Table S1. Summary data for Laysan albatross (A) and Newell's shearwater (B) feather and bone collagen samples. Time corresponds to the time periods described in text. CAS, California Academy of Sciences; USNM, National Museum of Natural History, Smithsonian Institution; BPBM, Bernice Pauahi Bishop Museum; NA, not applicable. ID indicates the museum catalog number or the sample ID assigned at Michigan State University prior to analysis. Year and location indicate when and where samples were collected. HI Fishery, Hawaii Fishery. NPO, North Pacific Ocean near Hawaiian Islands. All isotope values are expressed in per mil (‰); we report means of replicate injections and in parentheses are standard deviations of triplicates (italics) or differences between duplicates. Population averages, standard deviations, and 95% credible intervals (95% CI) are provided in bold. MEI, Multivariate ENSO Index, values calculated as described in Morra et al. (2019), classifications from NOAA. Bone collagen data are reprinted by permission from Springer Nature License: Springer Oecologia (Trophic declines and decadal-scale foraging segregation in three pelagic seabirds, Morra et al. 2019).

Time	Museum	ID	Year	Location	Feather			Bone			MEI
					$\delta^{15}N_{Glu}$	$\delta^{15}N_{Phe}$	$\Delta\delta^{15}N_{Glu-Phe}$	$\delta^{15}N_{Glu}$	$\delta^{15}N_{Phe}$	$\Delta\delta^{15}N_{Glu-Phe}$	
Historical	CAS	72618	1902	Laysan	-	-	-	19.6 *(0.3)*	5.3 *(0.5)*	14.4	73.5, neutral
Historical	CAS	72619	1902	Laysan	-	-	-	22.3 *(0.2)*	6.1 *(0.3)*	16.1	73.5, neutral
Historical	USNM	189392	1902	Laysan	20.0 (0.5)	4.7 (0.2)	15.4	20.9 (0.4)	5.7 (0.5)	15.1	73.5, neutral
Historical	USNM	240914	1913	Laysan	20.9 *(0.3)*	4.9 *(0.6)*	16.0	23.1 *(0.3)*	6.9 *(0.5)*	16.3	80.8, neutral
Historical	USNM	240915	1913	Laysan	20.4 *(0.3)*	5.5 *(0.3)*	15.0	22.8 *(0.6)*	6.9 *(0.4)*	16.0	80.8, neutral
Historical	USNM	240913	1913	Laysan	20.9 *(0.1)*	6.2 *(0.3)*	14.7	23.0 *(0.4)*	6.0 *(0.1)*	17.0	80.8, neutral
Historical	USNM	240916	1913	Laysan	21.0 *(0.2)*	3.5 *(0.1)*	17.5	22.1 *(0.6)*	6.2 *(0.6)*	15.9	80.8, neutral
Historical	USNM	300844	1923	Laysan	22.5 *(0.2)*	3.9 *(0.4)*	18.6	22.0 *(0.2)*	5.7 *(0.4)*	16.4	47.8, neutral
Historical	USNM	300851	1923	Lisianski	19.3 *(0.2)*	4.5 *(0.4)*	14.8	23.4 *(0.7)*	6.4 *(0.6)*	17.0	48.4, neutral
Historical	USNM	366372	1937	Aleutians	20.0 *(0.1)*	3.6 *(0.3)*	16.5	21.8 *(0.7)*	6.2 *(0.5)*	15.7	79.6, neutral
Historical	USNM	366960	1937	Midway	21.9 (0.1)	5.9 (0.4)	16.0	22.0 (0.6)	6.6 (0.3)	15.4	80.5, neutral
				Average	**20.8 *(1.0)***	**4.7 *(1.0)***	**16.0 *(1.3)***	**22.1 *(1.0)***	**6.2 *(0.5)***	**15.9 *(0.8)***	
				95% CI	**(20.0, 21.5)**	**(4.0, 5.4)**	**(15.1, 17.0)**	**(21.3, 22.8)**	**(5.7, 6.6)**	**(15.4, 16.5)**	
Post-2000	USNM	656772	2003	Fishery	20.6 *(0.1)*	6.5 (0.2)	14.0	20.0 (0.3)	5.4 (0.7)	14.7	44.1, neutral
Post-2000	USNM	656777	2010	Fishery	20.4 (0.4)	5.8 (0.3)	14.5	22.0 *(0.7)*	5.5 *(0.6)*	16.4	27.9, neutral
Post-2000	USNM	656775	2010	Fishery	21.2 *(0.3)*	4.2 *(0.6)*	17.0	22.4 *(0.0)*	6.5 (0.2)	15.9	27.9, neutral
Post-2000	USNM	656778	2010	Fishery	20.7 *(0.1)*	5.6 (0.5)	15.1	19.9 *(0.2)*	4.4 *(0.6)*	15.4	27.9, neutral
Post-2000	USNM	656790	2011	Fishery	19.9 (0.5)	3.1 (0.0)	16.7	21.7 *(0.6)*	7.2 *(0.4)*	14.6	13.0, moderate La Niña
Post-2000	USNM	656806	2011	Fishery	20.1 *(0.3)*	3.5 (0.7)	16.5	20.8 *(0.4)*	6.1 *(0.6)*	14.7	13.0, moderate La Niña
Post-2000	USNM	656804	2011	Fishery	-	-	-	20.5 *(0.3)*	5.3 *(0.6)*	15.2	13.0, moderate La Niña
Post-2000	USNM	656798	2011	Fishery	19.6 *(0.1)*	2.7 (0.1)	17.0	19.9 (0.1)	5.3 (0.3)	14.6	13.0, moderate La Niña
Post-2000	USNM	656782	2012	Fishery	20.9 (0.0)	5.4 (0.1)	15.5	20.9 *(0.2)*	5.0 *(0.6)*	15.9	37.2, neutral
Post-2000	USNM	656791	2013	Fishery	19.7 *(0.2)*	2.7 *(0.4)*	17.0	19.7 *(0.6)*	6.2 *(0.3)*	13.5	30.1, neutral
Post-2000	USNM	656789	2014	Fishery	19.7 (0.4)	3.1 (0.7)	16.6	21.9 *(0.3)*	7.5 *(0.6)*	14.3	45.8, neutral
				Average	**20.3 *(0.6)***	**4.3 *(1.5)***	**16.0 *(1.1)***	**20.9 *(1.0)***	**5.8 *(0.9)***	**15.0 *(0.8)***	

					δ^{15}N$_{Glu}$	δ^{15}N$_{Phe}$	Δδ^{15}N$_{Glu-Phe}$	δ^{15}N$_{Glu}$	δ^{15}N$_{Phe}$	Δδ^{15}N$_{Glu-Phe}$	
95% CI					**(19.6, 21.0)**	**(3.3, 5.1)**	**(15.5, 16.7)**	**(20.2, 21.5)**	**(5.2, 6.5)**	**(14.4, 15.6)**	

S1B. Newell's shearwater

					Feather			Bone			
Time	Museum	ID	Year	Location	δ^{15}N$_{Glu}$	δ^{15}N$_{Phe}$	Δδ^{15}N$_{Glu-Phe}$	δ^{15}N$_{Glu}$	δ^{15}N$_{Phe}$	Δδ^{15}N$_{Glu-Phe}$	MEI
Historical	BPBM	6692	1960	Kaua`i	23.4 (0.3)	6.0 (0.0)	17.4	-	-	-	26.4, neutral
Historical	USNM	493647	1964	NPO	17.6 (0.4)	-0.7 (0.5)	18.3	20.2 *(0.2)*	2.7 *(0.4)*	17.5	28.7, neutral
Historical	BPBM	145112	1964	Oahu	26.6 (0.2)	8.7 (0.1)	17.9	19.3 (0.4)	1.0 (0.1)	18.4	30.8, neutral
Historical	USNM	495240	1965	NPO	21.7 (0.1)	5.0 (0.1)	16.7	22.1 (0.4)	5.1 (0.2)	16.9	22.7, neutral
Historical	USNM	495847	1965	Kaua`i	*25.9 (0.1)*	8.7 *(0.4)*	17.2	20.7 *(0.1)*	2.8 *(0.6)*	17.9	22.7, neutral
Historical	USNM	496516	1966	NPO	25.5 (0.2)	8.7 (0.3)	16.8	20.7 *(0.4)*	3.8 (0.4)	16.9	47.4, weak El Niño
				Average	**23.4 *(3.4)***	**6.1 *(3.7)***	**17.4 *(0.6)***	**20.6 *(1.0)***	**3.1 *(1.5)***	**17.5 *(0.6)***	
				95% CI	**(19.1, 25.6)**	**(1.3, 8.4)**	**(16.6, 18.3)**	**(19.3, 21.6)**	**(1.3, 4.5)**	**(16.6, 18.4)**	
Post-2000	NA	A	2013	Kaua`i	23.8 *(0.0)*	9.5 (0.3)	14.3	19.6 *(0.5)*	3.7 *(0.4)*	15.9	35.6, neutral
Post-2000	NA	C	2013	Kaua`i	21.7 *(0.4)*	5.9 (0.6)	15.7	18.9 (0.1)	2.4 (0.4)	16.6	35.5, neutral
Post-2000	NA	E	2013	Kaua`i	23.0 *(0.5)*	9.3 *(0.5)*	13.7	18.5 (0.1)	2.2 (0.5)	16.3	35.6, neutral
Post-2000	NA	I	2013	Kaua`i	21.0 (0.2)	6.3 (0.2)	14.7	21.5 *(0.2)*	4.8 (0.5)	16.6	33.7, neutral
Post-2000	NA	B	2014	Kaua`i	25.0 (0.2)	8.3 (0.2)	16.7	19.6 (0.0)	3.6 (0.2)	16.0	35.9, neutral
Post-2000	NA	F	2014	Kaua`i	26.3 (0.2)	11.1 *(0.7)*	15.3	20.8 (0.1)	5.5 (0.4)	15.4	34.9, neutral
Post-2000	NA	G	2014	Kaua`i	24.4 *(0.5)*	9.4 (0.3)	15.0	19.0 *(0.6)*	2.3 (0.2)	16.7	37.4, neutral
Post-2000	NA	J	2014	Kaua`i	21.7 *(0.1)*	5.5 (0.5)	16.2	22.1 *(0.1)*	4.8 (0.3)	17.3	37.9, neutral
Post-2000	NA	H	2015	Kaua`i	24.8 *(0.4)*	7.9 (0.3)	16.9	18.5 *(0.1)*	1.8 (0.7)	16.7	53.1, moderate El Niño
Post-2000	NA	K	2016	Kaua`i	25.5 (0.1)	8.8 (0.2)	16.6	21.1 *(0.1)*	4.5 (0.3)	16.6	60.9, moderate El Niño
				Average	**23.7 *(1.8)***	**8.2 *(1.8)***	**15.5 *(1.1)***	**20.0 *(1.3)***	**3.5 *(1.3)***	**16.4 *(0.5)***	
				95% CI	**(22.5, 24.8)**	**(7.1, 9.3)**	**(14.8, 16.1)**	**(18.9, 20.8)**	**(2.6, 4.4)**	**(15.9, 16.8)**	

Code S1. R code to prepare dataset, run JAGS model (S3), and generate summary statistics and probability density distributions.

```
rm(list=ls())
# Select JAGS model file ("Morra_MEPS_Model.R")
model<-file.choose()

# Set Working Directory
setwd(dirname(model))
bird.raw<-read.csv("Morra_MEPS_data_2020.csv",head=TRUE,stringsAsFactors=FALSE)
# Remove cases with only one isotope
bird.raw<-bird.raw[!is.na(bird.raw$Glu)&!is.na(bird.raw$Phe),]

# Clean sample ID variable to use as individudal, note that some individuals have
# both bone and feather values but these are estimated independently in the model
bird.raw$Indi<-as.numeric(as.factor(paste(bird.raw$Sample.ID,bird.raw$Tissue)))

#Get rid of 0's for time peroid indicator variable
bird.raw$Time<-bird.raw$Time+1

#Reassign rep count to ensure no duplicates, note the numerical value given to each
# observation is irrelevent so long as it is not duplicated
nIndi<-max(bird.raw$Indi)
for (i in 1:nIndi){
  temp<-nrow(bird.raw[bird.raw$Indi==i,])
  bird.raw[bird.raw$Indi==i,"Rep"]<-1:temp
}
# Reassign factors to numerical values
bird.raw$Tissue<-as.numeric(as.factor(bird.raw$Tissue)) # 1=bone, 2=feather
bird.raw$Species<-as.numeric(as.factor(bird.raw$Species)) # 1=LAAL, 2=NESH

# Calculate dimensions needed for data array
nIndi<-max(bird.raw$Indi)
nRep<-max(bird.raw$Rep)
nSpecies<-max(bird.raw$Species)
nTime<-max(bird.raw$Time)
nTissue<-max(bird.raw$Tissue) # 1=feather, 2=bone
nIso<-2

# Create array with dimensions y[nIndi, nRep, nTime, nSpecies]
y<-array(NA, dim=c(nIndi, nRep, nTime, nSpecies, nTissue, nIso))
for (i in 1:nIndi){
   for (t in 1:nTime){
    for (s in 1:nSpecies){
     for (b in 1:nTissue){
     temp<-bird.raw[bird.raw$Indi==i&
                 bird.raw$Time==t&
                 bird.raw$Species==s&
                 bird.raw$Tissue==b,c("Glu", "Phe")]
     temp.reps<-nrow(temp)
     if (temp.reps>0){  # skip over empty portions of data array
```

```
      y[i,1:temp.reps,t,s,b,1:nIso]<-unlist(temp)
    }}}}}

# Gather items needed for JAGS
JAGS.time<-c()
JAGS.species<-c()
JAGS.tissue<-c()
for (i in 1:nIndi){
  JAGS.time[length(JAGS.time)+1]<-unique(bird.raw[bird.raw$Indi==i,"Time"])
  JAGS.species[length(JAGS.species)+1]<-unique(bird.raw[bird.raw$Indi==i,"Species"])
  JAGS.tissue[length(JAGS.tissue)+1]<-unique(bird.raw[bird.raw$Indi==i,"Tissue"])
}

jags.data <-list(y=y, nIso=nIso, ONES=diag(2), # ONES is an identity matrix needed for the
prior on variance terms
            nIndi=nIndi, nSpecies=nSpecies, nTime=nTime, nReps=nRep, time=JAGS.time,
            species=JAGS.species, tissue=JAGS.tissue, nTissue=nTissue)

params <- c( "pop.sigma", "obs.sigma", "pop.mu", "indi.mu",
        "delta.phe", "delta.glu.phe", "pop.glu.phe", "p.phe", "p.glu.phe",
        "LAAL", "NESH", "LAAL.tissue.diff.p", "NESH.tissue.diff.p", "NESH.time.diff.p",
        "LAAL.time.diff.p", "Species.LAAL_NESH.p")

library(jagsUI)
ni <-100000
nb <-10000
nt <-3
nc <-3
out <- jags(jags.data, inits = NULL, parameters.to.save = params, model.file = model,
n.chains = nc,
        n.thin = nt, n.iter = ni, n.burnin = nb, store.data = TRUE,
        parallel = TRUE)

#check results
times<-c("old","mid/mod","mod")
isotopes<-c("Phe","Glu-Phe")
tissues<-c("Bone","Feather")
species<-c("LAAL", "NESH")

#Graphing
LAAL<-array(out$sims.list$LAAL[,c(1,2),,],dim=c(90000,2,2,2),dimnames =
list(1:90000,times[c(1,3)],isotopes,tissues))
apply(LAAL,c(2,3,4),quantile,probs=c(0.5,0.025,0.975))
NESH<-array(out$sims.list$NESH,dim=c(90000,3,2,2),dimnames =
list(1:90000,times,isotopes,tissues))
apply(NESH,c(2,3,4),quantile,probs=c(0.5,0.025,0.975))

# Tissue Comparison
#LAAL
array(out$mean$LAAL.tissue.diff.p, dim=c(3,2), dimnames = list(times,isotopes))[1:2,]
#NESH
```

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```
array(out$mean$NESH.tissue.diff.p, dim=c(3,2), dimnames = list(times,isotopes))

# Time Period Comparison
#LAAL
array(out$mean$LAAL.time.diff.p, dim=c(2,2), dimnames = list(tissues,isotopes))
#LAAL
array(out$mean$NESH.time.diff.p, dim=c(2,2), dimnames = list(tissues,isotopes))

# Species Comparison
array(out$mean$Species.LAAL_NESH.p, dim=c(3,2,2), dimnames =
list(times,isotopes,tissues))

library(ggplot2)
temp1<-data.frame(LAAL[,"old","Phe","Feather"],"LAAL Old")
temp2<-data.frame(LAAL[,"mod","Phe","Feather"],"LAAL Mod")
temp3<-data.frame(NESH[,"old","Phe","Feather"],"NESH Old")
temp4<-data.frame(NESH[,"mid/mod","Phe","Feather"],"NESH Mod")
colnames(temp1)<-colnames(temp2)<-colnames(temp3)<-colnames(temp4)<-c("x","Group")
plot1.data<-rbind(temp1, temp2, temp3, temp4)

plot1<-ggplot(plot1.data) + geom_density(aes(x=x, fill=Group), colour=NA, alpha=0.9) +
  scale_x_continuous(name="Phe", limits=c(0,10))
plot1

temp1<-data.frame(LAAL[,"old","Glu-Phe","Feather"],"LAAL Old")
temp2<-data.frame(LAAL[,"mod","Glu-Phe","Feather"],"LAAL Mod")
temp3<-data.frame(NESH[,"old","Glu-Phe","Feather"],"NESH Old")
temp4<-data.frame(NESH[,"mid/mod","Glu-Phe","Feather"],"NESH Mod")
colnames(temp1)<-colnames(temp2)<-colnames(temp3)<-colnames(temp4)<-c("x","Group")
plot2.data<-rbind(temp1, temp2, temp3, temp4)
plot2<-ggplot(plot2.data) + geom_density(aes(x=x, fill=Group), colour=NA, alpha=0.9) +
  scale_x_continuous(name="Glu-Phe", limits=c(14,19))
plot2
```

Code S2. R code for JAGS model.

```
#JAGS model
model {
 for (s in 1:nSpecies){
  for (b in 1:nTissue){
   # Variance terms for observation model
   obs.prec[1:nIso, 1:nIso, s, b] ~ dwish(ONES, 2)
   obs.sigma[1:nIso, 1:nIso, s, b] <- inverse(obs.prec[1:nIso, 1:nIso, s, b])

   for (t in 1:nTime){
     pop.prec[1:2,1:2,t, s, b] ~ dwish(ONES, 2)
     pop.sigma[1:2,1:2,t, s, b] <- inverse(pop.prec[1:nIso, 1:nIso, t, s, b])
     for (r in 1:nIso){
       pop.mu[t, s, b, r] ~ dnorm(0, 0.01)
 }}}}

 # Observational model
 for (i in 1:nIndi){
  for (j in 1:nReps){
   for (t in 1:nTime){
    for (s in 1:nSpecies){
     for (b in 1:nTissue){
      y[i,j,t,s,b,1:nIso] ~ dmnorm(indi.mu[i,b,1:nIso], obs.prec[1:nIso, 1:nIso, s, b])
   }}}}}

 #Population/time model
 for (i in 1:nIndi){
  for (b in 1:nTissue){
   indi.mu[i,b,1:nIso] ~ dmnorm(pop.mu[time[i],species[i],tissue[i],1:nIso],
pop.prec[1:nIso,1:nIso,time[i], species[i], tissue[i]])
  }}

 #Population Summaries
 #LAAL[time, isotope, tissue]
 for (t in 1:nTime){
  for (b in 1:nTissue){
   LAAL[t,1,b]<-pop.mu[t,1,b,2] # Phe
   LAAL[t,2,b]<-pop.mu[t,1,b,1] - pop.mu[t,1,b,2] #Glu - Phe
   NESH[t,1,b]<-pop.mu[t,2,b,2] # Phe
   NESH[t,2,b]<-pop.mu[t,2,b,1] - pop.mu[t,2,b,2] #Glu - Phe
  }}

 for (t in 1:nTime){
  for (r in 1:nIso){
   LAAL.tissue.diff[t,r]<-LAAL[t,r,1]-LAAL[t,r,2]
   LAAL.tissue.diff.p[t,r]<-step(LAAL.tissue.diff[t,r])
   NESH.tissue.diff[t,r]<-NESH[t,r,1]-NESH[t,r,2]
   NESH.tissue.diff.p[t,r]<-step(NESH.tissue.diff[t,r])
  }}
```

```
  for (b in 1:nTissue){
   for (r in 1:nIso){
     LAAL.time.diff[b,r]<-LAAL[1,r,b]-LAAL[2,r,b]
     LAAL.time.diff.p[b,r]<-step(LAAL.time.diff[b,r])
     NESH.time.diff[b,r]<-NESH[1,r,b]-NESH[2,r,b]
     NESH.time.diff.p[b,r]<-step(NESH.time.diff[b,r])
     for (t in 1:nTime){
       Species.LAAL_NESH[t,r,b]<-LAAL[t,r,b]-NESH[t,r,b]
       Species.LAAL_NESH.p[t,r,b]<-step(Species.LAAL_NESH[t,r,b])
     }}}

}
```