Time-scales alter the inferred strength and temporal consistency of intraspecific diet specialization.

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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 between- and 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

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

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 that is more temporally inconsistent (temporally generalized) than is the average 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 best-performing 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).

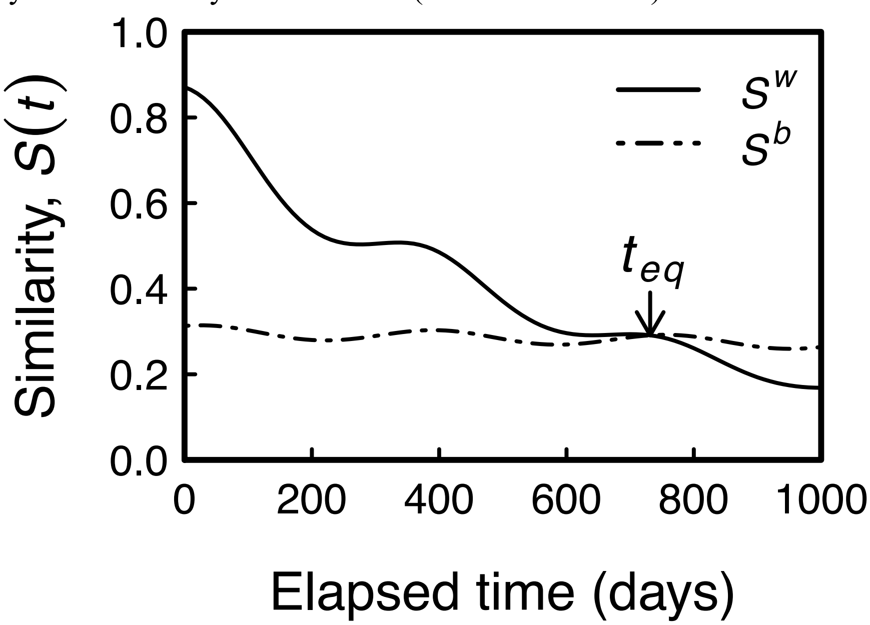

Figure S3.1. A hypothetical example illustrating the calculation of t_{eq} as a more intuitive measure of an individual's temporal consistency. t_{eq} reflects the number of elapsed days needed for the model-fit within-individual similarity of an individual's diet, S^w, to become equal in magnitude to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

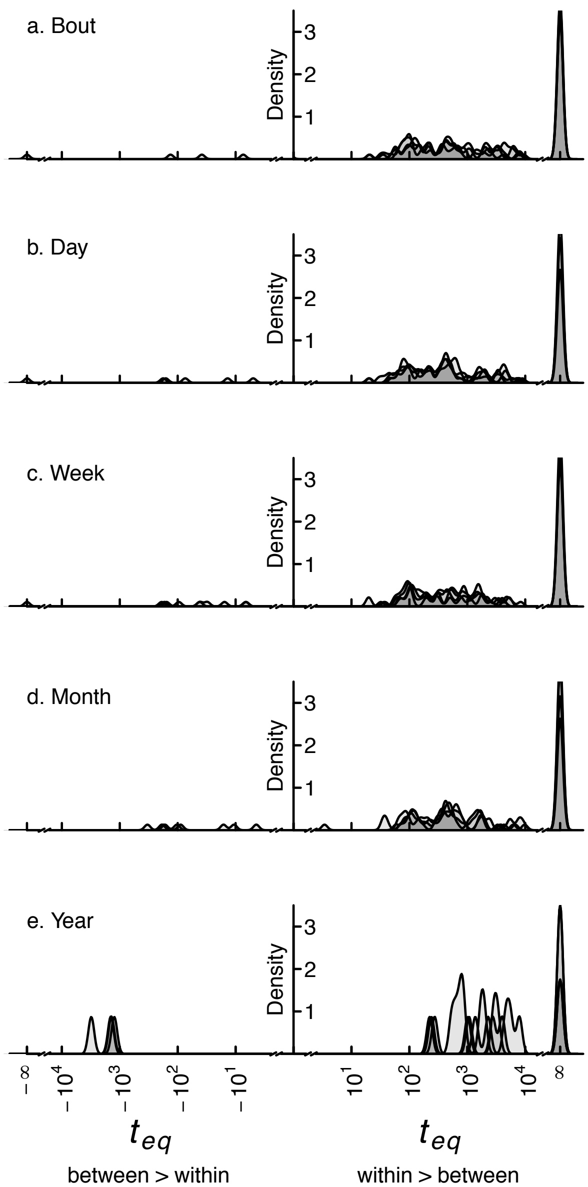

Figure S3.2. The relative frequency (probability density) of temporal specialists and temporal generalists illustrated by level of temporal aggregation and with each of the four indices of diet similarity superimposed. Individuals whose initial within-individual similarity is greater than their population's 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.

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

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
Week	S_J	623.5	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	S_J	695.3	1232.7	33.3	0
	S_{Ja}	741.3	1280.2	51.7	0
	S_{Je}	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

R-code to calculate t_{eq}

```
# 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(l*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){
		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 }
	}
	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,l=-0.002,m=0,a=0.1,f=1,p=45)
Bparms=c(S0=0.5,l=-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})}

# 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))
```