The following supplements accompany the article

Stable isotope mixing models elucidate sex and size effects on the diet of a generalist marine predator

Rhema H. Bjorkland*, Scott F. Pearson, Steve J. Jeffries, Monique M. Lance, Alejandro Acevedo-Gutiérrez, Eric J. Ward

*Corresponding author: bjorkland.rhema@epa.gov

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Supplement 1.

Table S1. Age, sex and location distribution of harbor seals in the study sample. Age categories are adults (A), and sub-adult(sad).

Date	Location	Age	Sex	Length	Weight	Pregnant	$\delta^{13}C$	$\delta^{15}N$
4/4/07	Bird Rocks	A	M	140	71.5	N	-14.39	16.95
4/5/07	Bird Rocks	A	M	149	74.5	N	-15.75	15.82
4/6/07	Bird Rocks	A	M	150	96.0	N	-16.70	15.89
4/6/07	Bird Rocks	A	F	152	90.0	N	-14.94	17.03
4/18/07	Padilla Bay	A	M	142	64.0	N	-14.77	15.26
4/19/07	Belle Rock	A	M	158	110.5	N	-15.80	15.04
4/20/07	Bird Rocks	A	M	156	86.0	N	-16.80	15.30
5/21/07	Padilla Bay	A	M	146	69.0	N	-12.03	16.43
5/21/07	Padilla Bay	A	M	135	54.0	N	-15.82	16.13
10/24/07	Vendovi beach	Sad	M	134	53.0	N	-15.56	16.49
10/24/07	Vendovi rks	AD	M	150	89.0	N	-15.95	15.82
10/24/07	Vendovi rks	AD	M	132	69.0	N	-16.10	16.18
11/5/07	Vendovi beach	AD	M	154	103.4	N	-18.52	14.75
11/19/07	Bird Rocks	AD	M	128	68.0	N	-15.68	15.60
11/19/07	Bird Rocks	AD	M	163	83.0	N	-14.89	16.37
11/20/07	Bird Rocks	AD	M	150	75.5	N	-17.68	14.97
11/20/07	Bird Rocks	AD	M	153	81.5	N	-14.69	17.28
1/16/08	Bird Rocks	AD	M	147.5	83.0	N	-16.25	15.51
2/25/08	Bird Rocks	AD	M	151	81.0	N	-17.91	15.37
4/4/07	Bird Rocks	A	F	147	76.5	Y	-14.74	15.87
4/17/07	Padilla Bay	A	F	139	55.5	N	-11.44	17.00
4/17/07	Padilla Bay	A	F	131	57.5	N	-16.18	15.60

4/17/07	Padilla Bay	A/Sad	F	128	48.5	N	-13.87	16.63
4/19/07	Padilla Bay	A	F	141	83.0	Y	-12.41	16.68
4/19/07	Padilla Bay	A	F	127	62.5	Y	-11.51	16.35
4/19/07	Padilla Bay	Sad	F	121	44.0	N	-11.50	16.89
5/21/07	Padilla Bay	A	F	143	77.5	Y	-13.86	16.96
5/21/07	Padilla Bay	A	F	143	70.0	Y	-13.29	16.62
5/21/07	Padilla Bay	A	F	154	103.0	Y	-14.56	16.62
5/21/07	Padilla Bay	Sad	F	129	47.0	N	-11.41	16.79
5/21/07	Padilla Bay	A	F	153	74.0	Y	-11.42	16.76
5/21/07	Padilla Bay	A	F	145	85.0	Y	-11.85	16.69

Supplement S2. R list object of all the data needed to run the mixing model

```
structure(list(consumer = structure(c-14.39, -15.75, -16.70, -14.94, -14.77, -15.80, -16.80, -12.03, -
15.82, -15.56, -15.95, -16.10, -18.52, -15.68, -14.89, -17.68, -14.69, -16.25, -17.91, -14.74, -11.44, -
16.18, -13.87, -12.41, -11.51, -11.50, -13.86, -13.29, -14.56, -11.41, -11.42, -11.85, -11.42, -14.71, -
13.46, 16.95, 15.82, 15.89,
17.03, 15.26, 15.04, 15.3, 16.43, 16.13, 16.49, 15.82, 16.18,
14.75, 15.6, 16.37, 14.97, 17.28, 15.51, 15.37, 15.87, 17, 15.6,
16.63, 16.68, 16.35, 16.89, 16.96, 16.62, 16.62, 16.79, 16.76,
16.69, 16.57, 15.93, 16.6), .Dim = c(32L, 2L), .Dimnames = list(
   c("1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "11",
   "12", "13", "14", "15", "16", "17", "18", "19", "20", "21",
   "22", "23", "24", "26", "27", "28", "29", "30", "31", "32",
   "34", "36", "37", "40"), c("carbon_corrected", "nitrogen"
   ))), N = 32L, num.prey = 4, alpha = c(1, 1, 1, 1 ), num.iso = 2,
   L = c(4.26969744969996, 4.31079912538551, 4.56434819146784,
   4.49980967033027, 4.15888308335967, 4.70501552095781, 4.45434729625351,
   4.23410650459726, 3.98898404656427, 3.97029191355212, 4.48863636973214,
   4.23410650459726, 4.63860496207433, 4.21950770517611, 4.4188406077966,
   4.32413265625498, 4.40060302024682, 4.4188406077966, 4.39444915467244,
   4.33729074083249, 4.01638302075239, 4.0517849478033, 3.88156379794344,
   4.4188406077966, 4.13516655674236, 3.78418963391826, 4.3502779363593,
   4.24849524204936, 4.63472898822964, 3.85014760171006, 4.30406509320417,
   4.44265125649032, 4.17438726989564, 3.88156379794344, 4.32413265625498
   ), Sex = c(2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
   2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1),
   u = structure(c(-19.45552,-16.49212, -18.79028, -13.6617,
    12.797, 13.83944, 12.14422, 13.2663,
v = structure(c(2.1289646, 0.8213492, 1.0913714, 2.1023952, 1.8882215, 0.4560949, 0.8777958,
0.7376972
   ), .Dim = c(4L, 2L))), .Names = c("consumer", "N", "num.prey",
"alpha", "num.iso", "L", "Sex", "u", "v"))
```

Supplement S3. JAGS object for the 2-sex mixing model with weight as a covariate

```
model = cat("
model {
  # p.global = estimated diet for smallest seals, with [,1] and [,2] = subscripting sex
  p.global[1:num.prey,1] ~ ddirch(alpha[1:num.prey]);
  p.global[1:num.prey,2] ~ ddirch(alpha[1:num.prey]);
  # p.end = estimated diet for largest seals, with [,1] and [,2] = subscripting sex
  p.end[1:num.prey,1] ~ ddirch(alpha[1:num.prey]);
  p.end[1:num.prey,2] ~ ddirch(alpha[1:num.prey]);

  # calculate slope (assumed constant among sexes) in each prey dimension
  for(i in 1:4) {
  B1[i,1] <- (p.end[i,1]-p.global[i,1])/0.2979597; # slope of C as derived param
  B1[i,2] <- 0; # set slope for N = 0
  }

  for(i in 1:N) {
    for(prey in 1:num.prey) {
      p[prey,i] <- p.global[prey, Sex[i]] + B1[prey,1] * L[i];
    }
  }

  # for each isotope and population, calculate the predicted mixtures
  for(iso in 1:num.iso) {
      mix.prcsn[iso] ~ dgamma(0.001,0.001);
      mix.var[iso] <- 1/mix.prcsn[iso];
    for(i in 1:N) {
      mix.mu[iso,i] <- inprod(u[,iso],p[,i]);
    }
  }

  # This section does the likelihood / posterior, N data points
  for(i in 1:N) {
    for(iso in 1:num.iso) {
      consumer[i,iso] ~ dnorm(mix.mu[iso, i], mix.prcsn[iso]);
    }
  }

}

", file = "model.txt")
```