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Supplementary Material

S1. Additional details for the four similarity indices

The classic <u>incidence-based Jaccard index</u> of similarity reflects the similarity of prey identities (the proportion of shared prey taxa) and is calculated as

$$S_J = \frac{A}{A+B+C},$$

where A is the total number of species present in the diets of both individuals, B is the number of unique species in the diet of the first individual, and C is the number of unique species in the diet of the second individual (Jaccard 1901).

The <u>frequency-based Jaccard index</u> of similarity reflects both prey identities and their occurrences, and is calculated as

$$S_{Ja} = \frac{UV}{U+V-UV},$$

where U is the sum of the proportional frequencies, p, of prey species in the diet of the first individual that it shares with the second individual $(U = \sum_{k=1}^{A} p_{1k})$ and V is the sum of the proportional frequencies of prey species in the diet of the second individual that it shares with the first individual $(V = \sum_{k=1}^{A} p_{2k})$ (Chao et al. 2005).

The <u>frequency-based Jaccard index estimator</u> is an extension of the frequency-based Jaccard index that considers the probability of having not observed prey species that are actually present and shared between the diets of two individuals; the other indices assume full and complete knowledge of each individual's diet. It is calculated as

$$S_{Je} = \frac{\hat{U}\hat{V}}{\hat{U} + \hat{V} - \hat{U}\hat{V}},$$

where \hat{U} and \hat{V} are estimators of U and V that take into account the number of prey species that are observed only once or twice in the diets of the two individuals (see Chao et al. 2005 for details).

Finally, the index of proportional similarity is calculated as $S_{PS} = 1 - 0.5 \sum_{k=1} |p_{1k} - p_{2k}| = \sum_{k=1} \min(p_{1k}, p_{2k})$

(Renkonen 1938; Schoener 1968). This individual-to-individual implementation of the *PS* index differs from its individual-to-population implementation in the *IS* index of individual diet specialization (Bolnick et al. 2002), but reflects the converse of its use in the dissimilarity-based E index, $\bar{S}_{PS} = 1 - E$ (Araújo et al. 2009; Araújo et al. 2008), and exhibits more favorable properties than do other indices of similarity not considered here (Gerrard and Barbour 1986; Schatzmann et al. 1986; Wolda 1981). We included the *PS* index in our analyses to permit comparisons to other studies of individual variation since the three Jaccard indices have not seen previous application in this context.

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Supplementary Material

S2. Summary of observational data, fitting example, and Akaike model weights.



Figure S2.1. The time-dependent temporal consistency of otter diets was estimated by regressing the similarity of an individual's diet at two time-points, *S*, on the length of time elapsed between observations, *t*. Observations were time-aggregated over periods of (*a*) hours (a bout of foraging activity), (*b*) a day (multiple bouts), (*c*) a week, (*d*) a month, and a year (for individuals with sufficient data), as illustrated by individual '*N*-1284-02-*S*' using the classic Jaccard index of similarity, *S_J*. Each point reflects the number of days having elapsed between the starting dates of a pair of aggregated observations. The true number of elapsed days is encompassed by each point's corresponding line segment. The fitted curves depict the seasonal model (M3).

	Bout	Day	Week	Month	Year	Pooled
Mean	19.6	20.6	26.5	41.3	152.5	393.6
Median	15.0	15.0	19.0	28.0	109.0	358.5
Std. dev.	17.2	18.8	25.6	43.4	146.2	166.4
Range	1-154	1-154	1-217	1-418	2-710	146-861

Table S2.1. Summary statistics of the number of feeding observations made per otter for each level of temporal aggregation.



Figure S2.2. Frequency distribution of all pairwise individual-to-individual diet similarity comparisons by index.

Time seele	Madal	Similarity Index					
1 ime-scale	Model	S_J	S_{Ja}	S_{Je}	S_{PS}		
Bout	M1	409.7	917.2	758.7	894.8		
	M2	47.3	54.9	62.8	11		
	M3	166.8	163.8	104.6	7.5		
	M4	0	0	0	0		
Day	M1	382.8	1187.4	730.1	928		
	M2	20	398.9	111.1	36.9		
	M3	314	0	62.7	237.		
	M4	0	231	0	0		

231.9

167.4

133.3

0

142.8

0

152.1

5

19.9

0

345.2

0

351.2

0.05

301.1

56.6

309.4

0

12.2

0

271.2

37.2

276.8

0

213.6

27.2

222.1

0

9.2

0

651.5

184.1

657.5

0

228.2

0

74.5

218.3

18.6

0

Week

Month

Year

M1

M2

M3

M4

M1

M2

M3

M4

M1

M2

Table S2.2. Comparisons of the performance of models M1-M4 in describing betweenindividual diet similarity as a function of the time having elapsed between sets of feeding observations and the level of temporal aggregation to which feeding observations had b d with si ven 16 a

Time-scale	Madal		Similari	ty Index	
Time-scale	WIUUEI	S_J	S_{Ja}	S_{Je}	S_{PS}
Bout	M1	0	0	0	0
	M2	0	0	0	0
	M3	0	0	0	0.02
	M4	1	1	1	0.97
Day	M1	0	0	0	0
	M2	0	0	0	0
	M3	0	1	0	0
	M4	1	0	1	1
Week	M1	0	0	0	0
	M2	0	0.51	0	0
	M3	0	0	0	0
	M4	1	0.49	1	1
Month	M1	0	0	0	0
	M2	0.92	0	0	1
	M3	0	0	0	0
	M4	0.08	1	1	0
Year	M1	0	0	0.01	0
	M2	1	1	0.99	1

Table S2.3. Comparisons of the performance of models M1-M4 in describing *between-individual* diet similarity as a function of the time having elapsed between sets of feeding observations and the level of temporal aggregation to which feeding observations had been aggregated. Values indicate Akaike weights derived from the dAICc scores of Table 2.2.

Table S2.4. Comparisons of the performance of models M1-M4 in describing *within-individual* diet similarity as a function of the time having elapsed between sets of feeding observations and the level of temporal aggregation to which feeding observations had been aggregated. Values for each similarity index indicate dAICc scores determined with the individuals of both sites combined. Successive model sets reflect the comparison of models after the exclusion of more complex models, performed in order to increase the number of otter individuals for which the models reached convergence.

Time-	Model	Model set	N7 1 1	Similarity Index				Best mode
scale	set	individuals	Model	S_J	S_{Ja}	S_{Je}	S _{PS}	individuals
Bout	M1-M4	11	M1	208	386.4	373.3	391.1	-
			M2	156	291	295.3	322	-
			M3	0	0	0	0	38
			M4	2.4	30.8	7.9	30.4	-
	M1-M3	31	M1	690.3	885.4	864	905.8	-
			M2	453.4	624.1	653	657.8	-
			M3	0	0	0	0	38
	M1-M2	61	M1	299.9	315.3	264.7	297.8	-
			M2	0	0	0	0	62
	M1	73	M1	-	-	-	-	-
Day	M1-M4	14	M1	313.9	545.6	507.9	492.5	-
			M2	249.6	394.2	396.7	333.9	-
			M3	0	0	0	0	44
			M4	19.6	124.2	102.2	61.9	-
	M1-M3	35	M1	673.7	899	856.7	873.5	-
			M2	480.2	651.9	660.4	607.2	-
			M3	0	0	0	0	44
	M1-M2	60	M1	226.3	266.9	228.7	290	-
			M2	0	0	0	0	61
	M1	73	M1	-	-	-	-	-

Week	M1-M4	11	M1	130.9	237.9	225.3	240.3	-
			M2	106.1	185	183.7	209.3	-
			M3	0	0	0	6.5	35
			M4	8.9	12	1.9	0	-
	M1-M3	29	M1	314.6	451.2	439.9	488.2	-
			M2	265.5	364.2	363.5	417.4	-
			M3	0	0	0	0	35
	M1-M2	60	M1	118.2	167.1	161.4	190.7	-
			M2	0	0	0	0	62
	M1	71	M1	-	-	-	-	-
Month	M1-M4	13	M1	148.5	142.3	124.4	166.9	-
			M2	141.5	133.1	116.3	137.1	-
			M3	0	6.8	6.9	3.2	-
			M4	11.4	0	0	0	18
	M1-M3	31	M1	306.5	343.2	324	366.3	-
			M2	259.2	282.1	280.3	276.9	-
			M3	0	0	0	0	36
	M1-M2	51	M1	97.5	95.6	78.6	152.2	-
			M2	0	0	0	0	53
	M1	57	M1	-	-	-	-	-
Vaar		Q	N / 1	2.2	11 5	15 4	0.1	
Year	IVI I -IVI 2	8	MI	5.5	11.5	15.4	0.1	-
			IVI2	U	U	0	U	δ
	M1	Q	M1	F	-	_	_	_
	1711)	1111	-	-	-	-	-

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Table S2.5. Comparisons of the performance of models M1-M4 in describing *within-individual* diet similarity as a function of the time having elapsed between sets of feeding observations and the level of temporal aggregation to which feeding observations had been aggregated. Values indicate Akaike weights derived from the dAICc scores of Table 2.4. Successive model sets reflect the comparison of models after the exclusion of more complex models, performed in order to increase the number of otter individuals for which the models reached convergence.

Time-	Model	Iodel Model set	N. J.I		Similar	Best model		
scale	set	individuals	wiodei-	S_J	S_{Ja}	S_{Je}	S_{PS}	individuals
Bout	M1-M4	11	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	0.76	1	0.98	1	38
			M4	0.24	0	0.02	0	-
	M1-M3	31	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	38
	M1-M2	61	M1	0	0	0	0	-
			M2	1	1	1	1	62
	M1	73	M1	-	-	-	-	-
Day	M1-M4	14	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	44
			M4	0	0	0	0	-
	M1-M3	35	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	44
	M1-M2	60	M1	0	0	0	0	-
			M2	1	1	1	1	61
	M1	73	M1	-	-	-	-	-

Week	M1-M4	11	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	0.99	1	0.72	0.04	35
			M4	0.01	0	0.28	0.96	-
	M1-M3	29	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	35
	M1-M2	60	M1	0	0	0	0	-
			M2	1	1	1	1	62
	M1	71	M1	-	-	-	-	-
Month	M1-M4	13	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	0.03	0.03	0.16	-
			M4	0	0.97	0.97	0.84	18
	M1-M3	31	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	36
	M1-M2	51	M1	0	0	0	0	-
			M2	1	1	1	1	53
	M1	57	M1	-	-	-	-	-
Year	M1-M2	8	M1	0.19	0	0	0.94	-
			M2	1	1	1	1	8
	M1	9	M1	-	-	-	-	-



Figure S2.3. Frequencies of the total number of foraging observations, aggregated by time-scale, made by all 74 studied sea otter individuals compared to the subset of individuals for which seasonal variation in diet self-similarity was detected.



Figure S2.4. Frequency of the total number of days over which all 74 studied sea otter individuals were observed compared to the subset of individuals for which seasonal variation in diet self-similarity was detected.

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Supplementary Material

S3. An alternative measure of diet specialization.

In combination with a model-fitting approach, the use of diet similarity for both betweenand within- individual comparisons permits an alternative definition and measure of diet specialization as the length of elapsed time needed for the within-individual similarity of an individual's diet, $S^w(t)$, to become equal in magnitude to the between-individual similarity of its population, $S^b(t)$ (Fig. 3.1). For the simple exponential model (M1) this time to equal similarity (t_{eq}) can be calculated as

$$t_{eq} = \frac{\left|\log(S_0^w/S_0^b)\right|}{\lambda^b - \lambda^w},$$

obtained by setting $S_0^w e^{\lambda^w t} = S_0^b e^{\lambda^b t}$ and solving for t. A solution is guaranteed either if $S_0^w > S_0^b$ and $\lambda^w < \lambda^b$ (resulting in $t_{eq} > 0$), or if $S_0^w < S_0^b$ and $\lambda^w > \lambda^b$ (resulting in $t_{eq} < 0$). The absolute value of the numerator may be taken for convenience. A positive t_{eq} value thereby reflects an individual that is more consistently self-similar (temporally specialized) in its prey choices than is the average individual to another. A negative t_{eq} value reflects an individual relative to another. The average t_{eq} value calculated across the population of individuals may therefore be used as a measure of the population's overall degree of specialization.

We obtained estimates of t_{eq} for each individual using the appropriate combination of bestperforming within- and between-individual models. For model combinations that included the more complicated plateauing and seasonal models (M2-M4), estimates of t_{eq} were obtained numerically in lieu of analytical solutions (see R-code below).



Figure S3.1. A hypothetical example illustrating the calculation of t_{eq} as a more intuitive measure of an individual's temporal consistency. t_{eq} reflects the number of elapsed days needed for the model-fit within-individual similarity of an individual's diet, S^w , to become equal in magnitude to the model-fit between-individual similarity of its population, S^b .



Figure S3.2. The relative frequency (probability density) of temporal specialists and temporal generalists illustrated by level of temporal aggregation and with each of the four indices of diet similarity superimposed. Individuals whose initial within-individual similarity is greater than their population's between-individual similarity, $S^{W}(0) > S^{b}(0)$, have positive t_{eq} values and may be considered temporal specialists, whereas individuals whose initial within-individual similarity is less than their population's between-individual similarity, $S^{W}(0) < S^{b}(0)$, have negative t_{eq} values and may be considered temporal generalists. Individuals with t_{eq} equaling ±infinity exhibit diet self-similarities that never converge on the between-individual similarity of their population.

Time-scale	Similarity Index	Mean	Standard deviation	% +Infinite	% -Infinite
Bout	S_J	966.8	1805.4	41.9	1.4
	S_{Ja}	1407.7	2039.0	45.9	0
	S_{Je}	1517.0	2246.7	41.9	0
	S_{PS}	1069.8	1619.9	47.3	0
Day	S_J	917.0	1548.3	33.8	1.4
	S_{Ja}	902.8	1635.0	48.6	0
	S_{Je}	1162.2	1760.1	43.2	0
	S_{PS}	1014.9	1636.4	43.2	0
Weals	C	(22.5	0/1 2	10 5	1 /
week	S_J	023.3	841.3	42.5	1.4
	S_{Ja}	940.6	1338.1	43.8	0
	S_{Je}	1167.8	1847.9	46.6	0
	S_{PS}	729.4	1021.6	50.7	0
Month	Sı	695 3	1232.7	333	0
1.10.1.	\tilde{S}_{Ia}	741.3	1280.2	51.7	Ő
	SIe	1588.3	2476.1	40.0	0
	S_{PS}	1034.5	1880.1	48.3	0
Year	S_J	749.9	1032.9	22.2	0
	S_{Ja}	1218.3	1927.3	44.4	0
	S_{Je}	1306.6	2117.6	44.4	0
	S_{PS}	2694.6	3656.9	22.2	0

Table S3.1. Summary statistics for the t_{eq} metric of individual specialization (in units of days) by level of temporal aggregation.

R-code to calculate *t_{eq}*

Define function to estimate Teq

```
# Define function to estimate Teq
EstTeq<-function(Wparms,Bparms,Prec=10^-8,Tmin=1,Tmax=10000,Step=1){
FullModel<-function(t,parms){with(as.list(parms),{S0*exp(I*t+a*sin(f*pi*t/182.5+ps))+P})}
if(FullModel(0,Wparms)==FullModel(0,Bparms)){return(list(Teq=0,Sign=0,sTeq=0))}
if(FullModel(0,Wparms)>FullModel(0,Bparms)){p1=Wparms; p2=Bparms; Sign=1}
if(FullModel(0,Wparms)<FullModel(0,Bparms)){p2=Wparms; p1=Bparms; Sign=-1}
Teq<-Tmin
while(Teq<=Tmax){</pre>
```

```
inte(Teq <= Tinax){
    Diff<-FullModel(Teq,p1) - FullModel(Teq,p2)
    if(Diff<Prec & Diff>0){out<-list(Teq=Teq,Sign=Sign);return(out)}
    if(Diff>Prec & Diff>0){ Teq<-Teq+Step }
    if(Diff<0){ Teq<-Teq-Step; Step<-Step/10 }</pre>
```

if(Teq>Tmax){warning('Solution not attained. Either none exists or Tmax is set too low.'); return(list(Teq=Inf,Sign=Sign,sTeq=Inf*Sign))}

}

Implement on an example Wparms=c(S0=0.8,I=-0.002,m=0,a=0.1,f=1,p=45) Bparms=c(S0=0.5,I=-0.001,m=0,a=0.05,f=1,p=45)

Est<-EstTeq(Wparms,Bparms)

```
#Define functions for within-individual and between-individual models
FullModelxw<-function(x){with(as.list(Wparms),{S0*exp(l*x+a*sin(f*pi*x/182.5+p))+m})}
FullModelxb<-function(x){with(as.list(Bparms),{S0*exp(l*x+a*sin(f*pi*x/182.5+p))+m})}</pre>
```

Plot functions curve(FullModelxw,0,1000,ylim=c(0,1),ylab=expression(S(t)),xlab='Days') curve(FullModelxb,0,1000,add=TRUE,lty=2) abline(v=Est\$Teq,lty=3) legend('topright',c('Within','Between', paste('Teq =',round(Est\$Sign*Est\$Teq,1))),lty=c(1,2,NA))

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Supplementary Material

S5. Sample-size effects on estimates of between- and within-individual similarity.

The number of feeding observations that can be made on a predator individual within a short period of time is often dictated more by the biology of the focal organism rather than the researcher's sampling effort. For example, on hourly time-scales a predator may only consume a small number of prey items. Therefore, larger sample sizes will typically be confounded by larger sampling time scales, and vice versa. In our study, the mean number of foraging observations made per individual roughly doubled at time-scales of a bout and a day (approx. 20 observations) to the time-scale of a month (approx. 41 observations) (Table S2.1).

The frequency-based Jaccard index estimator of similarity (S_{Je}) considers the probability of having not observed prey species that are actually present and shared between the diets of two individuals (Appendix S.1, Chao et al. 2005). It does so by taking into account the number of prey species that are observed only once or twice in the diets of the two individuals. The difference between the S_{Je} and the frequency-based Jaccard index S_{Ja} therefore reflects the degree to which the diets of two individuals may be under-sampled with respect to their true diets. However, the index remains sensitive to sample sizes and the underlying distribution of each individual's prey frequencies (Chao et al. 2005).

To assess the degree to which increasing sample sizes may have influenced our inferences of increasing temporal aggregation we therefore repeated the calculation of within- and between-individual diet similarities with each of the four indices (see Appendix S.1) after resampling each individual's foraging observations to different levels of sampling effort. Resampling was performed with replacement and was repeated ten times to calculate average within- and between individual pairwise similarities for sampling efforts corresponding to the observation of 10, 20, 30, 40 or 50 foraging observations per individual per time-scale. We conducted this analysis on data aggregated to the bout (Figs. S5.1-S5.2) and monthly (Figs. S5.3-S5.4) levels of temporal aggregation and used cubic smooth splines (R-package: *stats*) to visualize the time-dependence of the sampling effort effect.

These analyses confirm the appropriateness of the four parametric models (M1-M4), with the splines evidencing slow, and in some cases, apparently periodic declines in pairwise similarity over time. The analyses also indicate that sampling effort had little influence on the qualitative results reported in the main text. More specifically, although overall magnitudes of within- and between-individual diet similarity were decreased by decreasing sampling effort, the difference between low sampling effort (10-20 observations) and high sampling effort (40-50 observations) was (*i*) independent or only weakly-dependent on the number of elapsed days between observations (see Fig. S5.4b for example of weak-dependence), (*ii*) small (< 0.1 units of similarity), and (*iii*) roughly equivalent between levels of temporal aggregation will have increased overall estimates of individual diet specialization and will have decreased overall estimates of temporal consistency, the effects of temporal aggregation *per se* remain. Therefore the conclusions regarding the effects of temporal aggregation and the need to account for it in analyses of individual variation which we describe in the main text remain unchanged.



Figure S5.1. Cubic smoothing splines fit to the between-individual comparisons at the bout scale of temporal aggregation after the resampling of each individual's foraging observations.



Figure S5.2. Cubic smoothing splines fit to the witin-individual comparisons at the bout scale of temporal aggregation after the resampling of each individual's foraging observations.



Figure S5.3. Cubic smoothing splines fit to the between-individual comparisons at the month scale of temporal aggregation after the resampling of each individual's foraging observations.



Figure S5.4. Cubic smoothing splines fit to the within-individual comparisons at the month scale of temporal aggregation after the resampling of each individual's foraging observations.

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Supplementary Material

S4. Consequences of classifying prey into functional categories

Highest resolvable prey taxon	Functional category
Haliotus spp.	Abalone
Bivalve, unid.	Bivalve
Clam, unid.	Bivalve
Cockle, unid.	Bivalve
Gaper clam	Bivalve
Razor clam	Bivalve
Rock jingle	Bivalve
Scallop, unid.	Bivalve
Washington clam	Bivalve
Cancer spp.	Cancer crab
Logio sp., squid	Cephalopod
Octopus sp.	Cephalopod
Crab, unid.	Decapod
Decorator crabs	Decapod
Pugettia sp., Kelp crab	Kelp crab
Modiolus sp., Horse mussel	Mussel
Mytilus sp. or Musculus sp. mussel	Mussel
Algae	Other
Anemone	Other
Barnacle	Other
Chiton	Other
Coralline algae	Other
Crustacean, unid.	Other
Isopod	Other
Limpet	Other
Mollusk, <i>unid</i> .	Other
Nudibranch	Other
Ochre star	Other
Sea cucumber	Other
Sponge	Other
Tunicate	Other
<i>Emerita sp.</i> or <i>Blepharipoda sp.</i> sand crab	Other sand habitat
Sand dollar	Other sand habitat
Asteroidea seastar	Seastar
<i>Ophiuroidea</i> brittlestar	Seastar
Gastropod	Snail
Green urchin	Urchin
Purple urchin	Urchin
Red urchin	Urchin
Annelida worm	Worm
Fat innkeeper worm	Worm
Worm-like, unid.	Worm

Table S4.1. Sea otter prey items as used in the main text, and their categorization following Tinker et al. (2008; 2012).

Index	Montere	ey Peninsula ((<i>MON</i>)	Pt. Pie	Pt. Piedras Blancas (<i>PBL</i>)			
	Observed	Expected	р	Observed	Expected	р		
S_J	0.60	0.95-0.97	< 0.001	0.69	0.92-0.96	< 0.001		
S_{Ja}	0.59	0.99-1.00	< 0.001	0.74	0.99-1.00	< 0.001		
S_{Je}	0.61	0.99-1.00	< 0.001	0.76	0.99-1.00	< 0.001		
S_{PS}	0.31	0.89-0.90	< 0.001	0.40	0.90-0.92	< 0.001		

Table S4.2. As in Table 1 of main text, but with prey grouped into functional categories.



Figure S4.1. Frequency distribution of all pairwise individual-to-individual diet similarity comparisons by index using *prey grouped into functional categories*.



Figure S4.2. As in Figure 1 of main text, but with prey grouped into functional categories.



Figure S4.3. As in Figure 2 of main text, but with prey grouped into functional categories.



Figure S4.4. As in Figure 4 of main text, but with prey grouped into functional categories.



Figure S4.5. As in Figure S3.2, but with prey grouped into functional categories.

Time-scale	Madal		Similari	ty Index	
Time-scale	WIGUEI	S_J	S_{Ja}	S_{Je}	S_{PS}
Bout	M1	210.6	659	501	699.4
	M2	124.6	215.8	154.2	173.2
	M3	133.1	49.8	35	76.8
	M4	0	0	0	0
Day	M1	246.8	620.6	942.2	684.7
	M2	166.1	211	625.3	139.9
	M3	184.9	34	504.8	96
	M4	0	0	0	0
Week	M1	142.4	234.8	91.8	260.3
	M2	102.6	170.1	50.1	0
	M3	47.7	0	97.8	240.8
	M4	0	138.3	0	199.8
Month	M1	268	864.9	53.6	149.3
	M2	224.8	792.4	0	29
	M3	174.9	870.9	52.9	0
	M4	0	0	5.8	14.3
Year	M1	9.2	5.3	0.6	7.9
	M2	0	0	0	0

Table S4.3. As in Table S2.2 of main text, but with prey grouped into functional categories.

 Values reflect dAICc scores.

Time-	Model	Model set			Similar	ity Index		Best model
scale	set	individuals	Model	S_J	S_{Ja}	S_{Je}	S _{PS}	individuals
Bout	M1-M4	13	M1	302	367.5	331.7	346.1	-
			M2	224.2	287.1	264.5	287.6	-
			M3	0.2	0	0	0	45
			M4	0	59.2	19.3	81.9	-
	M1-M3	37	M1	624.8	970.7	900.3	905.3	-
			M2	393	712.6	687	653.7	-
			M3	0	0	0	0	45
	M1-M2	63	M1	293.2	341.6	277.1	334.8	-
			M2	0	0	0	0	63
	M1	74	M1	-	-	-	-	-
Day	M1-M4	15	M1	265.8	361.7	331.8	358.2	-
			M2	240	298.6	302.3	303.2	-
			M3	0	0	0	0	44
			M4	13.9	65.5	23.5	63.7	-
	M1-M3	35	M1	535.5	802	761.9	829.7	-
			M2	449.7	625.6	643	573.7	-
			M3	0	0	0	0	44
	M1-M2	62	M1	223.9	313	227.6	338.1	-
			M2	0	0	0	0	63
	M1	73	M1	-	-	-	-	-
Week	M1-M4	7	M1	68.7	174.8	177.6	182.1	-
			M2	52.6	141.9	146.8	123.3	-
			M3	0	0	0	0	32

Table S4.4. As in Table S2.4, but with *prey grouped into functional categories*. Values reflect dAICc scores.

			M4	2.3	9.8	8.4	1.6	-
	M1-M3	25	M1	359	459.6	456.5	494.4	-
			M2	312	373.7	369	394.5	-
			M3	0	0	0	0	32
	M1-M2	60	M1	100.1	169.5	171.4	218.2	-
			M2	0	0	0	0	62
	M1	71	M1	-	-	-	-	-
Month	M1-M4	13	M1	167.6	129.2	115.6	142.3	-
			M2	146.3	106.5	107.2	107.9	-
			M3	37.3	2.4	2.8	0	-
			M4	0	0	0	5	18
	M1-M3	31	M1	307.3	318.3	296.3	377.5	-
			M2	224.8	273.5	261.1	287.8	-
			M3	0	0	0	0	36
	M1-M2	46	M1	96.3	74.4	61.4	136.2	-
			M2	0	0	0	0	48
	M1	58	M1	-	-	-	-	-
Year	M1-M2	7	M1	1.7	16.2	6.4	201.4	-
			M2	0	0	0	0	7
	M1	9	M1	-	-	-	-	-

Timo coolo	Madal	Similarity Index						
1 Ime-scale	Model	S_J	S_{Ja}	S_{Je}	S_{PS}			
Bout	M1	0	0	0	0			
	M2	0	0	0	0			
	M3	0	0	0	0			
	M4	1	1	1	1			
Day	M1	0	0	0	0			
	M2	0	0	0	0			
	M3	0	0	0	0			
	M4	1	1	1	1			
Week	M1	0	0	0	0			
	M2	0	0	0	1			
	M3	0	1	0	0			
	M4	1	0	1	0			
Month	M1	0	0	0	0			
	M2	0	0	0.95	0			
	M3	0	0	0	1			
	M4	1	1	0.05	0			
Year	M1	0.01	0.07	0.42	0.02			
	M2	0.99	0.93	0.58	0.9			

Table S4.5. As in Table S2.3, but with *prey grouped into functional categories*. Values reflect

 Akaike weights based on the dAICc scores of Table S4.3.

Time- Mo scale s	Model	Model set individuals	Model-		Similar	Best model		
	set			S_J	S_{Ja}	S_{Je}	S_{PS}	individuals
Bout	M1-M4	13	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	0.47	1	1	1	45
			M4	0.53	0	0	0	-
	M1-M3	37	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	45
	M1-M2	63	M1	0	0	0	0	-
			M2	1	1	1	1	63
	M1	74	M1	-	-	-	-	-
Day	M1-M4	15	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	44
			M4	0	0	0	0	-
	M1-M3	35	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	44
	M1-M2	62	M1	0	0	0	0	-
			M2	1	1	1	1	63
	M1	73	M1	-	-	-	-	-
Week	M1-M4	7	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	0.76	0.99	0.99	0.69	32

Table S4.6. As in Table S2.4, but with *prey grouped into functional categories*. Values reflect

 Akaike weights based on the dAICc scores of Table S4.4.

			M4	0.24	0.01	0.01	0.31	-
	M1-M3	25	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	32
	M1_M2	60	M1	0	0	0	0	_
	1011-1012	00	MO	1	1	1	1	62
			IVI Z	1	1	1	1	02
	M1	71	M1	-	-	-	-	-
Month	M1-M4	13	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	0	0.23	0.19	0.92	-
			M4	1	0.77	0.81	0.08	18
	M1-M3	31	M1	0	0	0	0	-
			M2	0	0	0	0	-
			M3	1	1	1	1	36
	M1-M2	46	M1	0	0	0	0	
			M2	1	1	1	1	48
	2.61	50						
	MI	58	MI	-	-	-	-	-
Year	M1-M2	7	M1	0.42	0	0.04	0	_
			M2	1	1	1	1	7
	M1	9	M1	-	-	-	-	-

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