

# R code PA-CR model

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

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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
for (i in 1: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])
}

LS1[row_litter[k], col_litter[k]] <- 0.5 * (LS[row_litter[k], col_litter[k]] - 2)*(LS[row_litter[k],
LS2[row_litter[k], col_litter[k]] <- -1 * (LS[row_litter[k], col_litter[k]] - 1)*(LS[row_litter[k],
LS3[row_litter[k], col_litter[k]] <- 0.5 * (LS[row_litter[k], col_litter[k]] - 1)*(LS[row_litter[k],

# 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] * (-1) * (LS[row_litter[k], col_litter[k]] - 1)*(LS[row_litter[k], col_litter[k]] - 3) +
  gamma[7] * 0.5 * (LS[row_litter[k], col_litter[k]] - 1)*(LS[row_litter[k], col_litter[k]] - 2) +
  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] * (-1 * (LS[mother[i], t] - 1) * (LS[mother[i], t] - 3) + # LS2
        0.5 * (LS[mother[i], t] - 1) * (LS[mother[i], t] - 2)) + # LS3
        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] + Age3_4[i, t]) +
        theta[14] * Age5_19[i, t] +
        theta[15] * Age20[i, t] +

        theta[16] * (1 - Age0[i, t]) * Sex[i] + # Effect of sex = male f
        theta[17] * ((1 - Age0[i, t]) * (1 - Sex[i]) * mSpUnk[i] + # Effect of space use = NA
        Age1[i, t] * Sex[i] * mSpUnk[mother[i]]) + # Effect of maternal space use
        theta[18] * ((1 - Age0[i, t]) * (1 - Sex[i]) * mSpPel[i] + # Effect of space use = pelagic
        Age1[i, t] * Sex[i] * mSpPel[mother[i]]) + # Effect of maternal space use

      # Recapture
      logit(p[i, t]) <- lambda[1] +
        lambda[2] * (mSpUnk[i] * (1 - Sex[i]) + # all N
        mSpUnk[mother[i]] * Sex[i] * (Age1[i, t+1] + Age2[i, t+1])) + # all male dependence
        lambda[3] * (mSpPel[i] * (1 - Sex[i]) + # all p
        mSpPel[mother[i]] * Sex[i] * (Age1[i, t+1] + Age2[i, t+1])) + # all male dependence
        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
})

```

## 2. Process the data

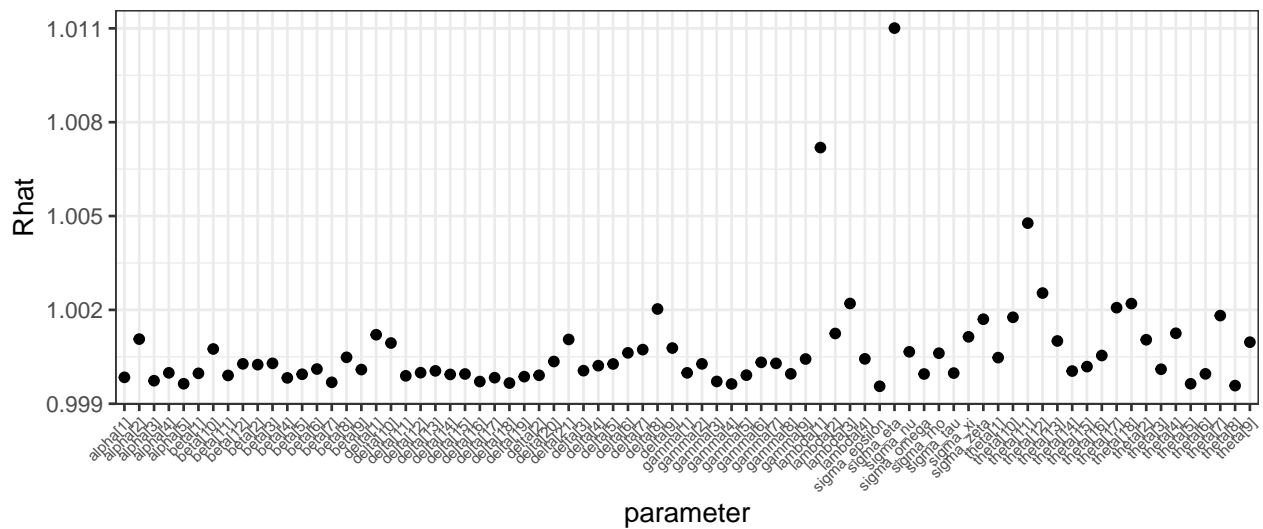
## 3. Run the model

## B. Inspect the results

### 1. Diagnostic plots

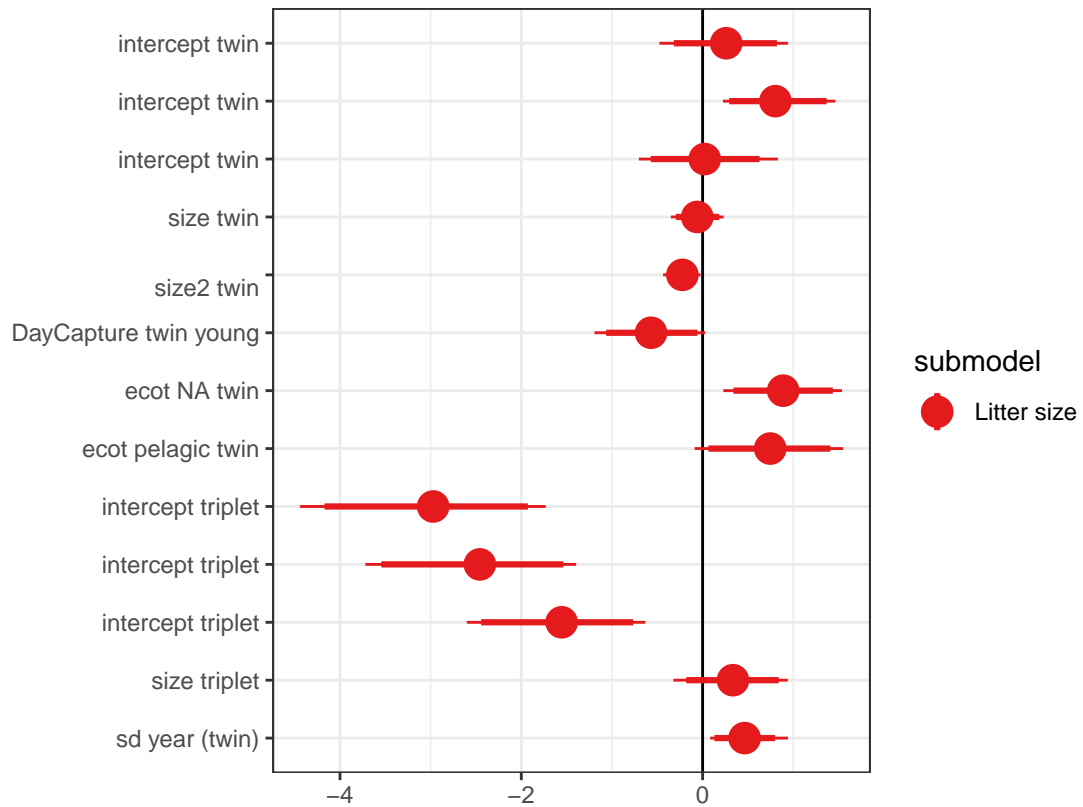
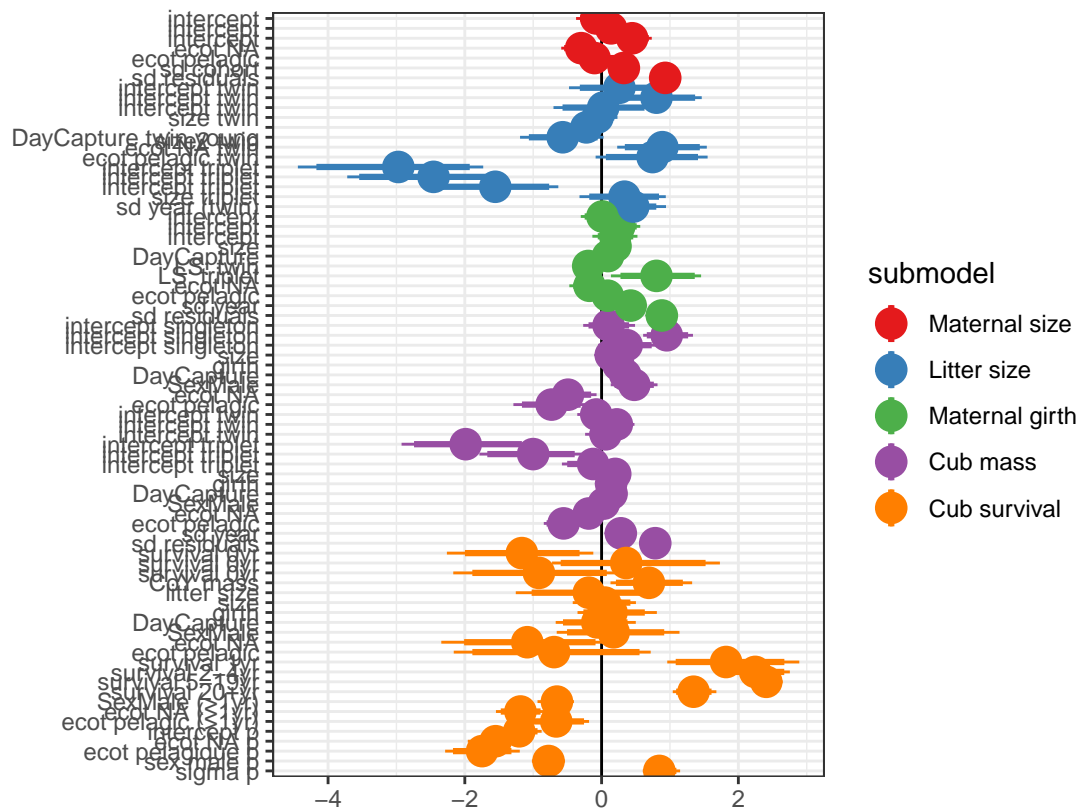
### 2. Rhat

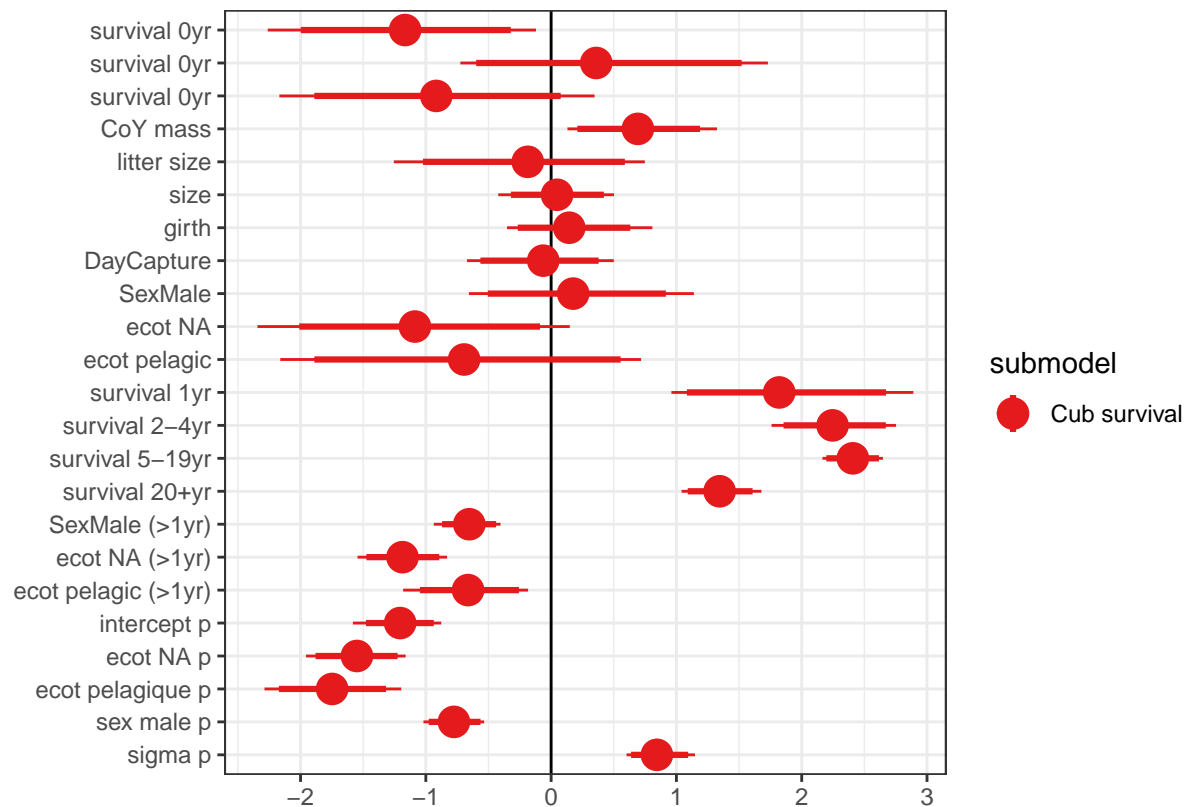
Calculate the Rhat value of each parameter, to make sure the chains have converged ( $Rhat < 1.1$ )



All Rhat are  $< 1.1$

### 3. Caterpillar plots





## C. Compute residuals

The residuals computed here will be used to plot the observations corrected for variables other than that on the x axis for the figures.

a. Cub mass for Fig. 2A

b. Cub mass for Fig. 2B

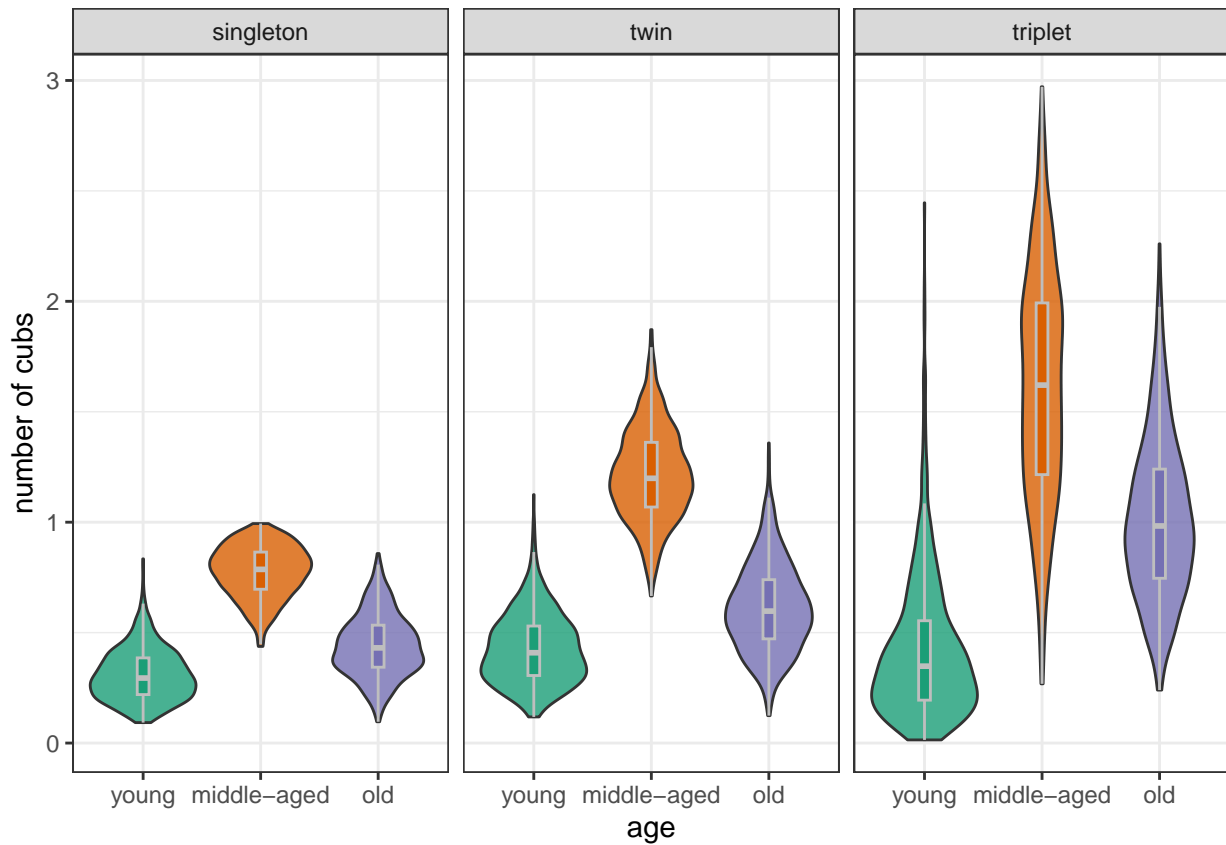
c. Cub mass for Fig. 2C

## D. Predict number of surviving cubs

Let's predict the number of surviving cubs by litter size and maternal age

We need to account for the fact that females who produce singleton/twin/triplet litters are not the same size on average. Let's compute the size of females corrected for the cohort random effect and the effect of the space-use strategy:

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



## E. Compute probabilities of direction (pd)

### 1. Pd and effect sizes

#### a. Maternal length

```
## [1] 178 213
## [1] 1.37871
##      2.5%      97.5%
## -0.4264643  3.1591493
## [1] 0.933
## [1] 1.960729
##      2.5%      97.5%
## -0.1311223  4.0995814
## [1] 0.966
## [1] 3.339439
##      2.5%      97.5%
## 1.121562  5.605809
## [1] 0.9985
## [1] -0.2983274
##      2.5%      97.5%
```



```
## -0.57634196 -0.02061026
## [1] 0.98125
## [1] -0.1042238
##      2.5%      97.5%
## -0.4529151  0.2664911
## [1] 0.70825
## [1] 0.1133352
##      2.5%      97.5%
## 0.02402668 0.27528545
```

#### **b. Litter size**

```
## [1] 1.688
## [1] 0.5289377
## [1] 0.1224279
##      2.5%      97.5%
## -0.03107809 0.27701748
## [1] 0.93875
## [1] 0.2090952
##      2.5%      97.5%
## 0.03307916 0.38189636
## [1] 0.99025
## [1] 0.08666729
##      2.5%      97.5%
## -0.1038202 0.2738608
## [1] 0.99025
## [1] -0.2226712
##      2.5%      97.5%
## -0.44503442 -0.01327327
## [1] 0.983
## [1] 0.97075
## [1] 0.9965
## [1] 0.96
## [1] 0.2593803
##      2.5%      97.5%
## 0.007015413 0.832116116
```

#### **c. Maternal girth**

```
## [1] 94 135
## [1] 1.777517
```

```

##          2.5%          97.5%
## -0.08527602  3.73335906

## [1] 0.9675
## [1] 0.4558738

##          2.5%          97.5%
## -1.855995  2.802063

## [1] 0.648
## [1] 1.321643

##          2.5%          97.5%
## -1.065840  3.786976

## [1] 0.8545
## [1] 1.436735

##          2.5%          97.5%
## -0.4406985  3.1938666

## [1] 0.93675
## [1] -5.784318

##          2.5%          97.5%
## -10.7086933 -0.9563209

## [1] 0.9885
## [1] 0.999
## [1] 0.907
## [1] 0.87075
## [1] 0.66075
## [1] 0.1920406

##          2.5%          97.5%
## 0.06021129 0.40962968

```

#### d. Cub mass

```

## [1] 3.00 31.25
## [1] 1.220548

##          2.5%          97.5%
## 1.110384 1.339997

## [1] 1
## [1] 1.48271

##          2.5%          97.5%
## 1.284317 1.699458

## [1] 1
## [1] 1.215447

##          2.5%          97.5%
## 1.070512 1.376433

```

```

## [1] 0.99975
## [1] 1.309397
##      2.5%      97.5%
## 1.143869 1.489855
## [1] 1
## [1] 1.201367
##      2.5%      97.5%
## 1.034060 1.388952
## [1] 0.99075
## [1] 1.093468
##      2.5%      97.5%
## 0.9428594 1.2618430
## [1] 0.875
## [1] 1.101892
##      2.5%      97.5%
## 1.024534 1.178438
## [1] 0.998
## [1] 1.054262
##      2.5%      97.5%
## 0.9651679 1.1496110
## [1] 0.878
## [1] 1.046729
##      2.5%      97.5%
## 0.9536279 1.1460931
## [1] 0.82325
## [1] 0.1975184
##      2.5%      97.5%
## 0.02568826 0.37502017
## [1] 0.989
## [1] 0.1511139
##      2.5%      97.5%
## -0.05238364 0.34621105
## [1] 0.93275
## [1] 0.04640455
##      2.5%      97.5%
## -0.1418984 0.2439453
## [1] 0.6885
## [1] 0.93675
## [1] 1

```

```

## [1] 0.99475
## [1] 0.99775
## [1] 1
## [1] 0.99625
## [1] 1.166981
##      2.5%    97.5%
## 1.043683 1.305583
## [1] 1
## [1] 0.99025
## [1] 0.94575
## [1] 0.99475
## [1] 1
## [1] 0.9945
## [1] 0.63925
## [1] 0.08466851
##      2.5%    97.5%
## 0.02281089 0.18855145

```

#### e. Litter mass

```

## singleton      twin    triplet
## 15.38750 25.23169 31.24473
## [1] 1.642374
##      2.5%    97.5%
## 1.492541 1.801179
## [1] 1
## [1] 1.239089
##      2.5%    97.5%
## 1.089774 1.401199
## [1] 0.99975

```

#### f. Cub survival

```

## [1] 0.9925
## [1] 0.3280594
##      2.5%    97.5%
## 0.1088579 0.5735900
## [1] 0.995
## [1] 0.2787698
##      2.5%    97.5%
## 0.03098407 0.53984559
## [1] 0.985

```

```
## [1] -0.04928959
##      2.5%      97.5%
## -0.2751187  0.1624413
## [1] 0.66625
## [1] 0.62625
## [1] -0.1862317
## [1] 0.5825
## [1] 0.0472786
## [1] 0.6875
## [1] 0.5525
## [1] 0.64375
## [1] 0.9575
## [1] 0.83125
```

#### g. Recapture probability

```
## [1] 0.2313914
##      2.5%      97.5%
## 0.1737597 0.2942490
## [1] 0.06135659
##      2.5%      97.5%
## 0.03853024 0.09083818
## [1] 0.05151737
##      2.5%      97.5%
## 0.02829964 0.08469957
## [1] 0.1224796
##      2.5%      97.5%
## 0.08872552 0.16188407
## [1] 0.8484879
##      2.5%      97.5%
## 0.6062677 1.1740871
```

#### h. Productivity by litter size

```
## [1] 0.1174675
##      2.5%      97.5%
## -0.1926263 0.4087787
## [1] 0.8125
## [1] 0.4410225
##      2.5%      97.5%
## 0.1159444 0.7643456
## [1] 0.99125
```

```
## [1] 0.1699285
##      2.5%      97.5%
## -0.1706343  0.5126746
## [1] 0.8325
## [1] 0.005329859
##      2.5%      97.5%
## -0.6805737  0.4609637
## [1] 0.5775
## [1] -0.397805
##      2.5%      97.5%
## -1.1397305  0.4784175
## [1] 0.8125
## [1] -0.4021119
##      2.5%      97.5%
## -0.974152012  0.001475672
## [1] 0.97375
```

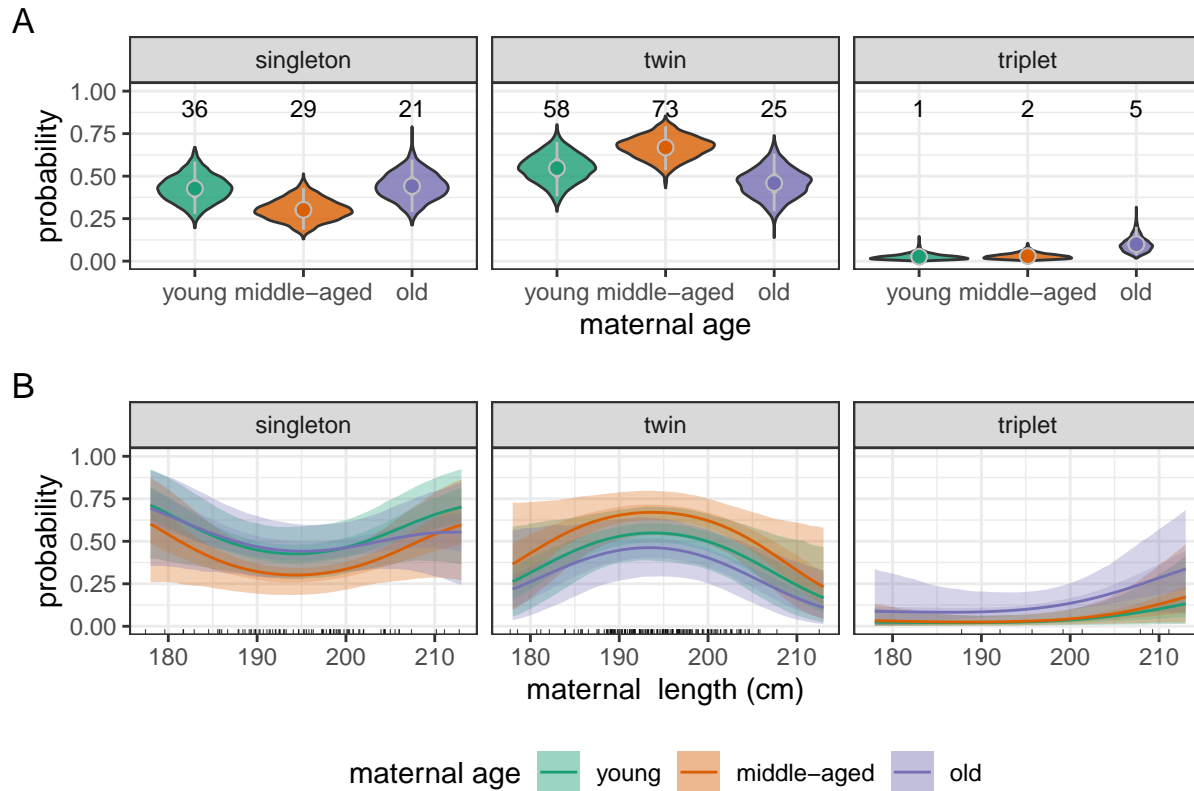
## 2. Variance explained by model

```
## [1] 0.132007
## [1] 0.2197837
## [1] 0.3834601
```

## F. 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.
```

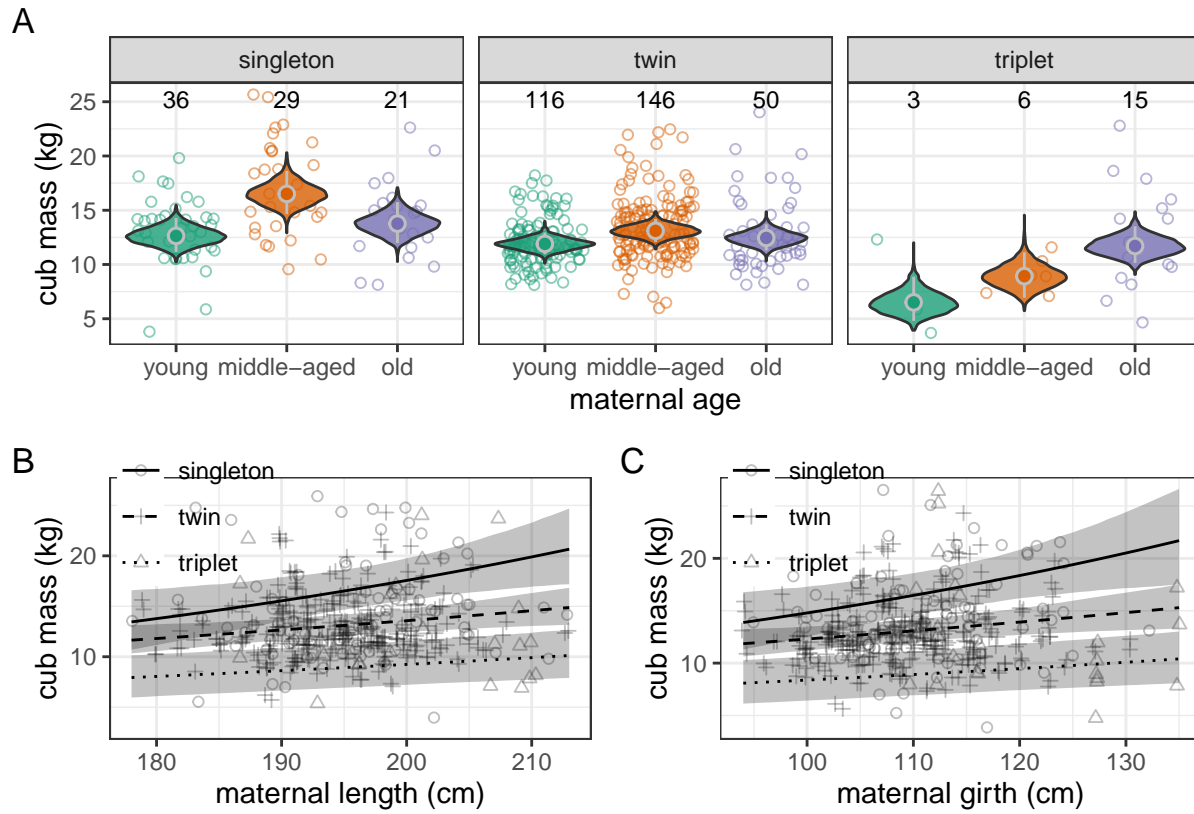


## 2. Figure 3: Determinants of cub mass

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

## Warning: A numeric 'legend.position' argument in 'theme()' was deprecated in ggplot2
## 3.5.0.
## i Please use the 'legend.position.inside' argument of 'theme()' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.

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

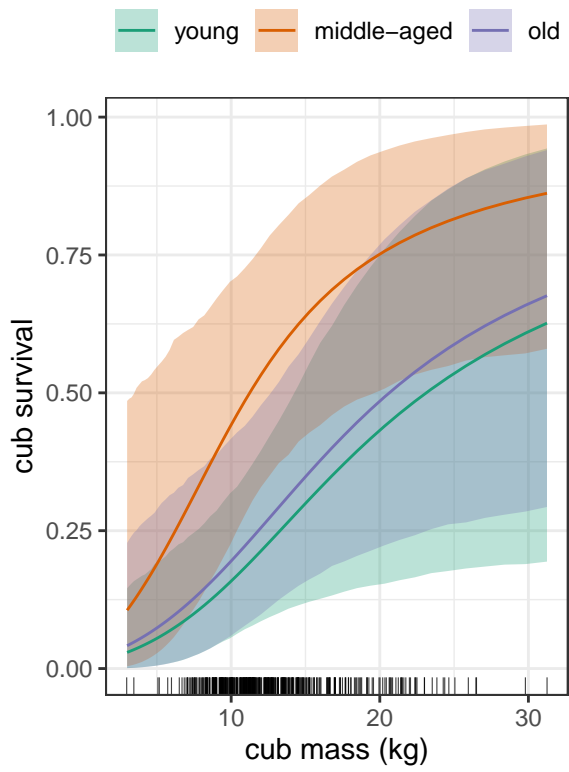


### 3. Figure 4: Determinants of cub survival

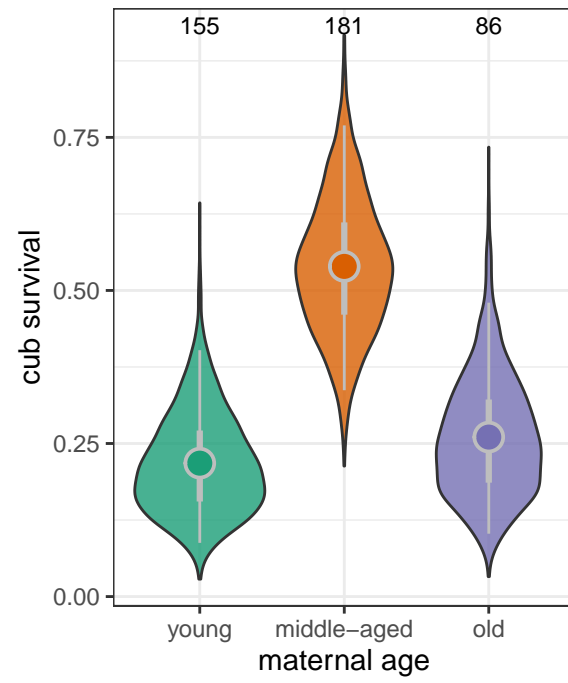
```
## 'summarise()' has grouped output by 'var'. You can override using the '.groups'
## argument.
```



A



B



4. Figure 6: Productivity by litter size

