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Supplementary file: Simulation study

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This is a simulation study included as a supplementary file of the paper titled: Multidecadal changes in home range characteristics of grey seals in a context of environmental changes and population growth in the Northwest Atlantic.

The goal of the simulation is to assess the capacity of the statistical approach used in the paper to tease apart inter- and intra-individual differences in home range characteristics, while accurately estimating the effects of population level variables, considering the data available. We use the example of home range area to illustrate how the model is able to achieve this.

Real case

Real data

The data comes from 123 grey seals captured in the Gulf of St-Lawrence (GSL) and equipped with satellite transmitters at 16 different deployment sites in the north, south and center of the GSL between 1992 and 2022. We extracted Argos locations from all transmitters, calculated each seal's monthly utilization distribution and estimated their monthly 95% home ranges. We then extracted information on the area, shape, and distribution of each monthly home range. See main text for additional details. Here we use the example of home range area in km^2 Figure 1.

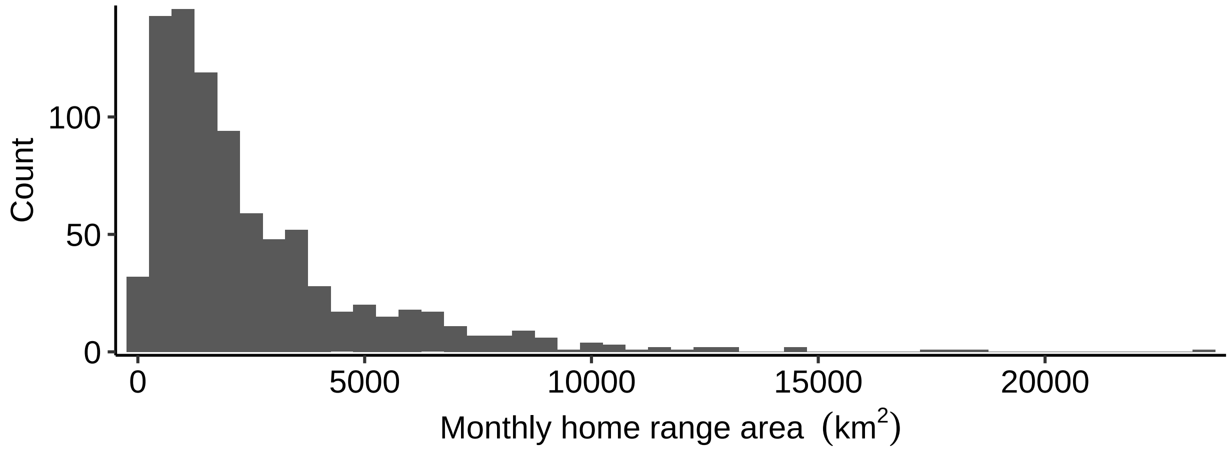

Figure 1: Distribution of monthly home range area in km^2 of grey seals in the Gulf of St-Lawrence between 1992 and 2022

Model with real data

We modeled temporal changes, population level effects and individual variation in home range characteristics using a Double Hierarchical Generalized Linear Model (DHGLM). With this type of model, we can specify fixed and random effects on the mean (*mu*) and the dispersion (*sigma*, i.e. residual variance) of the response variable. We fitted a random intercept of individual identity on both the mean and dispersion models. We could then estimate inter individual differences (i.e., individual differences in mean trait values) and intra individual variation (i.e., individuals' level of variability or dispersion). Code Block

```
# Write model formula
d_yr_area_form <- bf(
  # Mean model (mu)
  area ~ 0 + Intercept + scale(log(mean.loc.error)) + period +
    sexage + sexage:period + s(scale(deploy.yr), by = period) +
    (1|p|id) + (1|y|deploy.yr),
  # Dispersion model (sigma)
  sigma ~ 0 + Intercept + (1|p|id) + (1|y|deploy.yr),
  # Set the response distribution and link functions
  family = lognormal(link = "identity", link_sigma = "log"))

# Set model priors
d_yr_area_prior <- c(
  prior(lkj(1), class = "cor", group = "id"),
  prior(normal(7.7, 0.7), class = "b", coef = "Intercept"),
  prior(normal(0.5, 0.5), class = "b", coef = "scalelogmean.loc.error"),
  prior(normal(0, 0.7), class = "b", coef = "sexageadultM"),
  prior(normal(0, 0.7), class = "b", coef = "sexagejuvenileF"),
  prior(normal(0, 0.7), class = "b", coef = "sexagejuvenileM"),
  prior(normal(0, 0.7), class = "b", coef = "periodPost_breeding"),
  prior(normal(0, 0.7), class = "b", coef = "periodPost_breeding:sexageadultM"),
  prior(normal(0, 0.7), class = "b", coef = "periodPost_breeding:sexagejuvenileF"),
  prior(normal(0, 0.7), class = "b", coef = "periodPost_breeding:sexagejuvenileM"),
  prior(normal(0, 0.7), class = "b", coef = "periodPre_breeding"),
  prior(normal(0, 0.7), class = "b", coef = "periodPre_breeding:sexageadultM"),
  prior(normal(0, 0.7), class = "b", coef = "periodPre_breeding:sexagejuvenileF"),
  prior(normal(0, 0.7), class = "b", coef = "periodPre_breeding:sexagejuvenileM"),
  prior(normal(0, 0.7), class = "b", coef = "periodSummer"),
  prior(normal(0, 0.7), class = "b", coef = "periodSummer:sexageadultM"),
  prior(normal(0, 0.7), class = "b", coef = "periodSummer:sexagejuvenileF"),
  prior(normal(0, 0.7), class = "b", coef = "periodSummer:sexagejuvenileM"),
  prior(normal(0, 0.7), class = "b", coef = "sscaledeploy.yr:periodBreeding_1"),
  prior(normal(0, 0.7), class = "b", coef = "sscaledeploy.yr:periodPost_breeding_1"),
  prior(normal(0, 0.7), class = "b", coef = "sscaledeploy.yr:periodPre_breeding_1"),
  prior(normal(0, 0.7), class = "b", coef = "sscaledeploy.yr:periodSummer_1"),
  prior(normal(0, 1), class = "sd", coef = "Intercept", group = "id"),
  prior(normal(0, 1), class = "sd", coef = "Intercept", group = "deploy.yr"),
  prior(normal(0, 0.7), class = "b", coef = "Intercept", dpar = "sigma"),
  prior(normal(0, 1), class = "sd", coef = "Intercept", group = "deploy.yr",
        dpar = "sigma"),
  prior(normal(0, 1), class = "sd", coef = "Intercept", group = "id",
        dpar = "sigma"),
  prior(normal(0, 1), class = "sds", coef = "s(scale(deploy.yr), by = period)"))

# Run model
d_yr_area <- brm(
  d_yr_area_form,
  prior = d_yr_area_prior,
  data = hr.data,
  save_pars = save_pars(all = TRUE),
  sample_prior = TRUE,
```

```
  iter = 8000, cores = 3, chains = 3, warmup = 2000, thin = 1,
  control = list(adapt_delta = 0.99))

# Assigned model summary to an object
mod_sum <- summary(d_yr_area)
```

Simulation

Simulation parameters

We first defined the basic parameters from which we simulated data. To keep the simulated data as close to the 'reality' as possible, we mostly based the parameters used to simulate data on the estimates of the model with the real data. More specifically, we used the mean of the posterior distribution of each parameter estimated by the 'real' model. Code Block

We did this for population level parameters such as the population intercept and the effects of sexage class, period of the year, their interaction and mean location error. We then added an effect of year of deployment that resulted in a temporal trend in the simulated data. We also used the estimate of the model with the real data as the population intercept for the dispersion model. We then added some level of inter and intra year variation to the simulated data. We used the random intercepts of year of the mean and dispersion models.

These parameters were used to calculate the mean (*mu*) and standard deviation (*sigma*) on the log scale of a lognormal distribution from which we drew a value corresponding to our simulated home range area. We kept the same data structure as our real data, meaning we used the same combinations of population level variables (mean location error, sexage class, period of the year) and year of deployment present in our real data. Depending on the case, we added different level of inter and/or intra individual variation in the calculation of the mean and/or standard deviation.

```
### Define simulation parameters
## Define population level parameters
# Population intercept of mean model (mu)
beta_0 <- mod_sum$fixed["Intercept",]$Estimate

# Effect of mean location error
beta_1 <- mod_sum$fixed["scalelogmean.loc.error",]$Estimate

# Effect of period of the year
beta_2 <- c(
  "Breeding" = 0,
  "Post_breeding" = mod_sum$fixed["periodPost_breeding",]$Estimate,
  "Pre_breeding" = mod_sum$fixed["periodPre_breeding",]$Estimate,
  "Summer" = mod_sum$fixed["periodSummer",]$Estimate)

# Effect of sexage class
beta_3 <- c(
  "adult F" = 0,
  "adult M" = mod_sum$fixed["sexageadultM",]$Estimate,
  "juvenile F" = mod_sum$fixed["sexagejuvenileF",]$Estimate,
  "juvenile M" = mod_sum$fixed["sexagejuvenileM",]$Estimate)

# Interactive effect of period of the year and seaxage class
beta_4 <- c(
```

```
  "Breeding adult F" = 0,
  "Post_breeding adult F" = 0,
  "Pre_breeding adult F" = 0,
  "Summer adult F" = 0,
  "Breeding adult M" = 0,
  "Post_breeding adult M" = mod_sum$fixed["periodPost_breeding:sexageadultM",]$Estimate,
  "Pre_breeding adult M" = mod_sum$fixed["periodPre_breeding:sexageadultM",]$Estimate,
  "Summer adult M" = mod_sum$fixed["periodSummer:sexageadultM",]$Estimate,
  "Breeding juvenile F" = 0,
  "Post_breeding juvenile F" = mod_sum$fixed["periodPost_breeding:sexagejuvenileF",]$Estimate,
  "Pre_breeding juvenile F" = mod_sum$fixed["periodPre_breeding:sexagejuvenileF",]$Estimate,
  "Summer juvenile F" = mod_sum$fixed["periodSummer:sexagejuvenileF",]$Estimate,
  "Breeding juvenile M" = 0,
  "Post_breeding juvenile M" = mod_sum$fixed["periodPost_breeding:sexagejuvenileM",]$Estimate,
  "Pre_breeding juvenile M" = mod_sum$fixed["periodPre_breeding:sexagejuvenileM",]$Estimate,
  "Summer juvenile M" = mod_sum$fixed["periodSummer:sexagejuvenileM",]$Estimate)

# Effect of year of deployment (i.e. temporal trend)
# Write function that generates a type 2 response
year_trend <- function(x, a, b) {
  (a * x) / (b + x)}

# Assign effect on home range area to each year and center variable
beta_5 <- c(scale(year_trend(x = seq(min(hr.data$deploy.yr)-min(hr.data$deploy.yr),
                                 max(hr.data$deploy.yr)-min(hr.data$deploy.yr),
                                 1), 2, 15),
                  scale = F))
# Assign names to vector corresponding to the years
names(beta_5) <- seq(min(hr.data$deploy.yr), max(hr.data$deploy.yr), 1)


# Population intercepts of dispersion model (sigma)
beta_sigma_0 <- mod_sum$fixed["sigma_Intercept",]$Estimate

## Define group level parameters
# Grab random intercepts from model with real data
rand_eff <- ranef(d_yr_area)

# Extract year intercepts of mean model (mu)
year_mu <- rand_eff$deploy.yr[,,"Intercept"][,"Estimate"]
# Extract individual intercepts of mean model (mu)
id_mu <- rand_eff$id[,,"Intercept"][,"Estimate"]

# Extract year intercepts of dispersion model (sigma)
year_sigma <- rand_eff$deploy.yr[,,"sigma_Intercept"][,"Estimate"]
# Extract individual intercepts of dispersion model (sigma)
id_sigma <- rand_eff$id[,,"sigma_Intercept"][,"Estimate"]
```

Inter and intra individual variation

We considered four cases of inter and intra individual variations Figure 2.

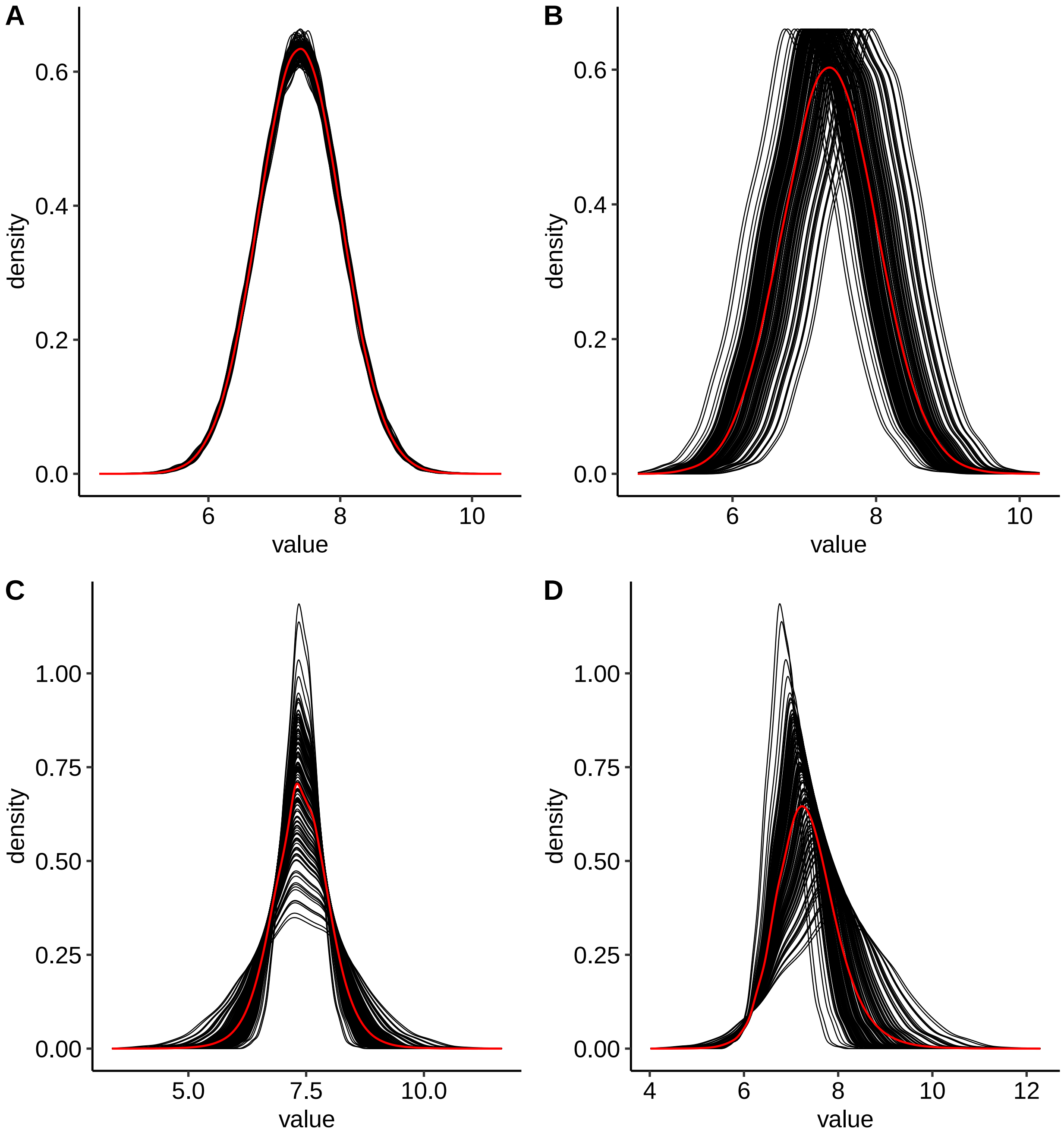

Figure 2: Simulated cases of inter (*mu*) and intra (*sigma*) individual variation. Black lines represent individuals' distribution while red lines represent the population's distribution. Value illustrates home range area on the log scale. A) Case 1: no inter and no intra individual variation, *i.e.* no difference in mean and standard deviation between individuals' distribution. B) Case 2: inter but no intra individual variation, *i.e.* differences in mean but not in standard deviation between individuals' distribution. C) Case 3: no inter but intra individual variation, *i.e.* no difference in mean but differences in standard deviation between individuals' distribution. D) Case 4: inter and intra individual variation, *i.e.* differences in mean and standard deviation between individuals' distribution.

Case 1: no inter nor intra individual variation

Case 1 represent the situation where there is no inter nor intra individual variation, *i.e.* no difference in mean and level of variability between individuals. Figure 2 A.

We first simulated some data.

```
# Get data set of predictor variables from real data
hr_sim <- hr.data %>%
  dplyr::select(id, deploy.yr, period, sexage, mean.loc.error)


## Simulate response var (home range area)
for (i in 1:length(hr_sim$id)) {

  # Calculate distribution mean
  mu <-
    # Population intercept
    beta_0 +
    # Population level effect: Mean location error
    beta_1 * log(hr_sim[i,]$mean.loc.error) +
    # Population level effect: Period of the year
    beta_2[hr_sim[i,]$period] +
    # Population level effect: Sexage class
    beta_3[hr_sim[i,]$sexage] +
    # Population level effect: Period of the year and sexage class interaction
    beta_4[paste(hr_sim[i,]$period, hr_sim[i,]$sexage)] +
    # Population level effect: temporal trend
    beta_5[as.character(hr_sim[i,]$deploy.yr)] +
    # Group level effect: Year intercept (Inter year var.)
    year_mu[as.character(hr_sim[i,]$deploy.yr)]

  # Calculate distribution standard deviation
  sigma <- exp(
    # Population intercept
    beta_sigma_0 +
      # Group level effect: Year intercept (Intra year var.)
      year_sigma[as.character(hr_sim[i,]$deploy.yr)])

  # Save distribution parameters (mu and sigma)
  hr_sim$mu[i] <- mu
  hr_sim$sigma[i] <- sigma

  # Simulate the response variable (area)
  hr_sim$area[i] <- rlnorm(1, meanlog = mu, sdlog = sigma)
}
```

We then ran the model with the simulated data.

```
## Run model
area_sim <- brm(
  d_yr_area_form,
  prior = d_yr_area_prior,
  data = hr_sim,
  save_pars = save_pars(all = TRUE),
  sample_prior = TRUE,
  iter = 8000, cores = 3, chains = 3, warmup = 2000, thin = 1,
  control = list(adapt_delta = 0.99))
```

We repeated the process a total of 100 times and visualized the estimates of inter and intra individual variation from the models Figure 3.

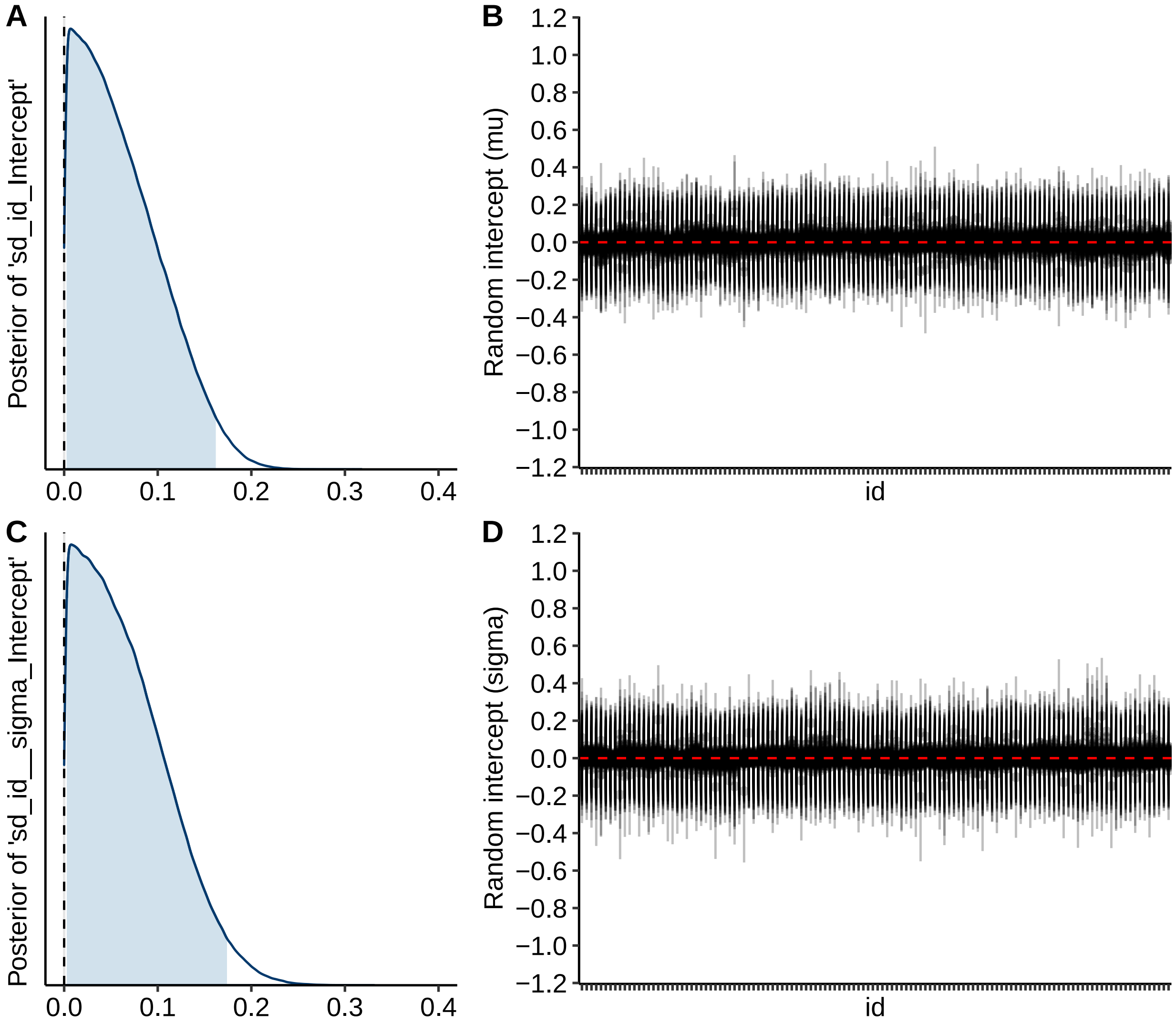

Figure 3: Estimates of inter and intra individual variation. A) Combined posterior distribution of models' estimates of inter individual variation with simulated value represented by the dashed line. The complete posterior distribution is represented while the shaded area represents the 95% CI. B) Models' estimates of individual random intercepts of mean models (*mu*). Mean estimates of each model are represented by the points while 95% CIs are represented by the lines. C) Combined posterior distribution of models' estimates of intra individual variation with simulated value represented by the dashed line. The complete posterior distribution is represented while the shaded area represents the 95% CI. D) Models' estimates of individual random intercepts of dispersion models (*sigma*). Mean estimates of each model are represented by the points while 95% CIs are represented by the lines.

Case 2: inter but no intra individual variation

Case 2 represent the situation where there is inter but not intra individual variation, *i.e.* differences in mean but not in the level of variability between individuals. Figure 2 B.

We first simulated some data.

```r
# Get data set of predictor variables from real data
hr_sim_inter <- hr.data %>%
  dplyr::select(id, deploy.yr, period, sexage, mean.loc.error)

# Generate random individual intercepts form a normal distribution
id_mu <- rand_eff$id[,,"Intercept"][,"Estimate"]
set.seed(1234); id_mu[1:124] <- rnorm(124, mean = 0, sd = 0.25)

## Simulate response var (home range area)
for (i in 1:length(hr_sim_inter$id)) {

  # Calculate distribution mean
  mu <-
    # Population intercept
    beta_0 +
    # Population level effect: Mean location error
    beta_1 * log(hr_sim_inter[i,]$mean.loc.error) +
    # Population level effect: Period of the year
    beta_2[hr_sim_inter[i,]$period] +
    # Population level effect: Sexage class
    beta_3[hr_sim_inter[i,]$sexage] +
    # Population level effect: Period of the year and sexage class interaction
    beta_4[paste(hr_sim_inter[i,]$period, hr_sim_inter[i,]$sexage)] +
    # Population level effect: temporal trend
    beta_5[as.character(hr_sim_inter[i,]$deploy.yr)] +
    # Group level effect: Individual intercept (Inter ind. var.)
    id_mu[hr_sim_inter[i,]$id] +
    # Group level effect: Year intercept (Inter year var.)
    year_mu[as.character(hr_sim_inter[i,]$deploy.yr)]

  # Calculate distribution standard deviation
  sigma <- exp(
    # Population intercept
    beta_sigma_0 +
      # Group level effect: Year intercept (Intra year var.)
      year_sigma[as.character(hr_sim_inter[i,]$deploy.yr)])

  # Save distribution parameters (mu and sigma)
  hr_sim_inter$mu[i] <- mu
  hr_sim_inter$sigma[i] <- sigma

  # Simulate the response variable (area)
  hr_sim_inter$area[i] <- rlnorm(1, meanlog = mu, sdlog = sigma)
}
```

We then ran the model with the simulated data.

```r
## Run model
area_sim_inter <- brm(
  d_yr_area_form,
  prior = d_yr_area_prior,
  data = hr_sim_inter,
  save_pars = save_pars(all = TRUE),
  sample_prior = TRUE,
  iter = 8000, cores = 3, chains = 3, warmup = 2000, thin = 1,
  control = list(adapt_delta = 0.99))
```

We repeated the process a total of 100 times and visualized the estimates of inter and intra individual variation from the models Figure 4.

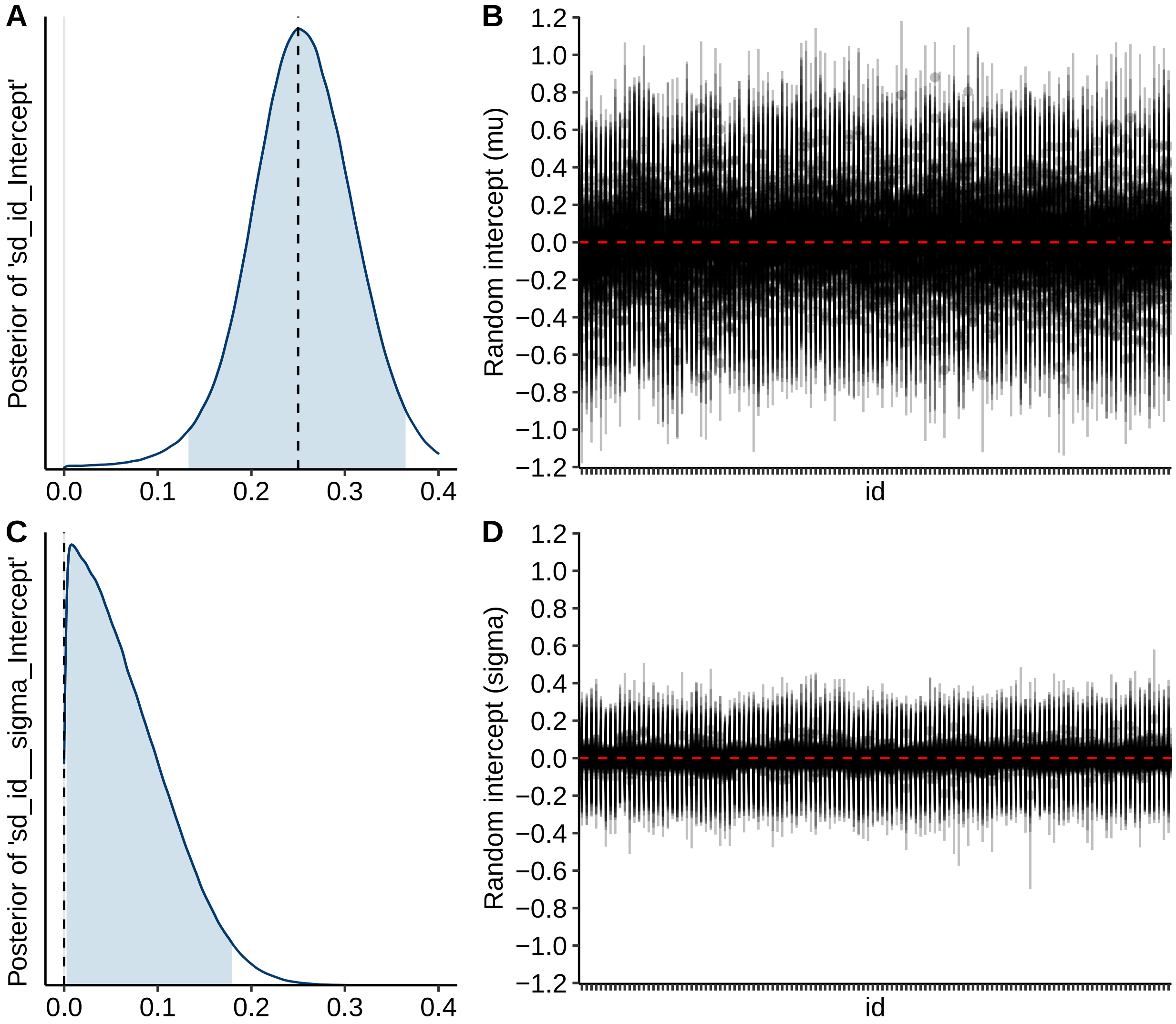

Figure 4: Estimates of inter and intra individual variation. A) Combined posterior distribution of models' estimates of inter individual variation with simulated value represented by the dashed line. The complete posterior distribution is represented while the shaded area represents the 95% CI. B) Models' estimates of individual random intercepts of mean models (*mu*). Mean estimates of each model are represented by the points while 95% CIs are represented by the lines. C) Combined posterior distribution of models' estimates of intra individual variation with simulated value represented by the dashed line. The complete posterior distribution is represented while the shaded area represents the 95% CI. D) Models' estimates of individual random intercepts of dispersion models (*sigma*). Mean estimates of each model are represented by the points while 95% CIs are represented by the lines.

Case 3: no inter but intra individual variation

Case 3 represent the situation where there is no inter but there is intra individual variation, *i.e.* no difference in mean but differences in the level of variability between individuals. Figure 2 C.

We first simulated some data.

```
# Get data set of predictor variables from real data
hr_sim_intra <- hr.data %>%
  dplyr::select(id, deploy.yr, period, sexage, mean.loc.error)

# Generate random individual intercepts form a normal distribution
id_sigma <- rand_eff$id[,,"sigma_Intercept"][,"Estimate"]
set.seed(1234); id_sigma[1:124] <- rnorm(124, mean = 0, sd = 0.25)


## Simulate response var (home range area)
for (i in 1:length(hr_sim_intra$id)) {

  # Calculate distribution mean
  mu <-
    # Population intercept
    beta_0 +
    # Population level effect: Mean location error
    beta_1 * log(hr_sim_intra[i,]$mean.loc.error) +
    # Population level effect: Period of the year
    beta_2[hr_sim_intra[i,]$period] +
    # Population level effect: Sexage class
    beta_3[hr_sim_intra[i,]$sexage] +
    # Population level effect: Period of the year and sexage class interaction
    beta_4[paste(hr_sim_intra[i,]$period, hr_sim_intra[i,]$sexage)] +
    # Population level effect: temporal trend
    beta_5[as.character(hr_sim_intra[i,]$deploy.yr)] +
    # Group level effect: Year intercept (Inter year var.)
    year_mu[as.character(hr_sim_intra[i,]$deploy.yr)]

  # Calculate distribution standard deviation
  sigma <- exp(
    # Population intercept
    beta_sigma_0 +
      # Group level effect: Year intercept (Intra year var.)
      year_sigma[as.character(hr_sim_intra[i,]$deploy.yr)] +
      # Group level effect: Individual intercept (Intra ind. var.)
      id_sigma[hr_sim_intra[i,]$id])

  # Save distribution parameters (mu and sigma)
  hr_sim_intra$mu[i] <- mu
  hr_sim_intra$sigma[i] <- sigma

  # Simulate the response variable (area)
  hr_sim_intra$area[i] <- rlnorm(1, meanlog = mu, sdlog = sigma)
}
```

We then ran the model with the simulated data.

```
## Run model
area_sim_intra <- brm(
  d_yr_area_form,
  prior = d_yr_area_prior,
  data = hr_sim_intra,
  save_pars = save_pars(all = TRUE),
  sample_prior = TRUE,
  iter = 8000, cores = 3, chains = 3, warmup = 2000, thin = 1,
  control = list(adapt_delta = 0.99))
```

We repeated the process a total of 100 times and visualized the estimates of inter and intra individual variation from the models Figure 5.

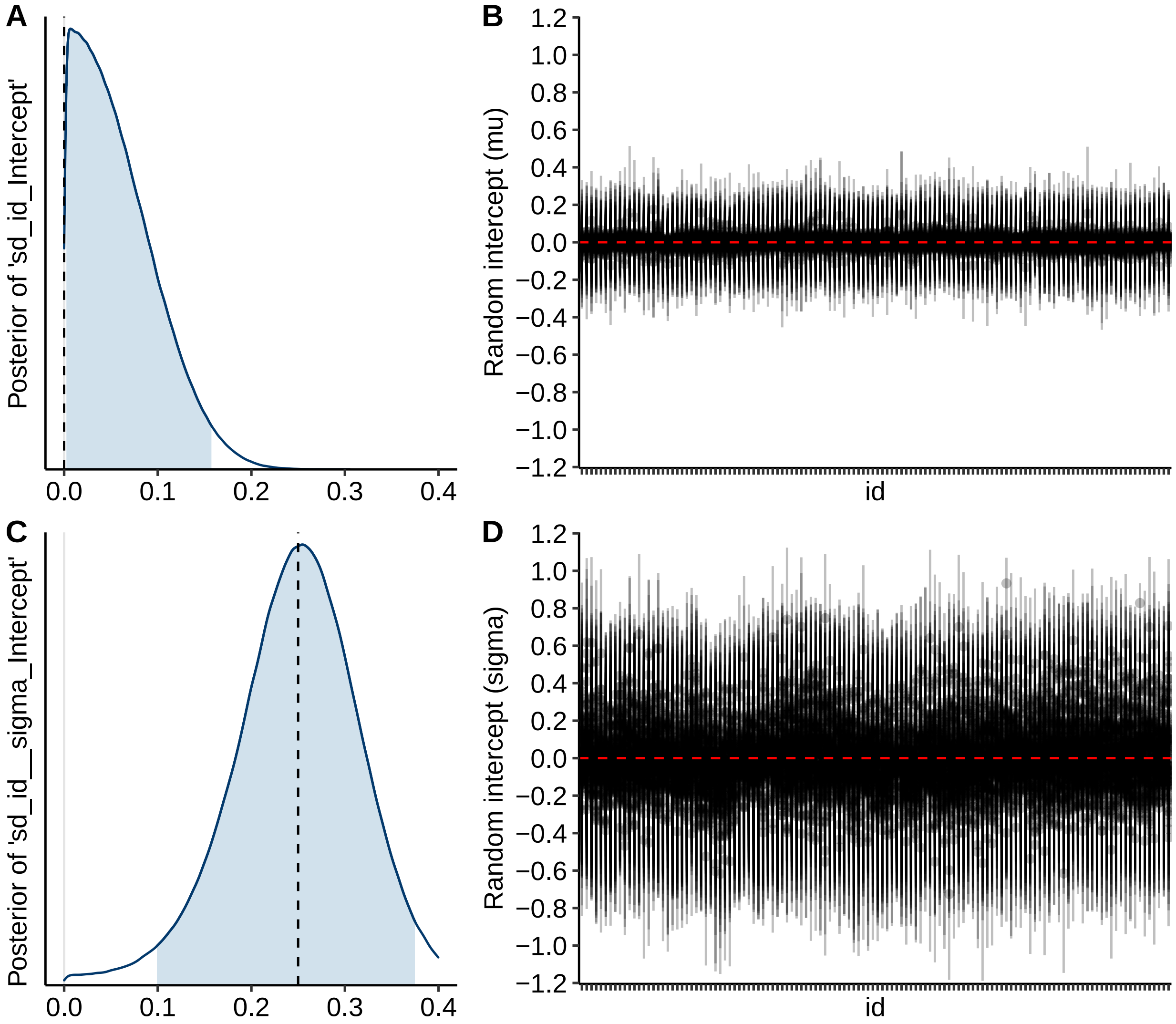

Figure 5: Estimates of inter and intra individual variation. A) Combined posterior distribution of models' estimates of inter individual variation with simulated value represented by the dashed line. The complete posterior distribution is represented while the shaded area represents the 95% CI. B) Models' estimates of individual random intercepts of mean models (*mu*). Mean estimates of each model are represented by the points while 95% CIs are represented by the lines. C) Combined posterior distribution of models' estimates of intra individual variation with simulated value represented by the dashed line. The complete posterior distribution is represented while the shaded area represents the 95% CI. D) Models' estimates of individual random intercepts of dispersion models (*sigma*). Mean estimates of each model are represented by the points while 95% CIs are represented by the lines.

Case 4: inter and intra individual variation

Case 4 represent the situation where there is inter and intra individual variation, *i.e.* differences in mean and in the level of variability between individuals. Figure 2 D.

We first simulated some data.

```r
# Get data set of predictor variables from real data
hr_sim_inter_intra <- hr.data %>%
  dplyr::select(id, deploy.yr, period, sexage, mean.loc.error)

# Generate random individual intercepts for mean, form a normal distribution
id_mu <- rand_eff$id[,,"Intercept"][,"Estimate"]
set.seed(1234); id_mu[1:124] <- rnorm(124, mean = 0, sd = 0.25)

# Generate random individual intercepts for sigma, form a normal distribution
id_sigma <- rand_eff$id[,,"sigma_Intercept"][,"Estimate"]
set.seed(1234); id_sigma[1:124] <- rnorm(124, mean = 0, sd = 0.25)

## Simulate response var (home range area)
for (i in 1:length(hr_sim_inter_intra$id)) {

  # Calculate distribution mean
  mu <-
    # Population intercept
    beta_0 +
    # Population level effect: Mean location error
    beta_1 * log(hr_sim_inter_intra[i,]$mean.loc.error) +
    # Population level effect: Period of the year
    beta_2[hr_sim_inter_intra[i,]$period] +
    # Population level effect: Sexage class
    beta_3[hr_sim_inter_intra[i,]$sexage] +
    # Population level effect: Period of the year and sexage class interaction
    beta_4[paste(hr_sim_inter_intra[i,]$period, hr_sim_inter_intra[i,]$sexage)] +
    # Population level effect: temporal trend
    beta_5[as.character(hr_sim_inter_intra[i,]$deploy.yr)] + +
    # Group level effect: Individual intercept (Inter ind. var.)
    id_mu[hr_sim_inter_intra[i,]$id] +
    # Group level effect: Year intercept (Inter year var.)
    year_mu[as.character(hr_sim_inter_intra[i,]$deploy.yr)]

  # Calculate distribution standard deviation
  sigma <- exp(
    # Population intercept
    beta_sigma_0 +
      # Group level effect: Year intercept (Intra year var.)
      year_sigma[as.character(hr_sim_inter_intra[i,]$deploy.yr)] +
      # Group level effect: Individual intercept (Intra ind. var.)
      id_sigma[hr_sim_intra[i,]$id])

  # Save distribution parameters (mu and sigma)
  hr_sim_inter_intra$mu[i] <- mu
  hr_sim_inter_intra$sigma[i] <- sigma

  # Simulate the response variable (area)
  hr_sim_inter_intra$area[i] <- rlnorm(1, meanlog = mu, sdlog = sigma)
}
```

We then ran the model with the simulated data.

```r
## Run model
area_sim_inter_intra <- brm(
  d_yr_area_form,
  prior = d_yr_area_prior,
  data = hr_sim_inter_intra,
  save_pars = save_pars(all = TRUE),
  sample_prior = TRUE,
  iter = 8000, cores = 3, chains = 3, warmup = 2000, thin = 1,
  control = list(adapt_delta = 0.99))
```

We repeated the process a total of 100 times and visualized the estimates of inter and intra individual variation from the models Figure 6.

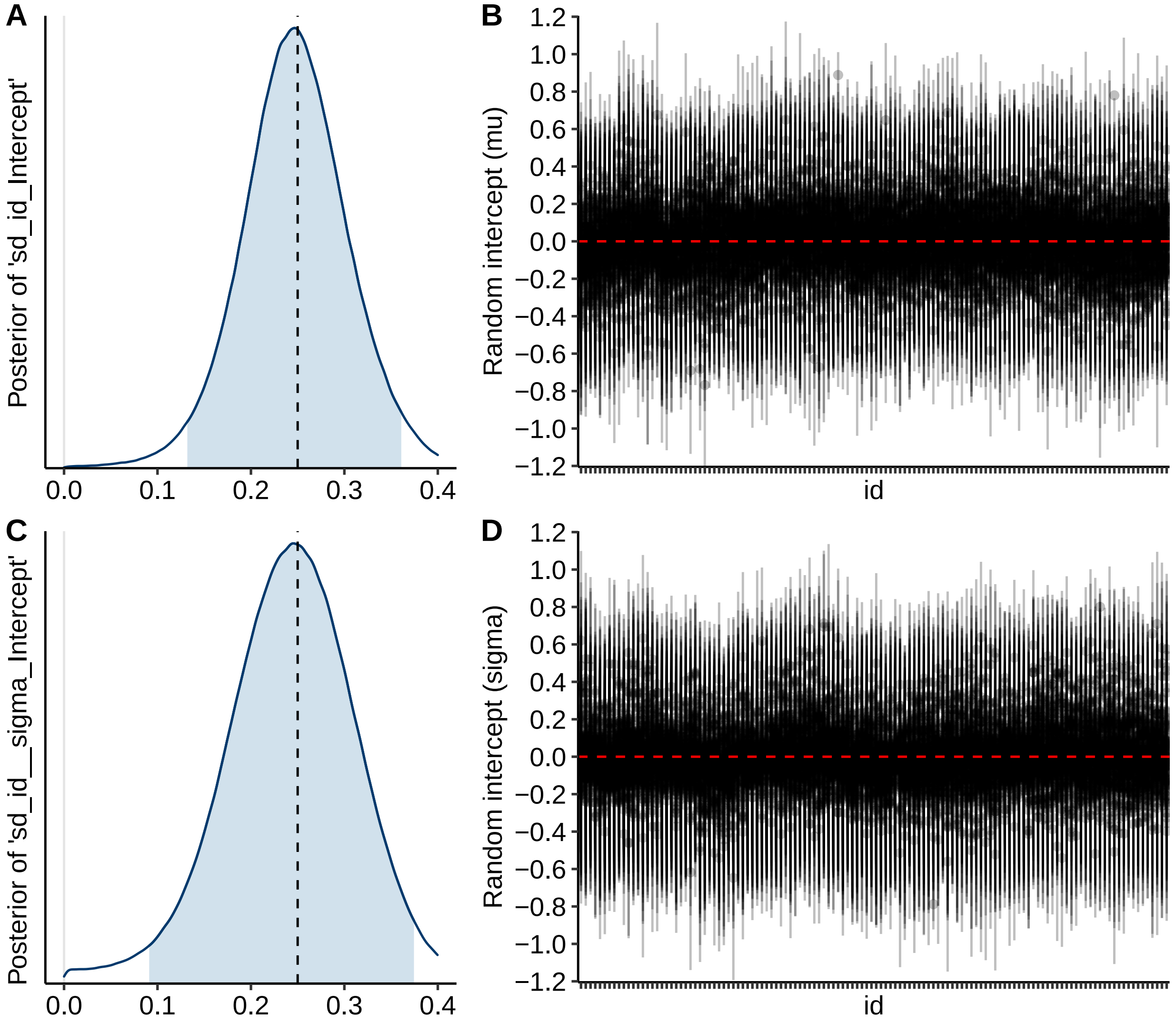

Figure 6: Estimates of inter and intra individual variation. A) Combined posterior distribution of models' estimates of inter individual variation with simulated value represented by the dashed line. The complete posterior distribution is represented while the shaded area represents the 95% CI. B) Models' estimates of individual random intercepts of mean models (*mu*). Mean estimates of each model are represented by the points while 95% CIs are represented by the lines. C) Combined posterior distribution of models' estimates of intra individual variation with simulated value represented by the dashed line. The complete posterior distribution is represented while the shaded area represents the 95% CI. D) Models' estimates of individual random intercepts of dispersion models (*sigma*). Mean estimates of each model are represented by the points while 95% CIs are represented by the lines.

Population-level effects

Ontological and seasonal effects

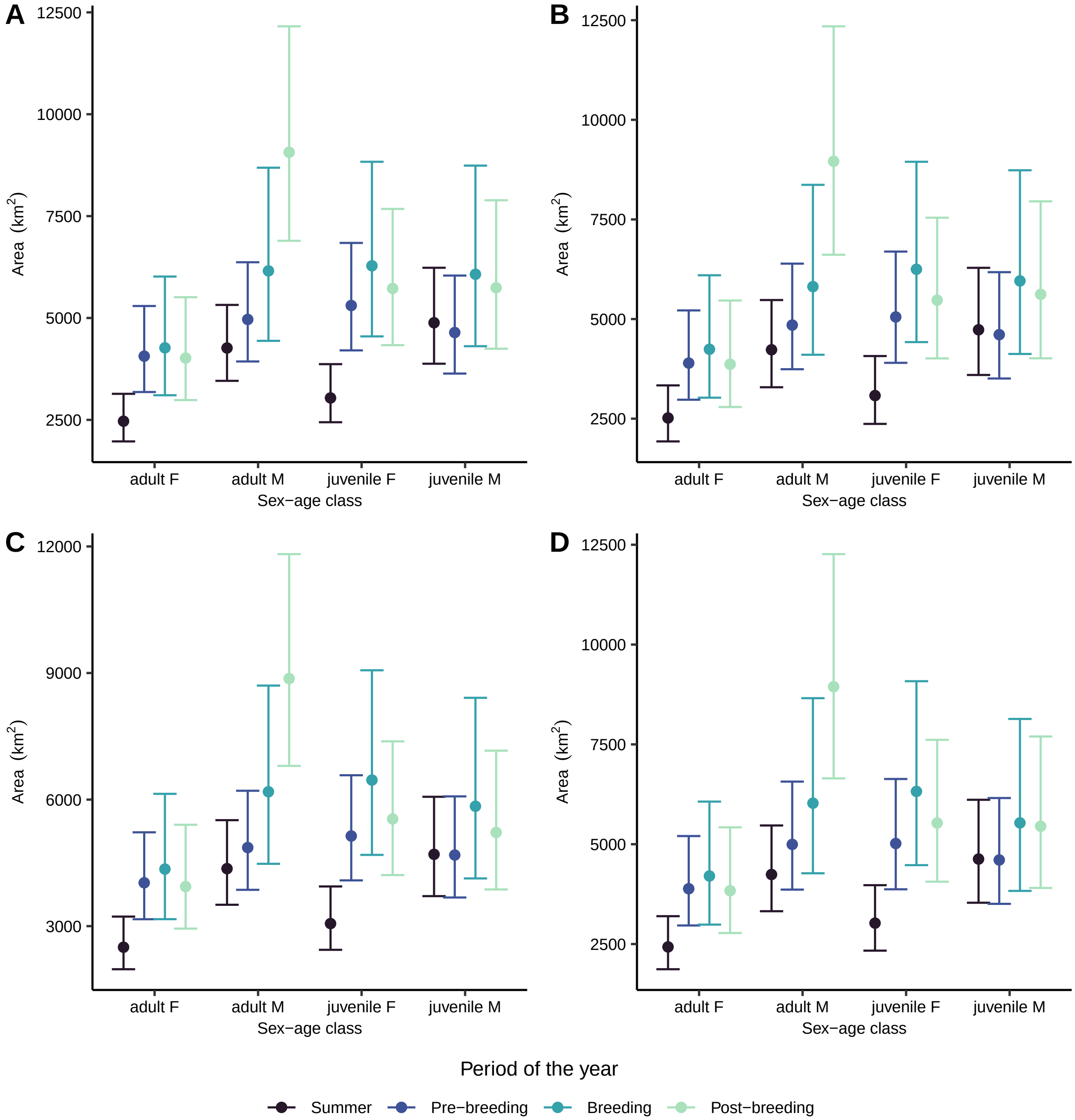

Figure 7: Ontological and seasonal variation in monthly home range area. Dots represent the mean predicted values of the response from the models. Error bars represent the mean lower and upper bounds of the 95% uncertainty intervals of the response. Colors represent the period of the year. A) Case 1: no inter and no intra individual variation. B) Case 2: inter but no intra individual variation. C) Case 3: no inter but intra individual variation. D) Case 4: inter and intra individual variation.

Temporal change

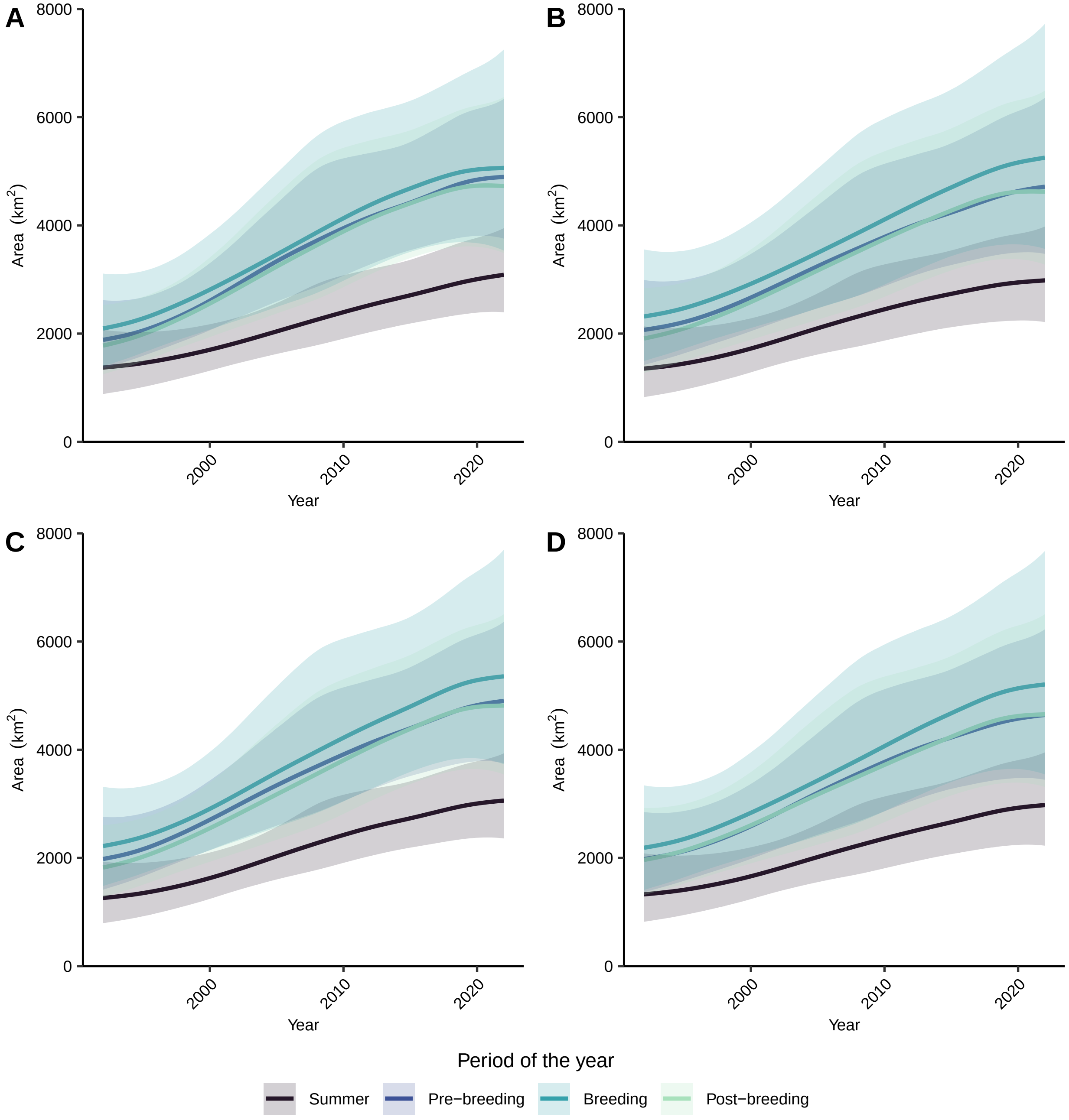

Figure 8: Temporal change in monthly home range area. Lines represent the mean predicted values of the response from the models. Shaded areas represent the mean lower and upper bounds of the 95% uncertainty intervals of the response. Colors represent the period of the year. A) Case 1: no inter and no intra individual variation. B) Case 2: inter but no intra individual variation. C) Case 3: no inter but intra individual variation. D) Case 4: inter and intra individual variation.

Simulated vs estimated parameters

Table 1: Simulated vs estimated paramaters. Estimates represent the mean of the combined posterior distributions and are presented with their 95% credible intervals (CI).

		Sim Case 1	Sim Case 2	Sim Case 3	Sim Case 4
Parameter	Simulated	Estimate ($\text{CI}_{95\%}$)	Estimate ($\text{CI}_{95\%}$)	Estimate ($\text{CI}_{95\%}$)	Estimate ($\text{CI}_{95\%}$)
Population-Level Effects:					
Intercept	-	7.84(7.62 - 8.06)	7.84(7.59 - 8.08)	7.84(7.62 - 8.06)	7.85(7.60 - 8.09)
Location error	0.75	0.56(0.47 - 0.65)	0.55(0.44 - 0.66)	0.55(0.46 - 0.64)	0.55(0.44 - 0.66)
Post-breeding	-0.15	-0.10(-0.37 - 0.18)	-0.10(-0.38 - 0.17)	-0.11(-0.38 - 0.16)	-0.10(-0.38 - 0.17)
Pre-breeding	-0.09	-0.09(-0.34 - 0.16)	-0.08(-0.33 - 0.17)	-0.08(-0.32 - 0.17)	-0.07(-0.32 - 0.18)
Summer	-0.57	-0.52(-0.77 - -0.27)	-0.53(-0.79 - -0.28)	-0.52(-0.77 - -0.27)	-0.54(-0.80 - -0.29)
Adult M	0.33	0.33(0.03 - 0.64)	0.36(0.03 - 0.69)	0.34(0.04 - 0.64)	0.34(0.01 - 0.67)
Juvenile F	0.37	0.38(0.08 - 0.69)	0.38(0.04 - 0.71)	0.38(0.07 - 0.68)	0.35(0.02 - 0.69)
Juvenile M	0.30	0.31(0.00 - 0.63)	0.32(-0.03 - 0.66)	0.31(0.00 - 0.62)	0.28(-0.06 - 0.63)
Post-breeding:Adult M	0.54	0.50(0.12 - 0.87)	0.49(0.10 - 0.87)	0.48(0.11 - 0.85)	0.47(0.09 - 0.85)
Pre-breeding:Adult M	-0.13	-0.09(-0.44 - 0.26)	-0.14(-0.50 - 0.22)	-0.12(-0.47 - 0.23)	-0.15(-0.51 - 0.20)
Summer:Adult M	0.21	0.19(-0.16 - 0.55)	0.19(-0.18 - 0.55)	0.20(-0.15 - 0.55)	0.21(-0.15 - 0.57)
Post-breeding:Juvenile F	-0.01	-0.04(-0.43 - 0.35)	-0.03(-0.43 - 0.36)	-0.01(-0.40 - 0.38)	-0.03(-0.43 - 0.37)
Pre-breeding:Juvenile F	-0.12	-0.12(-0.47 - 0.23)	-0.13(-0.49 - 0.23)	-0.12(-0.47 - 0.23)	-0.13(-0.48 - 0.23)
Summer:Juvenile F	-0.17	-0.19(-0.55 - 0.17)	-0.17(-0.54 - 0.19)	-0.19(-0.54 - 0.17)	-0.17(-0.54 - 0.20)
Post-breeding:Juvenile M	0.06	0.03(-0.38 - 0.43)	0.02(-0.39 - 0.43)	0.05(-0.35 - 0.45)	0.05(-0.36 - 0.46)
Pre-breeding:Juvenile M	-0.15	-0.13(-0.50 - 0.23)	-0.15(-0.51 - 0.22)	-0.16(-0.52 - 0.21)	-0.15(-0.52 - 0.22)
Summer:Juvenile M	0.35	0.33(-0.04 - 0.69)	0.32(-0.06 - 0.70)	0.31(-0.05 - 0.68)	0.35(-0.03 - 0.73)
Intercept sigma	-0.47	-0.48(-0.61 - -0.36)	-0.47(-0.59 - -0.35)	-0.48(-0.61 - -0.34)	-0.46(-0.59 - -0.33)
Group-Level Effects:					
~Id (Number of levels: 124)					
sd(Intercept)	0.00	0.06(0.00 - 0.14)	-	0.06(0.00 - 0.14)	-
	0.25	-	0.25(0.18 - 0.33)	-	0.25(0.17 - 0.32)
sd(sigma_Intercept)	0.00	0.07(0.00 - 0.16)	0.07(0.00 - 0.16)	-	-
	0.25	-	-	0.25(0.16 - 0.33)	0.24(0.15 - 0.33)
~Year (Number of levels: 16)					
sd(Intercept)	0.13	0.09(0.01 - 0.20)	0.11(0.01 - 0.26)	0.09(0.01 - 0.20)	0.11(0.02 - 0.26)
sd(sigma_Intercept)	0.24	0.21(0.12 - 0.34)	0.20(0.11 - 0.33)	0.20(0.09 - 0.36)	0.20(0.08 - 0.35)

Conclusions

We simulated data corresponding to four cases of presence or absence of inter and intra individual variation in monthly home range area. We simulated data using the same number of replications per individual and the same combinations of population level variables that were present in our real data. We then introduced (or not) individual variation when simulating the data. When we introduced individual variation, we used similar levels of variation that were found in our real model.

We then ran the double hierarchical generalized linear models (DGLMs) with the same formula and the same priors on the simulated datasets. We simulated some data and ran the model 100 times for each of the four cases. In all cases the models were able to accurately estimate the amount of individual variation present in the data. In cases were individual variation was completely absent from the data, they correctly did not detect it (case 1). In cases were only one of inter or intra individual variation was present, the models were able to tease apart inter and intra individual differences and accurately estimated the amount of variation present in the data (cases 2 and 3). Finally, when both inter and intra individual variation were present in the data, the models were able to detect and accurately estimate both of them.

Based on theses simulations, we concluded that the statistical approach used in this article, given the data available, allows us to accurately parse the inter and intra individual variation in monthly home range characteristics of grey seals. We are thus confident that the amounts of inter and intra individual variation found when we ran the model with the real data represent true variation in the data and not some methodological artifact.