Supporting information:
Size, foraging and food web structure
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1 Empirical information on foraging trait allometry

The DBM requires the body size of each species and four allometries; those of energetic content of individuals of each species, density of each species, the attack rate of each consumer on each resource species, and the handling time of each consumer on each resource species. We assumed that energetic content is linearly related with body mass and a common allometric scaling of density and body mass.

We searched the literature for empirically motivated and parameterised allometries of handling time and attack rate and, due to its importance for food web structure, we focused on allometry of handling times. For a function to be directly applicable to the model, it would need to 1) be parameterised from data that cover the range of organism sizes observed in real food webs (about 17 orders of magnitude); 2) include information about effects of a large range of resource sizes on the foraging of a single predator species. Various functions that appear in the literature are given in table S1 and none appear applicable.

2 Fifteen real food webs

Table S2 contains the original sources of predation matrices and common names used in this article. Only the scmown2 web in Cattin et al. (2004) was used. We did not model or analyse the Weddell Sea food web because the large number of species and links made the required computations exceed available processing resources. The predation matrices of each food web are presented in figure S1. Body sizes were compiled from a variety of sources (table S2).

These real food webs contain producers, herbivores, carnivores, parasites, and parasitoids. The organisms display a range of feeding interactions including predation, herbivory, bacterivory, parasitism, pathogenic, and parasitoid. For nine of the 15 webs there was information available about which interaction was represented by each individual feeding link.

3 Parameterising the Allometric DBMs

As the literature does not contain suitably parameterised allometries for attack rates and handling times, we used optimisation to fit the parameters. Two methods of optimisation were used: complete enumeration (CE)

Table S1: Empirical information on handling time allometries. In the first column H_{ij} is time for consumer j to handle resource i; absence of j indicates the study did not address variation in consumer size. Consumer size is M_j, resource size is M_i. All other letters in column 1 are constants. † indicates unavailable information.

Function	Resource size range (orders of magnitude)	Consumer size range (orders of magnitude)	Range of resource sizes for a particular consumer	Reference
$H_i = a + bM_i$	< 1	NA	Yes	(Woodward and Hildrew, 2002)
$\log(H_i) = a + bL_i$	< 1	NA	Yes	(Turesson et al., 2002)
$H_i = a + bM_i$	< 1	NA	Yes	(Spitze, 1985)
$H_i = aL_i^b$	< 2	< 1	Yes	(Dickman, 1988)
$H_{ij} = aM_i^b M_j^c + cM_i M_j^{-1}$	< 1	$\tilde{2}$	Yes	(Aljetlawi et al., 2004)
$H_{ij} = a(M_i/M_j)^b$	< 1	< 1	Yes	(our fit to Thompson (1975))
$H_{ij} = a(M_i/M_j)^b$	$\tilde{1}7$	$\tilde{1}2$	No	(unpublished data)
$H_j = a + bM_j - c\exp(dM_j)$	†	†	†	(Persson, 1987)
$H_j = aM_j^{2/3}$	NA	NA	NA	(Kooijman, 1993)

Table S2: The real food webs

Common food web name	Predation matrix source	Body size source	General ecosystem
Benguela Pelagic	(Yodzis, 1998)	(Yodzis, 1998)	Marine
Broadstone Stream	(Woodward and Hildrew, 2001; Woodward et al., 2005)	(Brose et al., 2005)	Freshwater
Broom	(Memmott et al., 2000)	(Brose et al., 2005)	Terrestrial
Capinteria	(Lafferty et al., 2006)		Marine (Salt Marsh)
Caricaie Lakes	(Cattin et al., 2004)	(Brose et al., 2005)	Freshwater
Coachella Valley	(Polis, 1991)	(Reide, unpublished)	Terrestrial (Desert)
EcoWEB41	(Cohen, 1989)	(Jonsson, 1998)	Marine
EcoWEB60	(Cohen, 1989)	(Jonsson, 1998)	Terrestrial
Grasslands	(Dawah et al., 1995)	(Brose et al., 2005)	Terrestrial
Mill Stream	(Ledger, Edwards, Woodward, unpublished)	(Brose et al., 2005)	Freshwater
Sierra Lakes	(Harper-Smith et al., 2005)	(Brose et al., 2005)	Freshwater
Skipwith Pond	(Warren, 1989)	(Brose et al., 2005)	Freshwater
Small Reef	(Opitz, 1996)	(Reide, unpublished)	Marine (Reef)
Tuesday Lake	(Jonsson et al., 2005)	(Brose et al., 2005)	Freshwater
Ythan	(Emmerson and Raffaelli, 2004)	(Emmerson and Raffaelli, 2004)	Marine (Estuarine)

and Nelder-Mead (Nelder and Mead, 1965) (NM). Complete enumeration searches a region of parameter space (table S3) for a set of parameter values that gave the best fit between model prediction and observed data. Nelder-Mead optimisation performs a search through parameter space starting at a set of initial parameter values, and ends at a set of parameter values with maximum explanatory power. To ensure that the results of Nelder-Mead optimisation were not affected by local optima, we repeated the procedure with various combinations of initial parameter values. CE and NM parameterisation produced generally similar results and we present only results of NM optimisation in the main text.

We chose to parameterise each food web separately, rather than parameterising all food webs simultaneously. This was due to the heterogeneity present across the food webs in ecosystem (table S3), in taxa, and in the types of interactions. For example, the Grasslands food web is mostly of host-parasitoid interactions, whereas others have herbivores and predators dominating. Table S4 gives the values of parameters fitted for each web when the ratio handling time function was used.

4 Structural food web properties

We examined twelve structural properties between model and observed food webs:

1. Proportion basal. Basal species are those that have no resources in the recorded food web. The *proportion* of all species that are basal is used to make this property comparable among food webs with different numbers of species.

2. Proportion intermediate. Intermediate species are those that have resources and consumers.

3. Top species. Top species have resources and no consumers.

4. Proportion herbivores. Herbivore species consume only basal species.

5. Mean trophic level. The average trophic level of the species in a food web. The trophic level of each species is computed using the short-weighted trophic level algorithm (Williams and Martinez, 2004).

6. Maximum trophic level. The maximum trophic level of the species in a food web.

Table S3: Parameter values and ranges used in the optimisation methods of parameterisation for the ADBM. † In the ADBM, diet breadth and therefore connectance are affected by the product *nab* (Beckerman et al., 2006). We chose to optimise parameter a to set connectance at the observed value, but could equally have used n or b, hence their arbitrary values.

Allometric function	Parameter	Value in complete enumeration method	Value in Nelder-Mead method	Comments
Energy: $E_i = eM_i$	e	1	1	Arbitrary. No effect on structure
Density: $N_i = nM_i^{n_i}$	n	1	1	Arbitrary†
	n_i	-0.75	-0.75	(Damuth, 1981)
Attack rate: $A_i = aM_i^{a_i}M_j^{a_j}$	a	Free	Free	The value is set so predicted = observed connectance
	a_i	Selected from -1 to 1 in 0.25 steps	Free	Value chosen to maximise fit of model to data
	a_j	Selected from -1 to 1 in 0.25 steps	Free	Value chosen to maximise fit of model to data
Ratio handling time function: $H_{ij} = \frac{h}{b - \frac{M_i}{M_j}}$	h	1	1	Arbitrary†
	b	Selected from 2^x where x is the vector from -8 to 2 in steps of 1	Free	Value chosen to maximise fit of model to data

Table S4: The parameter values for the ADBM with ratio handling time.

	Parameter			
Food web	a	a_i	a_j	b
Benguela Pelagic	1.89×10^{-2}	-4.91×10^{-1}	-4.65×10^{-1}	4.01×10^{-2}
Broadstone Stream	2.08×10^{-22}	-2.00×10^{0}	-1.85×10^{0}	8.43×10^{-2}
Broom	6.15×10^{-6}	-9.37×10^{-1}	1.05×10^{0}	2.72×10^{-2}
Capinteria	2.54×10^{-9}	-1.96×10^{0}	2.04×10^{0}	5.74×10^{-3}
Caricaie Lakes	3.27×10^{-6}	-4.67×10^{-1}	5.39×10^{-1}	4.12×10^{-2}
Coachella	1.20×10^{-5}	-7.67×10^{-1}	-3.67×10^{-1}	3.83×10^{-1}
EcoWEB41	1.89×10^{-6}	-1.93×10^{0}	2.11×10^{0}	8.86×10^{-2}
EcoWEB60	4.41×10^{3}	-5.06×10^{-1}	-4.81×10^{-1}	4.28×10^{-2}
Grasslands	3.88×10^{4}	1.00×10^{0}	1.00×10^{0}	1.00×10^{0}
Mill Stream	1.29×10^{-12}	-9.10×10^{-1}	-8.82×10^{-1}	6.72×10^{-3}
Sierra Lakes	5.97×10^{-10}	-2.11×10^{0}	-2.02×10^{0}	3.34×10^{-1}
Skipwith Pond	1.07×10^{-11}	-2.03×10^{0}	-2.04×10^{0}	4.70×10^{-1}
Small Reef	8.56×10^{-6}	-5.39×10^{-1}	5.80×10^{-1}	5.69×10^{-2}
Tuesday Lake	3.88×10^{-19}	-1.80×10^{0}	2.01×10^{0}	7.21×10^{-4}
Ythan	1.89×10^{-2}	-4.91×10^{-1}	-4.65×10^{-1}	4.01×10^{-2}
Grasslands	1.80×10^{-17}	-1.98×10^{0}	2.19×10^{0}	3.22×10^{-4}

7. Mean omnivory. The level of omnivory displayed by each species is the standard deviation of the trophic level of its resources. This is averaged across all the species in the food web.
8. Clustering coefficient (aka. transitivity) Watts and Strogatz (1998). This measures how close to a small world type of network is a food web.
9. Standard deviation of generalism. The generalism of a species is the number of resources its has. The standard deviation of this is taken across all species.
10. Standard deviation of vulnerability. The vulnerability of a species is the number of consumers it has. The standard deviation of this is taken across all species.
11. Diet similarity. The similarity of a two species' diets is the number of prey shared in common, divided by the pair's total number of prey. The maximum value for species was taken, and averaged over all species.
12. Mean path length. The mean of the shortest path length between all pairs of species in a food web.

For each food web and property, raw error was calculated as predicted - observed. Standardised error was raw error divided by the maximum raw error for each property. This gives each property the same weight when mean standardised error was calculated for each food web.

Mean diet contiguity was measured for each real web as the $\sum_{j=1}^{s} \frac{s_{max}-s_{real}}{s*(s_{max}-1)}$, where s_{max} is the maximum number of discrete contiguous ranges along the size axis and s_{real} is the realised number. A completely contiguous diet gives $s_{real} = 1$, whereas s_{max} is defined by the possible number of resources and the number of realised resources ($s_{max} =$ the number of realised resources if this is not too large relative to the possible number of resources). Hence, a mean diet contiguity of 1 indicates all consumers have a completely contiguous diet, whereas a value of 0 indicates that all consumers have diets that are as non-contiguous as possible.

5 Model complexity and performance

Statistical theory predicts that increasing the number of parameters alone can increase model performance. To explore the importance of model complexity, we examine the performance of each ADBM when the number and combination of fitted parameters is restricted. The full Ratio ADBM has three (a_i, a_j, b) and the full Power ADBM has four (a_i, a_j, h_i, h_j). We measured the performance of each ADBM when the combinations (and therefore numbers) of parameters were varied. We then modelled the effect of parameter combination on performance, taking into account the different performance among food webs. This was done by fitting a linear model of the form Performance = Food web + Parameter combination, where Performance is proportion of links correctly predicted, Food web is a factor, and Parameter combination is a factor. Performance was arcsine transformed before modelling.

Generally, fewer than all parameters were required to maintain near maximum predictive power (within 10% of the maximum). Across all the webs analysed, the Ratio model required only parameter b (table S5). This parameter defines how handling times relate to the mass ratio of predator and prey. The Power model required parameter h_i and at least one of the two predator specific parameters (a_j or h_j) (table S6). It therefore seems clear that model complexity is not primarily responsible for performance.

Table S5: Complexity and performance of the Ratio ADBM. The effect column shows the change in performance caused by that parameter combination, relative to the combination with maximum predictive power. They are the coefficients of the linear model Performance = Food web + Parameter combination, where Performance is arcsine transformed proportion of links correctly predicted, Food web is a factor, and Parameter combination is a factor. We do not use the model for hypothesis testing.

Presence (1) or absence (0) of parameter			Effect of parameter combination on model performance (relative to maximum)
a_i	a_j	b	
0	**0**	**1**	**-0.07**
0	1	0	-0.46
0	**1**	**1**	**0.00**
1	0	0	-0.40
1	**0**	**1**	**-0.02**
1	1	0	-0.28
1	**1**	**1**	**-0.01**

Table S6: Complexity and performance of the Power ADBM. See legend of table S5 for details.

Presence (1) or absence (0) of parameter				Effect of parameter combination on model performance (relative to maximum)
a_i	a_j	h_i	h_j	
0	0	0	1	-0.17
0	0	1	0	-0.24
0	**0**	**1**	**1**	**-0.02**
0	1	0	0	-0.17
0	1	0	1	-0.12
0	**1**	**1**	**0**	**-0.01**
0	**1**	**1**	**1**	**0.00**
1	0	0	0	-0.39
1	0	0	1	-0.12
1	0	1	0	-0.11
1	**0**	**1**	**1**	**-0.02**
1	1	0	0	-0.16
1	1	0	1	-0.11
1	**1**	**1**	**0**	**-0.01**
1	**1**	**1**	**1**	**0.00**

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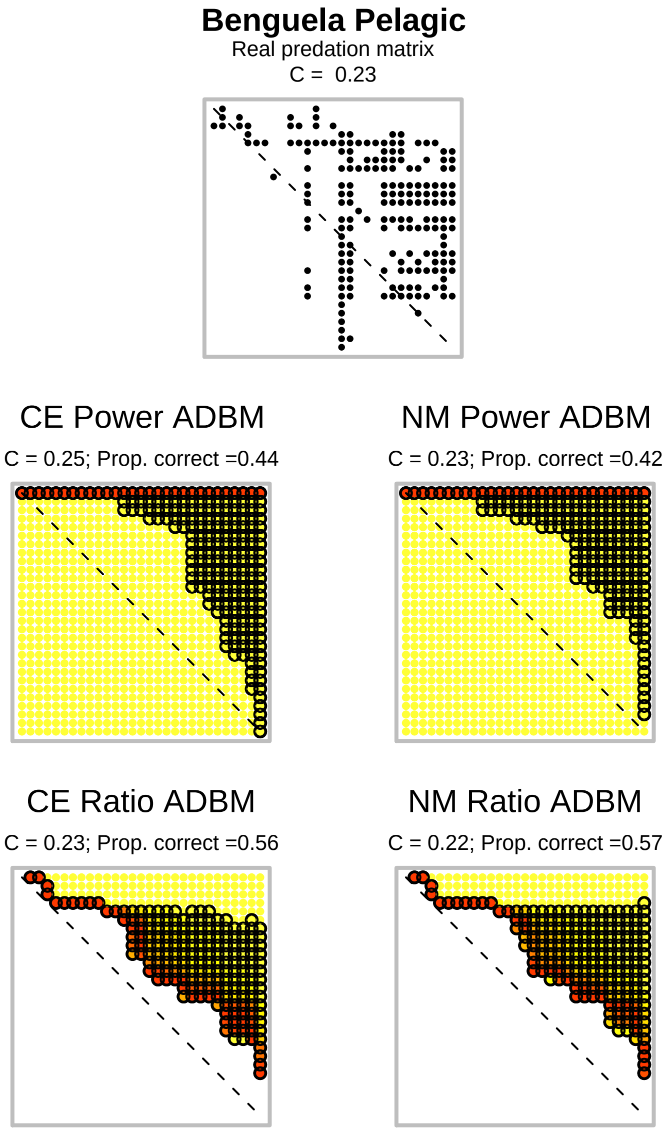
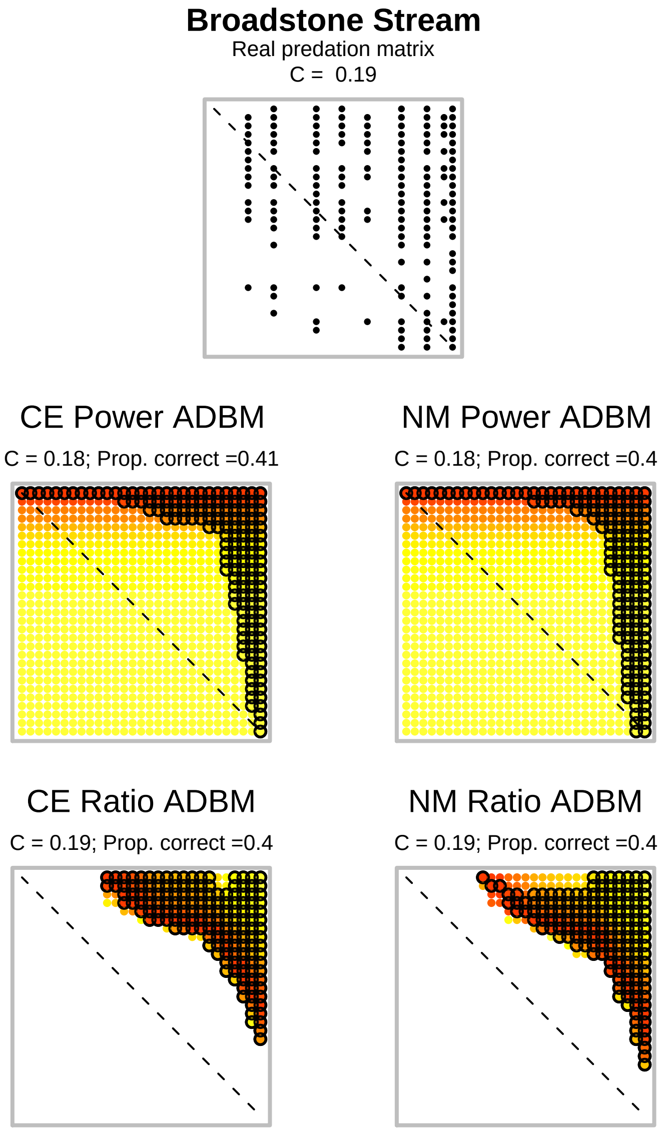
6 Figure legends

Figure S1: The real food webs and various models of them, each of them depicted by a predation matrix. Each predation matrix describes a food web, with resources in rows and consumers in columns. The rows and columns are ordered in increasing body size from left-to-right, and top-to-bottom. A black dot indicates the consumer in that column feeds upon the resource in that row. Hence dots in the upper right triangle indicate feeding links where consumers are larger than their resources. Colours from yellow to red indicate low to high resource profitability in the ADBM models. Here, consumer diets (columns) always include the darker red (most profitable) resources, and extend to different amounts into yellows (less profitable resources). The dashed diagonal line represents the position that cannibalistic links would occupy. Ratio indicates an ADBM with ratio handling time function, Power indicates the power handling time function. NM indicates parameterisation using the Nelder-Mead algorithm; CE indicates parameterisation by Complete Enumeration. Connectance (C) and proportion of links correctly predicted (prop. correct) are also given. This legend applies for figures S1 a-o.



Supplementary Figure S1a



Broadstone Stream
Real predation matrix
C = 0.19

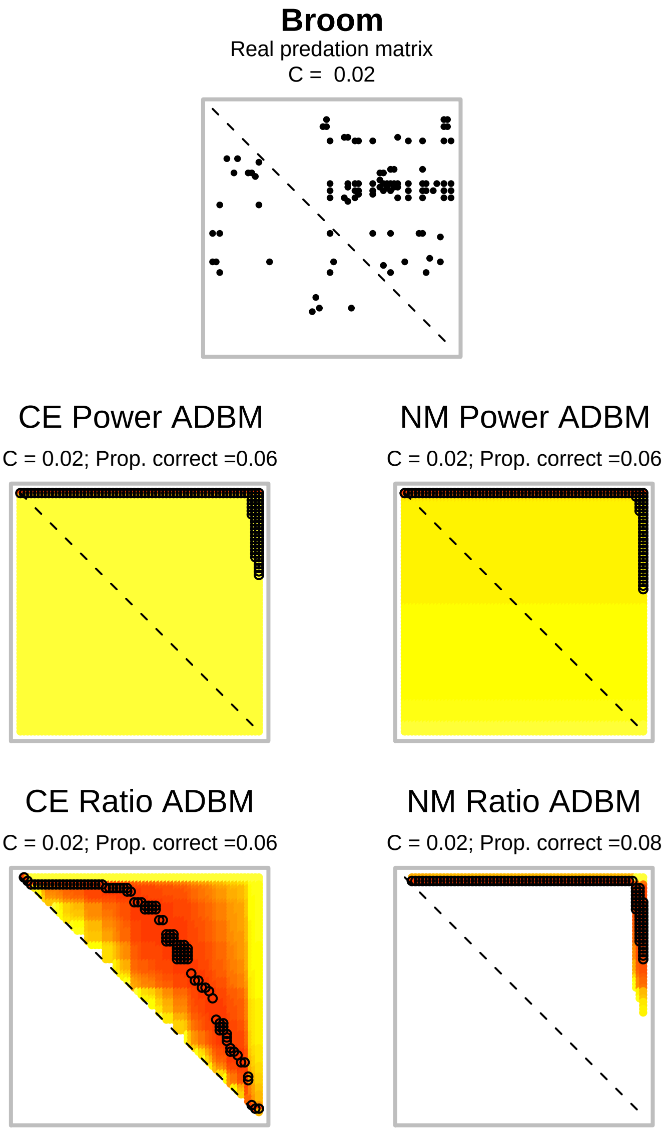
CE Power ADBM
C = 0.18; Prop. correct =0.41

NM Power ADBM
C = 0.18; Prop. correct =0.4

CE Ratio ADBM
C = 0.19; Prop. correct =0.4

NM Ratio ADBM
C = 0.19; Prop. correct =0.4

Supplementary Figure S1b



Broom
Real predation matrix
C = 0.02

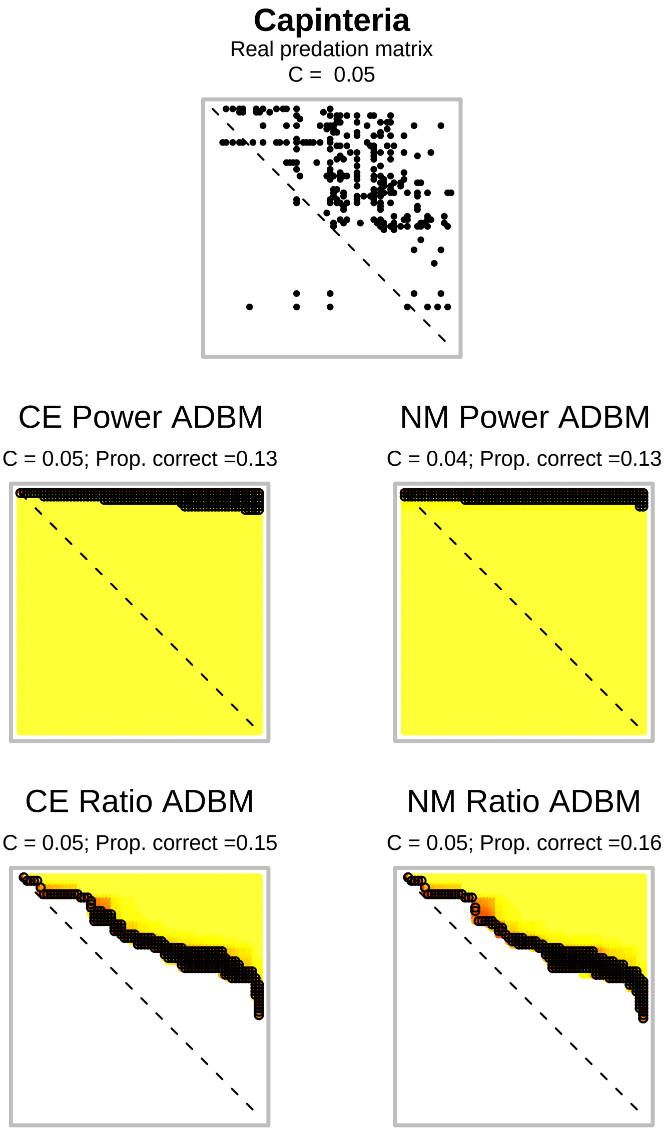
CE Power ADBM
C = 0.02; Prop. correct =0.06

NM Power ADBM
C = 0.02; Prop. correct =0.06

CE Ratio ADBM
C = 0.02; Prop. correct =0.06

NM Ratio ADBM
C = 0.02; Prop. correct =0.08

Supplementary Figure S1c



Capinteria
Real predation matrix
C = 0.05

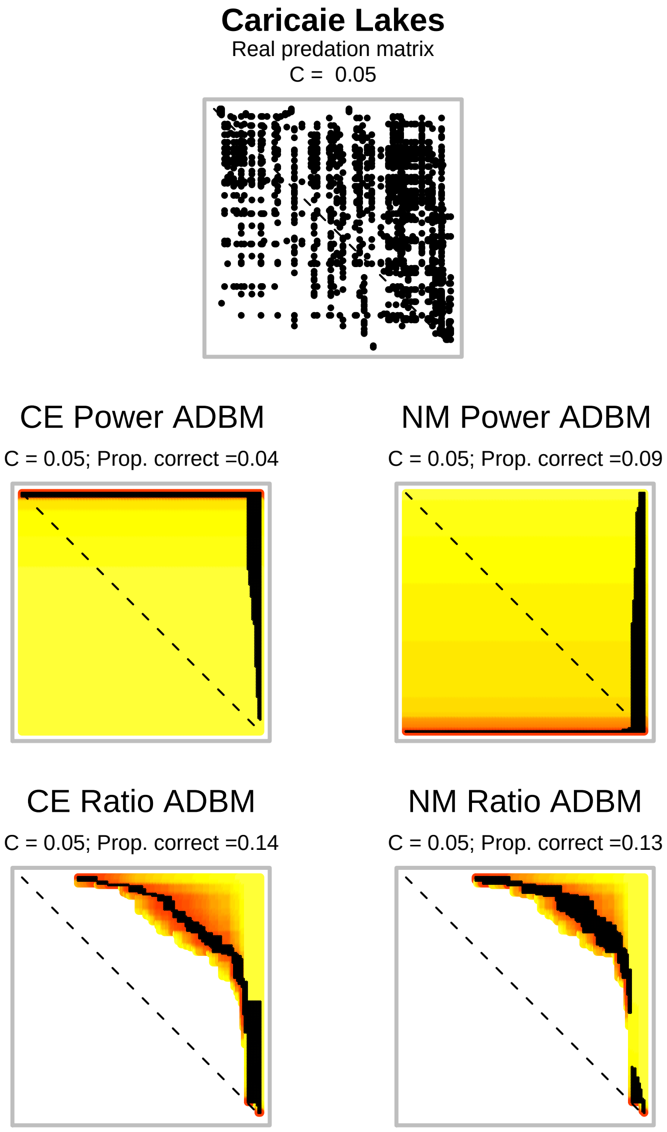
CE Power ADBM
C = 0.05; Prop. correct =0.13

NM Power ADBM
C = 0.04; Prop. correct =0.13

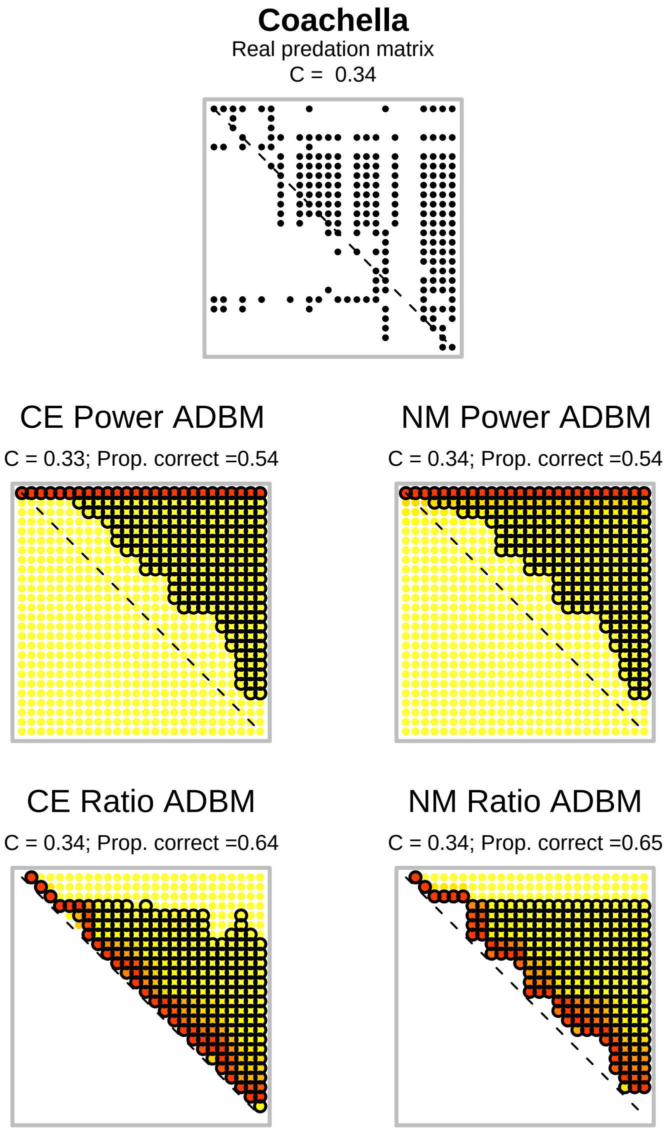
CE Ratio ADBM
C = 0.05; Prop. correct =0.15

NM Ratio ADBM
C = 0.05; Prop. correct =0.16

Supplementary Figure S1d



Supplementary Figure S1e



Coachella
Real predation matrix
C = 0.34

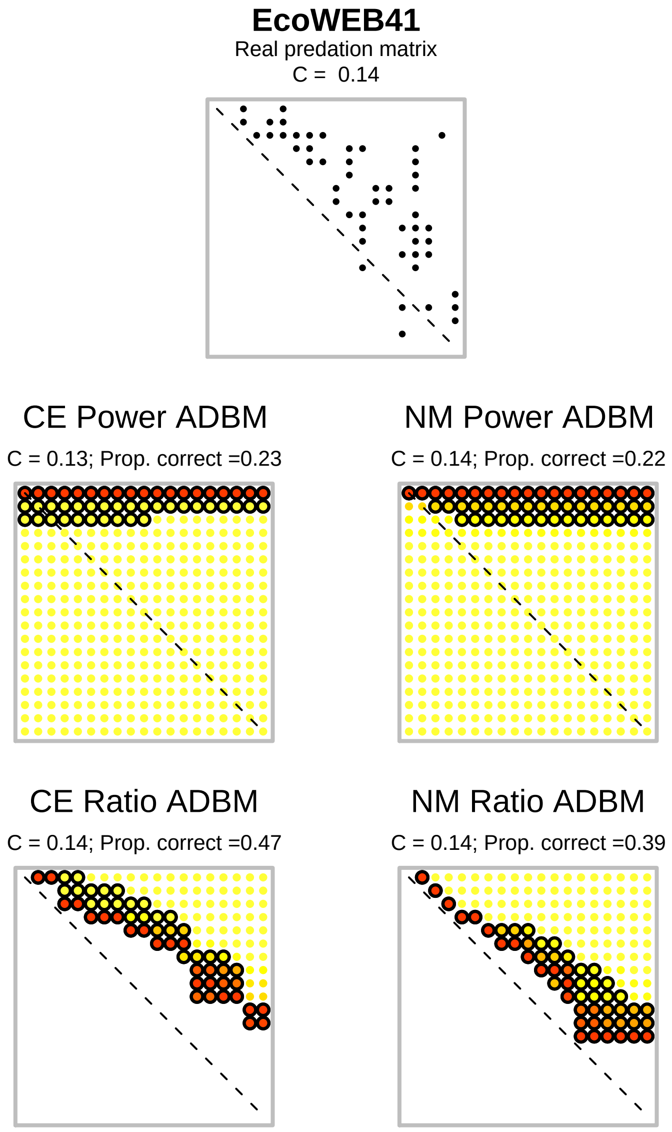
CE Power ADBM
C = 0.33; Prop. correct =0.54

NM Power ADBM
C = 0.34; Prop. correct =0.54

CE Ratio ADBM
C = 0.34; Prop. correct =0.64

NM Ratio ADBM
C = 0.34; Prop. correct =0.65

Supplementary Figure S1f



EcoWEB41
Real predation matrix
C = 0.14

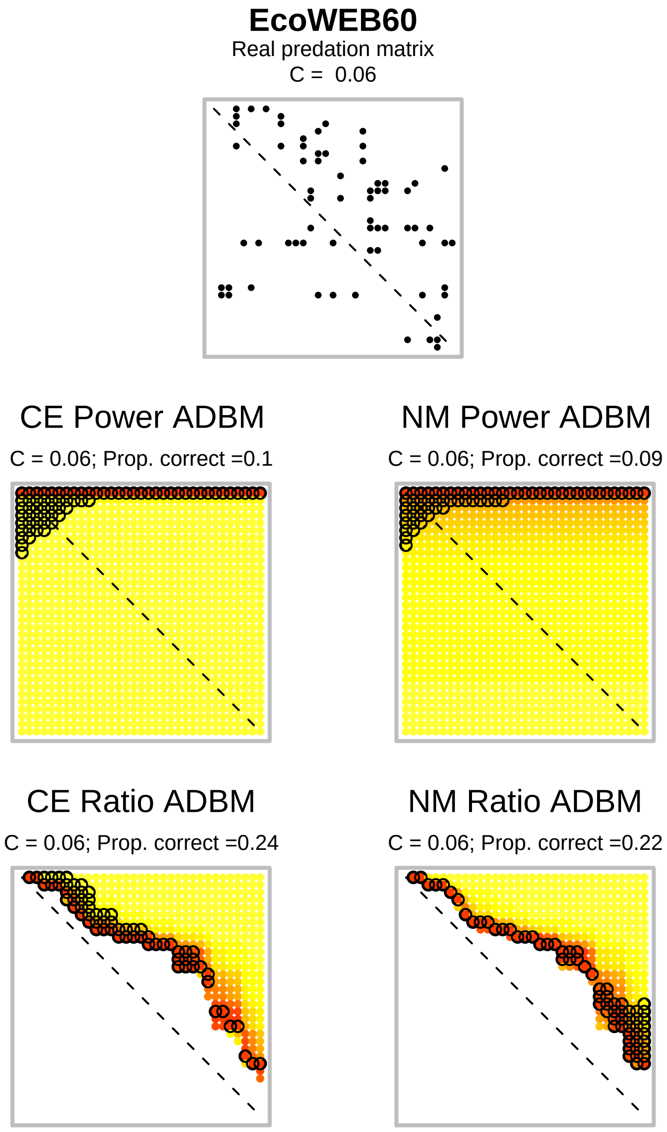
CE Power ADBM
C = 0.13; Prop. correct =0.23

NM Power ADBM
C = 0.14; Prop. correct =0.22

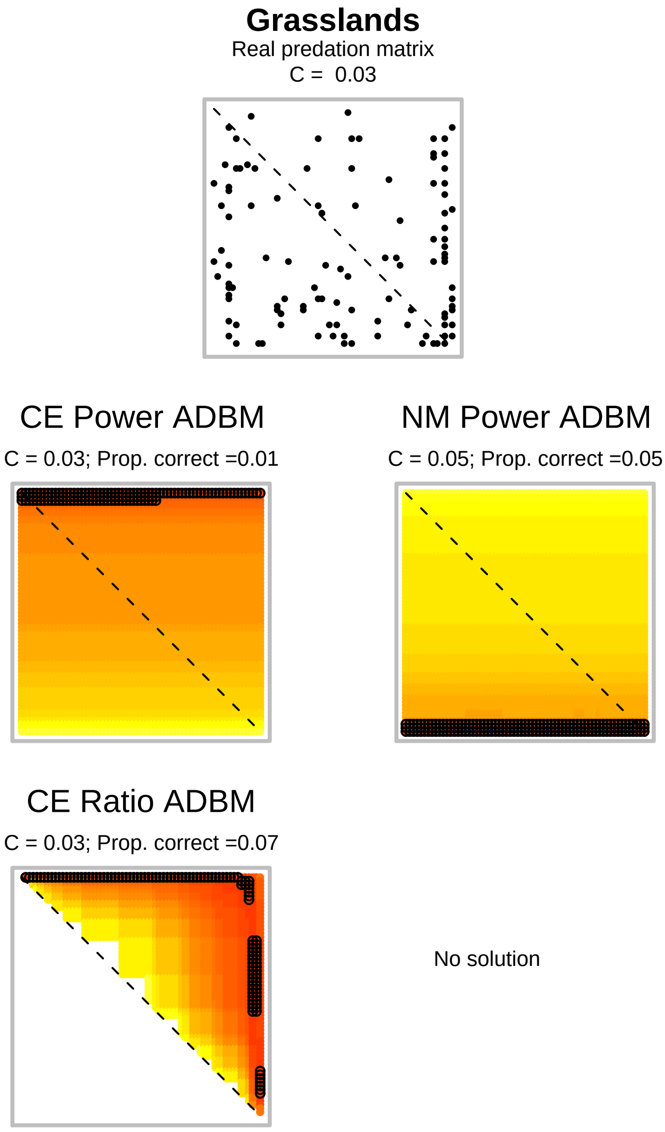
CE Ratio ADBM
C = 0.14; Prop. correct =0.47

NM Ratio ADBM
C = 0.14; Prop. correct =0.39

Supplementary Figure S1g



Supplementary Figure S1h



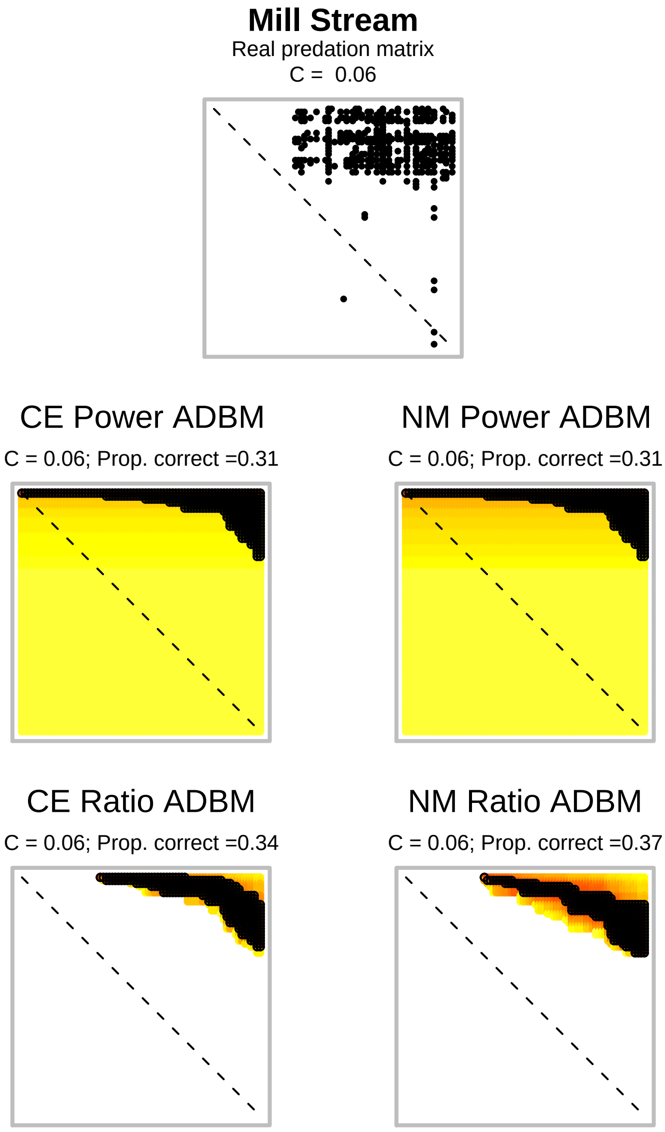
Grasslands
Real predation matrix
C = 0.03

CE Power ADBM
C = 0.03; Prop. correct =0.01

NM Power ADBM
C = 0.05; Prop. correct =0.05

CE Ratio ADBM
C = 0.03; Prop. correct =0.07

Supplementary Figure S1i



Mill Stream

Real predation matrix

C = 0.06

CE Power ADBM

C = 0.06; Prop. correct =0.31

NM Power ADBM

C = 0.06; Prop. correct =0.31

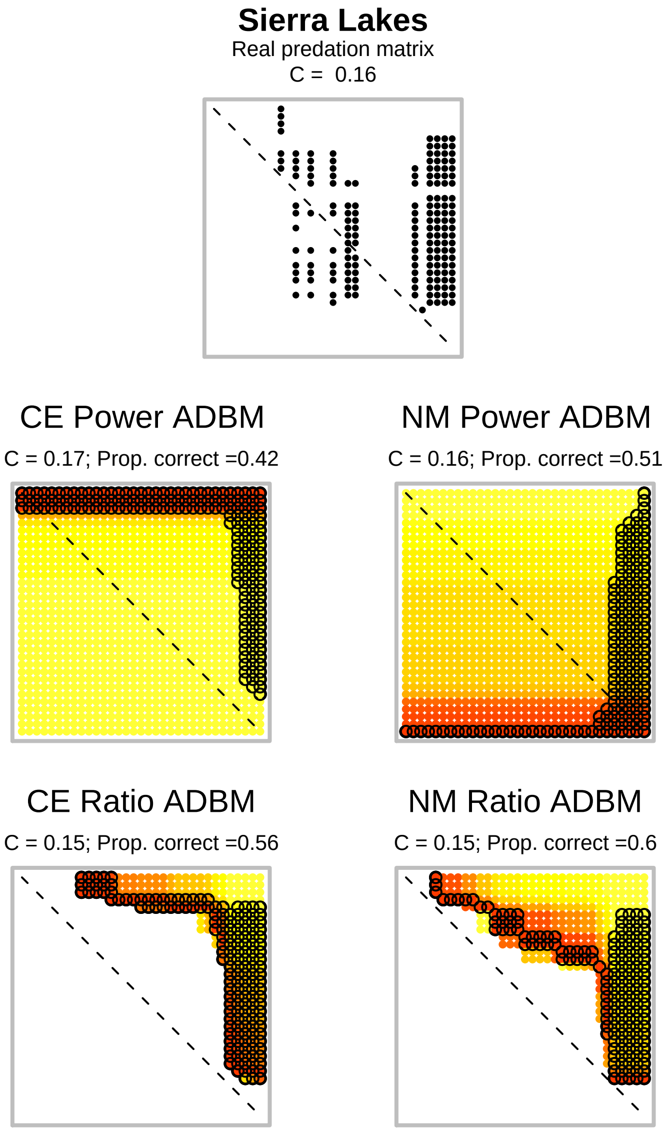
CE Ratio ADBM

C = 0.06; Prop. correct =0.34

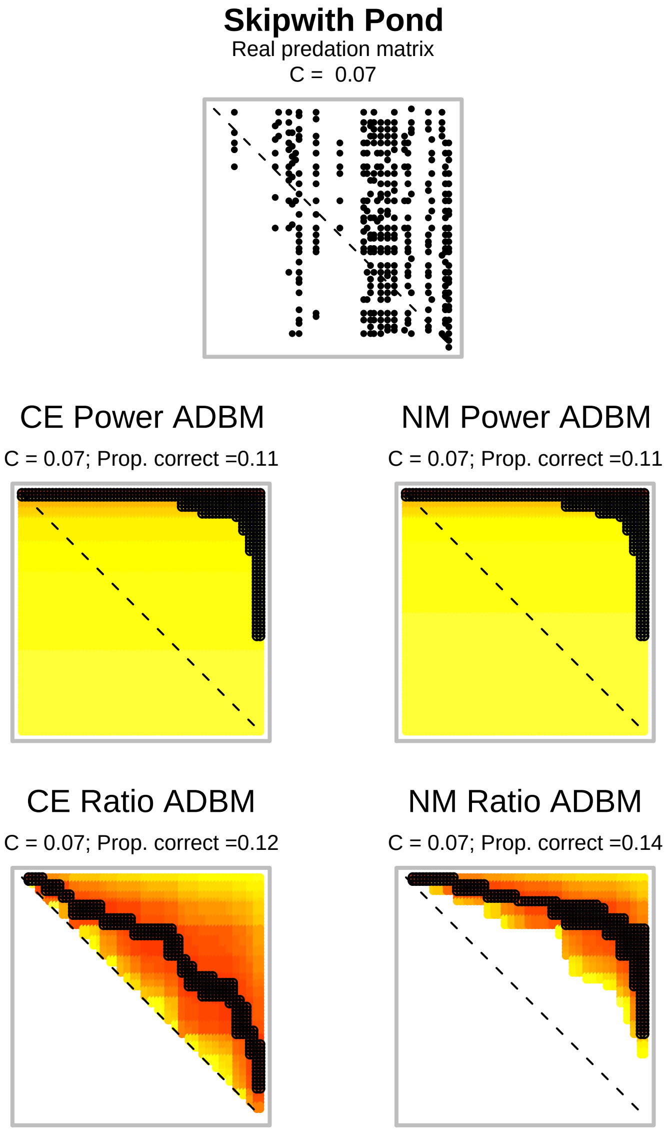
NM Ratio ADBM

C = 0.06; Prop. correct =0.37

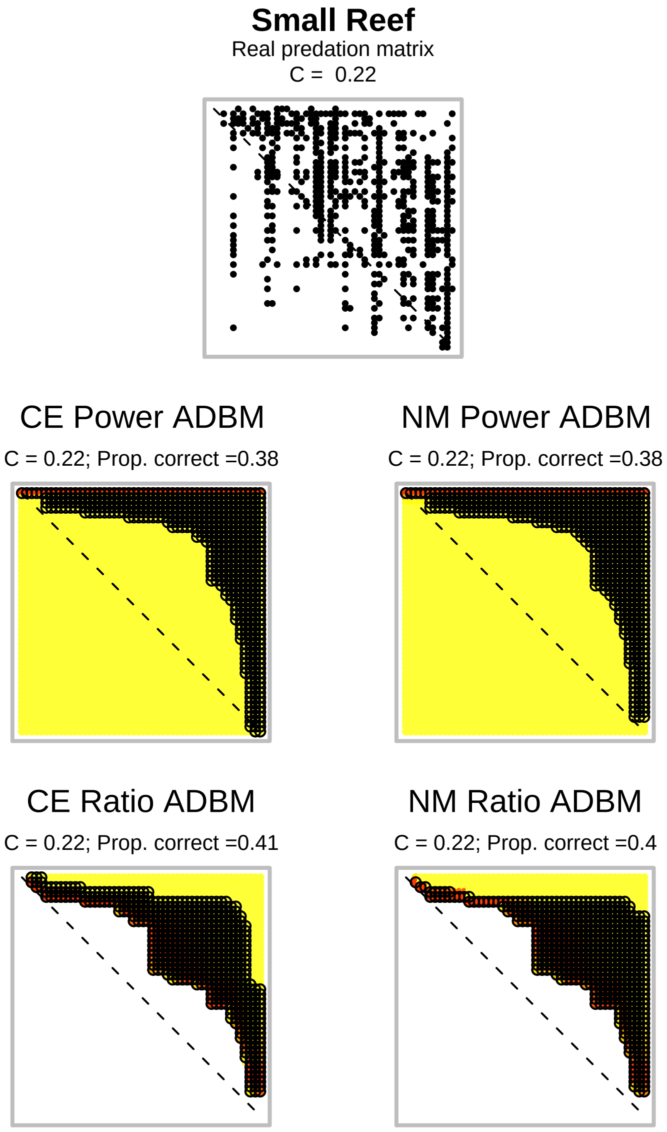
Supplementary Figure S1j



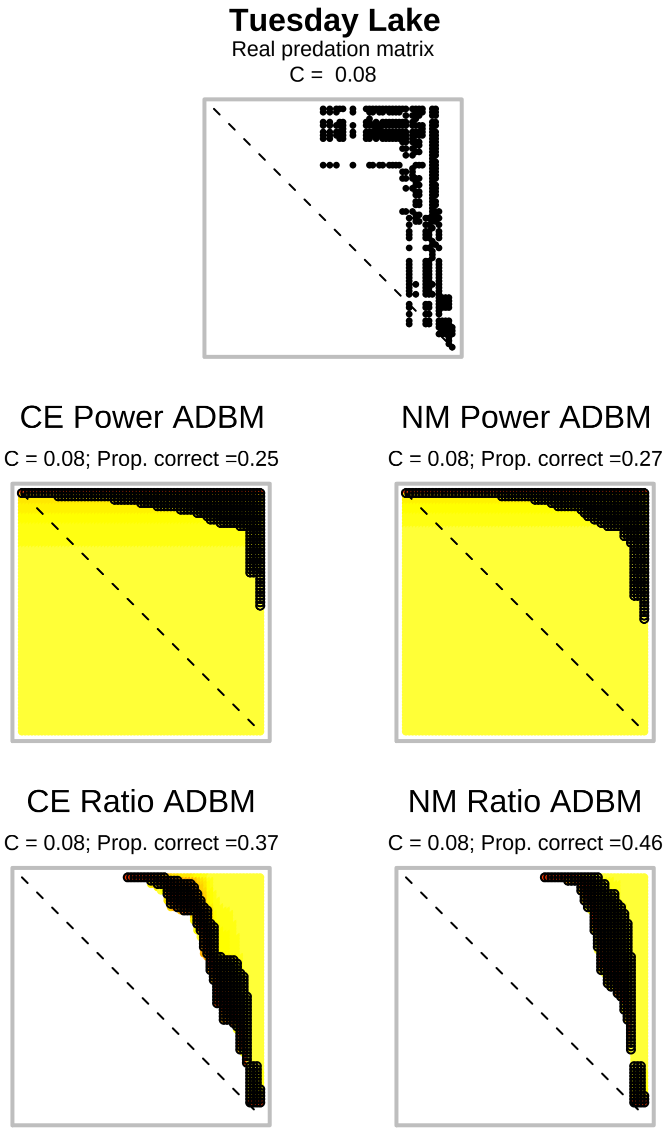
Supplementary Figure S1k



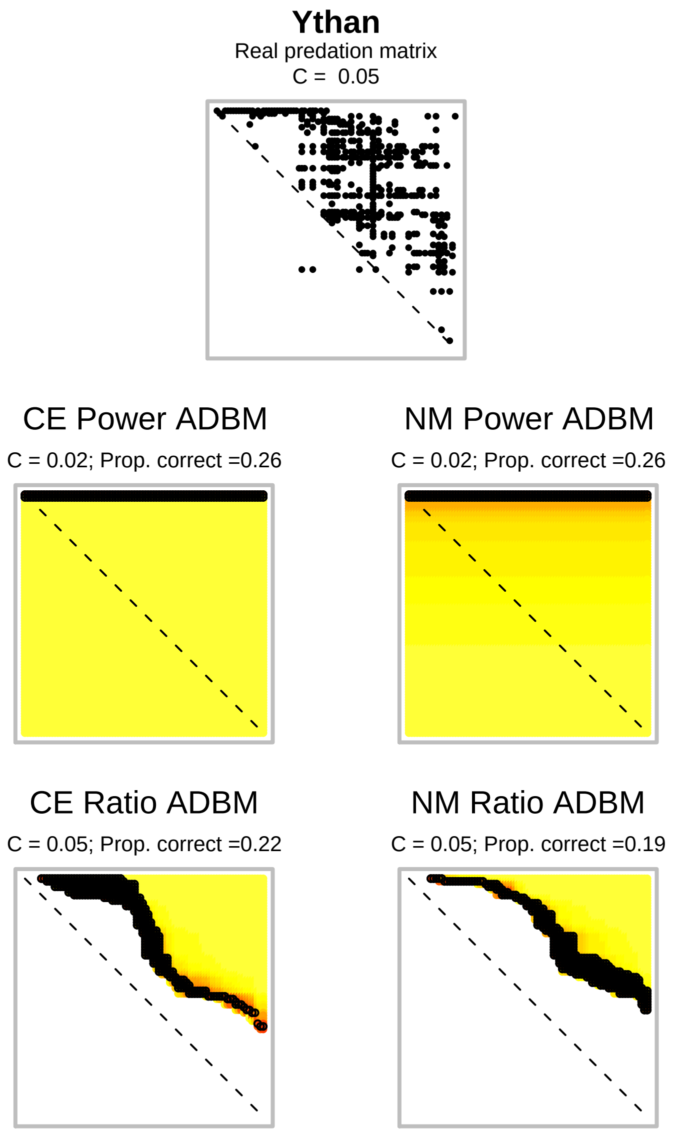
Supplementary Figure S1l



Supplementary Figure S1m



Supplementary Figure S1n



Supplementary Figure S1o