APPENDIX

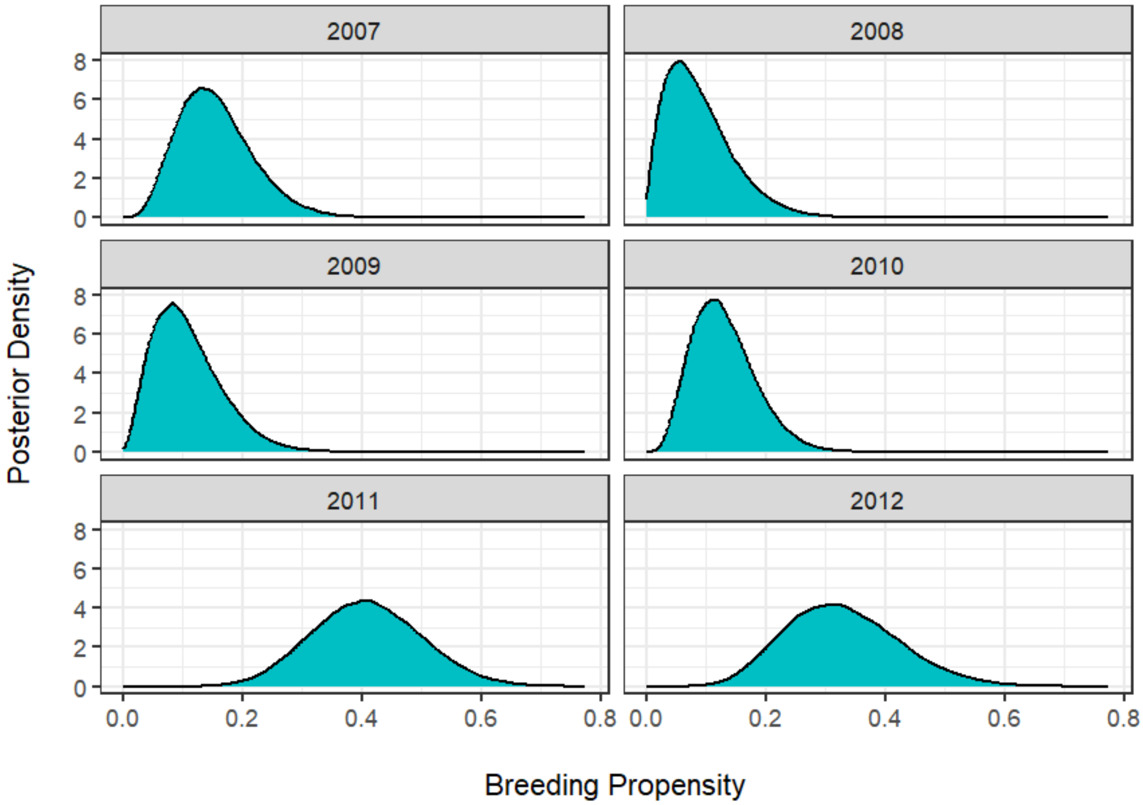

Fig. A1. Posterior distributions for annual breeding propensity of Kittlitz's murrelets in Icy Bay, Alaska, 2007–2012.

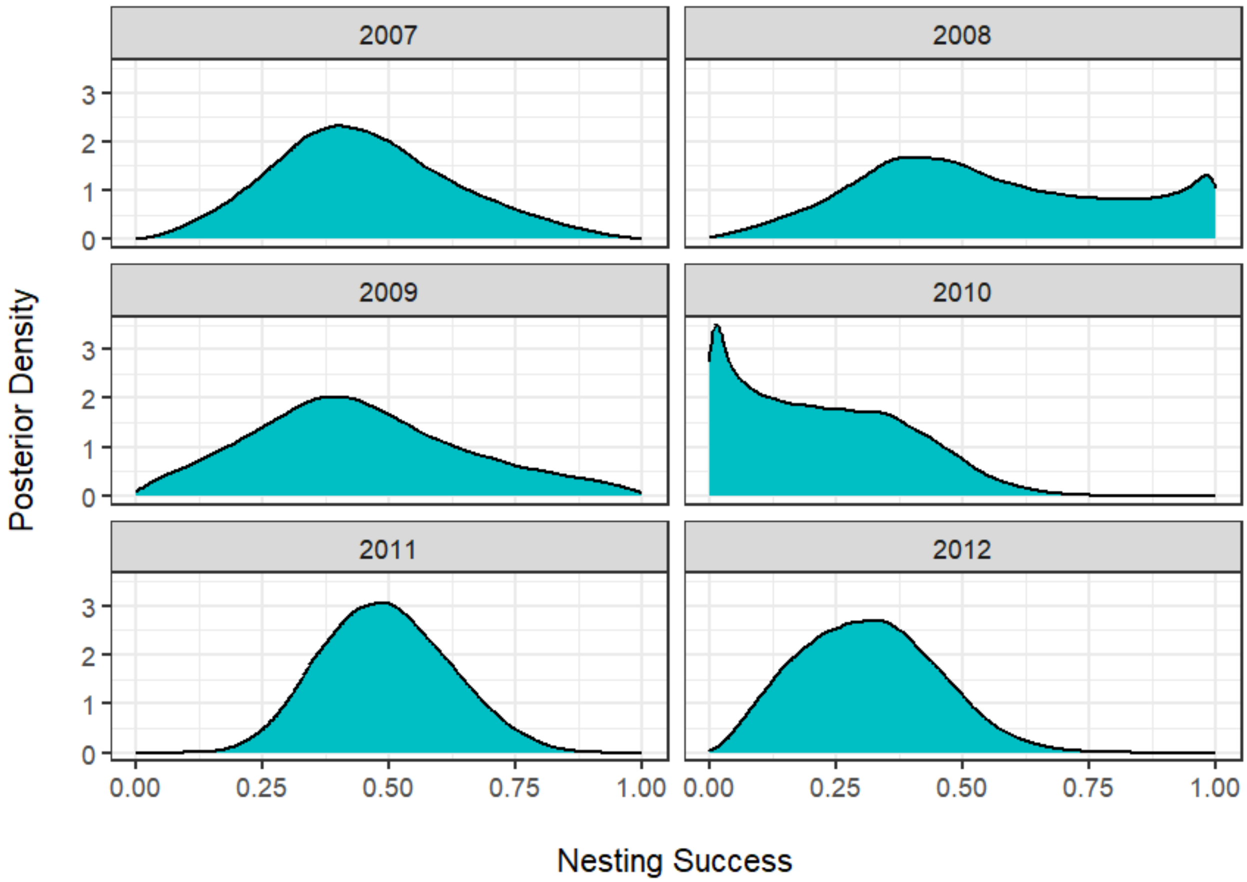

Fig. A2. Posterior distributions for annual nesting success of Kittlitz's murrelets in Icy Bay, Alaska, 2007–2012. Note: In 2008, we found only one nest and it was successful, and in 2010, we found four nests, but all of them failed. Consequently, our estimates of nesting success in those years were poor.

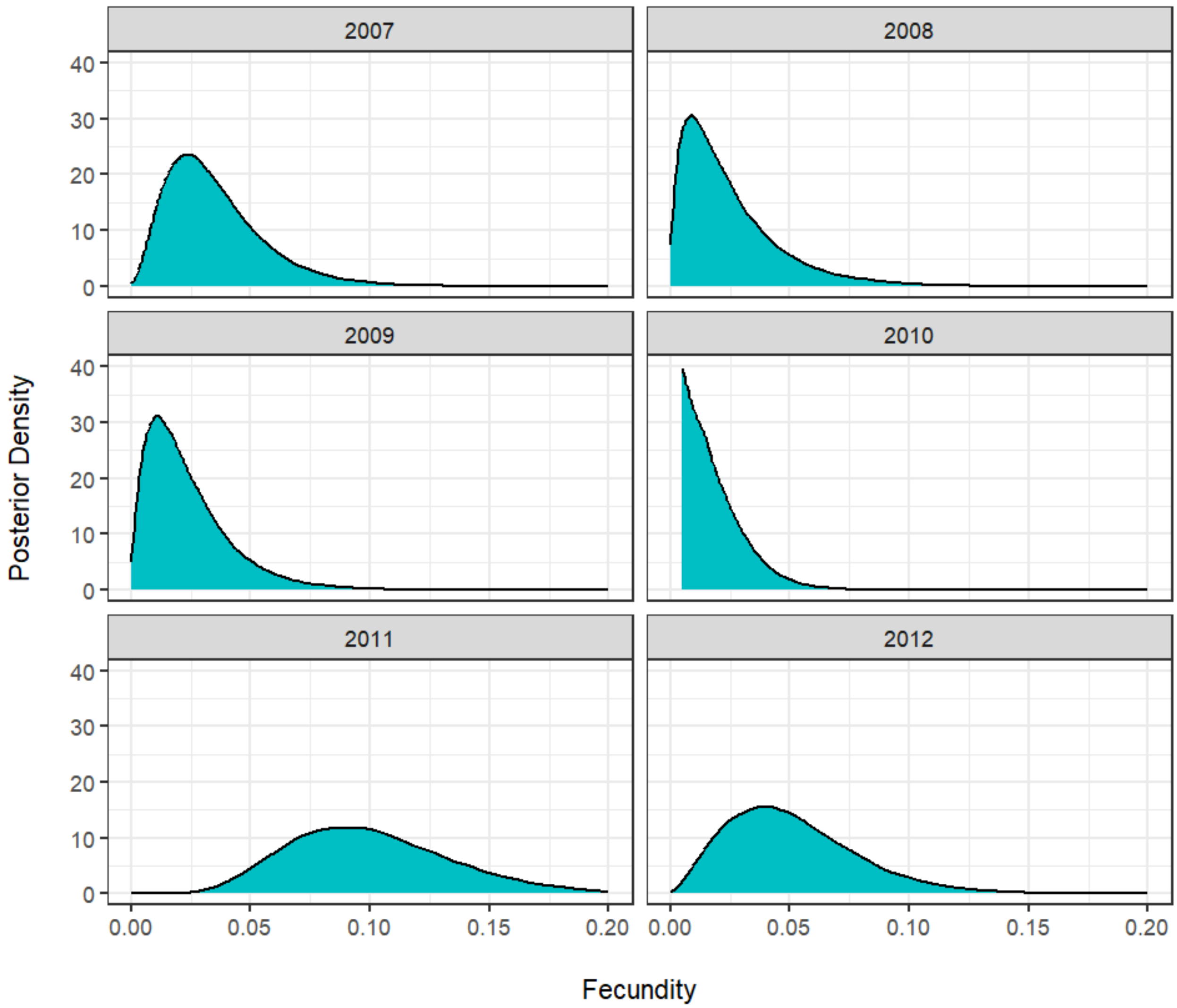

Fig. A3. Posterior distributions for annual fecundity of Kittlitz's murrelets in Icy Bay, Alaska, 2007–2012.

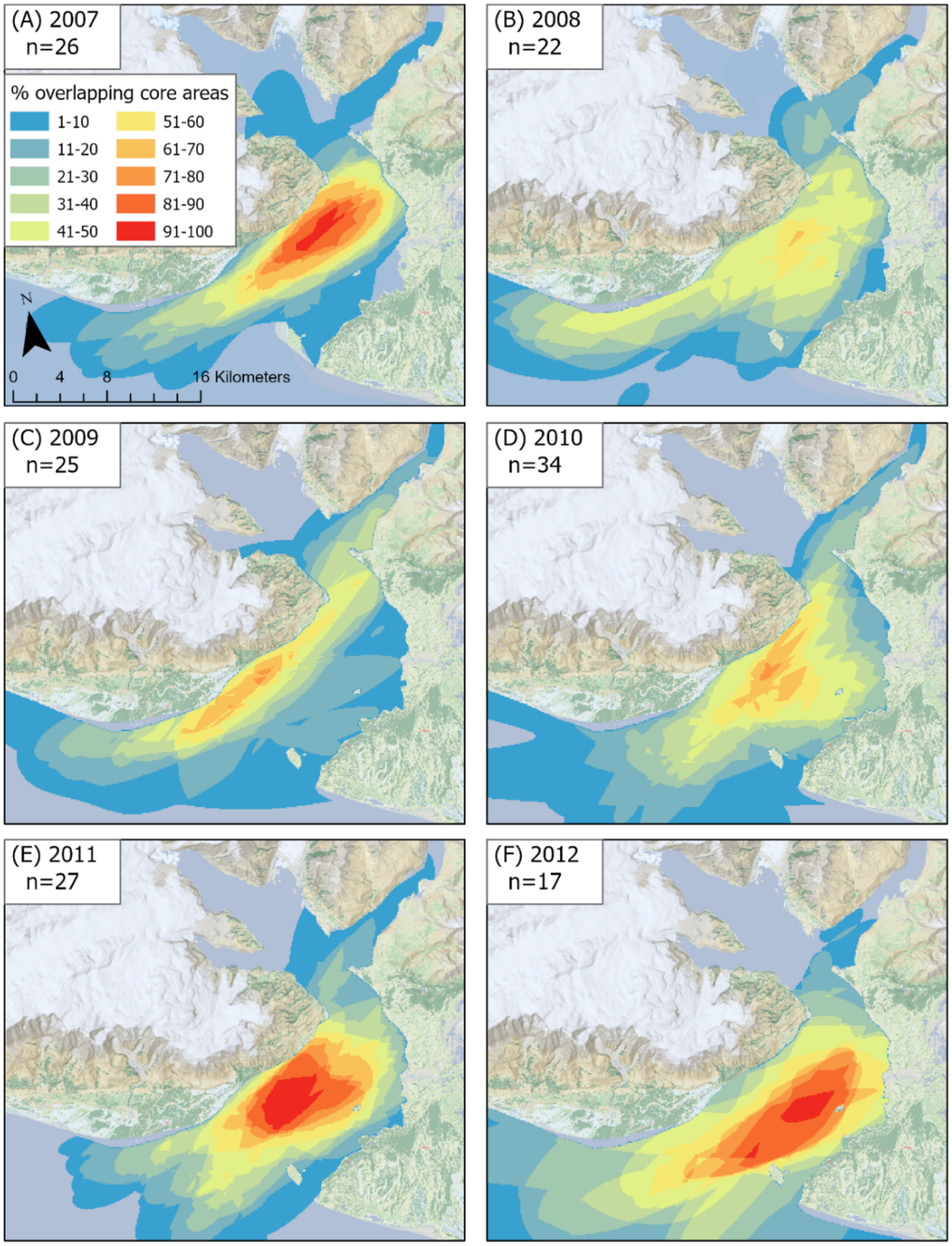

Fig. A4. Spatial representation of percentage of overlapping individual core use areas of Kittlitz's murrelets, Icy Bay, Alaska, 2007–2012. Cell size was 100 m. We normalized and fixed scales to allow comparison among years. Sample sizes indicate the number of murrelet marine core use areas in a given year.

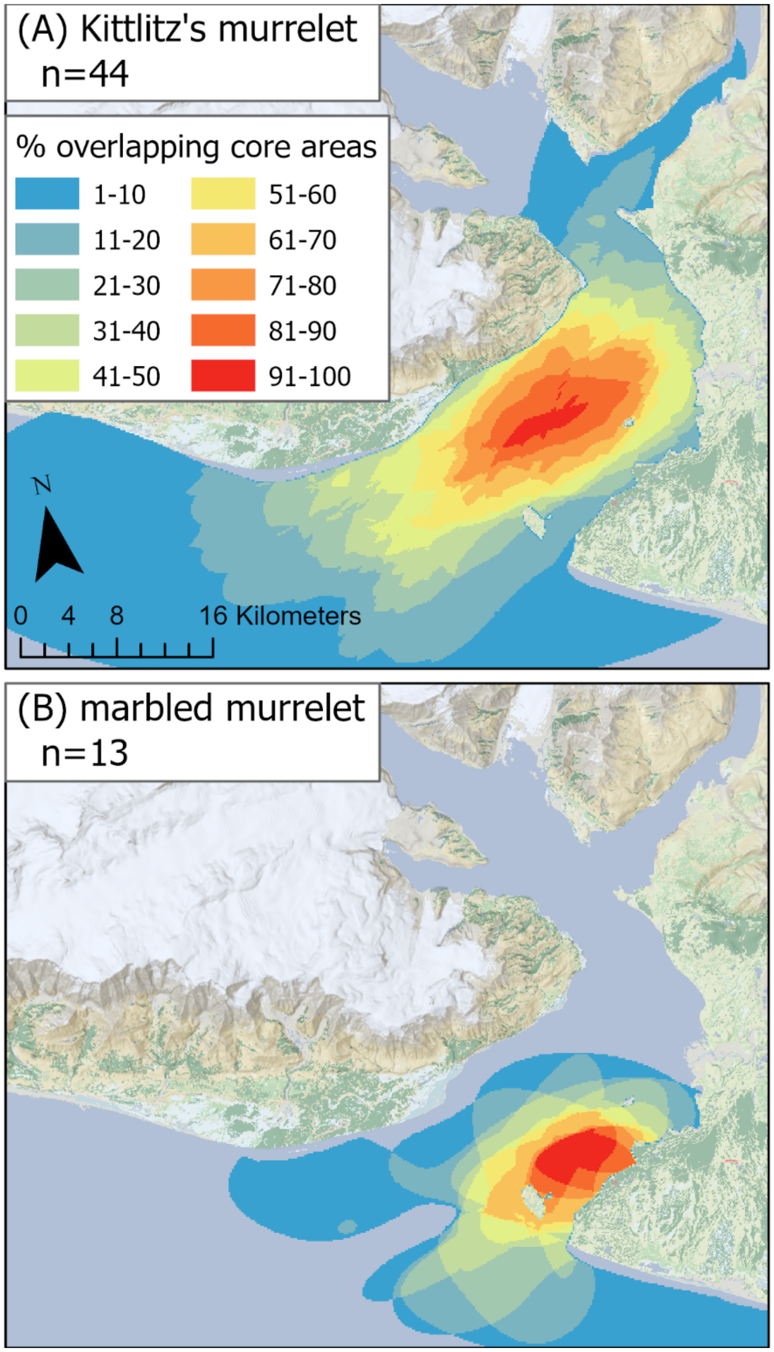

Fig. A5. Spatial representation of percentage of overlapping individual marine core use areas of (A) Kittlitz's murrelets (n=44) and marbled murrelets (n=13), Icy Bay, Alaska, 2011–2012. Cell size was 100 m. We normalized and fixed scales to allow comparison of marine core use areas between species.

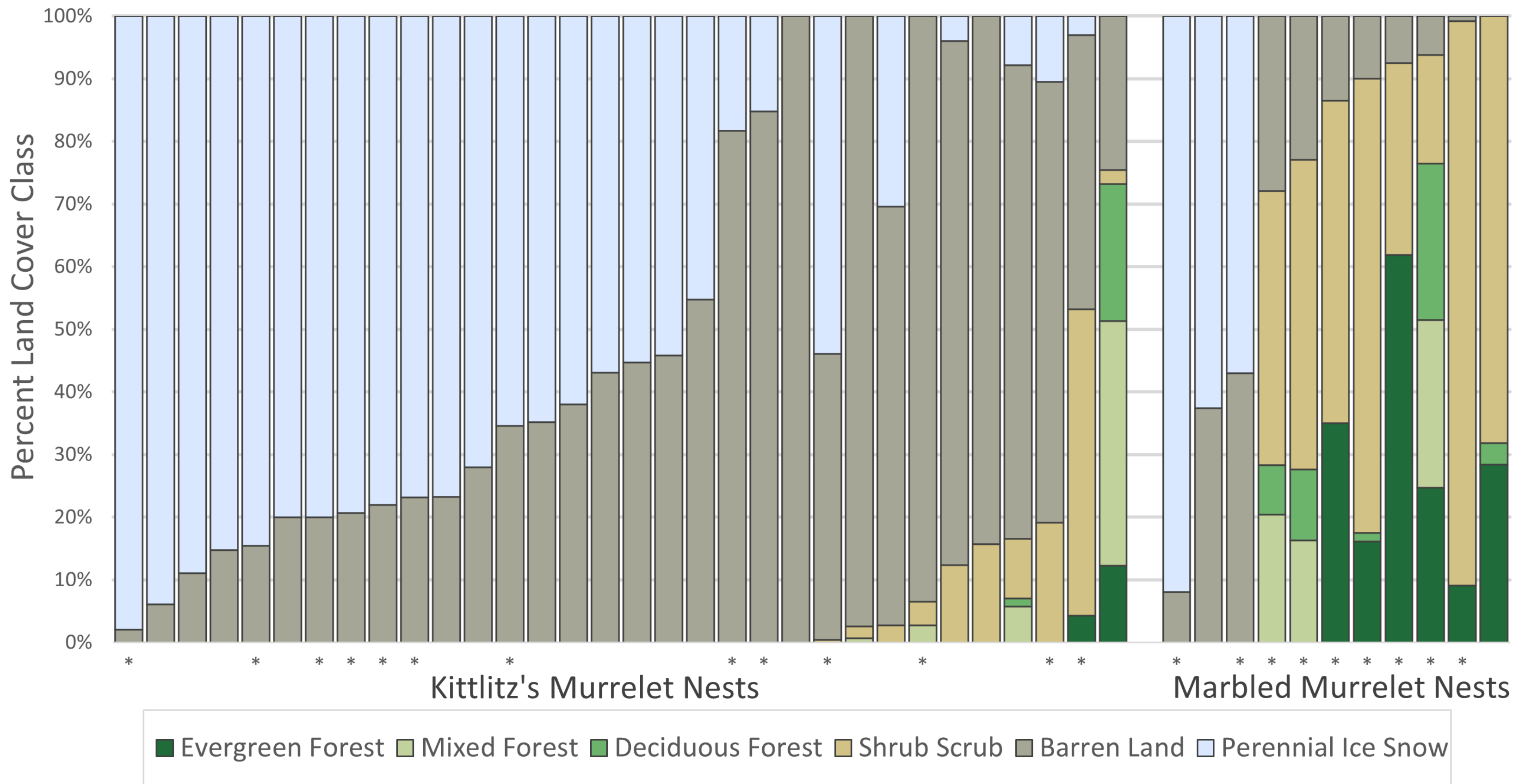

Fig. A6. Percent land cover class within 500 m of Kittlitz's murrelet (KIMU) and marbled murrelet (MAMU) nests, Icy Bay, Alaska, 2007–2012. Successful nests are denoted with an asterisk.

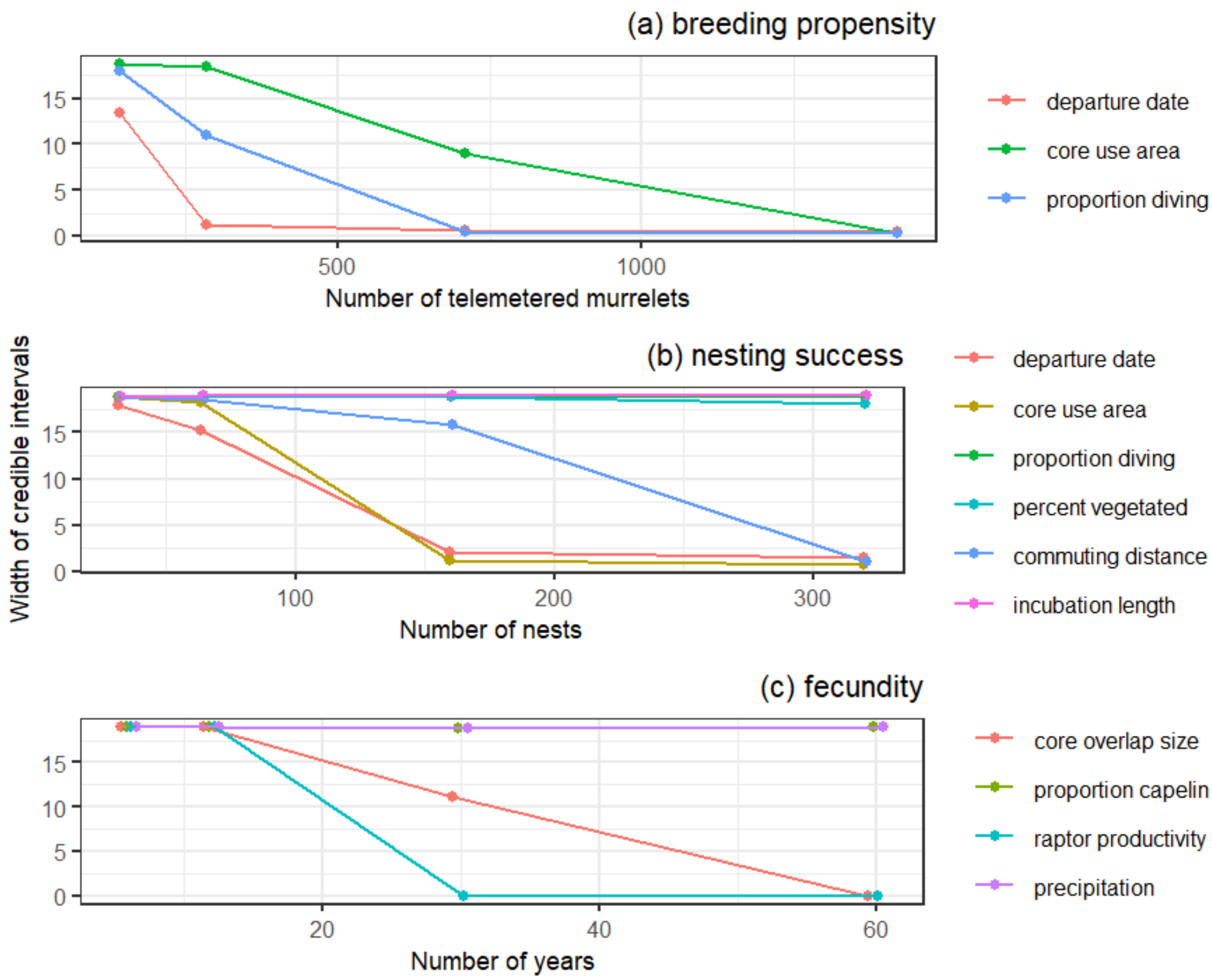

Fig. A7. The effect of sample size on precision of explanatory factor coefficients for (a) breeding propensity, (b) nesting success, and (c) fecundity. Precision was calculated as the difference in the 95% credible intervals. The points denote the number of replicates (1, 2, 5, and 10) of each dataset while holding the number of years modeled as a random effect constant for breeding propensity and nesting success (i.e., 6 years). Both points and lines are slightly offset for visibility.

JAGS code for models with explanatory factors to explain variation in breeding propensity, nesting success, and fecundity of Kittlitz's murrelets.

1. Model for breeding propensity

```
model{
 ### prior distributions
 # beta estimates
  b0.mu ~ dnorm( 0, 0.001)T(-10,10)    # intercept
  b1 ~ dnorm ( 0, 0.001)T(-10,10)   # maximum Julian date located
  b2 ~ dnorm ( 0, 0.001)T(-10,10)   # size of marine core use area
  b3 ~ dnorm ( 0, 0.001)T(-10,10)   # proportion flights diving

  # random effect for year
  b0.tau <- 1 / (b0.sd*b0.sd)
  b0.sd ~ dunif(0, 5)

  for( k in 1:nyears){
   b0[k] ~ dnorm(b0.mu, b0.tau)
  }

 # augmentation of switches for covariates (binary indicator)
  z1 ~ dbern( .5 )
```

```
  z2 ~ dbern( .5 )
  z3 ~ dbern( .5 )

 ### likelihood
   for (i in 1:nobs){
     repro[i] ~ dbern( bp[i])
     logit(bp[i]) <- b0[year[i]] + z1*b1*MaxJulDate[i] + z2*b2*HR50[i] + z3*b3*PropForage[i]
   }

 ### derived parameters
  logit(bp.2007) <- b0[1]
  logit(bp.2008) <- b0[2]
  logit(bp.2009) <- b0[3]
  logit(bp.2010) <- b0[4]
  logit(bp.2011) <- b0[5]
  logit(bp.2012) <- b0[6]
  bp.mu <- mean(bp)

}
```

2. Model for nesting success

```
model{
 ### prior distributions
 # beta estimates
  b0.mu ~ dnorm( 0, 0.001)T(-10,10)   # intercept
  b1 ~ dnorm ( 0, 0.001)T(-10,10)   # maximum Julian date located
  b2 ~ dnorm ( 0, 0.001)T(-10,10)   # size of marine core use area
  b3 ~ dnorm ( 0, 0.001)T(-10,10)   # proportion flights diving
  b4 ~ dnorm ( 0, 0.001)T(-10,10)   # percent nest vegetated
  b5 ~ dnorm ( 0, 0.001)T(-10,10)   # one-way commuting distance
  b6 ~ dnorm ( 0, 0.001)T(-10,10)   # mean incubation shift length

 # random effect for year
   b0.tau <- 1 / (b0.sd*b0.sd)
   b0.sd ~ dunif(0, 5)

   for( k in 1:nyears){
     b0[k] ~ dnorm(b0.mu, b0.tau)
   }

 # augmentation of switches for covariates (binary indicator)
 z1 ~ dbern( .5 )
```

```
z2 ~ dbern( .5 )

z3 ~ dbern( .5 )

z4 ~ dbern( .5 )

z5 ~ dbern( .5 )

z6 ~ dbern( .5 )


### likelihood

for (i in 1:nobs){

  nfate[i] ~ dbern( ns[i])

  logit(ns[i]) <- b0[year[i]] + z1*b1*depdate[i] + z2*b2*HR50[i] + z3*b3*forage[i]

 + z4*b4*veg[i] + z5*b5*commute[i] + z6*b6*incubate[i]

}


### derived parameters

logit(ns.2007) <- b0[1]

logit(ns.2008) <- b0[2]

logit(ns.2009) <- b0[3]

logit(ns.2010) <- b0[4]

logit(ns.2011) <- b0[5]

logit(ns.2012) <- b0[6]

ns.mu <- mean(ns)
```

```
}
```

3. Model for fecundity

```
model{
  ### prior distributions
  # beta estimates
  b0 ~ dnorm( 0, 0.001) T( -10, 10)
  b1 ~ dnorm( 0, 0.001) T( -10, 10)  # overlap of marine core use area
  b2 ~ dnorm( 0, 0.001) T( -10, 10)  # proportion of capelin biomass for rhinoceros auklets
  b3 ~ dnorm( 0, 0.001) T( -10, 10)  # raptor productivity
  b4 ~ dnorm( 0, 0.001) T( -10, 10)  # precipitation in cm

  sig ~ dunif( 0, 10 )
  tau <- 1/(sig * sig)

  # augmentation of switches for covariates (binary indicator)
  z1 ~ dbern( .5 )
  z2 ~ dbern( .5 )
  z3 ~ dbern( .5 )
  z4 ~ dbern( .5 )
```

```
### likelihood
 for (i in 1:nobs){
   fec[i] ~ dnorm( mu.fec[i], tau)
   mu.fec[i] <- b0 + z1*b1*overlap[i] + z2*b2*capelin[i] + z3*b3*raptor[i] + z4*b4*precip[i]
 }

 ### derived parameters

 mean.fec <- mean(mu.fec)

}
```