Appendix S1. *Algorithm for Estimating Intake Rates and Diet from Observational Data of Foraging Sea Otters.*

The southern sea otter (*Enhydra lutris nereis*) is the smallest of marine mammals, and is an apex predator in nearshore marine food webs of central California. Sea otters feed entirely on sub-tidal and inter-tidal benthic invertebrates (Riedman & Estes 1990), making dives of up to 100m in depth and over 5 min in duration to search for and capture invertebrate prey from the benthos. Sea otters have a highly diverse and individually variable diet (Estes *et al.* 1981; Ostfeld 1982; Kvitek & Oliver 1988; Estes *et al.* 2003). At high population densities they are capable of limiting the abundance of several of their prey populations, including sea urchins, leading to important indirect effects such as increased abundance of kelp (Estes & Palmisano 1974; Estes 1990). Sea otters provide a particularly good model for investigating variation in foraging behavior because their distribution is limited to the near-shore habitat where they are easily observed. More importantly, sea otters bring all captured prey to the surface to handle and consume, making it possible to quantify their foraging behavior and diet directly and non-invasively via shore-based observations. Such observations can be used to estimate species-specific prey intake rates for individual tagged sea otters, as described below.

Observational foraging data are collected from radio-tagged sea otters following well-established protocols (Ralls *et al.* 1995; Watt *et al.* 2000; Estes *et al.* 2003; Tinker *et al.* 2008). Field observations are collected 7 days per week throughout the study period, with teams of 1–2 observers making systematic searches of the study areas and sequentially targeting specific animals for foraging observations. Study animals are initially located by radio signal using standard telemetric techniques, and then visually monitored them from shore using a 50-80X spotting scopes (Questar Inc., Isanti, MN). Foraging bouts (defined as contiguous sequences of feeding dives made by the focal otter) typically last 1-4 hours, and data are recorded throughout the entire bout or for as many dives as possible. The information recorded includes date and time, precise location of each dive (determined by visual triangulation using GPS, compass and laser range-finder), duration of the subsurface dive interval (" DT") and the post-dive surface interval ("ST") for each feeding dive (in seconds), outcome of each dive (i.e. whether or not prey was captured), species of prey captured, number and size of prey items, per-item handling time (number of seconds required to handle and consume each item), whether or not tools were used to handle the prey, and ambient conditions (including sea-state, wind, etc.). Prey size is recorded as the estimated diameter of the shell or maximum body dimension (excluding appendages), categorized into 5cm size-classes. For observations where prey cannot be reliably identified to species, the items in question are assigned to the lowest possible taxonomic unit. Any items that cannot be reliably categorized to any taxonomic level are listed as "un-identified". Additional information recorded by observers includes numbers of prey items that were stolen by or from the focal animal and, in the case of females with dependent pups, the number of items that were shared with the pups.

When recording sea otter feeding behavior from shore, it is typical that a substantial proportion of dive records (10-50%) are incomplete in some way. The most common reason for an incomplete record is that prey type is unidentified, but in some cases the number of prey items or prey size cannot be reliably recorded. A common approach when analyzing data sets of this nature is to simply "throw away" all records with incomplete information and analyze just the remaining data. Such an approach makes the generally unrecognized assumption that the sub-set of the data used for analysis are perfectly representative of the incomplete records that were discarded. In the case of sea otter feeding data this assumption is usually violated, often to a substantial degree, because there are a variety of biases underlying which types of records are likely to be incomplete. In particular, dives that are far from shore, or have very short surface times, or include very small prey types are more likely to be missed or incomplete.

To account for these biases, we have adopted a Monte Carlo procedure that makes maximum use of incomplete records by taking advantage of the strong correlations that exist between dive parameters to account for the above mentioned biases while at the same time providing more robust estimates of uncertainty in each parameter. This algorithm is described elsewhere (e.g. Tinker et al 2008, Supplementary online materials) and consists of the following 5 steps:

Step 1. Use all collected data and maximum likelihood methods to fit appropriate probability distributions (indicated below in parentheses) to each of the following 6 parameters (or related sets of parameters): i) probability of successful prey capture on a dive (binomial); ii) probability that prey is identified, given that it is captured (binomial); iii) probability that captured prey is of type *i*, given that it is identified (multinomial); iv) dive and surface interval durations (log-normal) for unsuccessful dives, un-identified prey dives, and dives in which prey type *i* was captured; v) edible biomass for prey type *i* (log-normal), or size class (negative binomial) in the case of un-identified prey, stratified by surface interval (short, medium and long surface intervals = 1-45, 46-90, and >90 s respectively); vi) regression parameters and residual variance (normal) from a multiple regression of number of items consumed per dive (for prey type *i*) vs. dive surface interval and prey biomass (or prey size class in the case of un-identified prey). In general, the number of items consumed per dive is an increasing function of the time spent on the surface and a decreasing function of prey size (for most taxa, many small items or one large item can be handled and consumed in a given period of time). Note that numbers of items consumed per dive are not limited to integer values, as whole or partial items can be discarded, stolen or shared with a pup and these are discounted appropriately.

Step 2. Generate "simulated feeding bouts" of sequential dives for each individual at each study site in a manner that maintains the empirically-derived frequency distributions for each of the parameters described in step 1, as well as the co-variances between parameters. These simulated bouts include dives with no captured prey, and dives with captured but unidentified prey.

Step 3. For each simulated dive in which prey type is assigned as "unidentified", assign prey size and number of items based on the empirically-derived distributions and relationships for un-identified prey (see step 1). Next, randomly draw a prey type from the entire observed set of identified-prey captures for that individual having "sufficiently similar" dive and surface times, prey size values and number of items. Sufficiently similar is defined as having dive and surface times ± 30 seconds of the simulated dive and surface times, having the exact same size class, and having the exact same number of items in the case of simulated dives with ≤ 2 items, or ± 1 item in the case of simulated dives with > 2 items. If there are no observed dives for that individual that meet these criteria, then draw from the data set for all animals of the same sex and from the same study site. If there are still no observed dives that meet these criteria, then sequentially broaden the data set to include both sexes, and then other study sites.

Step 4. Repeat steps 1-3 for a large number of iterations (100,000). For each iteration, the number of bouts and dives per bout is limited to the observed sample size for each individual and study site.

Step 5 Using the resulting set of Monte Carlo simulations, summarize mean and variance in prey-specific intake rates (g minute^{-1}) for each individual, and estimate diet composition as the proportion of total consumed biomass accounted for by each prey type.

Note that in the special case of a data set in which all data records are complete (i.e. no unidentified prey and no missing data fields), the point estimates for prey intake rate and diet composition that would be calculated from a simple arithmetic summary of the raw data will be approximately equal to the mean values generated by the Monte Carlo simulations. Assuming a large enough sample size, the variance estimates in this special case will primarily reflect "process error" (e.g. actual variability in prey size and numbers of items captured per dive). In the more typical case of data

sets with substantial numbers of incomplete records (including unidentified prey and other missing data fields), the point estimates derived from a simple arithmetic summary of only the complete records will tend to differ from mean values generated by the Monte Carlo simulations, with the magnitude of the difference depending on the magnitude of the biases inherent in the data set (i.e. biases as to which records were incomplete). The variance estimates generated by the Monte Carlo simulations in this case incorporate both process error and sampling uncertainty: data sets with small sample sizes and/or a high proportion of missing values will result in larger variance estimates and thus wider confidence intervals around the point estimates.

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Appendix S2. *Equations, program links and/or source code for all statistics or analytical algorithms reported in the text*

Niche Width Statistics

We used the following equations to estimate Total Niche Width (TNW_S) and the Within-Individual Component of Niche Width (WIC_S):

$$\mathrm{TNW_s} = -\sum_j q_j \ln q_j$$

$$\mathrm{WIC_s} = \sum_i p_{i\cdot}\left(-\sum_j p_{ij} \ln p_{ij}\right)$$

where the elements p_{ij} describe the proportion of the *j*th resource category in the diet of individual *i*, variable $p_{i\cdot}$ is the proportion of all resources used by the population that are used by individual *i,* and q_j is the proportion of the *j*th resource category in the population's niche.

Citation: equations 4, 5 and 6 in Bolnick D.I., Yang L.H., Fordyce J.A., Davis J.M. & Svanbäck R. (2002). Measuring individual-level resource specialization. *Ecology*, 83, 2936-2941.

Proportion of Total Niche Width (TNW_S) contributed by within individual variation (WIC_S / TNW_S)

We used the following MATLAB function for calculating WIC_S / TNW_S:

```
function [PSI,PSI_btstr,meanPSI,sdPSI,PSI_CL,Prob_gen,Prob_HO,NicheW,NicheWr] = PSI_boot(data,n1,n2,H0)
% Function to calculate "Proportional Similarity Index" (PSI) and
% Niche Width statistics (including WICs/TNWs) using bootstrap resampling
% of an individual resource use matrix following the methods described in:
%  Bolnick, D. I., L. H. Yang, J. A. Fordyce, J. M. Davis, and R. Svanbäck.
%      2002. Measuring individual-level resource specialization.
%      Ecology 83:2936-2941.
%
% Input Arguments
% data = Matrix with individuals as rows and prey types as collumns,
%     with each cell representing the proportion of prey type j in the
%     the diet of individual i
% n1 = number of bootstrap replications
% n2 = number of individuals to be sampled (with replacement) at each
%      bootstrap replication
```

```
% H0 = Hypothesized "null" value for PSI
%
% Output Arguments
%  PSI = matrix of "raw" PSi values for each individual
%  PSI_btstr = bootstrap mean, lower CL and upper CL for PS for individuals
%  meanPSI = bootstrapped mean population-level PSI value
%  sd = standard deviation for population-level PSI value
%  PSI_CL = lower and upper 95% bootstrap confidence limits for mean PSI (col 1)
%           and 95% CL for population PSI (with sample uncertainty) (col 2)
%  Prob_gen = P value for each individual --> probability that individual
%            is selecting prey in proportion to pop'n frequency
%  Prob_HO = Probability that population PS value is no different than H0
%  NicheWr = replications of Niche Width Stats:
%   WICs = Within-ind component of Niche width
%   BICs = Between-ind component of Niche width
%   TNWs = Total Niche Width
%   WICs/TNWs = WIC/Total Niche Width... note: TNW can be derived as WIC * 1/(WIC/TNW)
%  NicheW = Niche Width Stats: mean (first row), std dev'n (second row),
%    and 95% CI (3rd and 4th rows) of:
%   WICs = Within-ind component of Niche width
%   BICs = Between-ind component of Niche width
%   TNWs = Total Niche Width
%   WICs/TNWs = WIC/Total Niche Width... note: TNW can be derived as WIC * 1/(WIC/TNW)
%%
J = size(data,2); % number of prey types
I = size(data,1); % number of individuals
PSI = zeros(I,1);
PSI_b = zeros(n1,I);
PSI_r = zeros(n1,I);
PSI_btstr = zeros(I,3);
Prob_H0 = zeros(n1,1);
PSi = zeros(n1,1);
PS = zeros(n2,1);
Ind_Sums = sum(data,2);
NicheWr = zeros(n1,5);
p = [];
pp = [];
q = [];
y = [];
for i = 1:I
    minpq = [];
```

```
    for j = 1:J
        term1 = data(i,j)/sum(data(i,:));
        term2 = sum(data(:,j))/sum(sum(data(:,:)));
        q(j) = term2;
        minpq = [minpq; min([term1 term2])];
        pp(i,j) = term1;
        y(i,j) = data(i,j)/sum(data(:,j));
    end
    p(i) = sum(data(i,:))/sum(sum(data(:,:)));
    PSI(i,1) = sum(minpq);
end
%%
for n = 1:n1
    p = [];
    pp = [];
    q = [];
    y = [];
    dat = data(unidrnd(I,n2,1),:);
    for i=1:n2
        minpq = [];
        for j = 1:J
            term1 = dat(i,j)/sum(dat(i,:));
            term2 = sum(dat(:,j))/sum(sum(dat(:,:)));
            q(j) = term2;
            minpq = [minpq; min([term1 term2])];
            pp(i,j) = term1;
            y(i,j) = dat(i,j)/(sum(dat(:,j))+ 1.0e-020);
        end
        p(i) = sum(dat(i,:))/sum(sum(dat(:,:)));
        PS(i,1) = sum(minpq);
    end
    indNW = mean((-1.*sum(pp(:,:).*log(pp(:,:)+1.0e-020),2)));
    WIC = sum(p(:).*(-1.*sum(pp(:,:).*log(pp(:,:)+1.0e-020),2)));
    BIC = -1*(sum(p(:).*log(p(:))))-(sum(q(:)'.*(-1.*sum(y(:,:).*log(y(:,:)+1.0e-020),1))));
    TNW = -1*sum(q(:).*log(q(:)+1.0e-020));
    NicheWr(n,:) = [WIC BIC TNW WIC/TNW indNW];
    [PHAT, PCL] = mle(PS);
    PSi(n,1)= PHAT(1);
    if PCL(1,1)<H0 && PCL(2,1)>H0
        Prob_H0(n,1) = 1;
    end
```

```
    for i = 1:I
        dat2 = [data(i,:); dat];
        Gen_R = cumsum(sum(dat2)./sum(sum(dat2)));
        datR = zeros(1,J);
        for c = 1:Ind_Sums(i)
            test = rand();
            j = 1;
            while j <= J
                if test <= Gen_R(j)
                    datR(j) = datR(j)+1;
                    j = J+1;
                else
                    j = j+1;
                end
            end
        end
        minpq = [];
        minpqR = [];
        for j = 1:J
            termR = datR(1,j)/sum(datR(1,:));
            term1 = dat2(1,j)/sum(dat2(1,:));
            term2 = sum(dat2(:,j))/sum(sum(dat2(:,:)));
            minpq = [minpq; min([term1 term2])]; %#ok<*AGROW>
            minpqR = [minpqR; min([termR term2])];
        end
        PSI_b(n,i) = sum(minpq);
        if sum(minpqR)<=sum(minpq)
            PSI_r(n,i) = 1;
        end
    end
end
[PHAT, PCL] = mle(PSi);
meanPSI = PHAT(1);
sdPSI = PHAT(2);
PSI_CL(:,1) = PCL(:,1);
PSI_CL(1,2) = prctile(PSi,2.5);
PSI_CL(2,2) = prctile(PSi,97.5);
Prob_HO = mean(Prob_H0);
for i = 1:I
    [PHAT, PCL] = mle(PSI_b(:,i));
    PSI_btstr(i,1) = PHAT(1);
```

```
    PSI_btstr(i,2) = PCL(1,1);
    PSI_btstr(i,3) = PCL(2,1);
end
Prob_gen = mean(PSI_r)';
NicheW(1,:) = mean(NicheWr(:,:));
NicheW(2,:) = std(NicheWr(:,:));
NicheW(3,:) = prctile(NicheWr(:,:),2.5);
NicheW(4,:) = prctile(NicheWr(:,:),97.5);
```

Average Density of Connections/Pairwise diet dissimilarity index (E)

We used DIETA to compute E (https://webspace.utexas.edu/dib73/TheBolnickLab/Programs/Programs.html)

Nestedness (NODF)

We used program ANINHADO to compute nestedness (www.guimaraes.bio.br)

Modularity (M)

We used program NETCARTO, kindly provided by Roger Guimerà.

Weighted nestedness (WNODF)

We used the following Matlab script for calculating WNODF:

```
% the r matrix has individuals in the rows and the resources in the columns

matrix=r;
row=size(r,1); % number of rows (individuals)
col=size(r,2); % number of columns (resources)

%% Creating the proportion matrix
N=sum(matrix'); % sums the marginal totals of rows

for i=1:row
    for j=1:col
        matrix(i,j)=matrix(i,j)/N(i); % defines proportion of each cell in relation to
                                      % the marginal total of the row
```

```
    end
end

%% Sorting the matrix by resource's strength
sum_resource=sum(matrix); % defines the marginal totals to columns
matrix2=matrix; % auxiliary matrix
matrix2(row+1,:)=sum_resource; % adds the marginal totals to columns in the end row of the matrix
degree=zeros(row+1,1);

for i=1:row
    for j=1:col
        if matrix(i,j)>0
            degree(i,1)=degree(i,1)+1; % counts the number of non-zeroed columns of the row i
                                       %   (degree of the row i)
        end
    end
end
matrix2(:,col+1)=degree; % adds the degree of the rows in the end column of the matrix

matrix2=sortrows(matrix2,-(col+1)); % sorts the matrix by the decreasing of degrees of rows
matrix2=matrix2';
matrix2=sortrows(matrix2,-(row+1)); % sorts the matrix by the decreasing of marginal totals of the columns
matrix2=matrix2';
matrix=matrix2(1:row, 1:col);

%% Computing WNODF

nrow=zeros(row);
ncol=zeros(col);

% how much of the columns can be predicted by rows

degreer=matrix2(:,col+1); % degrees of the rows

for i=1:row-1
    for j=2:row

        % if the rows with lower degrees have subsets of non-zeroed columns
        % comparing to the higher degree rows, and if the values are subsets
```

```
        % of the higher degree rows, it is counted 1 to compute the "nrow"
        % value between rows i and j

        if degreer(i,1)>degreer(j,1)
            count=0;
            for k=1:col
                if matrix(i,k)>0
                    if matrix(j,k)>0
                        if matrix(i,k)>matrix(j,k)
                            count=count+1;
                        end
                    end
                end
            end

            nrow(i,j)=count/degreer(j);

        end
    end
end

nrow=100.*nrow;

% how much of the rows can be predicted by columns
degreec=zeros(col,1);

% if the columns with lower degrees have subsets of non-zeroed rows
% comparing to the higher degree columns, and if the values are subsets
% of the higher degree columns, it is counted 1 to compute the "ncol"
% value between columns i and j

for i=1:row
    for j=1:col
        if matrix(i,j)>0 it % counts the number of non-zeroed rows of the column j (degree of the column j)
            degreec(j,1)=degreec(j,1)+1;
        end
    end
end
```

```
for i=1:col-1
    for j=2:col
        if degreec(i,1)>degreec(j,1)
            count=0;
            for k=1:row
                if matrix(k,i)>0
                    if matrix(k,j)>0
                        if matrix(k,i)>matrix(k,j)
                            count=count+1;
                        end
                    end
                end
            end

            ncol(i,j)=count/degreec(j);

        end
    end
end
ncol=100.*ncol;

WNODF_Row=sum(nrow(:)); % sums the "nrow" matrix
R=(row*(row-1))/2;
WNODF_Row=(WNODF_Row)/R; % calculates WNODF value to the rows

WNODF_Col=sum(ncol(:));  % sums the "ncol" matrix
C=(col*(col-1))/2;
WNODF_Col=(WNODF_Col)/C; % calculates WNODF value to the columns
```

Weighted Clustering coefficient (WCC)

We used the following Matlab script to calculate WCC

```
%100410 - metric for 2 measures of clustering
% each input matrix has individuals in the rows and the resources in the
% columnns

A=importdata('filename.txt'); % imports the file with input matrices filenames
```

```
Nnets=size(A,1); % define the number of nets
output=zeros(Nnets,1);

for net=1:Nnets

    name=A(net,1);

    r=dlmread(name{1,1});

    row=size(r,1); % number of rows (individuals)
    col=size(r,2); % number of columns (resources)

    %binary clustering coefficients for individuals

    %4-paths
    paths4=0;
    pathc4=0;

    for i=1:row %1  %looks for the 4-paths in the matrix
        for j=1:col %A(1)
            if r(i,j)>0
                for k=1:row %2
                    if k~=i && r(k,j)>0
                        for l=1:col %C (3)
                            if l~=j && r(k,l)>0
                                for m=1:row %(4)
                                    if m~=i && m~=k && r(m,l)>0 % with 4 linked nodes we have one 4-path
                                        SUMs=r(i,j)+r(k,j)+r(k,l)+r(m,l);
                                        SUMs=SUMs/4; % weighted clustering coefficient of 4-paths
                                        paths4=paths4+SUMs;

                                        count=0;
                                        for n=1:col
                                            if n~=j && n~=l && r(m,n)>0 && r(i,n)>0 % counts the 4-paths
that close

                                                SUMc=r(i,j)+r(k,j)+r(k,l)+r(m,l)+r(m,n)+r(i,n);
                                                count=count+1;
```

```
                                        end
                                    end
                                    if count>0
                                        count=count*6; % considers all focal nodes in the closed 4-path
                                        pathc4=pathc4+(SUMc/count); weighted clustering coefficient of
closed 4-paths

                                    end
                                end
                            end
                        end
                    end
                end
            end
        end
    end
    output(net)=pathc4/paths4 % WCC values of the read matrices, in the same order of filename.txt
end
```

Fractional Diet Composition Analysis (FDCA)

We used the following MATLAB script to generate binary matrices using Fractional diet composition analysis:

```
function [temp]=sliceoff(r,cutoff)
 % the input matrix has individuals in the rows and the resources in the columns

row=size(r,1); % number of rows (individuals)
col=size(r,2); % number of columns (resources)

% Slicing off the weighted matrix to generate binary matrices
% let's remove all resources the sum less or equal the cutoff

temp=r; % defines a temporary matrix (temp) equals the input matrix

for i=1:row
    SUM=0; % sums of diet percentage
    temp1=temp(i,:);  % auxiliary to diet of animal i
    [maxVal maxInd]=max(temp1); % defines the maximum percentage of anima i diet and its columns index
```

```
    % if the sum of diet percentages is lower than the cutoff and if we didn't
    % run all the animal diet, it defines the next maximum value of diet
    % percentage and its index, and sums to the diet of animal i until the
    % cutoff
    while (SUM < cutoff) && (size(temp1,2) > 0)
        if SUM < cutoff
            SUM = SUM + maxVal;
            temp(i,maxInd)=1; % changes to 1 the maximum values that enters in the diet cutoff
            temp1(maxInd)=0;
            [maxVal maxInd]=max(temp1);
        end
    end
    for j=1:col
        if temp(i,j)<1
            temp(i,j)=0; % changes to 0 all the values that don't enter in the diet cutoff
        end
    end
end

temp(:,find(sum(abs(temp)) == 0))=[]; % removes zeroed columns
```

Appendix S3 *Alternative explanations for dietary differences between SNI and MON/PBL.*

The lack of replicate low-density sites limits the strength of our inference regarding the factor(s) driving lower levels of diet diversity and specialization at San Nicolas Island (SNI) than at the two high-density mainland sites. The most likely alternative explanations include unconsidered environmental variables affecting prey availability (e.g., latitudinal differences between sites, with SNI being the southern-most), differences between sites in the degree of interspecific competition, and a "founder effect", whereby animals initially trans-located to SNI from the mainland were a non-random sample of individuals with unusually low level of individual-level variation in prey preferences. The interpretation of our results must be accompanied by this caveat. However, several lines of evidence argue against these alternative explanations and are more consistent with our hypothesis that across-site differences in individual specialization are driven by density-mediated behavioral responses.

An alternative explanation relying on latitudinal or site-specific differences in prey availability would predict that diets at SNI are less diverse because there is a lower abundance or diversity of available prey. This prediction is inconsistent with previously published subtidal community surveys which indicate that sea otter prey (both preferred and non-preferred types) are more abundant at SNI than at several central California sites (Tinker *et al.* 2008), and that the Channel Islands support a higher diversity of benthic invertebrates in general relative to central California (Blanchette *et al.* 2006).

Variation in interspecific competition could also conceivably contribute to variation in diet diversity, with stronger niche width constraints expected in areas with stronger interspecific competition. Sea otters at SNI do have more potential inter-specific competitors than do otters at MON or PBL, with both sheephead fish and lobsters (both of which are sea urchin predators) occurring in southern California but not in central California. Cowen (1983) has shown experimentally that sheephead can have a limiting influence on sea urchins at San Nicolas Island. However, this effect occurred patchily and much of the surrounding benthos remained urchin-dominated (Cowen, 1983). Furthermore, a 31-year data set on sub-tidal invertebrate abundance at SNI (USGS, unpublished data), which includes the time period prior to the arrival of sea otters, indicates that urchin populations remain much more abundant than at mainland sites (Tinker *et al.* 2008). Thus, as for sea otter populations in general (Estes et al. 2003), the influence of inter-specific competition for resources is likely to be minor relative to intra-specific competition .It therefore seems unlikely that sea otter diet diversity at SNI is strongly affected by interspecific competition, although there are insufficient data on multi-species interactions to entirely rule out this possibility.

For a founder effect to have occurred requires that all trans-located individuals happened to specialize on a single prey type (red urchins), and that this specialization has been passed on to subsequent offspring matrilineally (Estes *et al.* 2003). If this were the case, one would predict that dietary observations made immediately after the translocation (i.e. in the late 1980's) would also testify to low diet diversity and a lack of individual variation in the population. In contrast, Bentall (2005) reports that foraging observations recorded at SNI between 1988-1990 indicated a higher degree of diet diversity (Shannon-Weaver Index: H = 1.9) than exhibited by sea otters in the 2000's (H = 1.6, this study). In 1988-1990, individuals also included "sub-optimal" species, such as sand crabs, that were not observed in the diets of individuals in the 2000's (Bentall 2005). Moreover, the single original founder animal that was still alive and included our current data set was actually found to have the most diverse individual diet of any of the SNI study animals (Tinker *et al.* 2008). This suggests that she has retained foraging behaviors acquired prior to the translocation and thereby maintains a diet dissimilar to the more homogenous diets of the descendent population.

Finally, the strongest line of evidence running counter to alternative, density-independent explanations is provided by two historical data sets from central California recorded shortly after sea otters had re-colonized and were still at very low density. The data of Estes et al., (1981) were collected in 1977 from a site within 40 km of PBL, while the data from Ostfeld (1982) were collected in 1975 from a site within 35 km of MON). Neither data set provides individual-level information. Nevertheless, the population-level diet composition at these low-density sites in the 1970's were remarkably similar to that observed in our 2003-05 data from SNI in that all exhibit strongly skewed distributions, are relatively species poor, and are dominated by urchins (primarily red urchins, *Strongylocentrotus franciscanus*), unlike the two modern high-density sites (Figure S3). We believe this contrast provides compelling evidence that the diets recorded at SNI are representative of what sea otter diets were like at the PBL and MON when otter densities were lower and competition between individuals was weaker.

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Table S1. List of 75 prey species (or higher taxa) consumed by sea otters over the course of the study. Because it was often difficult to distinguish taxonomically and/or morphologically similar species from a distance, all prey were grouped into 14 functional groups (referred to as "prey types" in the text).

Functional Group	Prey Common Name	Latin Name
urchin	red urchin	*Strongylocentrotus fransicanus*
	purple urchin	*Strongylocentrotus purpuratus*
Cancer crab	Pacific rock crab	*Cancer antennarius*
	Dungeness crab	*Cancer magister*
	red rock crab	*Cancer productus*
	Cancer crab, un-ID	*Cancer sp.*
kelp crab	northern kelp crab	*Pugettia productus*
	graceful kelp crab	*Pugettia gracilis*
sand crab	spiny mole crab	*Blepharipoda occidentalis*
	Pacific sand crab	*Emerita analoga*
mussel	horse mussel	*Modiolus modiolus*
	california mussel	*Mytilus californianus*
	bay mussel	*Mytilus trossulus*
	mussel, un-ID	
clam	Nuttall's cockle	*Clinocarduim nuttallii*
	giant rock scallop	*Crassodoma gigantea*
	sunset clam	*Gari californica*
	Macoma clam	*Macoma spp.*
	surf clam	*Mactromeris spp.*
	softshell clam	*Mya arenaria*
	geoduck clam	*Panopea abrupta*
	scallop, un-ID	*Pectinidae spp. or Serripes spp.*
	rock jingle	*Pododesmus macroschisma*
	littleneck clam	*Leucoma staminea*

Functional Group	Prey Common Name	Latin Name
(clam, con't)	washington clam	*Saxidomus nuttalli*
	razor clam	*Siliqua patula*
	jackknife clam	*Taegelus californianus*
	tellin clam	*Tellina spp.*
	Pismo clam	*Tivela stultorum*
	gaper clam	*Tresus nuttalii*
	rough piddock	*Zirfaea pilspryi*
	clam, un-ID	
snail	top snail	*Calliostoma spp.*
	wavy turban snail	*Megastraea undosa*
	Nassa snail	*Nassa fossatus*
	moon snail	*Pollinices sp.*
	brown turban snail	*Chlorostoma brunnea*
	Monterey turban snail	*Chlorostoma montereyi*
	turban snail, un-ID	*Turbinidae*
	snail, un-ID	
abalone	black abalone	*Haliotis cracherodii*
	red abalone	*Haliotis rufescens*
	abalone, un-ID	
sea star	blood star	*Henricia sp.*
	brittle star	*Ophiuroidea*
	bat star	*Patiria miniata*
	ochre star	*Pisaster ochraceus*
	sunflower star	*Pychnopodia helianthoides*
	sea star, un-ID	
worm	pile worm	*Nereis sp.*
	polychaete, un-ID	*Polychaeta*
	peanut worm	*Sipunculus nudus*
	fat innkeeper worm	*Urechis caupo*
	worm, un-ID	

Functional Group	Prey Common Name	Latin Name
small invertebrates	acorn barnacle	*Balanus sp.*
(rocky benthos/kelp)	coraline algae	*Corallina sp., Clathromorphum sp.*
	gumboot chiton	*Cryptochiton stelleri*
	red sea cucumber	*Cucumaria sp.*
	isopod	*Idotea sp.*
	Katy chiton	*Katharina tunicata*
	owl limpet	*Lottia gigantea*
	mossy chiton	*Mopalia sp.*
	nudibranch	*Opisthobranchia*
	gooseneck barnacle	*Pollcipes polymerus*
	chiton, un-ID	*Polyplacophora sp.*
	Stenoplax chiton	*Stenoplax fallax*
	stalked tunicate	*Styela sp.*
	orange puffball sponge	*Tethya californiana*
	lined chiton	*Tonicella sp.*
sand dollar	sand dollar	*Dendraster excentricus*
octopus	octopus	*Octopus sp.*
lobster	spiny lobster	*Panulirus interruptus*

Table S2. Two-sided Wilcoxon rank sum tests assessing whether the central point of each distribution of rank preference correlations with no peripheral prey removed is significantly different from zero.

	All prey (ρ_{all})		Shared prey (ρ_{sh})	
Population	W	p-value	W	p-value
Between-module				
MBA	31427.5	<0.001	19853	<0.001
PBL	87894.5	<0.001	85123	<0.001
SNL	465	<0.001	465	<0.001
Within-module				
MBA	7604	<0.001	5104.5	<0.001
PBL	14952	<0.001	13503	<0.001
SNI	325	<0.001	325	<0.001

Table S3. Population-specific comparisons of within- versus between-module rank preference correlation distributions with no peripheral prey removed using two-sided Mann-Whitney test.

	All prey (ρall)		Shared prey (ρsh)	
Population	W	p-value	W	p-value
MBA	21664.5	< 0.001	16809.5	0.258
PBL	39884	0.076*	34000	0.189
SNI	518.5	0.016	337	0.512

* Significant under a one-sided test (p=0.038).

Table S4. Handling times for six of the most common prey types at the PBL and MON study sites. Standardized, least-squares mean values are shown (with standard errors) after controlling for the effects of prey size class and random individual otter effects. Data are summarized separately for "specialists" (sea otters that included the prey type in their core diets at f = 0.3) and "occasional users" (sea otters that did not include the prey in their core diets, but that did capture and consume the prey occasionally), and the statistical significance of the difference between these two groups is indicated by the associated F and P values from the General Linear model. For prey types where these groups were significantly different, the % difference in handling efficiency (= handling time^{-1}) of specialists relative to generalists is also shown.

	Specialists		Occasional Users		Comparison		% difference in
Prey type	L.S. mean	Std. err	L.S. mean	Std. err	F	P	handling efficiency
abalone	210.0351	32.433	189.8515	26.3396	0.2334	0.6307	n.s.
Cancer crab	170.8106	5.4303	179.0545	11.1113	0.4443	0.5053	n.s.
kelp crab	88.8037	9.727	139.7506	4.1466	23.2144	0.00001	57.37024471
clam	39.6143	3.9151	59.4676	4.1248	12.1872	0.0005	50.11649834
urchin	30.3188	2.0186	36.7412	1.4163	6.7831	0.0097	21.18289642
snail	13.0867	1.0837	18.5603	2.2908	4.665	0.0325	41.82567034

Figure S1. Map of coastal California showing geographic locations of study sites, as well as the range extent and local linear density of the southern sea otter population (based on 2010 range-wide survey data; USGS, unpublished data).

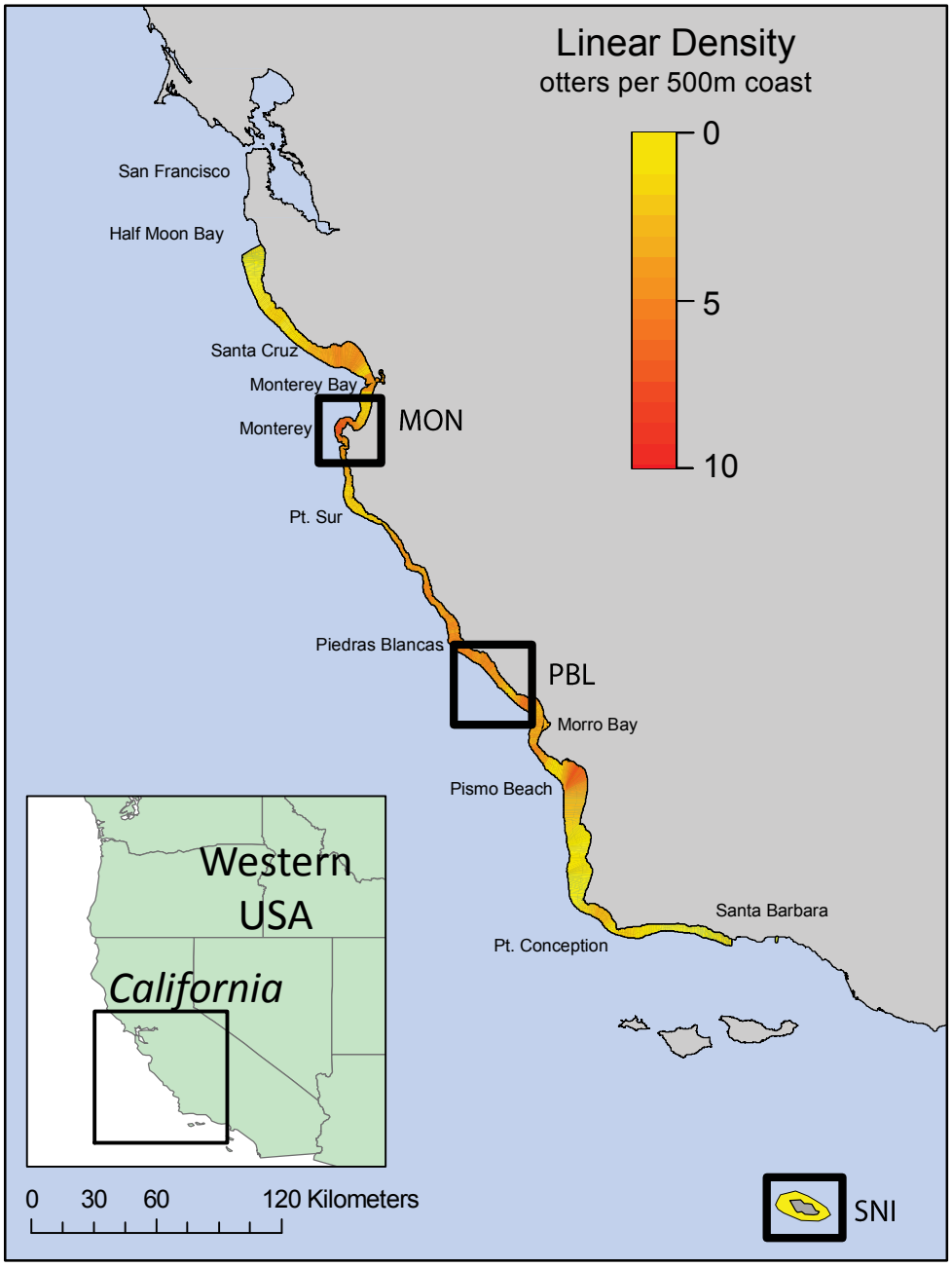
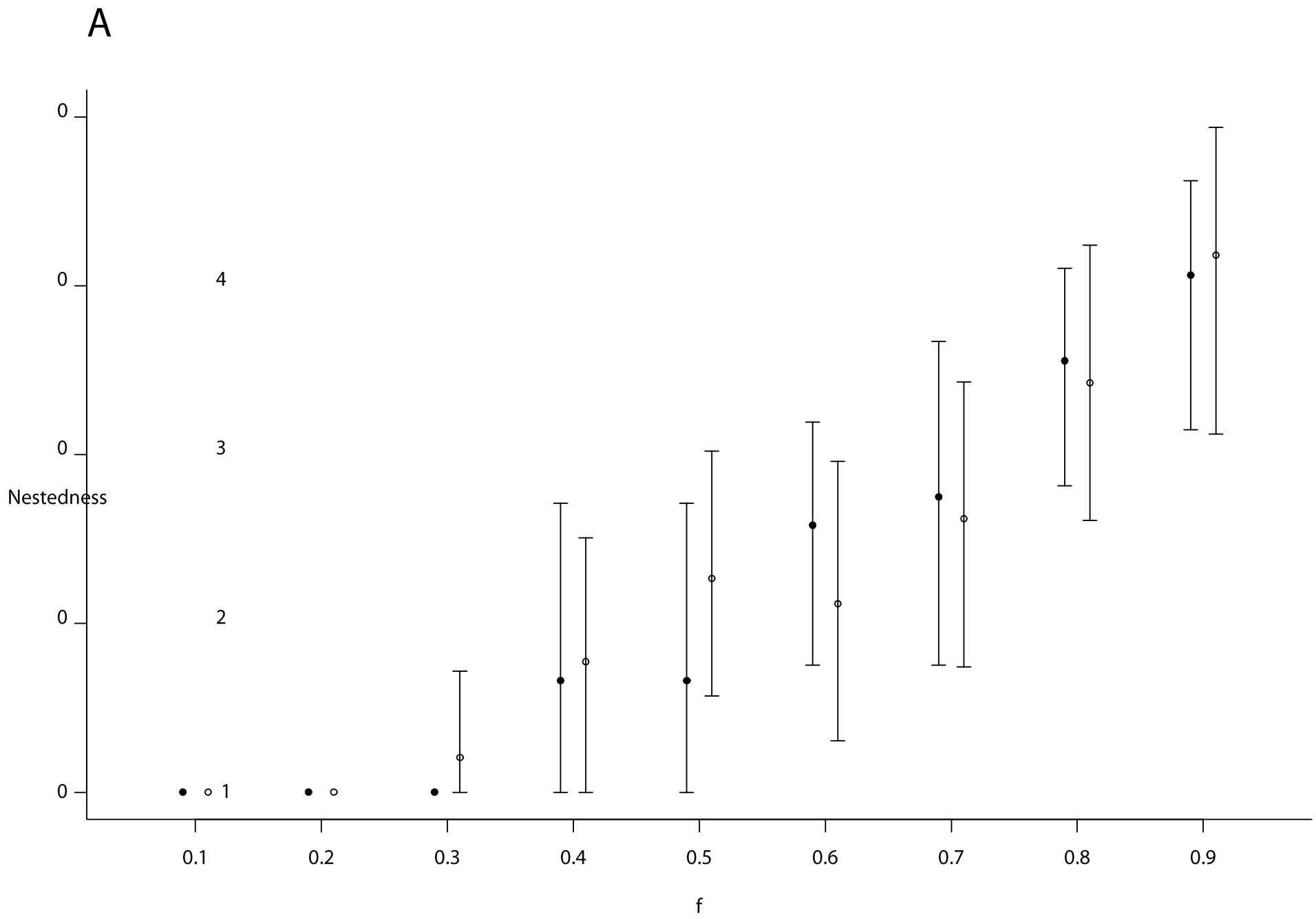


Figure S2. Variation in indices of Nestedness (Panels A and B) and Modularity (Panels C and D) as a function of the fraction (f) of the diet considered, with marginal prey types excluded when $f<1$. Error bars represent the 95% Bootstrap Confidence Intervals for the indices, calculated so as to normalize for sample size differences among study sites as described in the Methods section. Panel A shows a comparison of Nestedness for SNI (closed symbols) vs. PBL (open symbols); Panel B shows a comparison of Nestedness for SNI (closed symbols) vs. MON (open symbols); Panel C shows a comparison of Modularity for SNI (closed symbols) vs. PBL (open symbols); and Panel D shows a comparison of Modularity for SNI (closed symbols) vs. MON (open symbols).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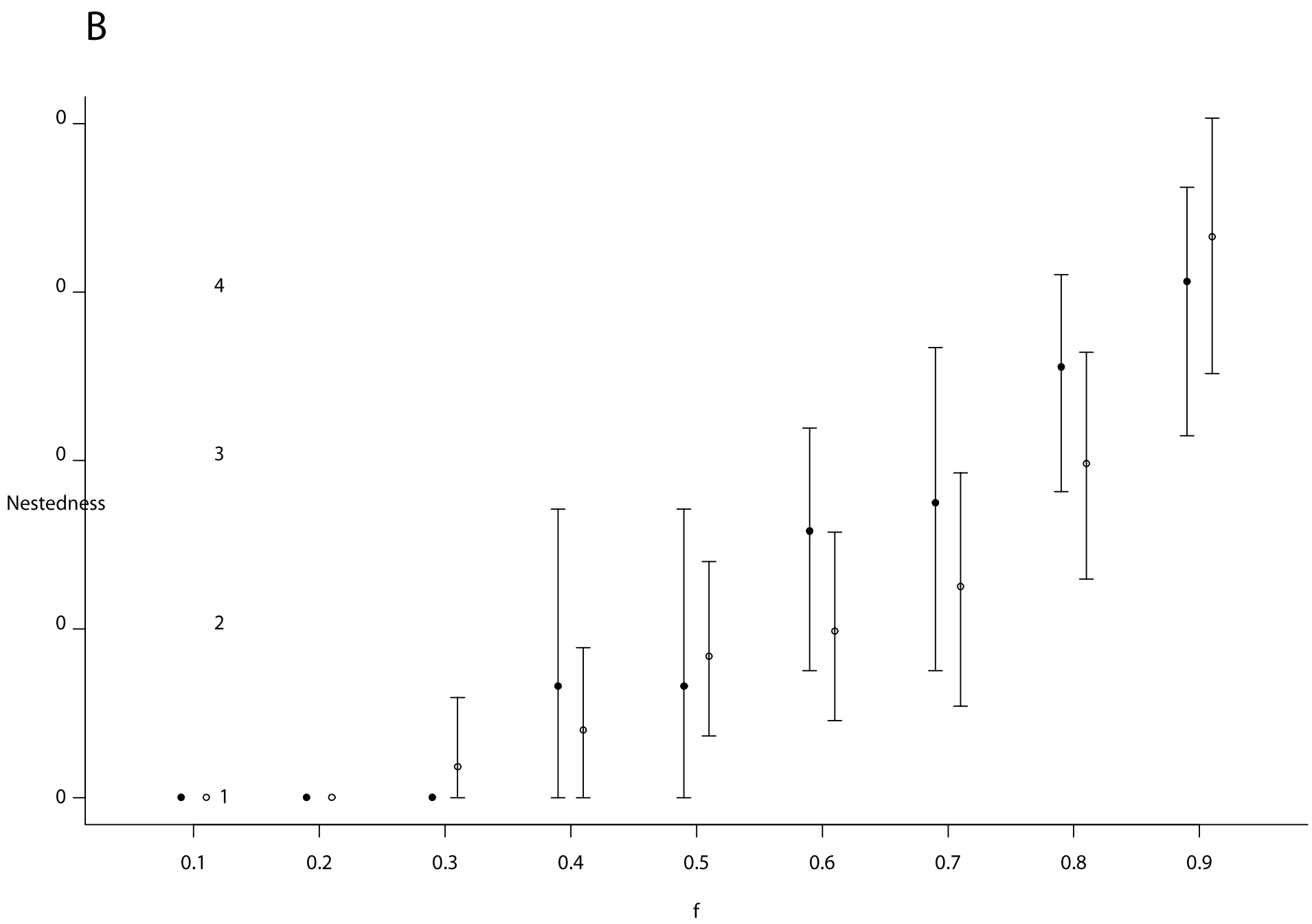
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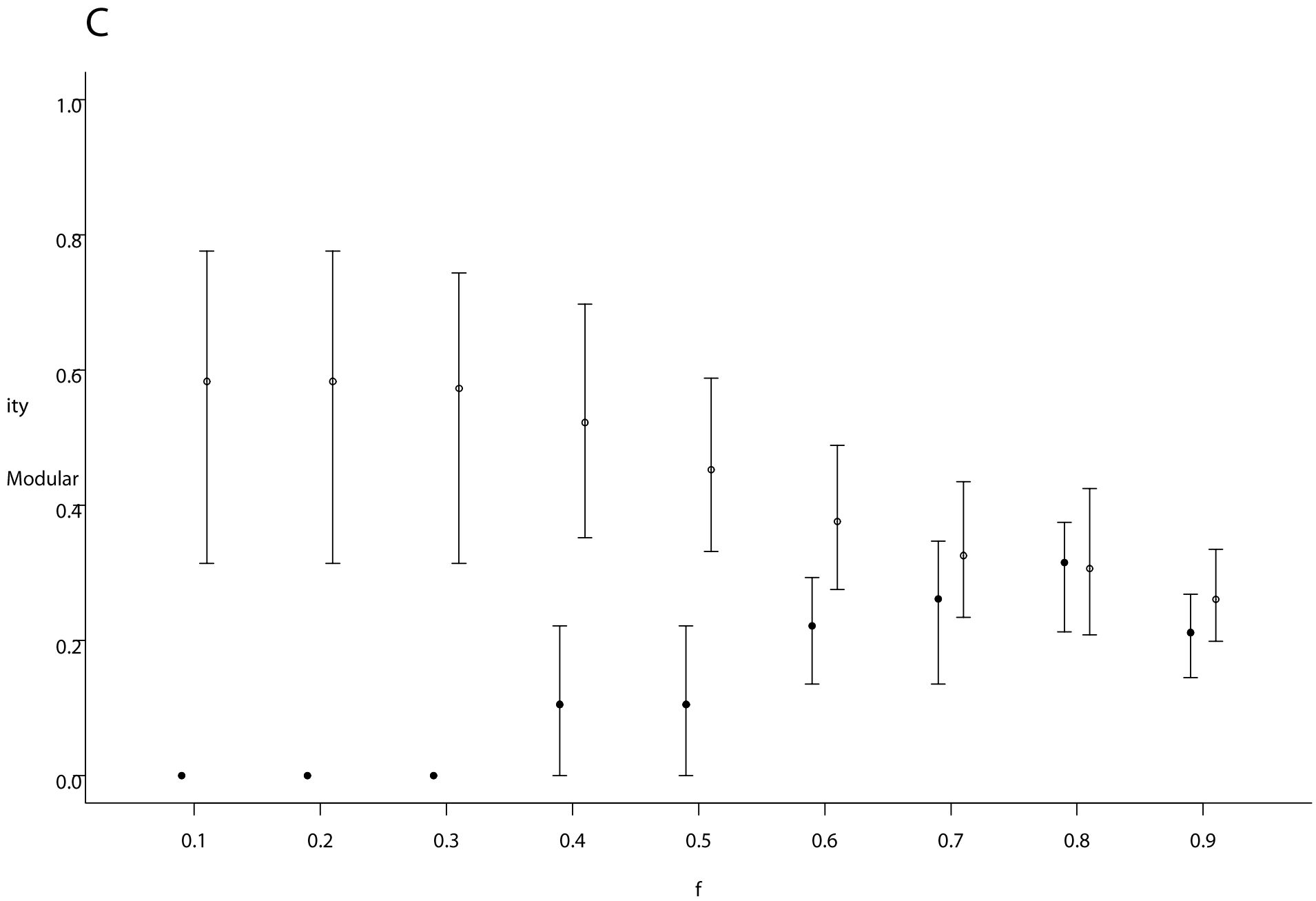
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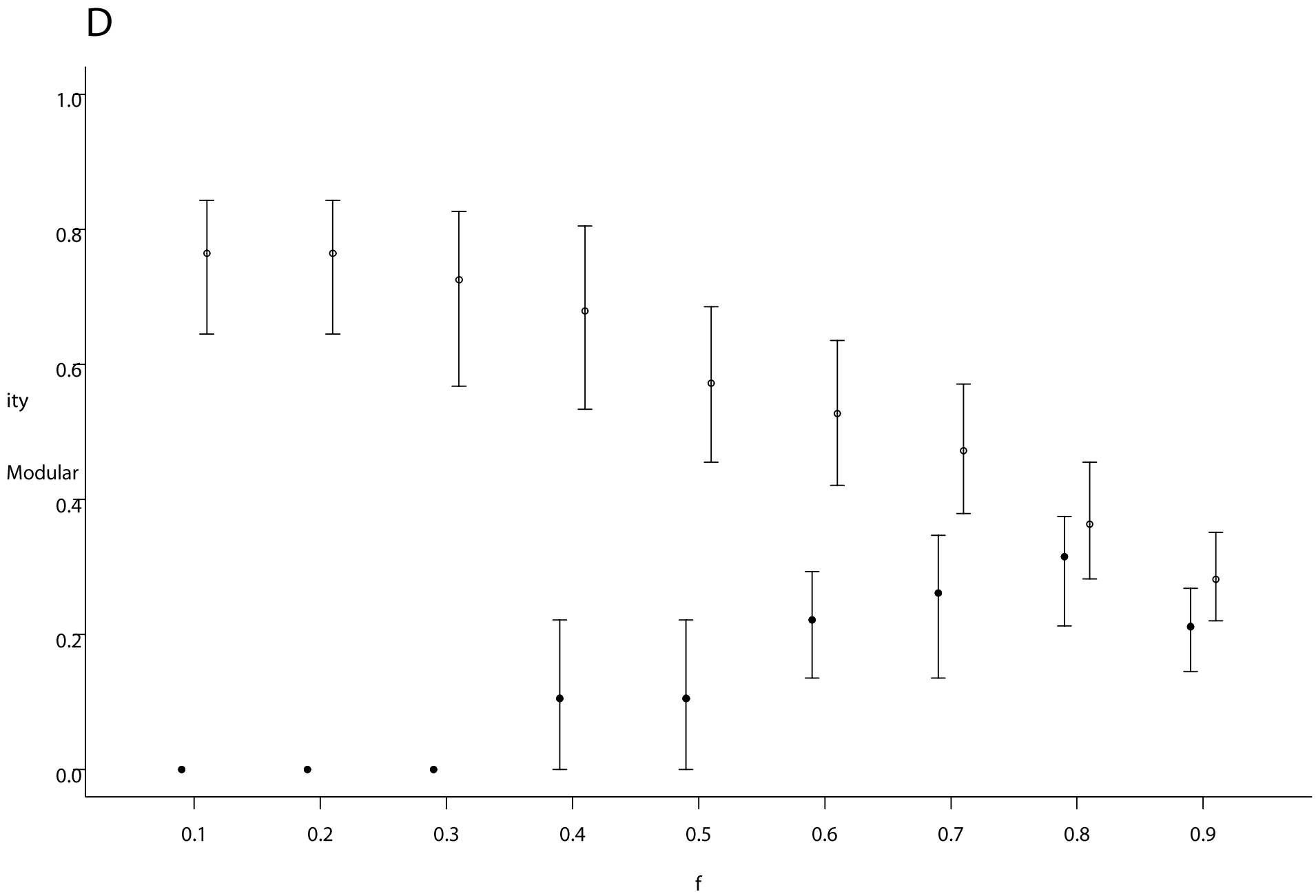
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Figure S3. Comparison of diet composition and diversity for five sea otter populations in California. Populations vary by population density and by geographic region. Panels on left (A, C and E) show diet histograms recorded from low-density, recently re-colonized populations, while panels on right (B and D) show diet histograms recorded from high-density, long-established populations. The top two panels (A and B) show data from northern central California (panel A data reported by Ostfeld 1982, panel B data from MON site, current study), while the middle two panels (C and D) show data from southern central California (panel C data reported by Estes et al. 1981, panel D data from PBL site, current study). Data for panel E were recorded from otters in southern California at San Nicolas Island (SNI site, current study). The frequency of prey types in the diet is measured as the relative proportion of successful dives in which each prey type was recorded (excluding dives with un-identifiable prey), and sample sizes indicate the number of recorded prey capture dives included in each data set.

References:

Estes J.A., Jameson R.J. & Johnson A.M. (1981). Food selection and some foraging tactics of sea otters. In: Worldwide Furbearer Conference Proceedings, Volume 1 (eds. Chapman JA & Pursley D). University of Maryland Press Baltimore, Maryland, pp. 606-641.

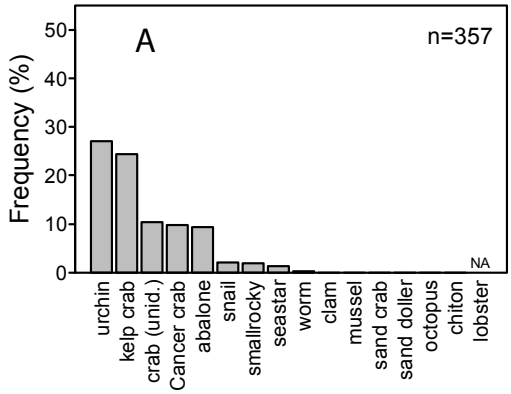
Ostfeld R.S. (1982). Foraging strategies and prey switching in the California sea otter. Oecologia, 53, 170-178.

Low Otter Density

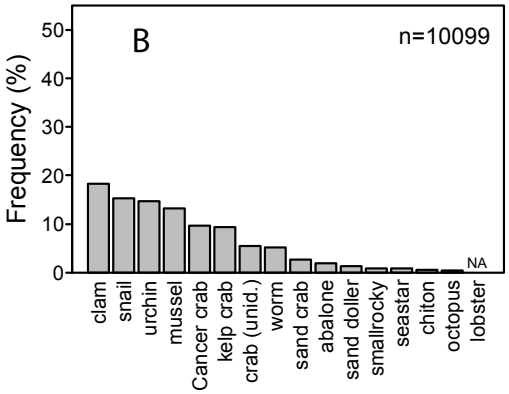
High Otter Density

Northern Central Coast

Pt. Santa Cruz, Santa Cruz County
1977

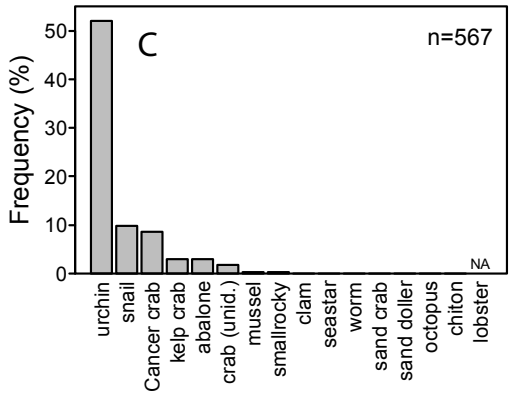


Monterey Penninsula
2000's

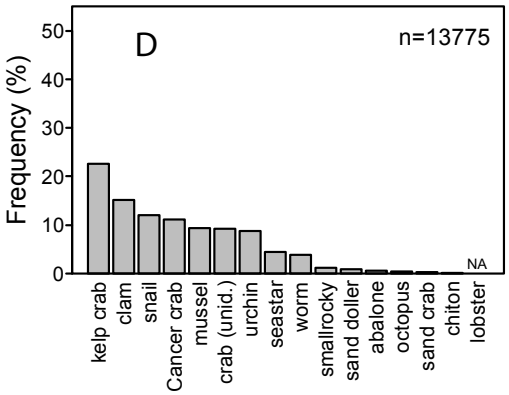


Southern Central Coast

Pt. Buchon
1975



Pt. Piedras Blancas − Pt. Estero
2000's



San Nicolas Island

San Nicolas Island
2000's