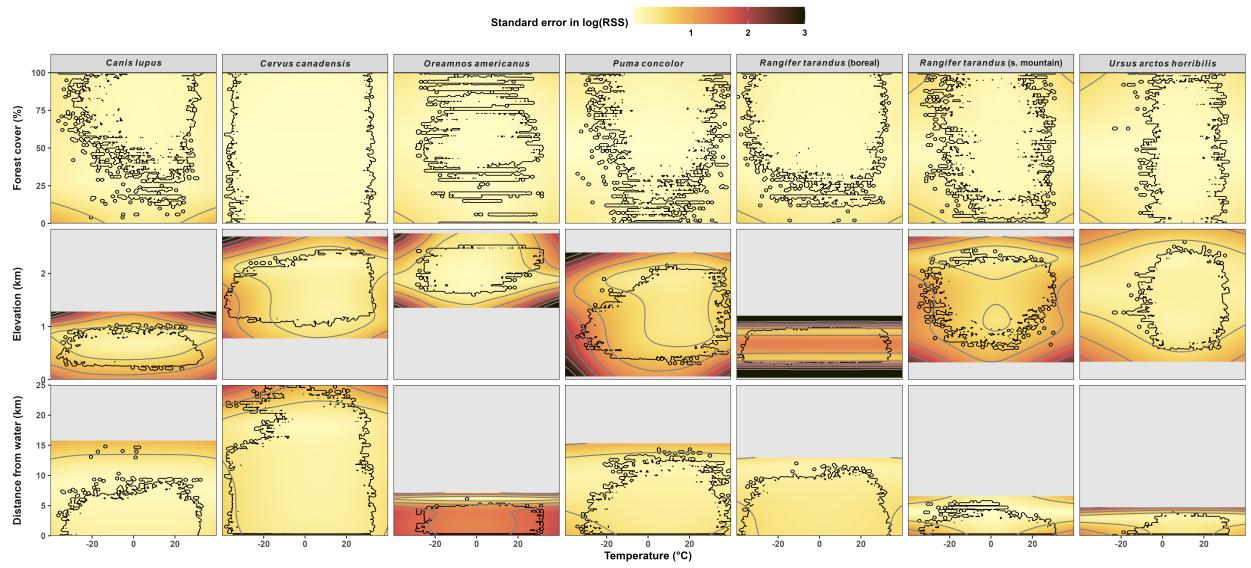


Figure B15: Estimated standard error in the relative selection strength (RSS) for forest cover (%), elevation (km), and distance from water (km) as a function of temperature (see Fig. 3 in the main text). The black contours indicate the extent of each species' observed data. For ease of readability, the color bar values were capped to a maximum of 3 (original maximum was 7.00).

3 Model selection

Table B2: Changes in deviance explained (ΔDE) and Akaike Information Criterion (ΔAIC) from including temperature in the models estimating probability of movement ($P(M)$) and speed when moving (Speed) as well as in species-level Hierarchical Resource Selection Functions (HRSF). Unlike conventional marginal AIC (Akaike, 1974), The AIC values provided by the `mgcv` package for R are calculated using the models' estimated effective degrees of freedom and the Bayesian variance-covariance matrices, which avoids issues related to random effects or Restricted Maximum Likelihood (REML).

Model	Species	ΔDE	ΔAIC
$P(M)$	All	0.5%	5927
Speed	All	0.2%	1682
HRSF	<i>Canis lupus</i>	9.2%	6566
HRSF	<i>Cervus canadensis</i>	4.6%	4448
HRSF	<i>Oreamnos americanus</i>	18.6%	813
HRSF	<i>Puma concolor</i>	8%	966
HRSF	<i>Rangifer tarandus</i> (boreal)	5.3%	5637
HRSF	<i>Rangifer tarandus</i> (s. mountain)	12%	342
HRSF	<i>Ursus arctos horribilis</i>	17.7%	914

3.1 Analyses of Deviance

Here we produce approximate p-values for analyses of deviance (a form of generalized likelihood ratio tests) following the methods of Section 3.3 in Wood (2017). We use an F test rather than a χ^2 test for the Gamma models because the scale parameter for the Gamma distribution is estimated rather than known or fixed (as in the case of binomial or Poisson distributions – see table 3.1 on page 104 of Wood, 2017).

```
# P(moving)
anova(readRDS('../models/binomial-gam-without-temperature.rds'),
      readRDS('../models/binomial-gam.rds'),
      test = 'Chisq')

## Analysis of Deviance Table
##
## Model 1: moving ~ s(animal, bs = "re") + species + s(tod_pdt, by = species,
##           k = 5, bs = "cc") + s(doy, by = species, k = 5, bs = "cc") +
##           ti(doy, tod_pdt, by = species, k = 5, bs = c("cc", "cc")) +
##           s(log(dt), k = 3) + s(log(dt), species, k = 3, bs = "fs")
## Model 2: moving ~ s(animal, bs = "re") + species + s(tod_pdt, by = species,
##           k = 5, bs = "cc") + s(doy, by = species, k = 5, bs = "cc") +
##           s(temp_c, by = species, k = 5, bs = "tp") + ti(doy, tod_pdt,
##           by = species, k = 5, bs = c("cc", "cc")) + ti(temp_c, tod_pdt,
##           by = species, k = 5, bs = c("tp", "cc")) + ti(temp_c, doy,
##           by = species, k = 5, bs = c("tp", "cc")) + s(log(dt), k = 3) +
##           s(log(dt), species, k = 3, bs = "fs")
##   Resid. Df Resid. Dev      Df Deviance  Pr(>Chi)
## 1    1476577     1129510
## 2    1476436     1123326 141.59      6184 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

# speed when moving
anova(readRDS('../models/gamma-gam-without-temperature.rds'),
      readRDS('../models/gamma-gam.rds'),
      test = 'F')

## Analysis of Deviance Table
##
## Model 1: speed_est ~ s(animal, bs = "re") + species + s(tod_pdt, by = species,
##                 k = 5, bs = "cc") + s(doy, by = species, k = 5, bs = "cc") +
##                 ti(doy, tod_pdt, by = species, k = 5, bs = c("cc", "cc")) +
##                 s(log(dt), k = 3) + s(log(dt), species, k = 3, bs = "fs")
## Model 2: speed_est ~ s(animal, bs = "re") + species + s(tod_pdt, by = species,
##                 k = 5, bs = "cc") + s(doy, by = species, k = 5, bs = "cc") +
##                 s(temp_c, by = species, k = 5, bs = "tp") + ti(doy, tod_pdt,
##                 by = species, k = 5, bs = c("cc", "cc")) + ti(temp_c, tod_pdt,
##                 by = species, k = 5, bs = c("tp", "cc")) + ti(temp_c, doy,
##                 by = species, k = 5, bs = c("tp", "cc")) + s(log(dt), k = 3) +
##                 s(log(dt), species, k = 3, bs = "fs")
##   Resid. Df Resid. Dev      Df Deviance      F     Pr(>F)
## 1    223798     37934
## 2    223710     37649  87.751   285.11 17.456 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

# HRSFs
anova(readRDS('../models/rsf-Canis_lupus-2025-01-20.rds'),
      readRDS('../models/rsf-Canis_lupus-no-temperature-2025-01-20.rds'),
      test = 'Chisq')

```

```

## Analysis of Deviance Table
##
## Model 1: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##                 k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##                 bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                 s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                 s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                 ti(forest_perc, temperature_C, k = 4, bs = "cr") + ti(elevation_m,
##                 temperature_C, k = 4, bs = "cr") + ti(dist_water_m, temperature_C,
##                 k = 4, bs = "cr") + s(temperature_C, k = 4, bs = "cr") +
##                 s(temperature_C, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
## Model 2: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##                 k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##                 bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                 s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                 s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
##   Resid. Df Resid. Dev      Df Deviance  Pr(>Chi)
## 1    639545     39183
## 2    639643     45920 -97.944  -6736.8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

anova(readRDS('../models/rsf-Cervus canadensis-2025-01-20.rds'),
      readRDS('../models/rsf-Cervus canadensis-no-temperature-2025-01-20.rds'),
      test = 'Chisq')

## Analysis of Deviance Table
##
## Model 1: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##   k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##   bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   ti(forest_perc, temperature_C, k = 4, bs = "cr") + ti(elevation_m,
##   temperature_C, k = 4, bs = "cr") + ti(dist_water_m, temperature_C,
##   k = 4, bs = "cr") + s(temperature_C, k = 4, bs = "cr") +
##   s(temperature_C, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
## Model 2: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##   k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##   bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
##   Resid. Df Resid. Dev      Df Deviance Pr(>Chi)
## 1    1436458     19199
## 2    1436594    23816 -136.27   -4617.1 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(readRDS('../models/rsf-Oreamnos americanus-2025-01-20.rds'),
      readRDS('../models/rsf-Oreamnos americanus-no-temperature-2025-01-20.rds'),
      test = 'Chisq')

## Analysis of Deviance Table
##
## Model 1: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##   k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##   bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   ti(forest_perc, temperature_C, k = 4, bs = "cr") + ti(elevation_m,
##   temperature_C, k = 4, bs = "cr") + ti(dist_water_m, temperature_C,
##   k = 4, bs = "cr") + s(temperature_C, k = 4, bs = "cr") +
##   s(temperature_C, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
## Model 2: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##   k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##   bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
##   Resid. Df Resid. Dev      Df Deviance Pr(>Chi)
## 1    70696     1576.8
## 2    70694    2387.3 2.1921   -810.56

```

```

anova(readRDS('../models/rsf-Puma concolor-2025-01-20.rds'),
      readRDS('../models/rsf-Puma concolor-no-temperature-2025-01-20.rds'),
      test = 'Chisq')

## Analysis of Deviance Table
##
## Model 1: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##                      k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##                      bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      ti(forest_perc, temperature_C, k = 4, bs = "cr") + ti(elevation_m,
##                      temperature_C, k = 4, bs = "cr") + ti(dist_water_m, temperature_C,
##                      k = 4, bs = "cr") + s(temperature_C, k = 4, bs = "cr") +
##                      s(temperature_C, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
## Model 2: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##                      k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##                      bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
##   Resid. Df Resid. Dev      Df Deviance Pr(>Chi)
## 1     324734    4076.5
## 2     324772    5099.7 -38.033  -1023.3 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

anova(
  readRDS('../models/rsf-Rangifer tarandus boreal-2025-01-21.rds'),
  readRDS('../models/rsf-Rangifer tarandus boreal-no-temperature-2025-01-20.rds'),
  test = 'Chisq')

## Analysis of Deviance Table
##
## Model 1: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##                      k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##                      bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      ti(forest_perc, temperature_C, k = 4, bs = "cr") + ti(elevation_m,
##                      temperature_C, k = 4, bs = "cr") + ti(dist_water_m, temperature_C,
##                      k = 4, bs = "cr") + s(temperature_C, k = 4, bs = "cr") +
##                      s(temperature_C, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
## Model 2: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##                      k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##                      bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##                      s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
##   Resid. Df Resid. Dev      Df Deviance Pr(>Chi)
## 1     1452896     48216
## 2     1452959     53927 -62.606  -5711.3 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

anova(readRDS('../models/rsf-Rangifer tarandus southern mountain-2025-01-20.rds'),
      readRDS('../models/rsf-Rangifer tarandus southern mountain-no-temperature-2025-01-20.rds'),
      test = 'Chisq')

```

```

## Analysis of Deviance Table
##
## Model 1: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##   k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##   bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   ti(forest_perc, temperature_C, k = 4, bs = "cr") + ti(elevation_m,
##   temperature_C, k = 4, bs = "cr") + ti(dist_water_m, temperature_C,
##   k = 4, bs = "cr") + s(temperature_C, k = 4, bs = "cr") +
##   s(temperature_C, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
## Model 2: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##   k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##   bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
##   Resid. Df Resid. Dev      Df Deviance  Pr(>Chi)
## 1     132580    2026.1
## 2     132589  2384.5 -8.8792 -358.34 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

anova(readRDS('../models/rsf-Ursus arctos horribilis-2025-01-20.rds'),
      readRDS('../models/rsf-Ursus arctos horribilis-no-temperature-2025-01-20.rds'),
      test = 'Chisq')

```

```

## Analysis of Deviance Table
##
## Model 1: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##   k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##   bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   ti(forest_perc, temperature_C, k = 4, bs = "cr") + ti(elevation_m,
##   temperature_C, k = 4, bs = "cr") + ti(dist_water_m, temperature_C,
##   k = 4, bs = "cr") + s(temperature_C, k = 4, bs = "cr") +
##   s(temperature_C, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
## Model 2: detected ~ s(forest_perc, k = 4, bs = "cr") + s(elevation_m,
##   k = 4, bs = "cr") + s(dist_water_m, k = 4, bs = "cr") + s(animal,
##   bs = "re") + s(forest_perc, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(elevation_m, animal, k = 4, bs = "fs", xt = list(bc = "cr")) +
##   s(dist_water_m, animal, k = 4, bs = "fs", xt = list(bc = "cr"))
##   Resid. Df Resid. Dev      Df Deviance  Pr(>Chi)
## 1     99164    2356.7
## 2     99165  3275.0 -1.1525 -918.26 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

References

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- Akaike H (1974) A new look at the statistical model identification. *IEEE Transactions on Automatic Control*, **19**, 716–723.
- Wood SN (2017) Generalized additive models: An introduction with R, Second edition edn. CRC Press/Taylor & Francis Group, Boca Raton.