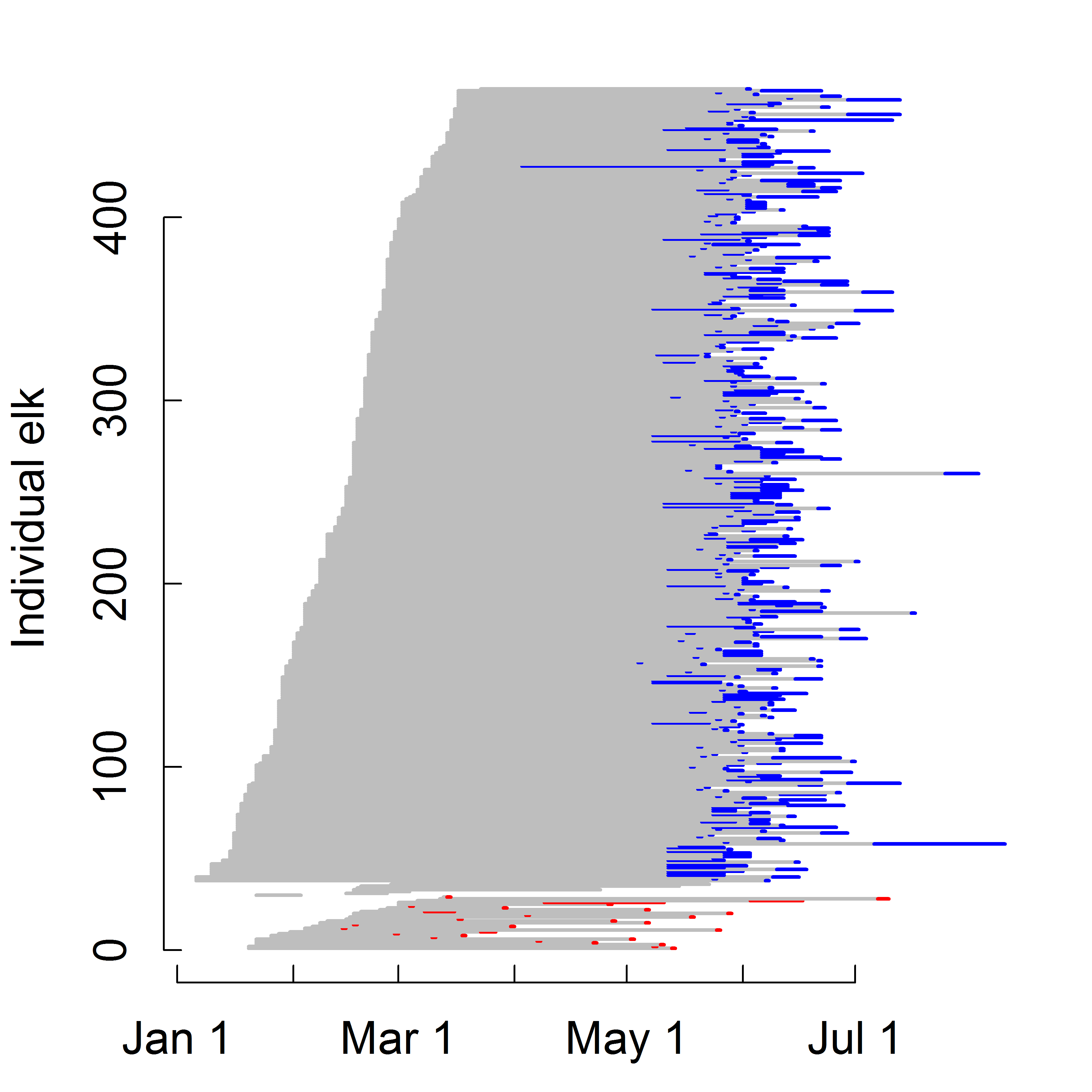
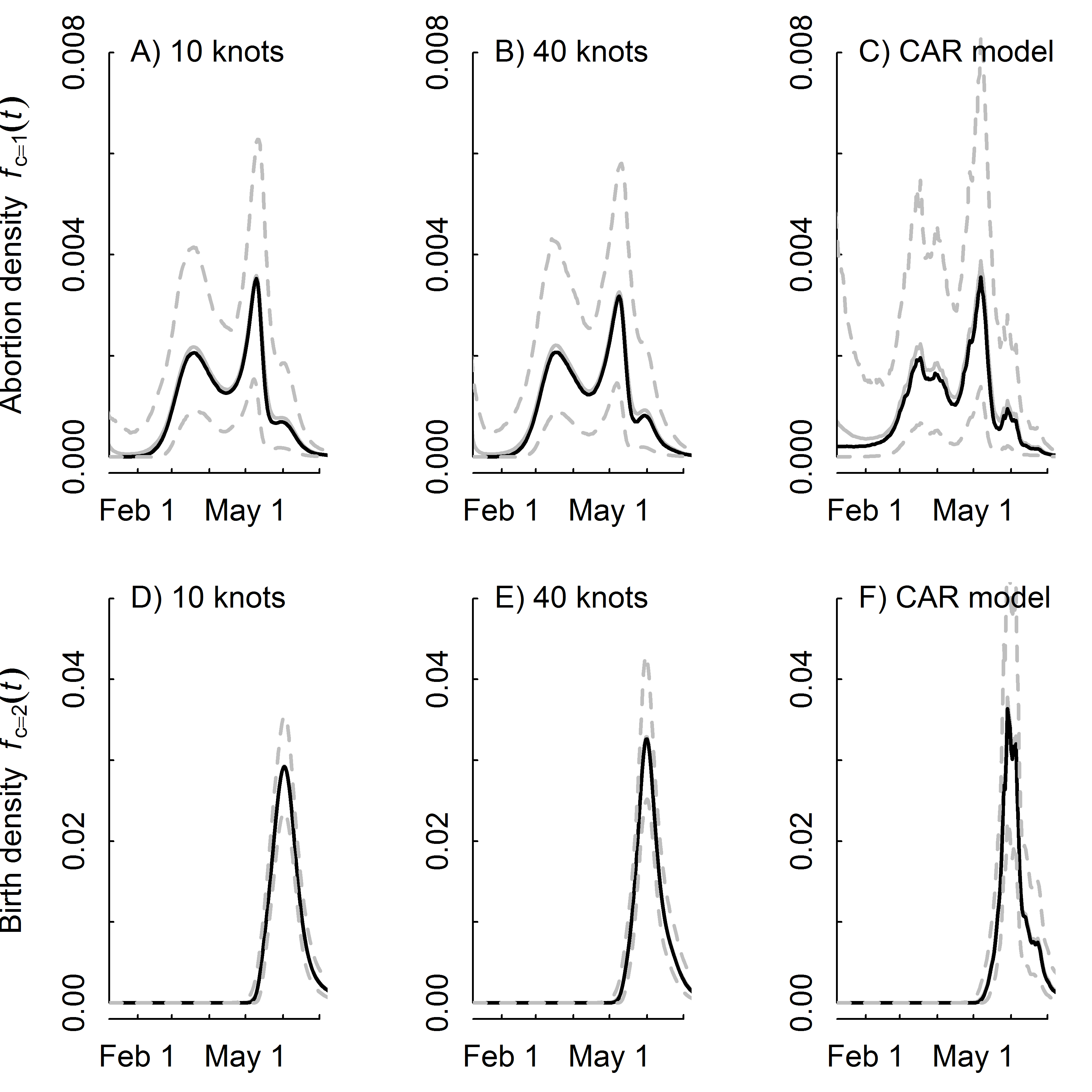
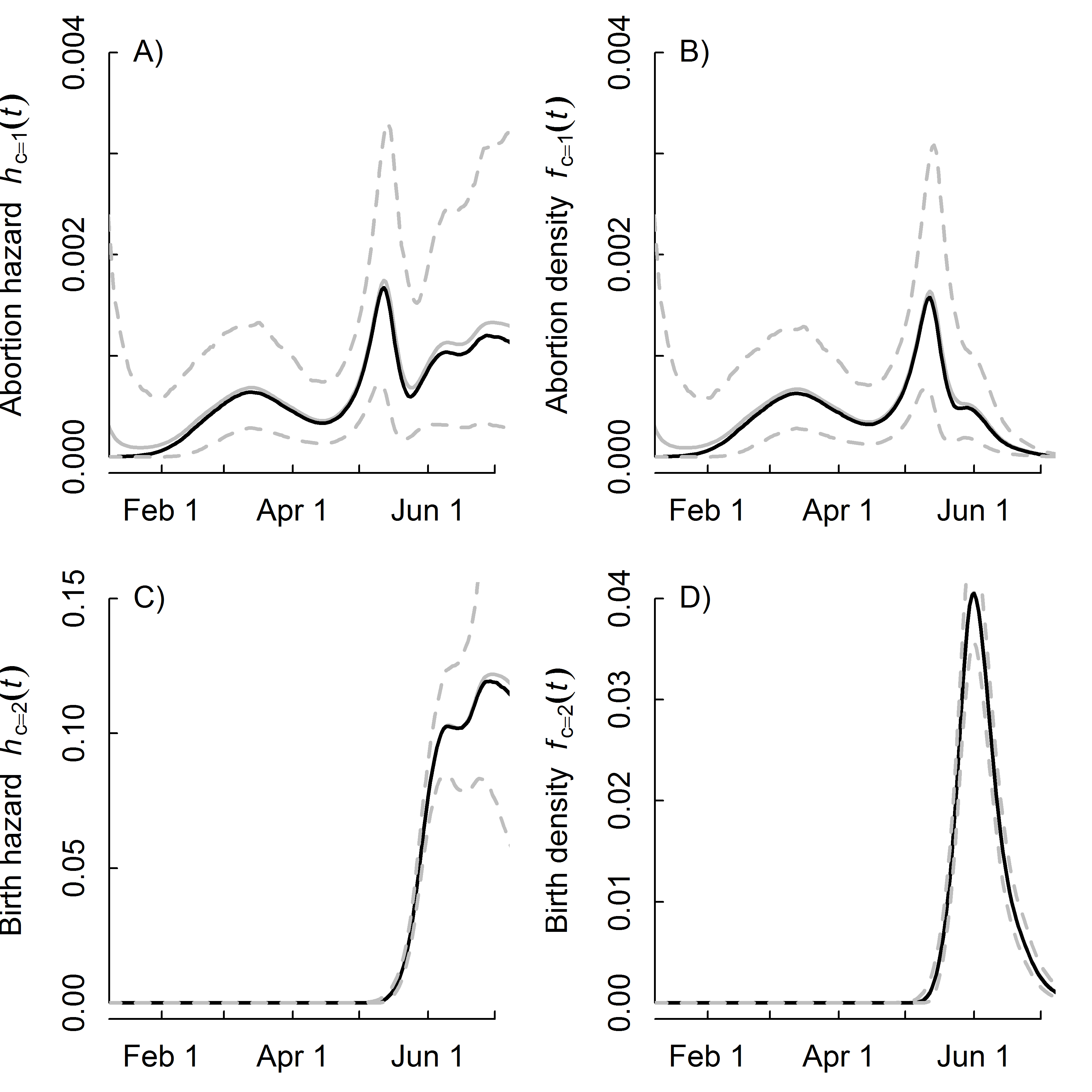
# Supplementary Information:



**Figure S1**. Raw data on the reproductive events of all pregnant elk in the study. Grey lines extend from the capture date to the time interval when the reproductive event occurred. Red and blue lines indicate time intervals when VITs were expelled due to abortions or normal birth events, respectively.



**Figure S2**. Comparison of reproductive event densities using different smoothing functions and only seropositive elk. Grey and black solid lines are the predicted posterior mean and medians. Dotted lines are the predicted posterior 95% credible intervals.



**Figure S3**. Results using seropositive and seronegative elk and the 40 knot spline model. Grey and black solid lines are the predicted posterior mean and medians. Dotted lines are the predicted posterior 95% credible intervals.

**Table S2**. Comparison of elk abortion timing across models when using all pregnant elk (n = 429). Models had different smoothing functions for the total hazard of a reproductive event, but the sub-model of the probability of an abortion relative to a live birth was a logistic regression in all cases.

##   
##   
## |Model |DIC |pD |5% |25% |75% |95% |  
## |:---------|:------|:----|:------|:------|:------|:-----|  
## |10 knots |2823.5 |12.6 |19-Feb |16-Mar |15-May |5-Jun |  
## |40 knots |2821.1 |14.1 |18-Feb |17-Mar |13-May |5-Jun |  
## |CAR model |2829.7 |33.2 |31-Jan |13-Mar |12-May |4-Jun |

DIC: Deviance information criteria  
pD: Estimate of model complexity  
5-95%: Estimated day of the year when *X*% of the abortions have occurred.

**Appendix S1:** Model code.  
Hazard spline model that is not partitioned by event type (10knots) -----------------------------------------------------

# Priors  
 gamma0 ~ dnorm(0, 1.0E-6)  
 sigmab ~ dunif(0,3)  
 taub <- pow(sigmab, -2)  
 for (l in 1:num.knots){b[l] ~ dnorm(0,taub)}  
   
 # Likelihood for the total hazard  
 for (j in 1:records) {  
 for (k in left[j]:(right[j]-1)) {  
 # unit cumulative hazard  
 UCH[j,k] <- exp(gamma0 + mre110[k])  
 }   
   
 SLR[j] <- exp(-sum(UCH[j,left[j]:(right[j]-1)])) # total prob of not having an event   
   
 # Bernoulli draw for "surviving"  
 noevent[j] ~ dbern(SLR[j])   
 }  
  
# Calculate the baseline hazard  
 for (i in 1:D) {  
 Haz\_b[i] <- exp(gamma0 + mre110[i]) # baseline hazard  
 # Spline part  
 mre110[i] <- b[1]\*Z[i,1]+b[2]\*Z[i,2]+b[3]\*Z[i,3]+b[4]\*Z[i,4]+b[5]\*Z[i,5]+  
 b[6]\*Z[i,6]+b[7]\*Z[i,7]+b[8]\*Z[i,8]+b[9]\*Z[i,9]+b[10]\*Z[i,10]  
 }

## Hazard spline model that is partitioned by event type (10knots)

# Priors  
sigmab ~ dunif(0,3)  
taub <- pow(sigmab, -2)  
gamma0 ~ dnorm(0, 1.0E-6)  
beta ~ dunif(0,2) # slope for the probability of an abortion  
alpha ~ dunif(50, 200) # offset for the transition from abortion to birth  
K ~ dunif(0,0.5) # lower asymptote for the prob. of an abortion  
for (l in 1:num.knots){b[l] ~ dnorm(0,taub)}  
  
#Derived parameters  
for (i in 1:D) {  
 Haz\_b[i] <- exp(gamma0 + mre110[i]) # baseline hazard  
  
 mre110[i] <- b[1]\*Z[i,1]+b[2]\*Z[i,2]+b[3]\*Z[i,3]+b[4]\*Z[i,4]+b[5]\*Z[i,5]+  
 b[6]\*Z[i,6]+b[7]\*Z[i,7]+b[8]\*Z[i,8]+b[9]\*Z[i,9]+b[10]\*Z[i,10]  
  
 prob.ab[i] <- 1 + (K - 1) / (1 + exp(-beta\*(i - alpha))) # probability of abortion   
 Haz\_a[i] <- prob.ab[i] \* Haz\_b[i] # abortion hazard  
 Haz\_l[i] <- (1-prob.ab[i]) \* Haz\_b[i] # live birth hazard  
}   
  
# Likelihood for the total hazard  
for (j in 1:records) {  
 for (k in left[j]:(right[j]-1)) {UCH[j,k] <- exp(gamma0 + mre110[k])}   
 SLR[j] <- exp(-sum(UCH[j,left[j]:(right[j]-1)])) # total prob of not having an event   
 noevent[j] ~ dbern(SLR[j])   
}  
  
# Likelihood on partitioning the event types  
for (m in 1:n.events) {  
 b.type[m] ~ dbern(p.a[m])  
 p.a[m] <- 1 + (K - 1) / (1 + exp(-beta\*(event.day[m] - alpha)))  
}

Estimating the design matrix *Z* for the splines was done in R as follows:

Z\_K<-(abs(outer(covariate,knots,"-")))^3   
OMEGA\_all<-(abs(outer(knots,knots,"-")))^3   
svd.OMEGA\_all<-svd(OMEGA\_all)   
sqrt.OMEGA\_all<-t(svd.OMEGA\_all$v %\*%   
(t(svd.OMEGA\_all$u)\*sqrt(svd.OMEGA\_all$d)))   
Z<-t(solve(sqrt.OMEGA\_all,t(Z\_K)))

## Conditional autoregressive model with event-type partitioning

# Priors  
 gamma0 ~ dnorm(0, 1.0E-6)  
 beta ~ dunif(0,2) # slope for the probability of an abortion  
 alpha ~ dunif(50, 200) # offset for the transition from abortion to birth  
 K ~ dunif(0,0.5) # lower asymptote for the prob. of an abortion  
 sd.rho ~ dunif(0,10) # hyperprior  
 tau.rho <- pow(sd.rho, -2)   
 rho[1] ~ dnorm(0, 1.0E-6)  
 for (i in 2:D) {rho[i]~dnorm(rho[i-1],tau.rho)}  
   
 #Derived quantities  
 for (i in 1:D) {  
 Haz\_b[i] <- exp(gamma0 + rho[i]) # overall baseline  
 prob.ab[i] <- 1 + (K - 1) / (1 + exp(-beta\*(i - alpha))) # probability of abortion   
 Haz\_a[i] <- prob.ab[i] \* Haz\_b[i] # abortion hazard  
 Haz\_l[i] <- (1-prob.ab[i]) \* Haz\_b[i] # live birth hazard  
 }   
  
 # Likelihood  
 for (j in 1:records) {  
 for (k in left[j]:(right[j]-1)) {  
 UCH[j,k] <- exp(gamma0 + rho[k]) # unit hazard over the interval  
 }   
 SLR[j] <- exp(-sum(UCH[j,left[j]:(right[j]-1)]))# total prob of not having an event   
 noevent[j] ~ dbern(SLR[j])   
 }  
   
 # Likelihood on partitioning the event types  
 for (m in 1:n.events) {  
 b.type[m] ~ dbern(p.a[m])  
 p.a[m] <- 1 + (K - 1) / (1 + exp(-beta\*(event.day[m] - alpha)))  
 }