

R code PA-CR model

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This code generates the results and the main figures presenter in the manuscript “Offspring number, size, and survival: state-dependent optimization of litter size in a long-lived capital breeder” *Ecological monographs*

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A. Run the model

1. Build the model

```
PA_CR <- nimbleCode({
  # ++++++ priors ++++++
  # Length
  for (i in 1:n_coef_mL) {
    alpha[i] ~ dnorm(0, sd = 5)
  }
  sigma_tau ~ dunif(0, 10)

  # Cohort random effect
  for (i in 1:n_cohort) {
    zeta[i] ~ dnorm(0, sd = sigma_zeta)
  }
  sigma_zeta ~ dunif(0, 10)

  # Litter size
  for (i in 1:n_coef_LS) {
    beta[i] ~ dnorm(0, sd = 1.5)
  }

  # Girth
  for (i in 1:n_coef_mG) {
    gamma[i] ~ dnorm(0, sd = 5)
  }
  sigma_xi ~ dunif(0, 10)

  # Cub mass
  for (i in 1:n_coef_M) {
    delta[i] ~ dnorm(0, sd = 5)
  }
  sigma_epsilon ~ dunif(0, 10)

  # Yearly random effects
  for (i in 1:n_year) {
```

```

eta[i] ~ dnorm(0, sd = sigma_eta)
rho[i] ~ dnorm(0, sd = sigma_rho)
nu[i] ~ dnorm(0, sd = sigma_nu)
}
sigma_eta ~ dunif(0, 10)
sigma_rho ~ dunif(0, 10)
sigma_nu ~ dunif(0, 10)

# Recapture
for (i in 1:n_coef_p) {
  lambda[i] ~ dnorm(0, sd = 1.5)
}

# Survival
theta[1] ~ dnorm(0, sd = 1.5)
theta[2] ~ dnorm(0, sd = 1)
for (i in 3:n_coef_phi) {
  theta[i] ~ dnorm(0, sd = 1.5)
}

# Yearly random effects on recapture
for (t in 1:(n_year-1)) {
  omega[t] ~ dnorm(0, sd = sigma_omega)
}
sigma_omega ~ dunif(0, 10)

# ***** model & likelihood *****

# length, girth and litter size
for (k in 1:n_litters) {
  # Length
  mu_mL[k] <- alpha[1] * mAgeY[row_litter[k], col_litter[k]] +
    alpha[2] * mAgeM[row_litter[k], col_litter[k]] +
    alpha[3] * mAge0[row_litter[k], col_litter[k]] +
    alpha[4] * mSpUnk[row_litter[k]] +
    alpha[5] * mSpPel[row_litter[k]] +
    zeta[cohort[k]]
  mL[row_litter[k], col_litter[k]] ~ dnorm(mu_mL[k], sd = sigma_tau)

  # Litter size
  log(q[k, 1]) <- 0

  log(q[k, 2]) <- beta[1] * mAgeY[row_litter[k], col_litter[k]] +
    beta[2] * mAgeM[row_litter[k], col_litter[k]] +
    beta[3] * mAge0[row_litter[k], col_litter[k]] +
    beta[4] * mL[row_litter[k], col_litter[k]] +
    beta[5] * mL[row_litter[k], col_litter[k]]^2 +
    beta[6] * mAgeY[row_litter[k], col_litter[k]] * DOY[row_litter[k], col_litter[k]] +
    beta[7] * mSpUnk[row_litter[k]] +
    beta[8] * mSpPel[row_litter[k]] +
    eta[col_litter[k]]

```

```

log(q[k, 3]) <- beta[9] * mAgeY[row_litter[k], col_litter[k]] +
  beta[10] * mAgeM[row_litter[k], col_litter[k]] +
  beta[11] * mAge0[row_litter[k], col_litter[k]] +
  beta[12] * mL[row_litter[k], col_litter[k]]

LS[row_litter[k], col_litter[k]] ~ dcat(s[k, 1:3])
for (i in 1:3) {
  s[k, i] <- q[k, i]/sum(q[k, 1:3])
}

# Girth
mu_mG[k] <- gamma[1] * mAgeY[row_litter[k], col_litter[k]] +
  gamma[2] * mAgeM[row_litter[k], col_litter[k]] +
  gamma[3] * mAge0[row_litter[k], col_litter[k]] +
  gamma[4] * mL[row_litter[k], col_litter[k]] +
  gamma[5] * DOY[row_litter[k], col_litter[k]] +
  gamma[6] * LS2[row_litter[k], col_litter[k]] +
  gamma[7] * LS3[row_litter[k], col_litter[k]] +
  gamma[8] * mSpUnk[row_litter[k]] +
  gamma[9] * mSpPel[row_litter[k]] +
  rho[col_litter[k]]
mG[row_litter[k], col_litter[k]] ~ dnorm(mu_mG[k], sd = sigma_xi)
}

# Cub mass
for (k in 1:n_cubs) {

  mu_M[k] <- delta[1] * LS1[mother[k], col_cub[k]] * mAgeY[mother[k], col_cub[k]] +
    delta[2] * LS1[mother[k], col_cub[k]] * mAgeM[mother[k], col_cub[k]] +
    delta[3] * LS1[mother[k], col_cub[k]] * mAge0[mother[k], col_cub[k]] +

    delta[4] * LS1[mother[k], col_cub[k]] * mL[mother[k], col_cub[k]] +
    delta[5] * LS1[mother[k], col_cub[k]] * mG[mother[k], col_cub[k]] +
    delta[6] * LS1[mother[k], col_cub[k]] * DOY[mother[k], col_cub[k]] +
    delta[7] * LS1[mother[k], col_cub[k]] * Sex[k] +
    delta[8] * LS1[mother[k], col_cub[k]] * mSpUnk[mother[k]] +
    delta[9] * LS1[mother[k], col_cub[k]] * mSpPel[mother[k]] +

    delta[10] * LS2[mother[k], col_cub[k]] * mAgeY[mother[k], col_cub[k]] +
    delta[11] * LS2[mother[k], col_cub[k]] * mAgeM[mother[k], col_cub[k]] +
    delta[12] * LS2[mother[k], col_cub[k]] * mAge0[mother[k], col_cub[k]] +

    delta[13] * LS3[mother[k], col_cub[k]] * mAgeY[mother[k], col_cub[k]] +
    delta[14] * LS3[mother[k], col_cub[k]] * mAgeM[mother[k], col_cub[k]] +
    delta[15] * LS3[mother[k], col_cub[k]] * mAge0[mother[k], col_cub[k]] +

    delta[16] * (LS2[mother[k], col_cub[k]] + LS3[mother[k], col_cub[k]]) * mL[mother[k], col_cub[k]] +
    delta[17] * (LS2[mother[k], col_cub[k]] + LS3[mother[k], col_cub[k]]) * mG[mother[k], col_cub[k]] +
    delta[18] * (LS2[mother[k], col_cub[k]] + LS3[mother[k], col_cub[k]]) * DOY[mother[k], col_cub[k]] +
    delta[19] * (LS2[mother[k], col_cub[k]] + LS3[mother[k], col_cub[k]]) * Sex[k] +
    delta[20] * (LS2[mother[k], col_cub[k]] + LS3[mother[k], col_cub[k]]) * mSpUnk[mother[k]] +
    delta[21] * (LS2[mother[k], col_cub[k]] + LS3[mother[k], col_cub[k]]) * mSpPel[mother[k]] +

```

```

    nu[col_cub[k]]

    M[k] ~ dnorm(mu_M[k], sd = sigma_epsilon)
  }

  for (i in 1:n_ind) {
    for (t in f[i]:(n_year-1)) {
      # Survival
      logit(phi[i, t]) <-
        theta[1] * Age0[i, t] * mAgeY[mother[i], t] +
        theta[2] * Age0[i, t] * mAgeM[mother[i], t] +
        theta[3] * Age0[i, t] * mAge0[mother[i], t] +

        theta[4] * Age0[i, t] * M[i] +
        theta[5] * Age0[i, t] * (LS2[mother[i], t] + LS3[mother[i], t]) +
        theta[6] * Age0[i, t] * mL[mother[i], t] +
        theta[7] * Age0[i, t] * mG[mother[i], t] +
        theta[8] * Age0[i, t] * DOY[mother[i], t] +
        theta[9] * Age0[i, t] * Sex[i] +
        theta[10] * Age0[i, t] * mSpUnk[mother[i]] +
        theta[11] * Age0[i, t] * mSpPel[mother[i]] +

        theta[12] * Age1[i, t] +
        theta[13] * Age2[i, t] +
        theta[14] * Age3_4[i, t] +
        theta[15] * Age5_19[i, t] +
        theta[16] * Age20[i, t] +

        theta[17] * (1 - Age0[i, t]) * Sex[i] +
        theta[18] * ((1 - Age0[i, t]) * (1 - Sex[i]) * mSpUnk[i] +
                     Age1[i, t] * Sex[i] * mSpUnk[mother[i]]) +
        theta[19] * ((1 - Age0[i, t]) * (1 - Sex[i]) * mSpPel[i] +
                     Age1[i, t] * Sex[i] * mSpPel[mother[i]])

      # Effect of sex = male f
      # Effect of space use = NA
      # Effect of maternal space use
      # Effect of space use = pelagic
      # Effect of maternal space use

      # Recapture
      logit(p[i, t]) <- lambda[1] +
        lambda[2] * (mSpUnk[i] * (1 - Sex[i]) +
                     mSpUnk[mother[i]] * Sex[i] * (Age0[i, t+1] + Age1[i, t+1] + Age2[i, t+1])) + # all N
        lambda[3] * (mSpPel[i] * (1 - Sex[i]) +
                     mSpPel[mother[i]] * Sex[i] * (Age0[i, t+1] + Age1[i, t+1] + Age2[i, t+1])) + # all p
        lambda[4] * Sex[i] * (Age3_4[i, t+1] + Age5_19[i, t+1] + Age20[i, t+1]) +
        omega[t]
    }
  }

  for (i in 1:n_ind) {
    # latent state at the first capture
    z[i, f[i]] <- 1

    for (t in (f[i]+1):n_year) {
      # State process

```

```

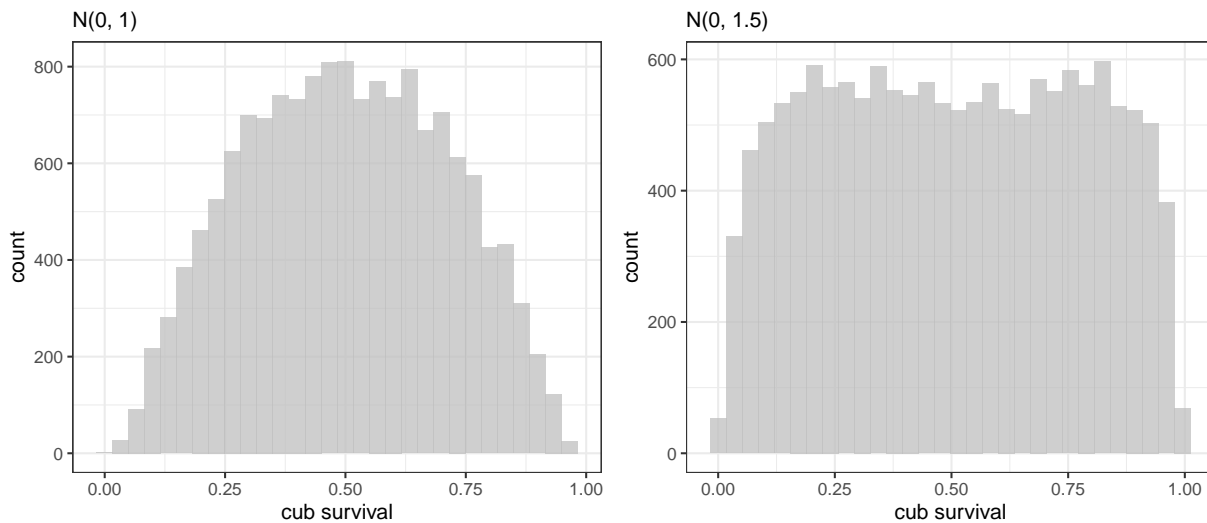
z[i, t] ~ dbern(phi[i, t-1] * z[i, t-1])

# Observation process
y[i, t] ~ dbern(p[i, t-1] * z[i, t])

} # t
} # i
})

```

Here, I use a relatively informative prior for theta[2] (survival of cubs of middle-aged females) because otherwise, I get unrealistically high survival (mean = 0.77). This informative prior is $N(0, 1)$, to compare to the less informative $N(0, 1.5)$:



2. Process the data

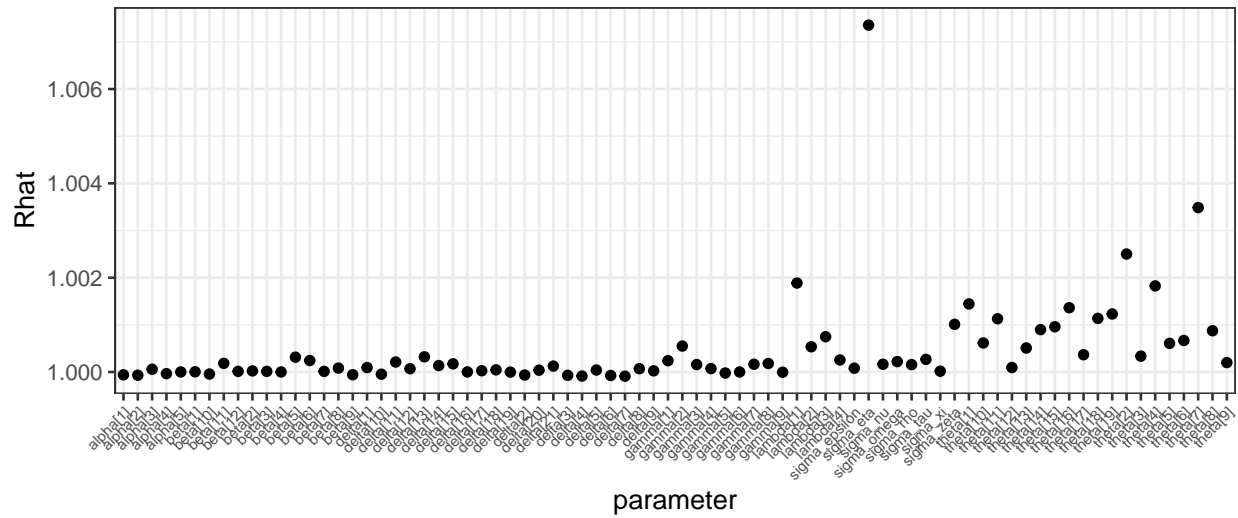
Using litter_size as value column: use value.var to override.

B. Inspect the results

1. Trace plots

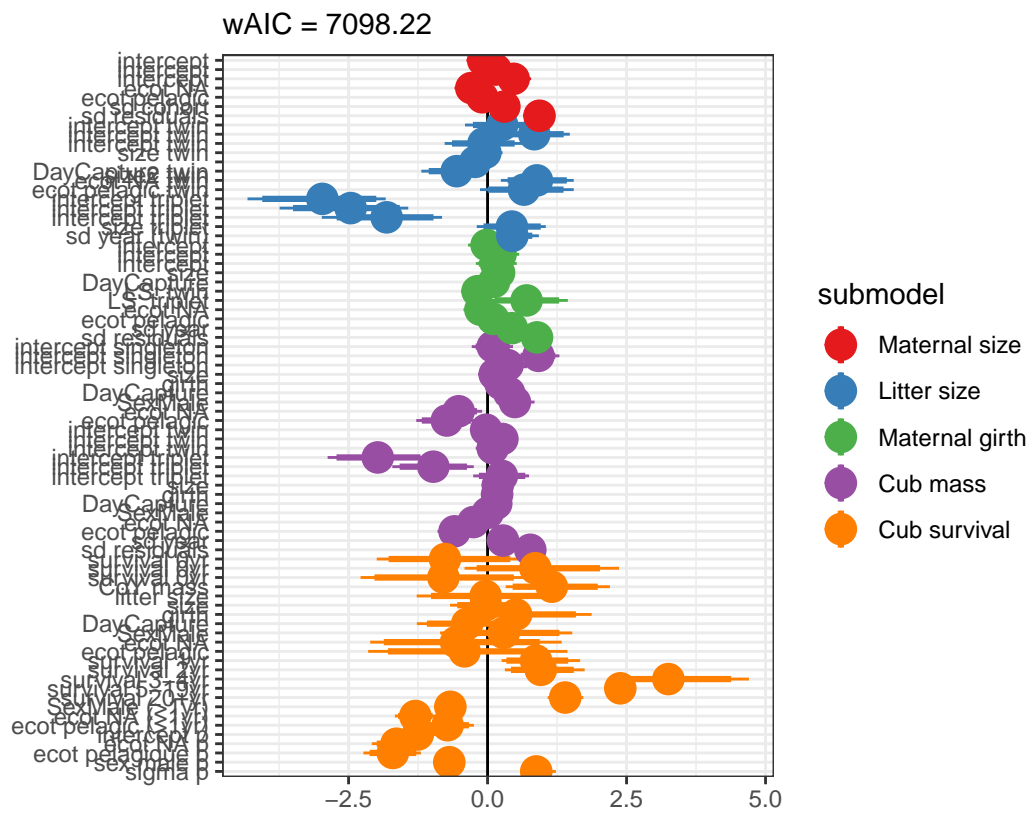
2. Rhat

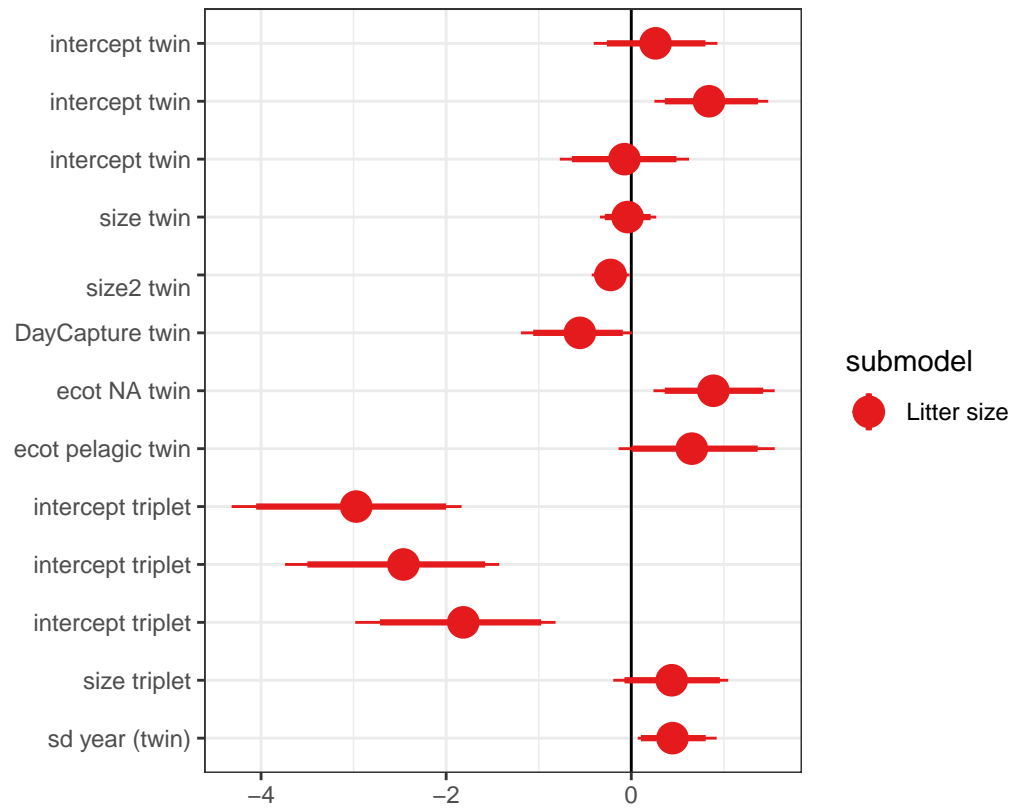
Calculate the Rhat value of each parameter, to make sure the chains have converged (Rhat < 1.1)

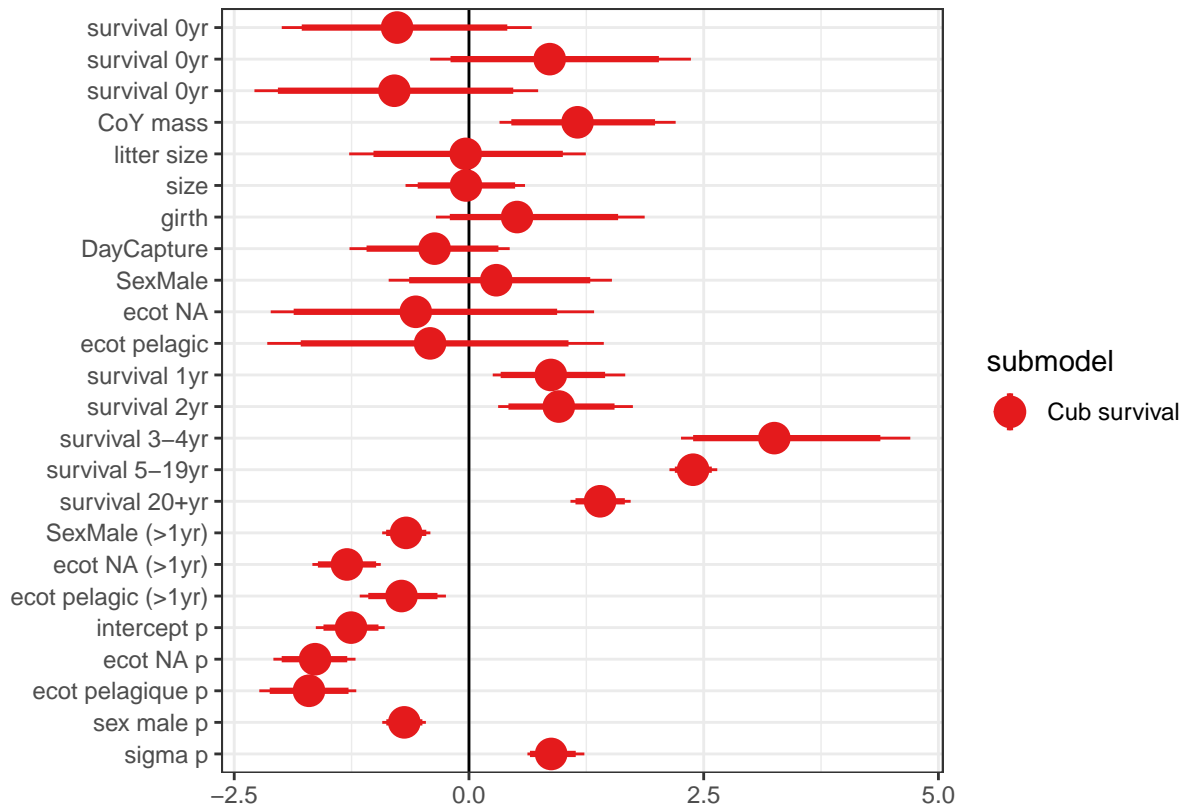


All Rhat are < 0.01

3. Caterpillar plots

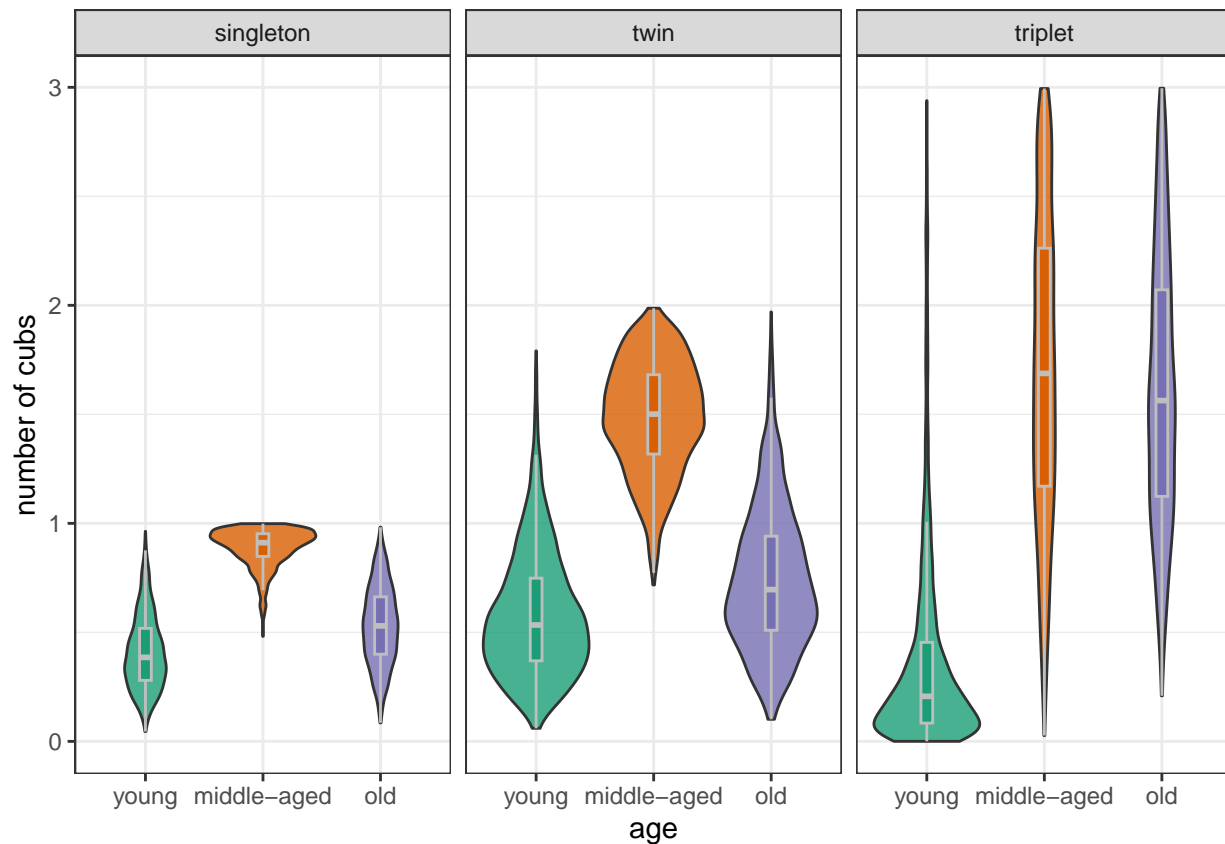






C. Compute residuals and predictions

1. Predict number of surviving CoYs by litter size and maternal age



2. Compute residuals

The residuals computed here will be used to plot the observations corrected for other variables for the figures.

a. Cub mass

b. Cub mass for plot length

c. Cub mass for plot girth

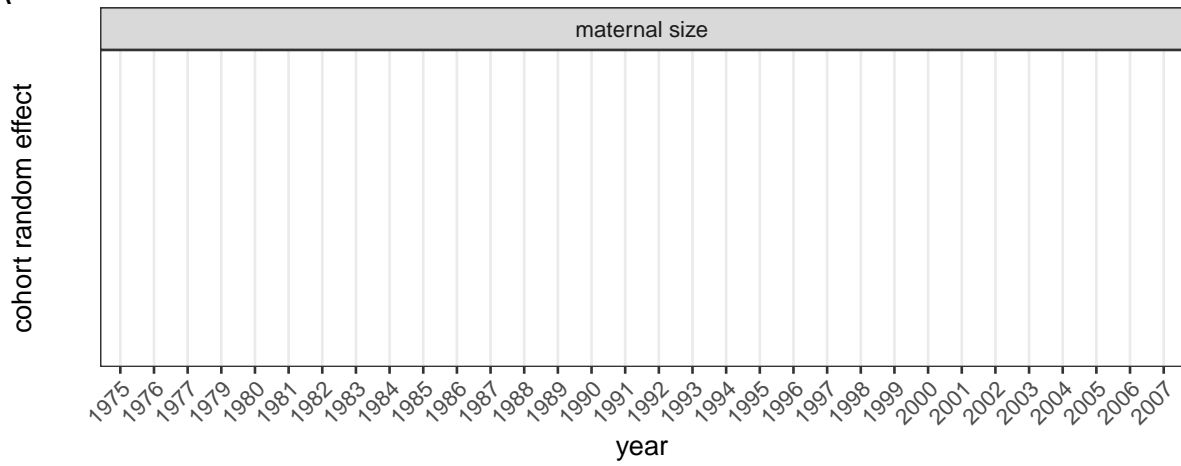
3. Plot random effects

Here I convert the random effects to the natural scale for continuous variables, and to the probability scale for probabilities.

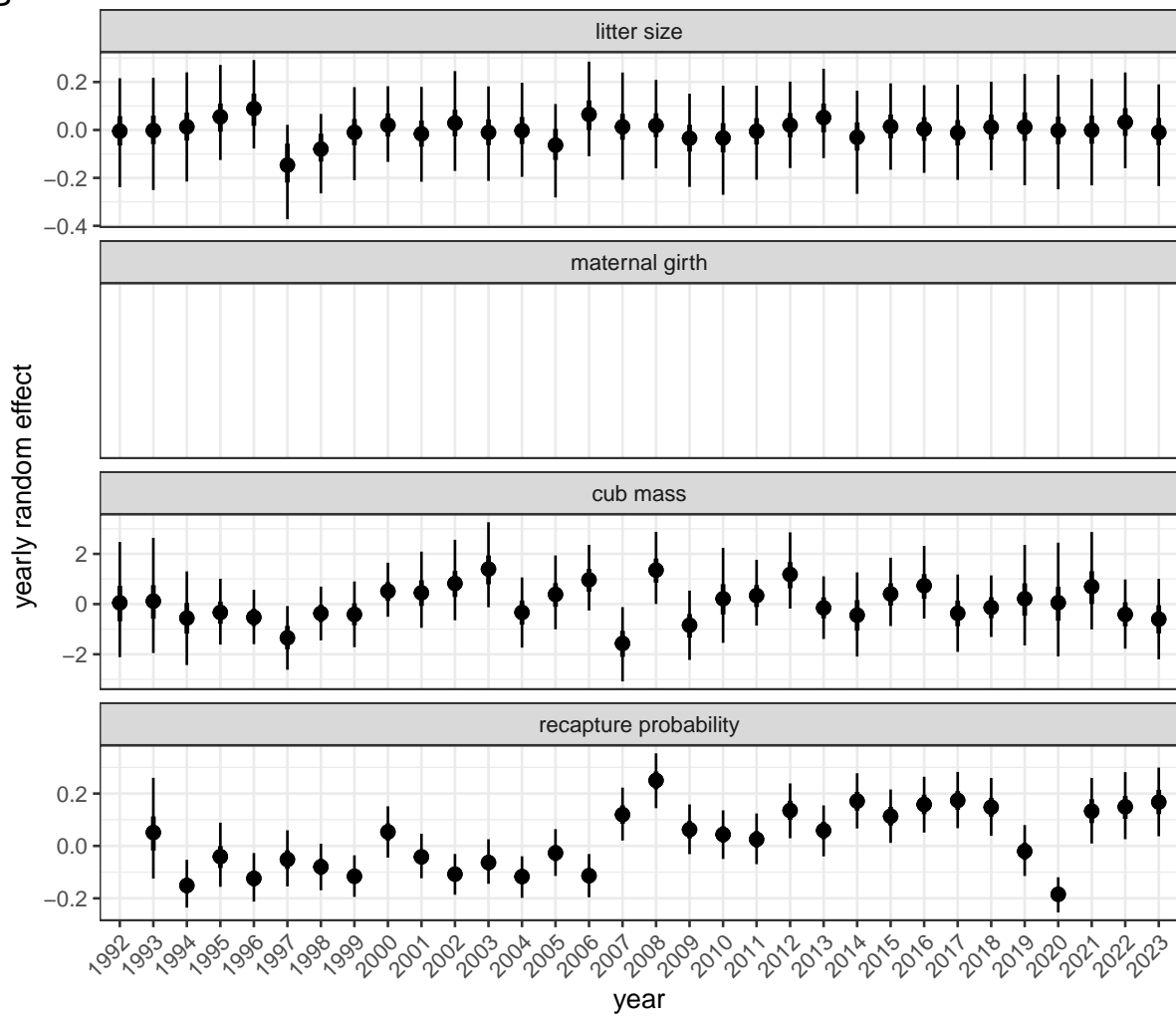
```
## Warning: Removed 57600 rows containing non-finite values ('stat_summary()').  
## Warning in max(f): aucun argument pour max ; -Inf est renvoyé  
## Warning: Computation failed in 'stat_summary()'  
## Caused by error in 'seq_len()':  
## ! l'argument doit être convertible automatiquement en un entier non négatif  
## Warning: Removed 57600 rows containing non-finite values ('stat_summary()').  
## Warning in max(f): aucun argument pour max ; -Inf est renvoyé
```

```
## Warning: Computation failed in 'stat_summary()'
## Caused by error in 'seq_len()':
## ! l'argument doit être convertible automatiquement en un entier non négatif
## Warning: Removed 59400 rows containing non-finite values ('stat_summary()').
## Removed 59400 rows containing non-finite values ('stat_summary()').
```

A



B



D. Compute pd and other quantities

1. Pd and effect sizes

a. Maternal length

```
## [1] 178 213
## [1] 1.40679
##      2.5%      97.5%
## -0.4167219  3.2173274
## [1] 0.9372778
## [1] 2.106713
##      2.5%      97.5%
## -0.1090095  4.3281067
## [1] 0.9692778
## [1] 3.513503
##      2.5%      97.5%
## 1.180246 5.859049
## [1] 0.9984444
## [1] -0.2922503
##      2.5%      97.5%
## -0.576971752 -0.006194798
## [1] 0.9774444
## [1] -0.09573022
##      2.5%      97.5%
## -0.4653858  0.2794673
## [1] 0.6937222
## [1] 0.1034846
##      2.5%      97.5%
## 0.003769299 0.266616013
```

b. Litter size

```
## [1] 1.683128
## [1] 0.5246046
## [1] 0.1238265
##      2.5%      97.5%
## -0.02789276  0.28134005
## [1] 0.9426667
## [1] 0.2311631
##      2.5%      97.5%
## 0.04933139 0.40490237
## [1] 0.9928889
```

```

## [1] 0.1073366
##      2.5%      97.5%
## -0.09022869  0.29710050
## [1] 0.9928889
## [1] -0.2233224
##      2.5%      97.5%
## -0.44226679 -0.01357876
## [1] 0.9802222
## [1] 0.9671667
## [1] 0.9968333
## [1] 0.9408889
## [1] 0.2435904
##      2.5%      97.5%
## 0.00506527 0.83786956

```

c. Maternal girth

```

## [1] 94 135
## [1] 1.75087
##      2.5%      97.5%
## -0.1581915  3.6946741
## [1] 0.9627222
## [1] 0.5389617
##      2.5%      97.5%
## -1.867172  2.945123
## [1] 0.672
## [1] 1.211908
##      2.5%      97.5%
## -1.20585  3.62550
## [1] 0.8360556
## [1] 1.31124
##      2.5%      97.5%
## -0.5003124  3.1149878
## [1] 0.9257222
## [1] -5.056817
##      2.5%      97.5%
## -10.1877712  0.1005879
## [1] 0.9735556
## [1] 0.9995
## [1] 0.9495

```

```
## [1] 0.7733889
## [1] 0.6990556
## [1] 0.2029323
##      2.5%      97.5%
## 0.06546549 0.43956391
```

d. Cub mass

```
## [1] 3.00 31.25
## [1] 15.03992
## [1] 12.61359
## [1] 10.27669
## [1] 1.193169
##      2.5%      97.5%
## 1.078368 1.316664
## [1] 0.9998889
## [1] 1.468266
##      2.5%      97.5%
## 1.270327 1.689124
## [1] 1
## [1] 1.231172
##      2.5%      97.5%
## 1.089171 1.383222
## [1] 0.9998889
## [1] 1.302466
##      2.5%      97.5%
## 1.139436 1.487960
## [1] 1
## [1] 1.196805
##      2.5%      97.5%
## 1.032235 1.379900
## [1] 0.9915556
## [1] 1.091756
##      2.5%      97.5%
## 0.9390356 1.2591582
## [1] 0.8769444
## [1] 1.098853
##      2.5%      97.5%
## 1.027109 1.174189
## [1] 0.9969444
```

```

## [1] 1.059594
##      2.5%      97.5%
## 0.9693416 1.1558857
## [1] 0.8985556
## [1] 1.038683
##      2.5%      97.5%
## 0.9436946 1.1397700
## [1] 0.7757222
## [1] 0.1908134
##      2.5%      97.5%
## 0.02397041 0.36598753
## [1] 0.9868333
## [1] 0.1384435
##      2.5%      97.5%
## -0.05778246 0.33205612
## [1] 0.9195556
## [1] 0.05236989
##      2.5%      97.5%
## -0.1328365 0.2416246
## [1] 0.7080556
## [1] 0.9378889
## [1] 0.9995556
## [1] 0.9951667
## [1] 0.9997778
## [1] 1
## [1] 0.9973889
## [1] 1.173139
##      2.5%      97.5%
## 1.050121 1.307514
## [1] 1
## [1] 0.9931111
## [1] 0.9818889
## [1] 0.9964444
## [1] 0.9999444
## [1] 0.9978889
## [1] 0.5064444
## [1] 0.08095135

```

```
##      2.5%      97.5%
## 0.02033751 0.18476288
```

e. Litter mass

```
## singleton      twin   triplet
## 15.03992 25.22717 30.83007

## [1] 1.68056

##      2.5%      97.5%
## 1.518991 1.854655

## [1] 1

## [1] 1.222878

##      2.5%      97.5%
## 1.084425 1.377194

## [1] 0.9992222
```

f. Cub survival

```
## [1] 0.9967778
## [1] 0.3487018

##      2.5%      97.5%
## 0.03995184 0.63904210

## [1] 0.9855556
## [1] 0.351673

##      2.5%      97.5%
## 0.000958976 0.681853722

## [1] 0.9755
## [1] 0.002971179

##      2.5%      97.5%
## -0.3504390 0.3507407

## [1] 0.5092222
## [1] 0.5208333
## [1] -0.02778369
## [1] 0.5378333
## [1] -0.03442667
## [1] 0.8321667
## [1] 0.7951667
## [1] 0.6773333
## [1] 0.7650556
## [1] 0.6895556
```


g. Recapture probability

```
## [1] 0.2234877
##      2.5%      97.5%
## 0.1651372 0.2905332
## [1] 0.05424124
##      2.5%      97.5%
## 0.03151335 0.08687671
## [1] 0.05086043
##      2.5%      97.5%
## 0.02716686 0.08462128
## [1] 0.1269051
##      2.5%      97.5%
## 0.09006323 0.17069503
## [1] 0.8724887
##      2.5%      97.5%
## 0.619182 1.224541
```

h. Productivity by litter size

```
## [1] 0.1711728
##      2.5%      97.5%
## -0.2482271 0.6812235
## [1] 0.7722222
## [1] 0.599932
##      2.5%      97.5%
## 0.1520810 0.9442597
## [1] 0.9944444
## [1] 0.2095511
##      2.5%      97.5%
## -0.2878088 0.7940797
## [1] 0.7894444
## [1] 0.2071466
##      2.5%      97.5%
## -0.8836952 0.9143302
## [1] 0.8172222
## [1] -0.2158487
##      2.5%      97.5%
## -1.1130376 0.9472112
## [1] 0.6433333
## [1] -0.8712762
```

```
##      2.5%      97.5%
## -1.7891654 -0.1388365
## [1] 0.9944444
```

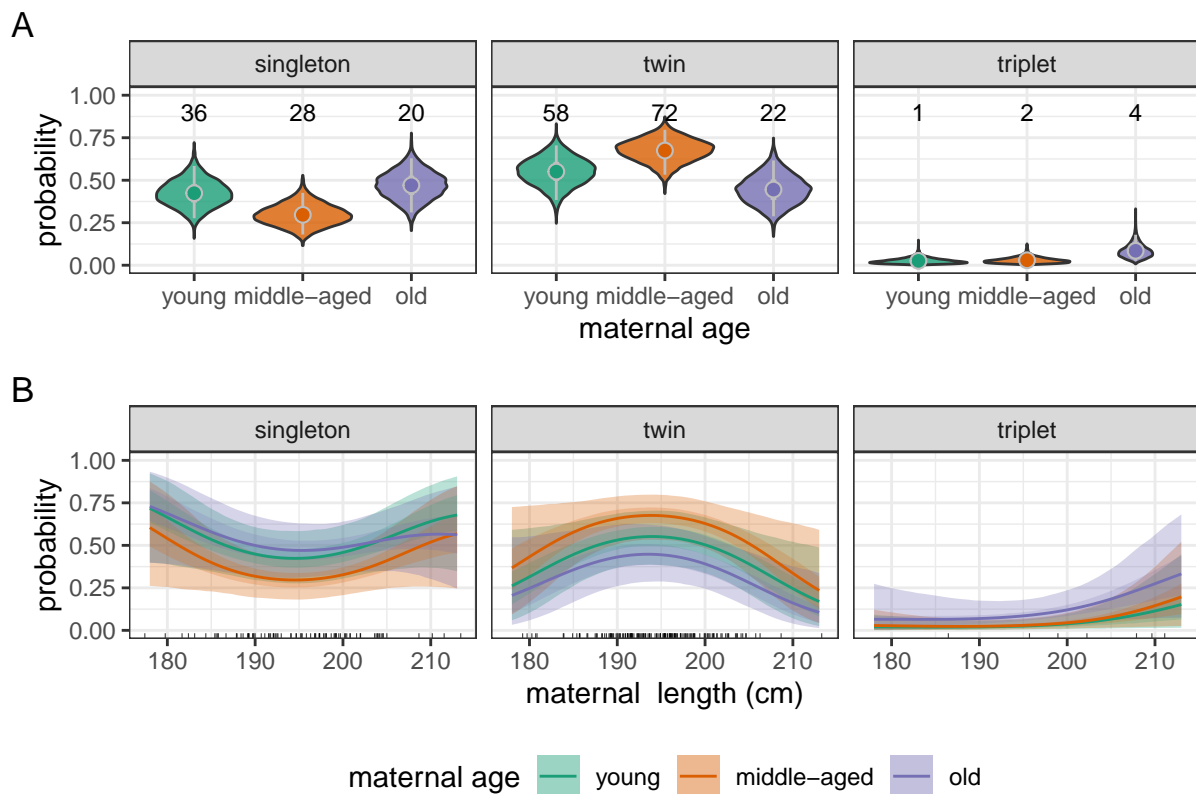
2. Variance explained by model

```
## [1] 0.1249375
## [1] 0.2066141
## [1] 0.4091651
```

E. Plot main figures

1. Figure 2: Effects on litter size

```
## 'summarise()' has grouped output by 'var', 'litter_size'. You can override
## using the '.groups' argument.
```

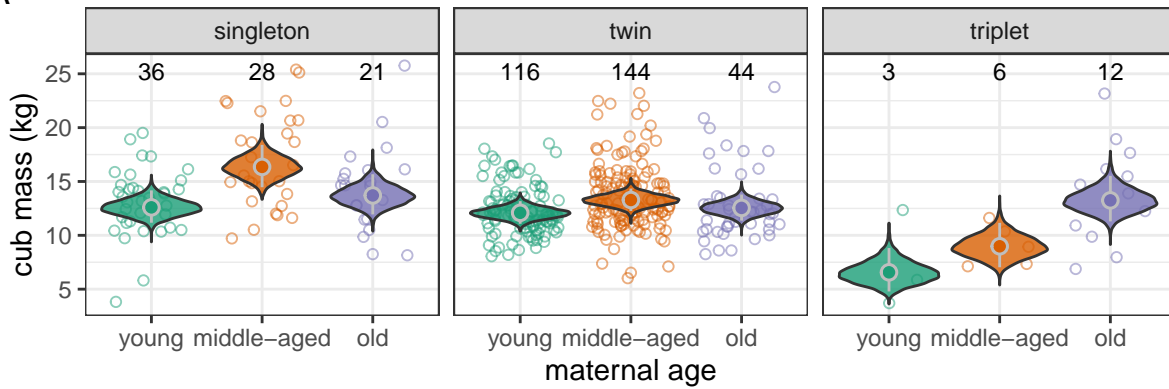


2. Figure 3: Determinants of cub mass

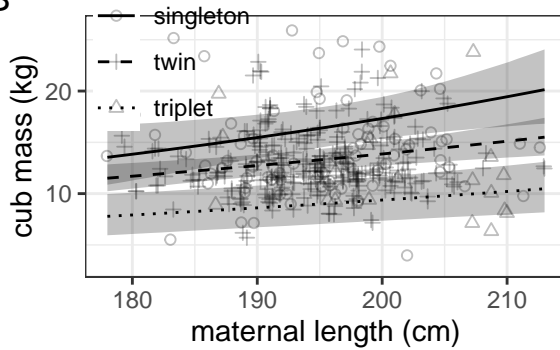
```
## 'summarise()' has grouped output by 'var'. You can override using the '.groups'
## argument.
## 'summarise()' has grouped output by 'var'. You can override using the '.groups'
## argument.
## Warning: Removed 1 rows containing missing values ('geom_point()').
```

```
## Removed 1 rows containing missing values ('geom_point()').
```

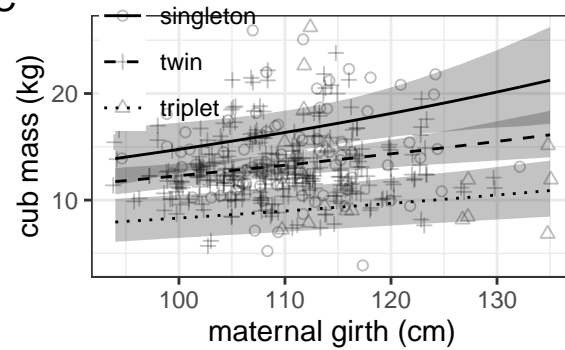
A



B



C



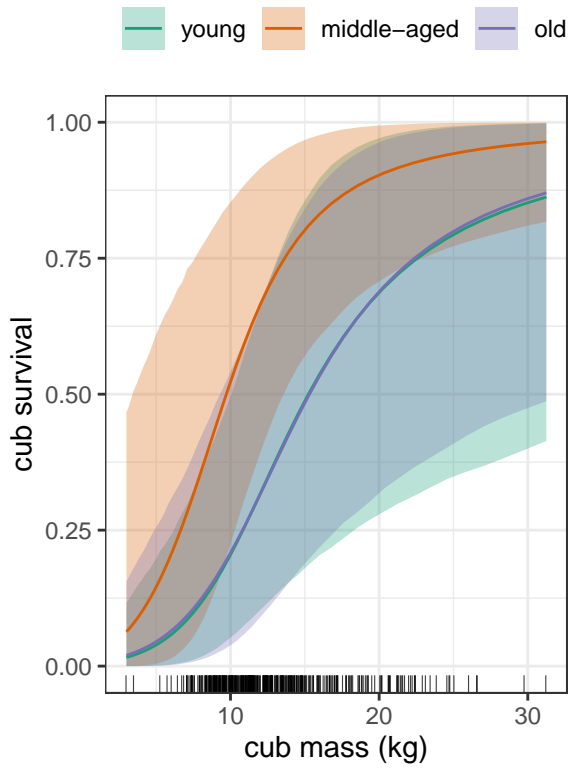
```
## Warning: Removed 1 rows containing missing values ('geom_point()').
```

```
## Removed 1 rows containing missing values ('geom_point()').
```

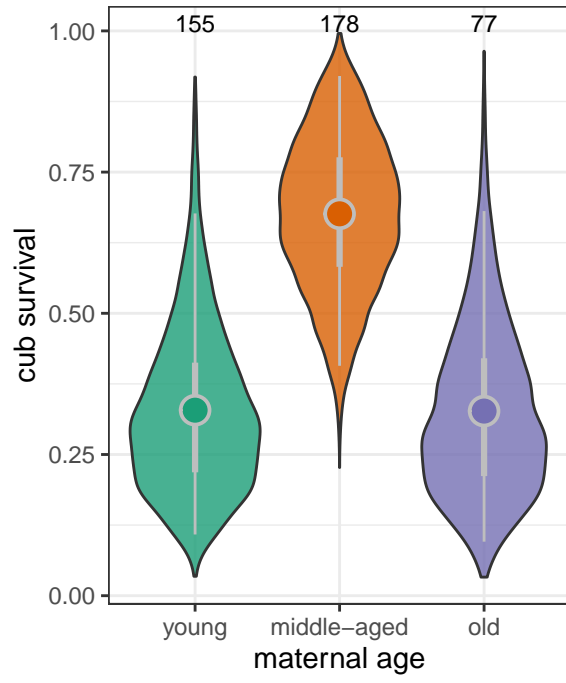
3. Figure 4: Determinants of cub survival

```
## 'summarise()' has grouped output by 'var'. You can override using the '.groups'
## argument.
```

A



B



4. Figure 6: Productivity by litter size

