# Decadal changes in blood $\delta^{13}$ C values, at-sea distribution and weaning mass of southern elephant seals from Kerguelen Islands.

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## Supplementary Materials S3: Mixture model set up on pup blood $\delta^{13}$ C values

### 1) Code of mixture model taking into account $\delta^{13}C$ trend

```
data {
 int<lower = 1> n obs;
                                 // n obs = number of data points
  int<lower = 1> n year; // n year = number of years
 vector[n obs] DELTA13C; // DELTA13C = observations
  int<lower = 1, upper = n_year> YEAR[n_obs];
                                 // YEAR[n obs] = indicator of year
 vector[n year] STDYEAR;
 }
parameters {
 ordered[2] unscaled_mu;
 vector<lower = 0.0>[2] sigma;
 real<lower = 0.0> sigma year;
  real unscaled_intercept; // intercept of logistic regression
  real unscaled slope; // slope of logistic regression
 vector[n year] unscaled epsilon; // residuals for year effect
  }
// mu = locations of mixture components
// sigma = scales of mixture components
transformed parameters {
 real intercept;
 real slope;
 vector[2] mu;
 vector[n year] epsilon;
```

```
vector[n obs] theta;
  vector[2] mu_year[n_year];
 vector[2] prop[n year];
 vector[2] log npdf[n obs];
 vector[2] marginal proba[n obs];
 real R sq;
 mu = rep_vector(-20, 2) + 5.0 * unscaled_mu;
  intercept = 1.5 * unscaled_intercept;
 slope = log(2) / 2 * unscaled slope;
  epsilon = rep vector(intercept, n year) + slope * STDYEAR + sigma year *
unscaled epsilon;
  theta = inv logit(epsilon[YEAR]);
  for(j in 1:n year) {
   prop[j, 2] = inv logit(epsilon[j]);
   prop[j, 1] = 1 - inv logit(epsilon[j]);
   mu year[j, 1] = mu[1] - 0.09 \times (j - 1);
   mu year[j, 2] = mu[2] - 0.09 * (j - 1);
    }
  for (i in 1:n obs) {
  // decrease of 0.09 permill per year
   for (k in 1:2) {
    log npdf[i, k] = normal lpdf(DELTA13C[i]| mu year[YEAR[i], k],
sigma[k]);
   marginal proba[i, k] = exp(log npdf[i, k]);
    }
 marginal_proba[i] = marginal_proba[i] / sum(marginal_proba[i]);
  }
  R_sq = 1 - square(sigma_year) * variance(unscaled_epsilon) /
variance(epsilon);
```

```
// mu_year = year specific d13C value (per strategy, per year)
// prop = proportion of mixtures (per mu, per year)
// R_sq = R^2 of a linear regression adjusted on probability to belong to a
foraging strategy
model {
  unscaled mu \sim normal(0.0, 1.0);
  sigma ~ normal(0.0, 1.0);
  sigma year ~ normal(0.0, 1.0);
  unscaled intercept ~ normal(0.0, 1.0);
  unscaled slope ~ normal(0.0, 1.0);
  unscaled epsilon ~ normal(0.0, 1.0);
// individual likelihoods, as sum of component contributions
  for (i in 1:n obs) {
    target += log mix(theta[i], log npdf[i, 2], log npdf[i, 1]);
    }
}
generated quantities {
  vector[n_obs] log_lik;
  int G[n obs];
  vector[n obs] y rep;
  for(i in 1:n obs) {
    log_lik[i] = log_mix(theta[i], log_npdf[i, 2], log_npdf[i, 1]);
    G[i] = categorical rng(marginal proba[i]);
    y rep[i] = normal rng(mu year[YEAR[i], G[i]], sigma[G[i]]);
    }
```

}

}



#### 2) Distribution of raw data and the fitted model

Figure S5. Empirical distribution of the blood  $\delta^{13}$ C values of pups superimposed with the probability density functions of the mixture model. The blue curve represents the probability density function of pups assigned to the Antarctic habitat, whereas the red one corresponds to individuals assigned to the sub-Antarctic habitat.



#### 3) Annual proportions of the two estimated groups

Figure S6. Annual percentages of pups presumably born from female southern elephant seals that foraged either in the Antarctic (light grey) or in sub-Antarctic (dark grey) zones. Groups of pups were established based on a mixture model taking into account the temporal trend in blood  $\delta^{13}$ C.

No significant change has been detected in the annual proportion of females' foraging strategies, suggesting that the balance between the two foraging habitats remained unchanged over the study period. We should however be cautious with this interpretation, as our results suggest that the two foraging strategies displayed by females whose pups were blood-sampled on southeast Kerguelen Island are of similar importance within the population. Tracking data at the opposite suggest that more females forage in the sub-Antarctic habitat. This is subjective and "data-biased", depending on thresholds set up to split the two foraging

strategies. Datasets thus do not have the same sample sizes, and we have to keep in mind that sampled individuals are not necessarily representative of the whole population. We therefore tried to get rid of subjectivity by implementing non-informative priors in our mixture models. However, and regardless of the relative importance of the two foraging habitats, our mixture models showed that the percentage of individuals assigned to a given foraging strategy stays relatively stable over time.