Supplementary Information for

HETEROTROPHIC EUKARYOTES SHOW A FAST-SLOW CONTINUUM, NOT A GLEANER-EXPLOITER TRADE-OFF

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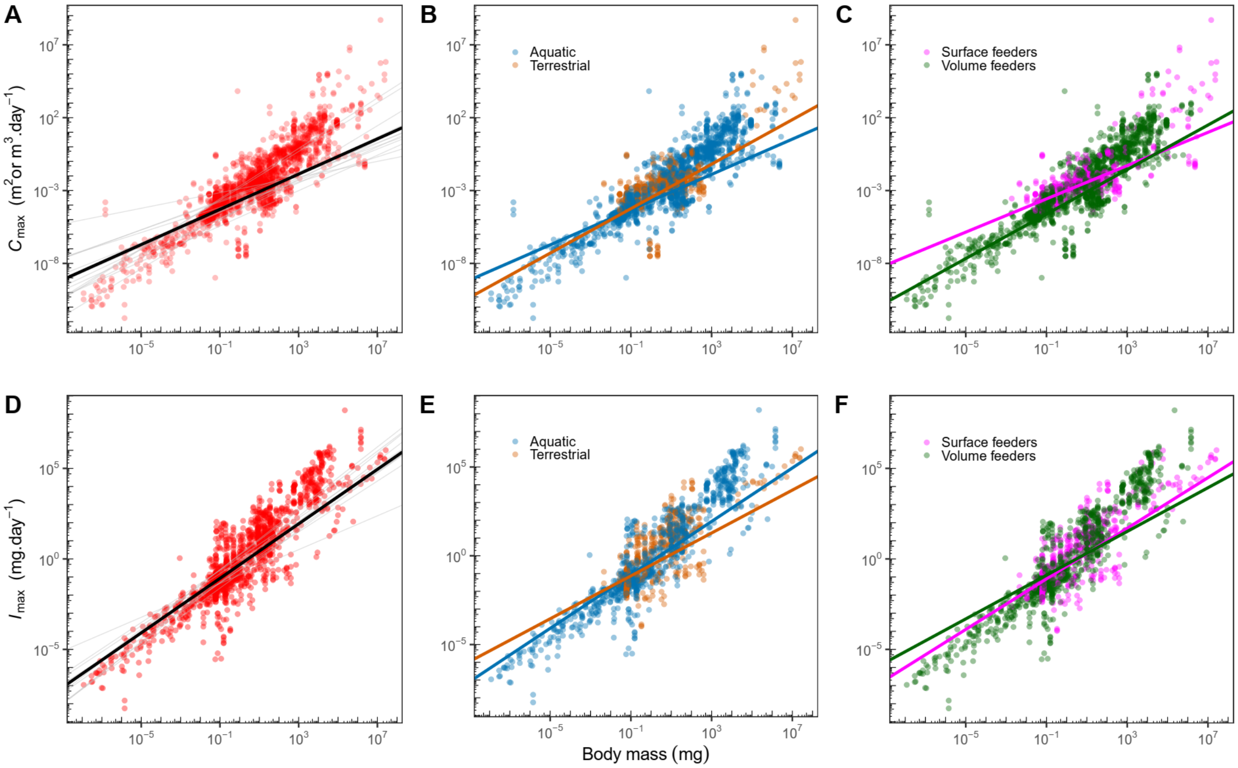

Fig. S1. The relationships between C_{max}, I_{max} and body mass, across habitats and feeding dimensionality. Here within-group patterns are not depicted for clarity except in A and D (thin grey lines), though it is captured in the models. There is very limited variation in these relationships across environments (aquatic/terrestrial) and feeding dimensionality (surface/volume feeders).

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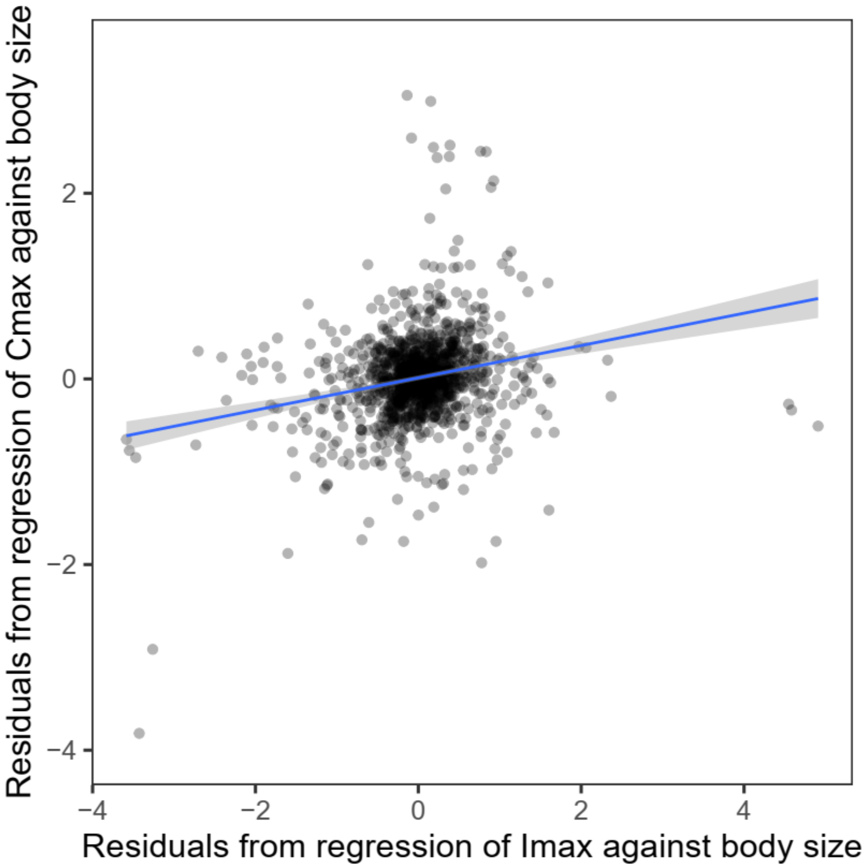

Fig. S2. Residual analysis. Residuals from the regressions between C_{max} and body mass, and I_{max} and body mass are regressed against each other, and they are weekly but positively related to one another ($R^2 = 0.05$, $p < 0.001$). This result is not sensitive to the extreme points on either axis. The regressions against body mass accounted for species- and taxonomic group- level variation in the data with random effects, so the residuals here have accounted for this variation. Therefore, we used an OLS regression in this case.

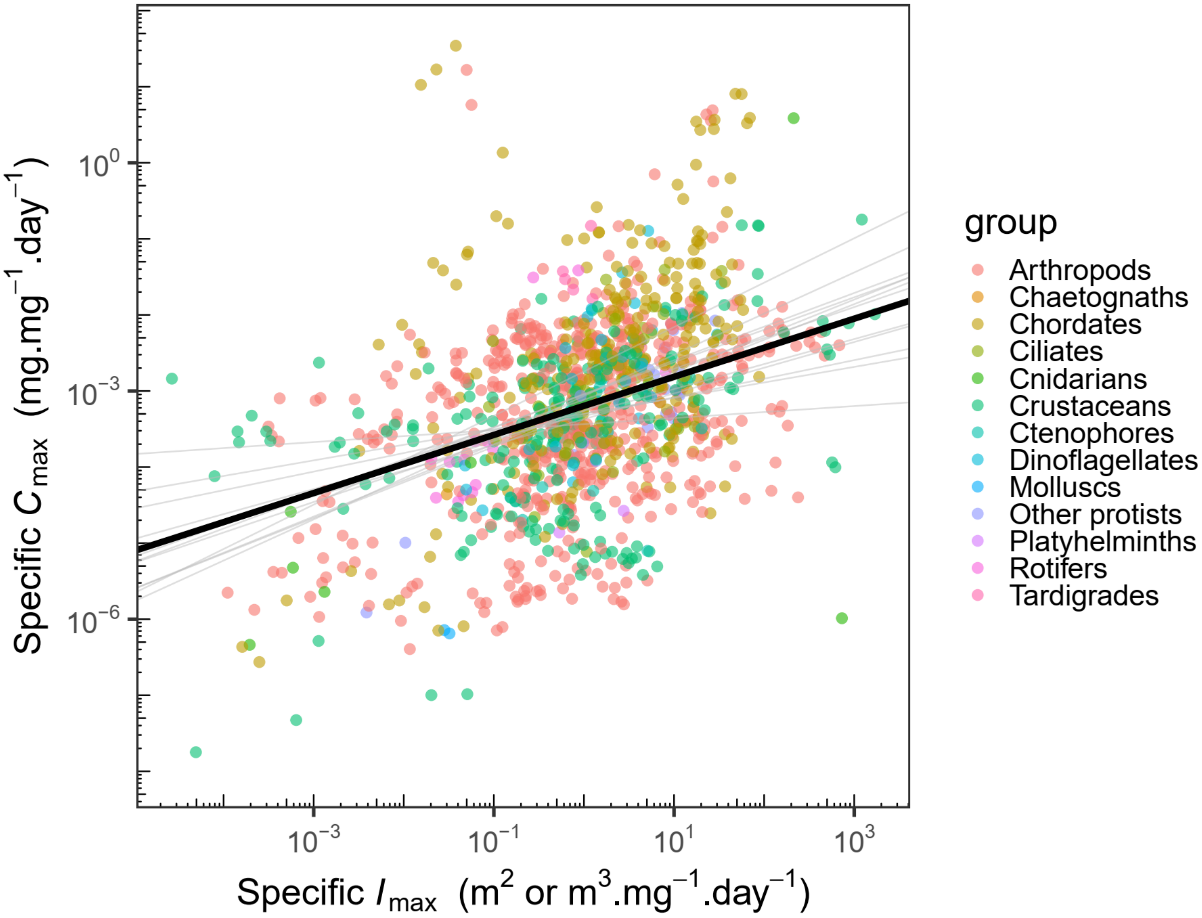

Fig. S3. Specific C_{max} (i.e. size-corrected C_{max}) is positively related to specific I_{max} in all taxonomic groups we modelled (the thin grey lines).

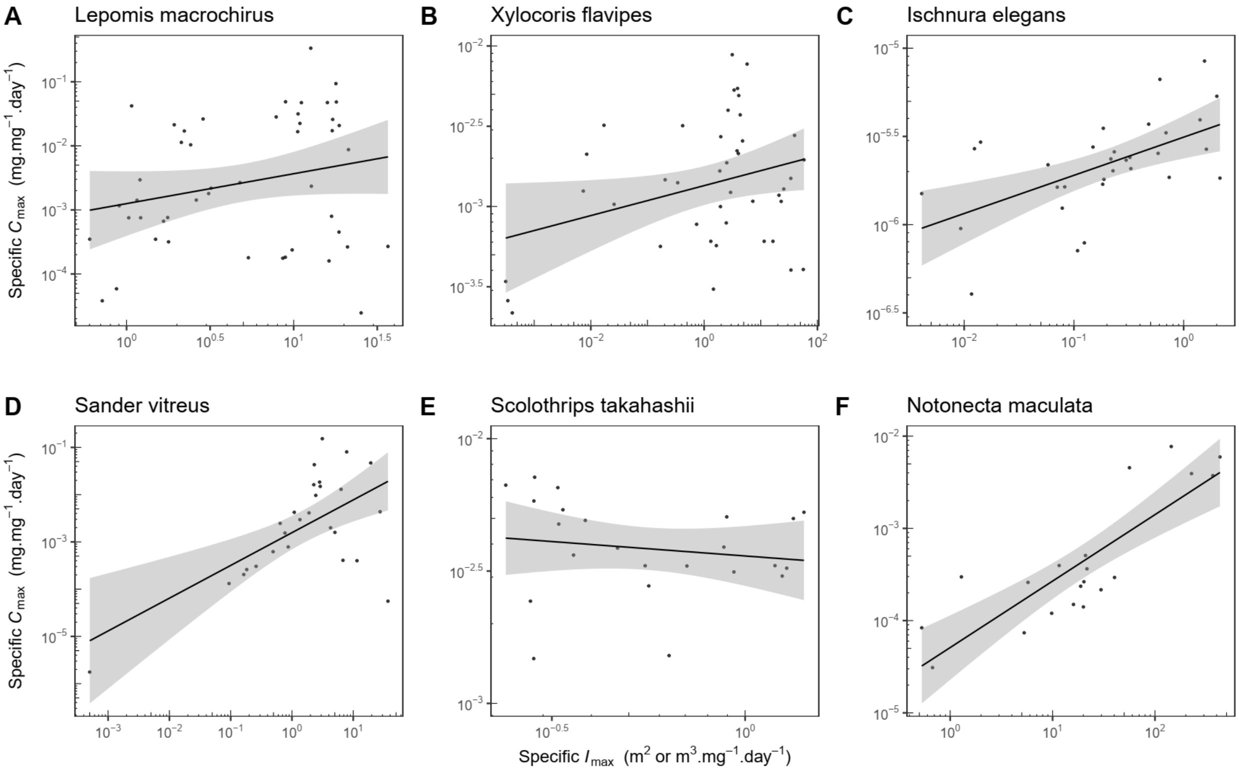

Fig. S4. Specific C_{max} is positively related to specific I_{max} even at an intraspecific level. We investigated the 6 species for which we had 20 or more measurements to understand whether the gleaner-exploiter trade-off appears at an intraspecific level. In 5 of the 6 species here, the regressions show a positive relationship, consistent with across-species patterns and contrary to the trade-off expectation. The sole exception, *Scolothripe takahashii* (panel E), shows a weak, non-significant negative relationship. While this does constitute evidence against a trade-off at the intraspecific level, it is relatively weak evidence, as discussed in the main text.

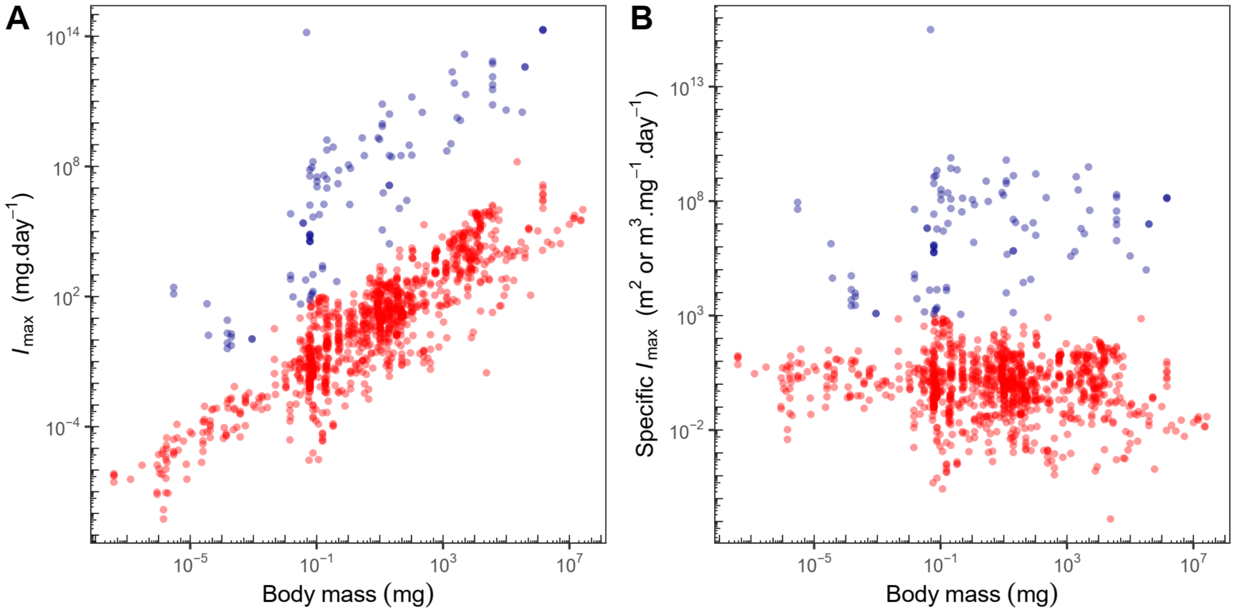

Fig. S5. Maximum ingestion rate (A) and specific maximum ingestion rate (B) as functions of body mass for the data in the Uiterwaal et al. data set (1). The blue points are observations where the estimated specific maximum ingestion rates exceeds 10^3 d^{-1}. These data were excluded from the analyses.

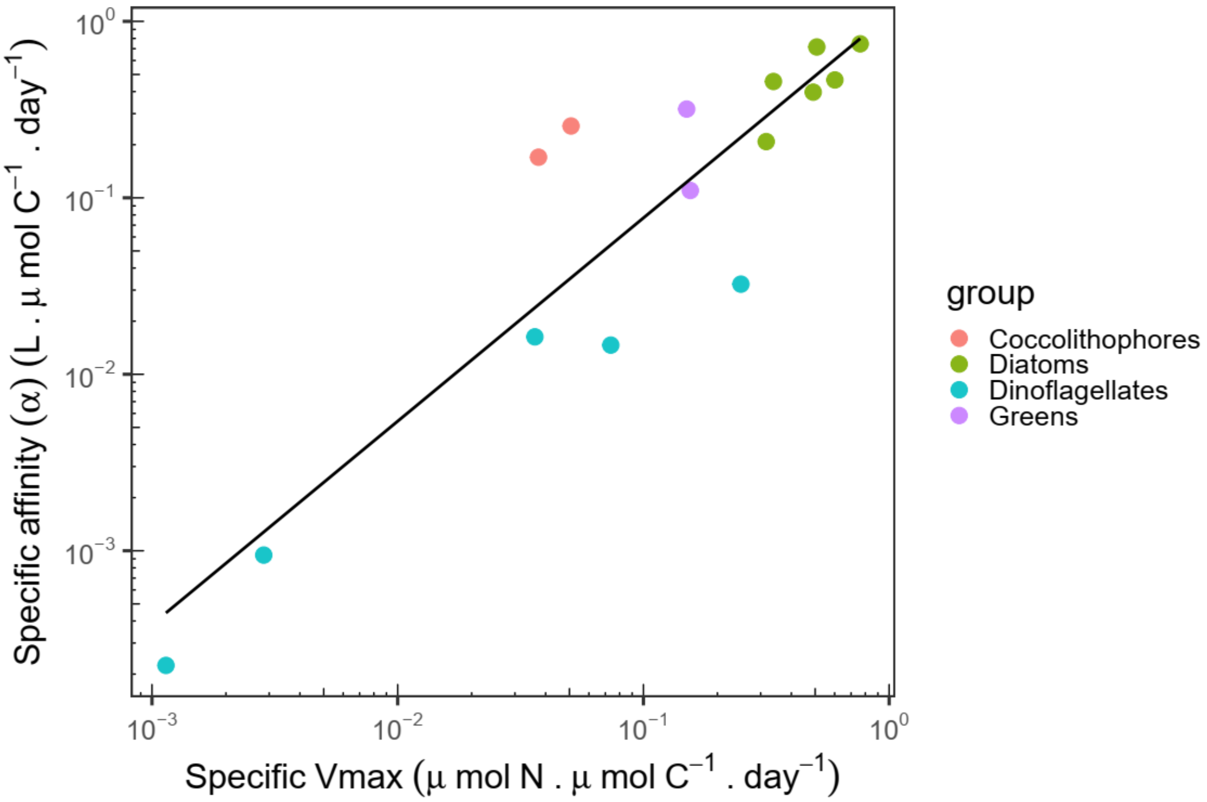

Fig. S6. Relation between specific affinity (α, L.µmol C^{-1}.d^{-1}) for nitrogen and specific maximum uptake rate (V_{max}, µmol N.µmol C^{-1}.d^{-1}) of nitrogen for phytoplankton belonging to different taxa. Note that affinity and Vmax have been normal per unit carbon, and not biomass as was done for the eukaryotes. However, these should produce very similar results. The data were compiled by Litchman et al. (2), and the affinity was computed here as the ratio of the V_{max} and the half saturation constant, the two parameters reported by Litchman et al. (2007). The regression line shown is $\log_{10}(\alpha) = 0.036 + 0.89 \log_{10}(V_{\mathrm{max}})$, $R^2 = 0.74$.

Bibliography for figures

1. Uiterwaal SF, Lagerstrom IT, Lyon SR, DeLong JP (2018) Data paper: FoRAGE (Functional Responses from Around the Globe in all Ecosystems) database: a compilation of functional responses for consumers and parasitoids. *bioRxiv* (December):43.
2. Litchman E, Klausmeier CA, Schofield OM, Falkowski PG (2007) The role of functional traits and trade-offs in structuring phytoplankton communities: Scaling from cellular to ecosystem level. *Ecol Lett* 10(12):1170–1181.

Table S1. Regression results for maximum clearance rate against maximum ingestion rate.

Note that p-values depicted here are not entirely accurate because of technical challenges associated with calculating degrees of freedom in mixed models.

Response variable:	$\log_{10}(C_{\max})$
Predictor variables:	
(a) *Fixed effects*:	$\log_{10}(I_{\max})$
(b) *Random intercepts*:	species, taxonomic group
(c) *Random slopes*:	taxonomic groups have different $\log_{10}(C_{\max})$ vs. $\log_{10}(I_{\max})$ slopes

	$\log_{10}(C_{\max})$		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-3.51	-4.22 – -2.80	**<0.001**
$\log_{10}(I_{\max})$	0.52	0.30 – 0.73	**<0.001**
Random Effects			
σ^2	0.28		
$\tau_{00\ \text{species}}$	0.84		
$\tau_{00\ \text{group}}$	1.21		
$\tau_{11\ \text{group.log10}(I\text{max})}$	0.10		
$\rho_{01\ \text{group}}$	-0.32		
ICC	0.90		
N_{species}	361		
N_{group}	13		
Observations	1206		
Marginal R^2 / Conditional R^2	0.408 / 0.944		

Table S2. Regression results for maximum clearance rate against body mass. Note that p-values depicted here are not entirely accurate because of technical challenges associated with calculating degrees of freedom in mixed models.

Response variable: $\log_{10}(C_{\max})$

Predictor variables:

(a) *Fixed effects*: $\log_{10}$(body mass)
(b) *Random intercepts*: species, taxonomic group
(c) *Random slopes*: taxonomic groups have different $\log_{10}(C_{\max})$ vs. $\log_{10}$(body mass) slopes

	$\log_{10}(C_{\max})$		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-3.69	-4.24 – -3.14	**<0.001**
$\log_{10}$(body mass)	0.60	0.45 – 0.76	**<0.001**
Random Effects			
σ^2	0.31		
$\tau_{00\ \text{species}}$	0.85		
$\tau_{00\ \text{group}}$	0.67		
$\tau_{11\ \text{group.log10(body mass)}}$	0.05		
$\rho_{01\ \text{group}}$	0.07		
ICC	0.85		
N_{species}	453		
N_{group}	13		
Observations	2114		
Marginal R^2 / Conditional R^2	0.497 / 0.927		

Table S3. Regression results for maximum ingestion rate against body mass. Note that p-values depicted here are not entirely accurate because of technical challenges associated with calculating degrees of freedom in mixed models.

Response variable: $\log_{10}(I_{\max})$

Predictor variables:

(a) *Fixed effects*: $\log_{10}$(body mass)

(b) *Random intercepts*: species, taxonomic group

(c) *Random slopes*: taxonomic groups have different $\log_{10}(I_{\max})$ vs. $\log_{10}$(body mass) slopes

	$\log_{10}(I_{\max})$		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-0.32	-0.74 – 0.10	0.133
$\log_{10}$(body mass)	0.75	0.64 – 0.86	**<0.001**
Random Effects			
σ^2	0.46		
$\tau_{00\ \text{species}}$	0.74		
$\tau_{00\ \text{group}}$	0.29		
$\tau_{11\ \text{group.log10(body mass)}}$	0.02		
$\rho_{01\ \text{group}}$	0.50		
ICC	0.72		
N_{species}	378		
N_{group}	13		
Observations	1392		
Marginal R^2 / Conditional R^2	0.682 / 0.911		

Table S4. Maximum clearance rate and maximum ingestion rate are positively related to each other even after accounting for body size, demonstrated using our first method. Here we size-corrected all estimates of maximum clearance rate and maximum ingestion rate by dividing them by organismal body mass, in mg. These new *specific* maximum clearance rate and *specific* maximum ingestion rate estimates were then regressed against each other. Note that in this case, we were faced with fitting problems (singular fits) using *lmer*() and so we instead present results from a Bayesian hierarchical model here. This model was fit with *rstanarm*() and used weakly informative priors. Quantitative results of the *lmer*() and *rstanarm*() fits were very similar, but the Bayesian hierarchical model results are more robust in this case.

Response variable: $\log_{10}$(specific $C_{\max}$)

Predictor variables:

(a) *Fixed effects*: $\log_{10}$(specific $I_{\max}$)
(b) *Random intercepts*: species, taxonomic group
(c) *Random slopes*: taxonomic groups have different $\log_{10}$(specific $C_{\max}$) vs. $\log_{10}$(specific $I_{\max}$) slopes

	$\log_{10}$(specific $C_{\max}$)	
Predictors	*Estimates*	*CI (95%)*
(Intercept)	-3.19	-3.50 – -2.94
$\log_{10}$(specific $I_{\max}$)	0.39	0.20 – 0.67
Random Effects		
σ^2	0.33	
$\tau_{00\ \text{species}}$	0.89	
$\tau_{00\ \text{group}}$	0.12	
$\tau_{11\ \text{group.log10(specific}\ I\text{max)}}$	0.08	
$\rho_{01\ \text{group}}$	0.37	
ICC	0.77	
N $_{\text{species}}$	361	
N $_{\text{group}}$	13	
Observations	1206	
Marginal R^2 / Conditional R^2	0.124 / 0.799	

Table S5. Maximum clearance rate and maximum ingestion rate are positively related to each other even after accounting for body size, demonstrated using a second method. Here, we first calculated the residuals from the regressions between $C_{\max}$ and body mass, and between $I_{\max}$ and body mass. We then regressed these results against each other. As random effects were accounted for in the original regressions from which the residuals were obtained, there was no need for random effects here and so we used OLS regression instead.

Response variable: Residuals from regression of $\log_{10}(C_{\max})$ vs $\log_{10}$(body size)

Predictor variables:

(a) *Fixed effects*: Residuals from regression of $\log_{10}(I_{\max})$ vs $\log_{10}$(body size)
(b) *Random intercepts*: none
(c) *Random slopes*: none

	Residuals from $C_{\max}$ size regression		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	0.01	-0.02 – 0.04	0.411
Residuals from $I_{\max}$ size regression	0.17	0.13 – 0.21	**<0.001**
Observations	1206		
R^2 / R^2 adjusted	0.051 / 0.051		

Table S6. Maximum clearance rate and maximum ingestion rate are positively related to each other even after accounting for body size, demonstrated using a third method. Here we used a multiple regression with body mass as a covariate. *p*-values in this table are more accurate because they were assessed using a more conservative F-test, based on the Kenward-Roger approximation for the denominator degrees of freedom.

Response variable: $\log_{10}(C_{\max})$

Predictor variables:
(a) *Fixed effects*: $\log_{10}(I_{\max})$, $\log_{10}$(body mass)
(b) *Random intercepts*: species, taxonomic group
(c) *Random slopes*: taxonomic groups have different $\log_{10}(C_{\max})$ vs. $\log_{10}(I_{\max})$ slopes

	$\log_{10}(C_{\max})$		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-3.45	-3.97 – -2.94	**<0.001**
$\log_{10}(I_{\max})$	0.34	0.17 – 0.52	**<0.001**
$\log_{10}$(body mass)	0.32	0.26 – 0.39	**<0.001**
Random Effects			
σ^2	0.28		
$\tau_{00\ \text{species}}$	0.66		
$\tau_{00\ \text{group}}$	0.54		
$\tau_{11\ \text{group.log10}(I\text{max})}$	0.06		
$\rho_{01\ \text{group}}$	-0.21		
ICC	0.85		
N_{species}	361		
N_{group}	13		
Observations	1206		
Marginal R^2 / Conditional R^2	0.617 / 0.943		

Table S7. Regression results for maximum clearance rate against body mass and habitat. Note that p-values depicted here are not entirely accurate because of technical challenges associated with calculating degrees of freedom in mixed models.

Response variable: $\log_{10}(C_{\max})$

Predictor variables:

(a) *Fixed effects*: $\log_{10}$(body mass), habitat, $\log_{10}$(body size) * habitat

(b) *Random intercepts*: species, taxonomic group

(c) *Random slopes*: taxonomic groups have different $\log_{10}(C_{\max})$ vs. $\log_{10}$(body mass) slopes

	$\log_{10}(C_{\max})$		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-3.71	-4.25 – -3.16	**<0.001**
$\log_{10}$(body mass)	0.58	0.42 – 0.75	**<0.001**
habitat [Terrestrial]	0.23	-0.17 – 0.62	0.263
$\log_{10}$(body mass) * habitat [Terrestrial]	0.16	0.04 – 0.28	**0.011**
Random Effects			
σ^2	0.31		
$\tau_{00\ \text{species}}$	0.81		
$\tau_{00\ \text{group}}$	0.65		
$\tau_{11\ \text{group.log10(body mass)}}$	0.06		
$\rho_{01\ \text{group}}$	0.01		
ICC	0.85		
N $_{\text{species}}$	453		
N $_{\text{group}}$	13		
Observations	2114		
Marginal R^2 / Conditional R^2	0.497 / 0.927		

Table S8. Regression results for maximum clearance rate against body mass and feeding dimensionality. Note that p-values depicted here are not entirely accurate because of technical challenges associated with calculating degrees of freedom in mixed models.

Response variable: $\log_{10}(C_{\max})$

Predictor variables:

(a) *Fixed effects*: $\log_{10}$(body mass), dimension, $\log_{10}$(body size) * dimension
(b) *Random intercepts*: species, taxonomic group
(c) *Random slopes*: taxonomic groups have different $\log_{10}(C_{\max})$ vs. $\log_{10}$(body mass) slopes

	$\log_{10}(C_{\max})$		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-3.00	-3.56 – -2.44	**<0.001**
$\log_{10}$(body mass)	0.57	0.41 – 0.73	**<0.001**
dimension [Volume feeders]	-0.85	-1.09 – -0.61	**<0.001**
$\log_{10}$(body mass) * dimension [Volume feeders]	0.03	-0.05 – 0.10	0.479
Random Effects			
σ^2	0.31		
$\tau_{00\ \text{species}}$	0.77		
$\tau_{00\ \text{group}}$	0.59		
$\tau_{11\ \text{group.log10(body mass)}}$	0.04		
$\rho_{01\ \text{group}}$	0.30		
ICC	0.84		
N_{species}	453		
N_{group}	13		
Observations	2114		
Marginal R^2 / Conditional R^2	0.524 / 0.926		

Table S9. Regression results for maximum ingestion rate against body mass and habitat. Note that p-values depicted here are not entirely accurate because of technical challenges associated with calculating degrees of freedom in mixed models.

Response variable:	$\log_{10}(I_{\max})$
Predictor variables:	
(a) *Fixed effects*:	$\log_{10}$(body mass), habitat, $\log_{10}$(body mass) * habitat
(b) *Random intercepts*:	species, taxonomic group
(c) *Random slopes*:	taxonomic groups have different $\log_{10}(I_{\max})$ vs. $\log_{10}$(body mass) slopes

	$\log_{10}(I_{\max})$		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-0.32	-0.76 – 0.11	0.143
$\log_{10}$(body mass)	0.79	0.67 – 0.90	**<0.001**
habitat [Terrestrial]	-0.20	-0.57 – 0.16	0.274
$\log_{10}$(body mass) * habitat [Terrestrial]	-0.15	-0.26 – -0.04	**0.010**
Random Effects			
σ^2	0.46		
$\tau_{00\ \text{species}}$	0.70		
$\tau_{00\ \text{group}}$	0.31		
$\tau_{11\ \text{group.log10(body mass)}}$	0.02		
$\rho_{01\ \text{group}}$	0.73		
ICC	0.72		
N_{species}	378		
N_{group}	13		
Observations	1392		
Marginal R^2 / Conditional R^2	0.684 / 0.912		

Table S10. Regression results for maximum ingestion rate against body mass and feeding dimensionality. Note that p-values depicted here are not entirely accurate because of technical challenges associated with calculating degrees of freedom in mixed models.

Response variable: $\log_{10}(I_{\max})$

Predictor variables:

(a) *Fixed effects*: $\log_{10}$(body mass), dimension, $\log_{10}$(body mass) * dimension

(b) *Random intercepts*: species, taxonomic group

(c) *Random slopes*: taxonomic groups have different $\log_{10}(I_{\max})$ vs. $\log_{10}$(body mass) slopes

	$\log_{10}(I_{\max})$		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-0.40	-0.87 – 0.07	0.092
$\log_{10}$(body mass)	0.70	0.56 – 0.84	**<0.001**
dimension [Volume feeders]	0.11	-0.17 – 0.39	0.449
$\log_{10}$(body mass) * dimension [Volume feeders]	0.08	-0.01 – 0.18	0.089
Random Effects			
σ^2	0.46		
$\tau_{00\ \text{species}}$	0.71		
$\tau_{00\ \text{group}}$	0.28		
$\tau_{11\ \text{group.log10(body mass)}}$	0.02		
$\rho_{01\ \text{group}}$	0.63		
ICC	0.72		
N species	378		
N group	13		
Observations	1392		
Marginal R^2 / Conditional R^2	0.688 / 0.911		

Table S11. Regression results for specific maximum clearance rate against specific maximum ingestion rate and habitat. Note that p-values depicted here are not entirely accurate because of technical challenges associated with calculating degrees of freedom in mixed models.

Response variable: $\log_{10}$(specific $C_{\max}$)

Predictor variables:

(a) *Fixed effects*: $\log_{10}$(specific $I_{\max}$), habitat, $\log_{10}$(specific $I_{\max}$) * habitat
(b) *Random intercepts*: species, taxonomic group
(c) *Random slopes*: taxonomic groups have different $\log_{10}$(specific $C_{\max}$) vs. $\log_{10}$(specific $I_{\max}$) slopes

	$\log_{10}$(specific $C_{\max}$)		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-3.36	-3.68 – -3.05	**<0.001**
$\log_{10}$(specific $I_{\max}$)	0.43	0.25 – 0.62	**<0.001**
habitat [Terrestrial]	0.76	0.47 – 1.05	**<0.001**
$\log_{10}$(specific $I_{\max}$) * habitat [Terrestrial]	-0.11	-0.26 – 0.04	0.141
Random Effects			
σ^2	0.33		
$\tau_{00\ \mathrm{species}}$	0.80		
$\tau_{00\ \mathrm{group}}$	0.18		
$\tau_{11\ \mathrm{group.log10(specific}\ I\mathrm{max)}}$	0.05		
$\rho_{01\ \mathrm{group}}$	0.67		
ICC	0.76		
N_{species}	361		
N_{group}	13		
Observations	1206		
Marginal R^2 / Conditional R^2	0.188 / 0.805		

Table S12. Regression results for specific maximum clearance rate against specific maximum ingestion rate and feeding dimensionality. Note that p-values depicted here are not entirely accurate because of technical challenges associated with calculating degrees of freedom in mixed models.

Response variable: $\log_{10}(\text{specific } C_{\text{max}})$

Predictor variables:

(a) *Fixed effects*: $\log_{10}(\text{specific } I_{\text{max}})$, dimension, $\log_{10}(\text{specific } I_{\text{max}})$ * dimension

(b) *Random intercepts*: species, taxonomic group

(c) *Random slopes*: taxonomic groups have different $\log_{10}(\text{specific } C_{\text{max}})$ vs. $\log_{10}(\text{specific } I_{\text{max}})$ slopes

	$\log_{10}(\text{specific } C_{\text{max}})$		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-2.67	-3.02 – -2.32	**<0.001**
$\log_{10}(\text{specific } I_{\text{max}})$	0.39	0.20 – 0.58	**<0.001**
dimension [Volume feeders]	-0.72	-0.93 – -0.51	**<0.001**
$\log_{10}(\text{specific } I_{\text{max}})$ * dimension [Volume feeders]	-0.01	-0.14 – 0.12	0.909
Random Effects			
σ^2	0.33		
$\tau_{00 \text{ species}}$	0.79		
$\tau_{00 \text{ group}}$	0.18		
$\tau_{11 \text{ group.log10(specific } I\text{max)}}$	0.05		
$\rho_{01 \text{ group}}$	0.90		
ICC	0.76		
N_{species}	361		
N_{group}	13		
Observations	1206		
Marginal R^2 / Conditional R^2	0.172 / 0.800		

Table S13. Specific growth rate increases with increases in specific maximum ingestion rate, consistent with our assumption. We used OLS regression for this analysis and neglected group-level variation, as only 5 groups were represented and 3 of them had 2 points or less. One species was represented twice, all other measurements were on distinct species.

Response variable:	$\log_{10}$(specific growth rate)
Predictor variables:	
(a) *Fixed effects*:	$\log_{10}$(specific $I_{\max}$)
(b) *Random intercepts*:	none
(c) *Random slopes*:	none

	$\log_{10}$(specific growth rate)		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	-0.42	-0.56 – -0.29	**<0.001**
$\log_{10}$(specific $I_{\max}$)	0.58	0.37 – 0.78	**<0.001**
Observations	47		
R^2 / R^2 adjusted	0.415 / 0.402		