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## Supplementary Information:

2

# Simultaneously estimating food web connectance and structure with uncertainty

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## 1 ABC methods

6 In the upcoming sections, we explain the Markov chain Monte Carlo and sequential Monte Carlo used to  
7 parameterise the ADBM.

### 1.1 Markov chain Monte Carlo ABC

10 Rejection ABC does not learn anything from rejection or acceptance events. It can therefore be inefficient,  
11 particularly when there is a high proportion of rejections. This may arise if prior distributions are wide and  
12 the observed data are informative as they may constrain the posterior distributions relative to the priors.

13 MCMC ABC attempts to overcome this shortcoming by learning from rejections and acceptances, and thereby  
14 focus tested sets of parameter values in regions of parameter space that have higher posterior probability, but  
15 still explore other parts of parameter space.

16 Based on Marjoram et al. (2003), the MCMC method is as follows:

17 *Properties:*

18 As in rejection ABC except with the addition:

- 19 • A proposal distribution  $K(\theta|\theta')$  which is a normal distribution

20 *Initialisation:*

- 21     • Run the rejection method to choose a set of parameter values from  $\theta_0 \sim \pi(\theta)$  within the distance  
 22       tolerance

23    *Sampling:*

24    for  $i = 1 \dots n$

- 25     • Simulate  $\theta' \sim K(\theta_i | \theta_{i-1})$   
 26     • Compute model result  $x_i = \text{model}(\theta')$   
 27     • Compute summary statistics  $s(x')$   
 28     • Calculate  $\alpha = \frac{K_h(d(s(x'), s(y)))\pi(\theta')K(\theta', \theta^{i-1})}{K_h(d(s(x^{i-1}), s(y)))\pi(\theta^{i-1})K(\theta^{i-1}, \theta')}$   
 29       – Simulate  $u \sim U(0, 1)$   
 30       – If  $u \leq \alpha$ ,  $\theta^i = \theta'$  else,  $\theta^i = \theta^{i-1}$

31    *Output:*

32    Construct posterior distribution using the correlated  $\theta_1, \dots, \theta_n$ .

### 33    **1.1.1 Burn in**

- 34    There is a possibility that the posterior distribution is influenced by the initial set of parameter values  $\theta_0$ .  
 35    We therefore discard the first half of Markov chain and use only the second half.

### 36    **1.1.2 Thinning**

- 37    In the MCMC approach, the accepted parameter values are correlated as in some cases  $\theta^i = \theta^{i-1}$ ; which  
 38    reduces the independence of sampled parameter values in the posterior distribution. The Markov chains are  
 39    thinned to reduce the dependence (autocorrelation  $< 0.05$ ) which lowers number parameter values in the  
 40    posterior distribution. The chain length was chosen such that the chain length was approximately 1000 after  
 41    thinning.

### 42    **1.1.3 Convergence**

- 43    It is important to look into the convergence of the chains before drawing conclusions about the posterior  
 44    distributions. The convergence was checked using Gelman-Rubin diagnostics. The value obtained from the  
 45    Gelman-Rubin diagnostics should be less than 1.1 for convergence (Gelman and Rubin 1992).

46    **1.2 Sequential Monte Carlo ABC**

47    Sequential Monte Carlo ABC two main features: i. weighted resampling from the set of parameter values  
 48    already drawn; ii. successive reduction in the distance threshold. This approach gives a set of posterior  
 49    distribution where the successive posterior distribution is narrower than the previous one. SMC is more  
 50    efficient than the rejection method when the posterior distribution is a lot narrower than the prior distribution.  
 51    In SMC the parameters are uncorrelated and therefore do not require burn-in or assessment of convergence.

52    *Properties:*

53    As in rejection ABC except with the addition:

- 54       • A proposal distribution  $K(\theta|\theta')$  which is a normal distribution  
 55       • A decreasing sequence of tolerance thresholds  $\epsilon_1, \dots, \epsilon_T$

56    *Initialisation:*

57    At iteration  $t = 1$ ,

- 58       • for  $i = 1, \dots, N$ ,  
 59           – until distance  $d(S(x), S(y)) < \epsilon_1$   
 60           \* simulate model parameter  $\theta_i^{(1)} \sim \pi(\theta)$  and model output  $x = \text{model}(\theta_i^{(1)})$ .  
 61       • Set equal probabilities  $w_i^1 = 1/N$  for parameter values.  
 62       • Take variance of proposal distribution  $\tau_2^2$  as twice the empirical variance of the  $\theta_1^{(1)}$ 's.

63    *Sampling:*

64    At iteration  $2 \leq t \leq T$ ,

- 65       • for  $i = 1, \dots, N$ ,  
 66           – until distance  $d(S(x), S(y)) < \epsilon_t$   
 67           \* pick  $\theta_i^*$  from the  $\theta_j^{(t-1)}$ 's with probabilities  $w_j^{(t-1)}$   
 68           \* generate model parameter  $\theta_i^{(t)} \sim K(\theta|\theta_i^*; \tau_t^2)$  and model output  $x = \text{model}(\theta_i^{(t)})$ .  
 69           – Set  

$$w_i^{(t)} \propto \frac{\pi(\theta_i^{(t)})}{\sum_{j=1}^N w_j^{t-1} K(\theta_i^{(t)}|\theta_j^{(t-1)}; \tau_t^2)}$$
  
 70           – Take  $\tau_{t+1}^2$  as twice the weighted empirical variance of the  $\theta_i^{(t)}$ 's

71 Output:

- 72 Construct a sequence of converging posterior distributions using the parameter values:  $\theta_1^t, \dots, \theta_n^t$  for all  
73  $1 \leq t \leq T$

## 74 2 Choice of threshold value of distance

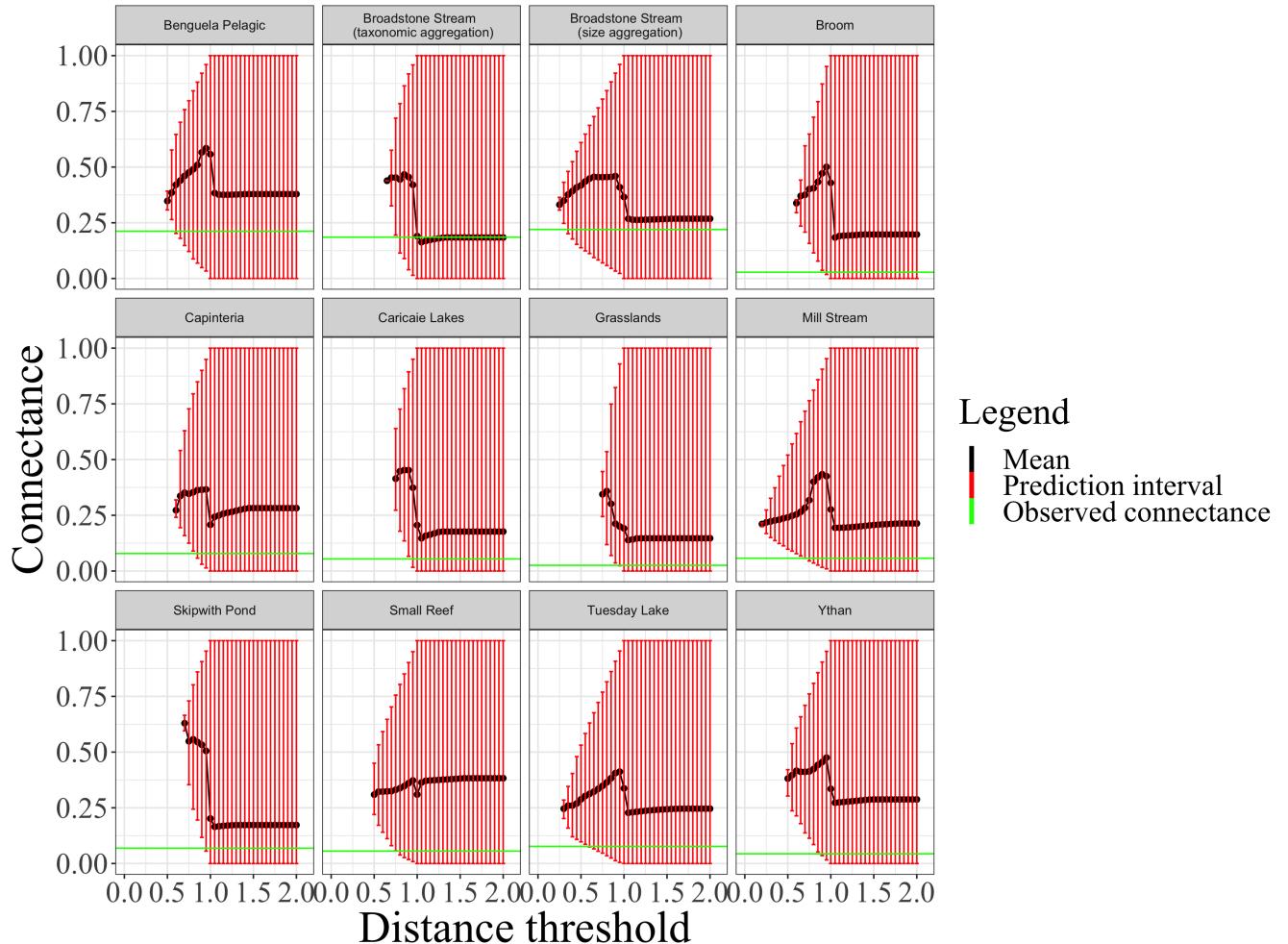


Figure S1: The prediction interval of the predicted connectance increases with increasing distance threshold. The green line and black line represent the observed connectance and mean of predicted connectance respectively.

<sup>75</sup> **3 Figure legends**

- <sup>76</sup> Figure S2-S13: (a) Observed and predicted predation matrices of the given food web. Body size increases  
<sup>77</sup> from left to right and top to bottom along the predation matrix. Black circles show where there were observed  
<sup>78</sup> trophic links. The intensity of the pink circles shows the proportion of 1000 predicted food webs that had  
<sup>79</sup> a trophic link between the corresponding species. This type of overlay is shown for two example predicted  
<sup>80</sup> in panel (c). (b) The histogram of the number of times a link was predicted across the 1000 independently  
<sup>81</sup> predicted food webs. The red bar shows the number of pairs of species for which a trophic link was never  
<sup>82</sup> predicted. (c) Two predicted predation matrices correspond to the minimum and the maximum value of  
<sup>83</sup> estimated  $b$ , and their sum.
- <sup>84</sup> Figure S14-S25: Marginal prior and marginal posterior distribution of the ADBM parameters for 12 food  
<sup>85</sup> webs estimated using rejection ABC. The black vertical line in (d) corresponds to the value of  $b$  (=2) above  
<sup>86</sup> which the most profitable prey item is larger in respect to the predator size.

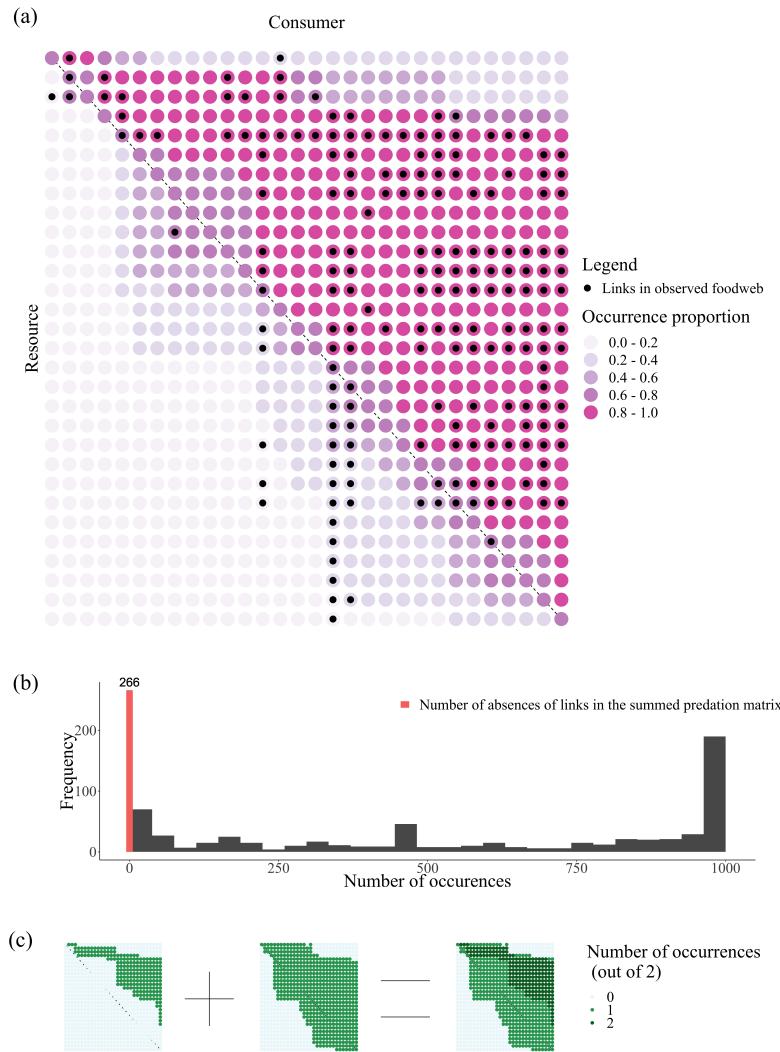


Figure S2: Benguela Pelagic

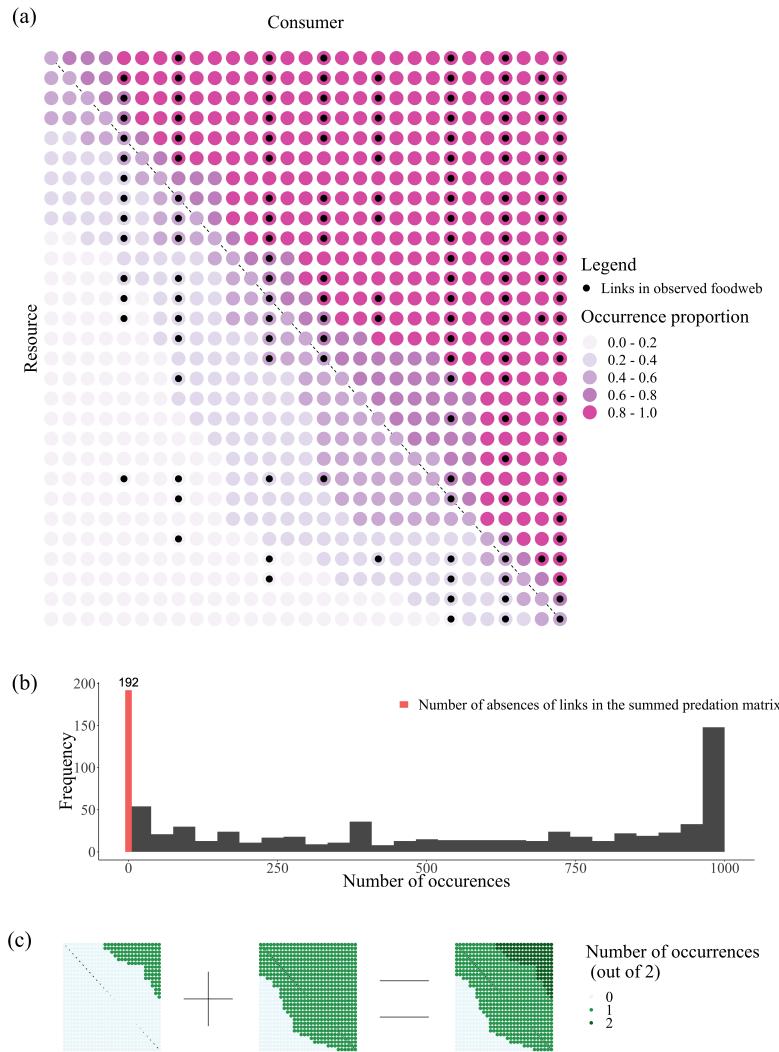


Figure S3: Broadstone Stream (taxonomic aggregation)

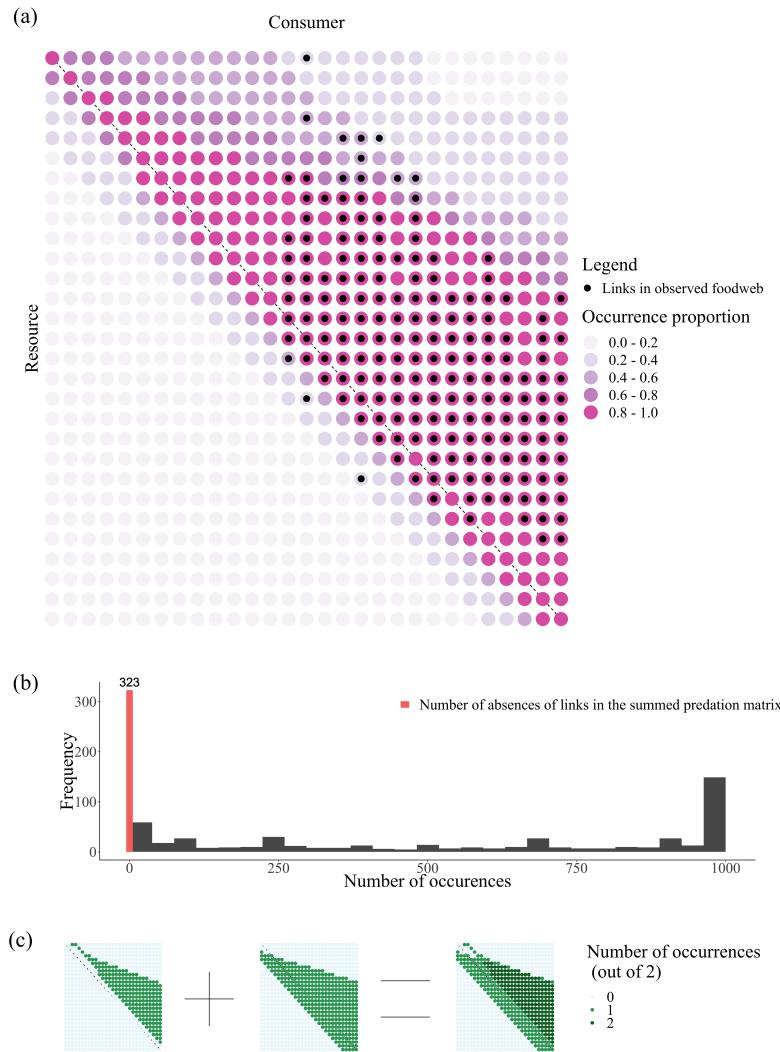


Figure S4: Broadstone Stream (size aggregation)

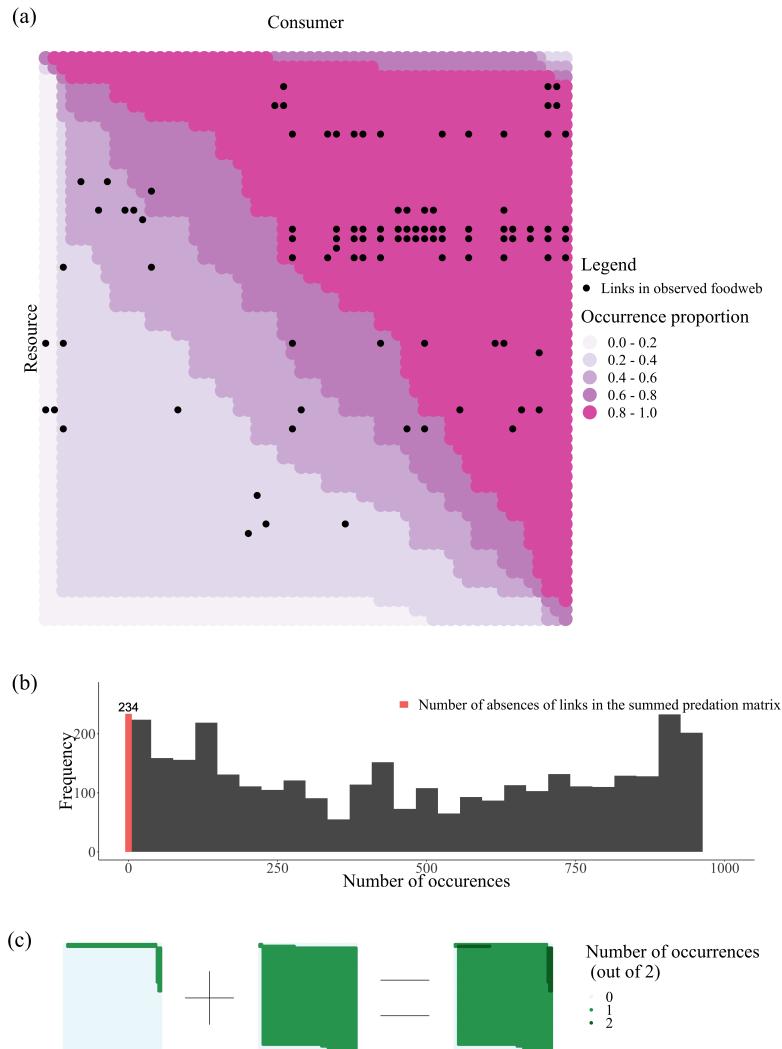


Figure S5: Broom

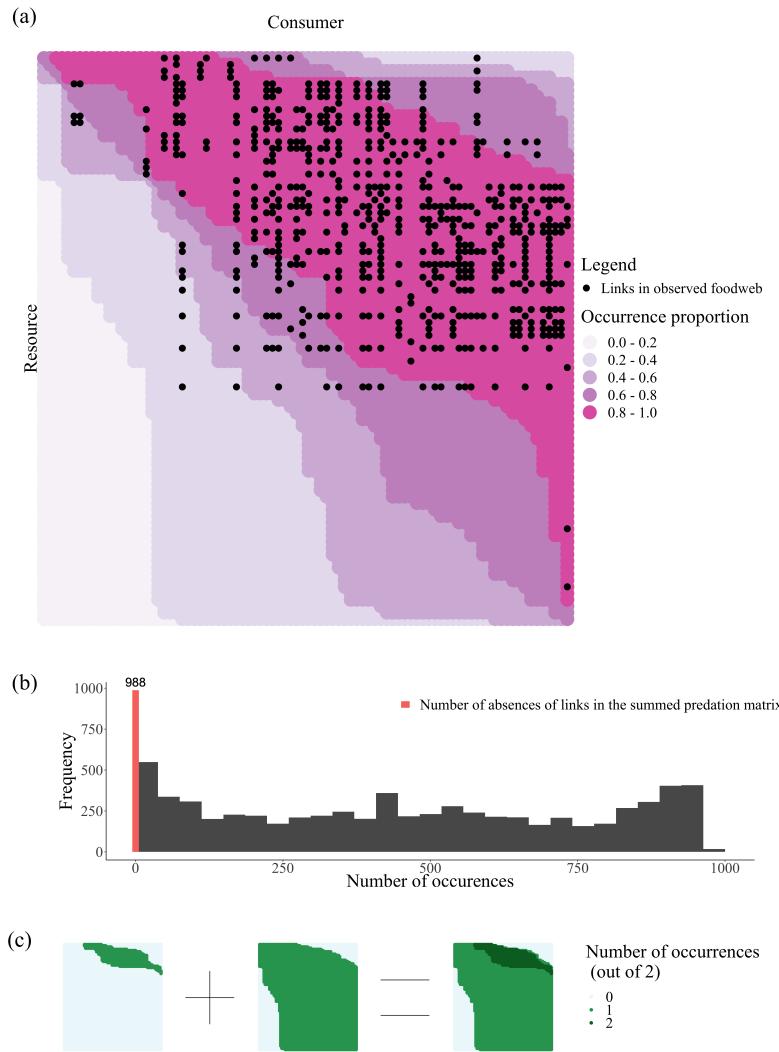


Figure S6: Capinteria

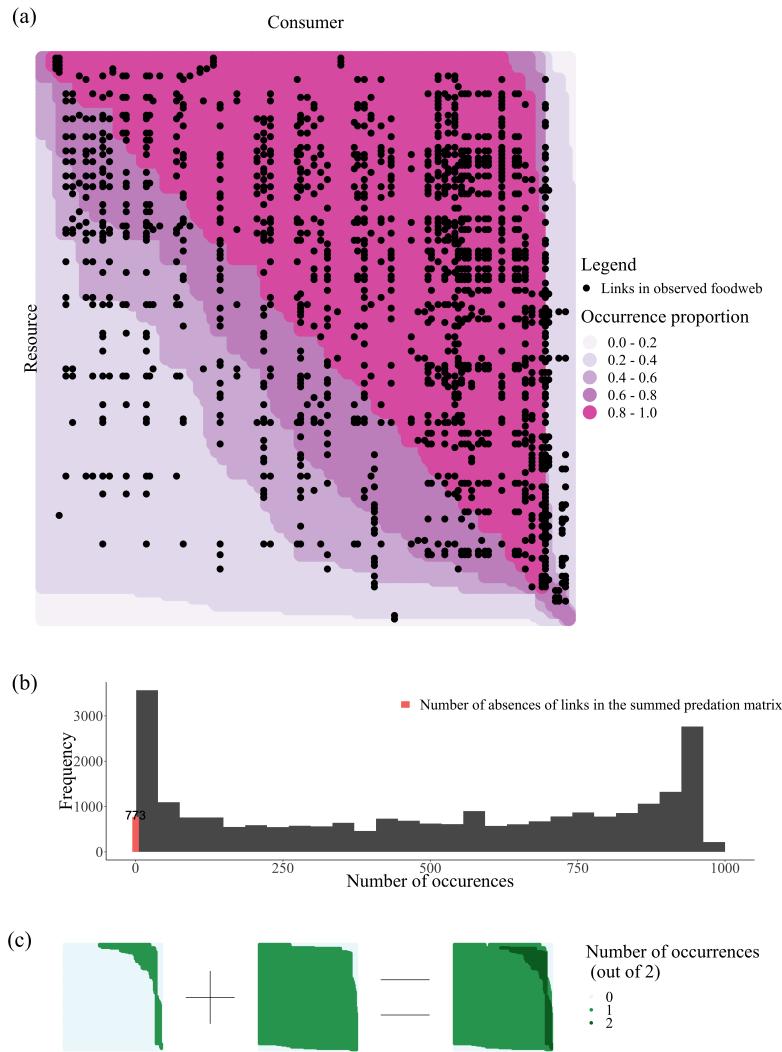


Figure S7: Caricaie Lakes

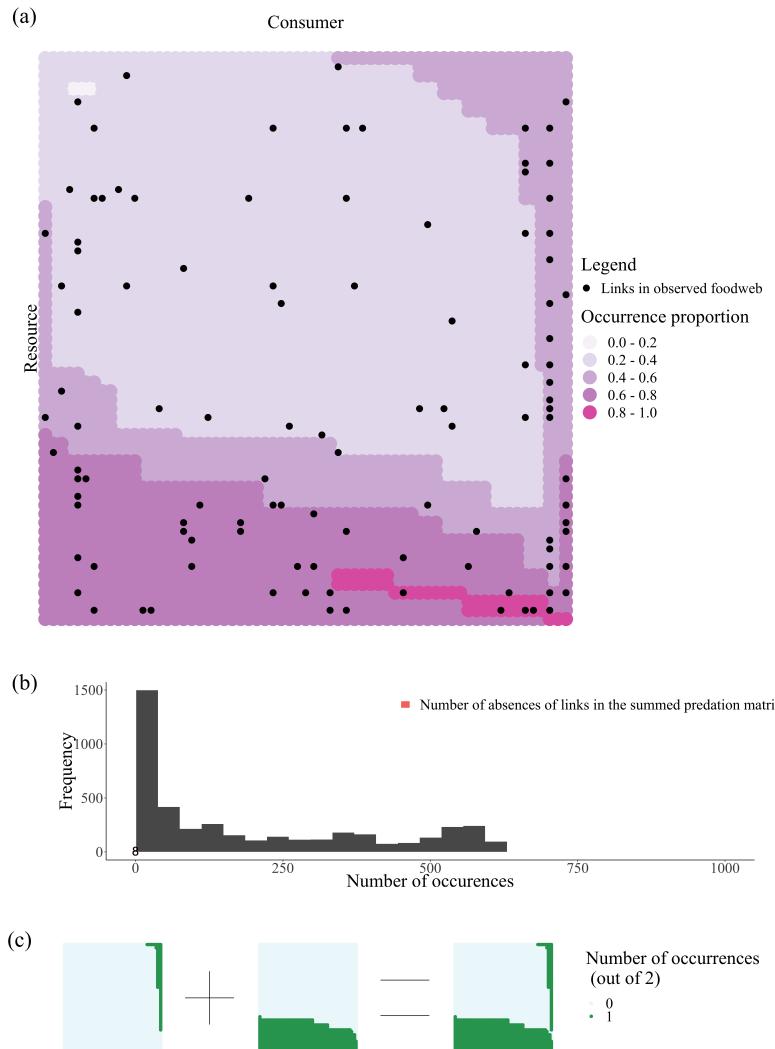


Figure S8: Grasslands

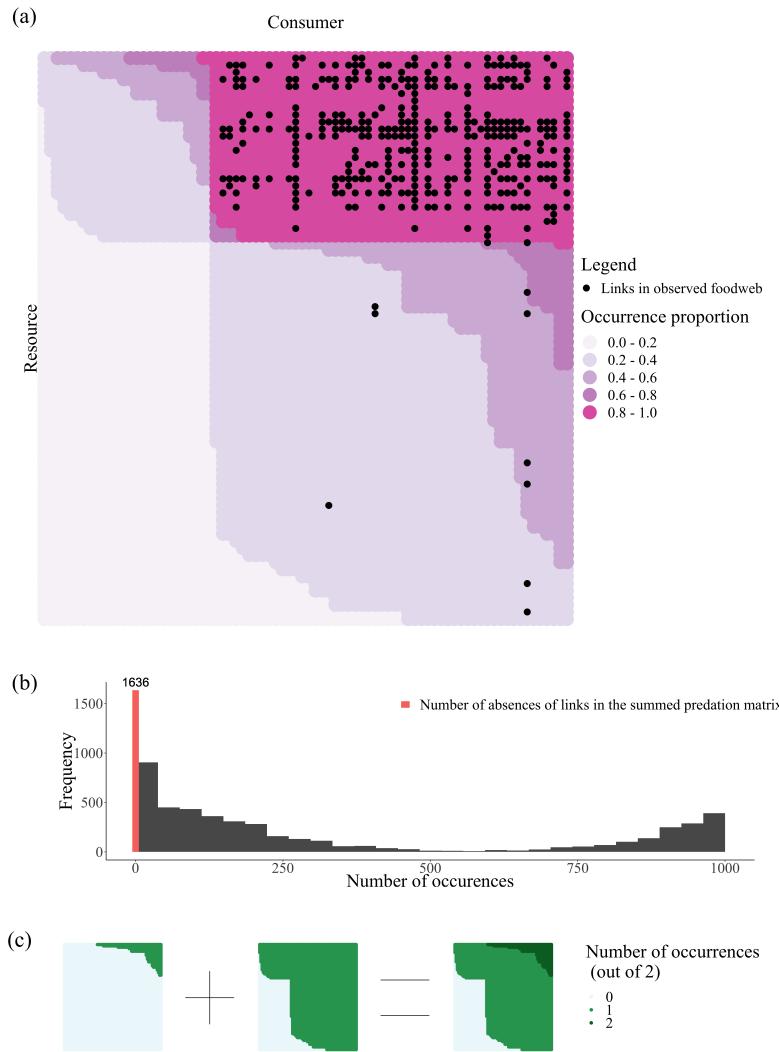


Figure S9: Mill Stream

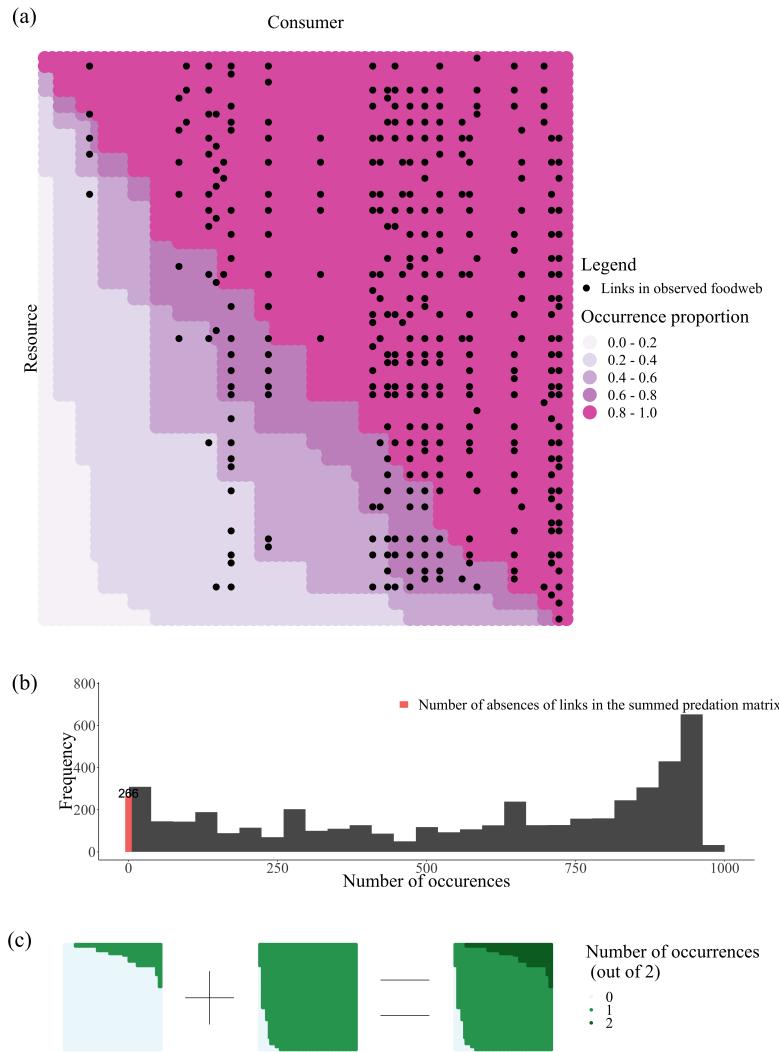


Figure S10: Skipwith Pond

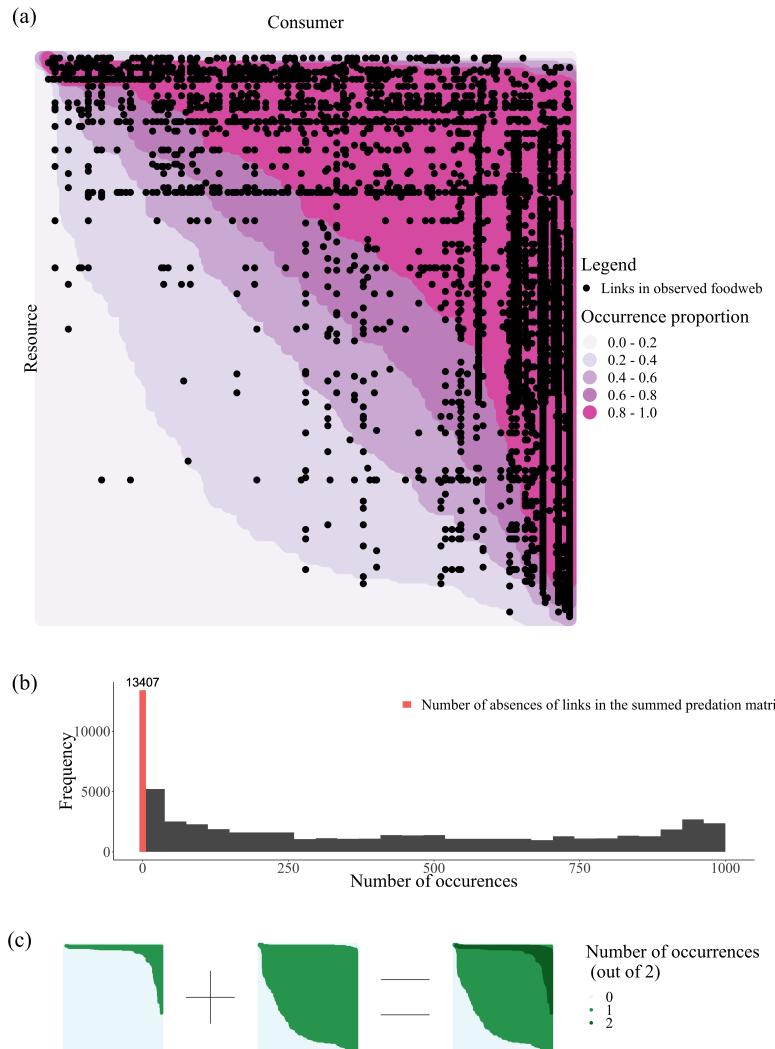


Figure S11: Small Reef

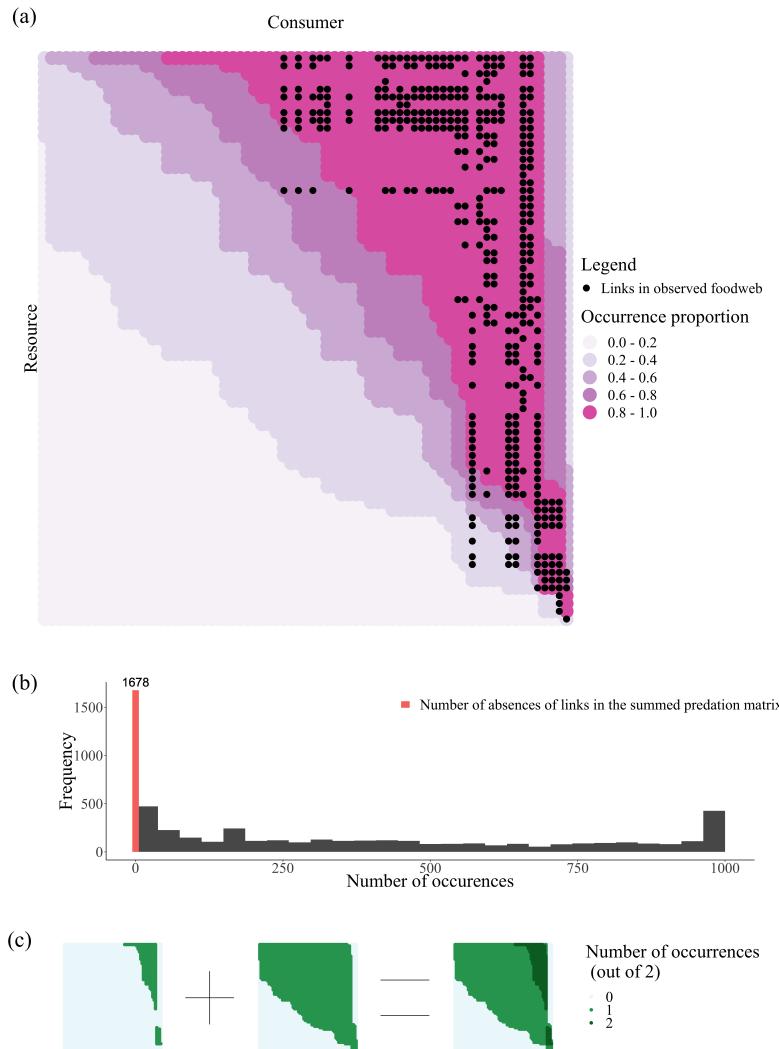


Figure S12: Tuesday Lake

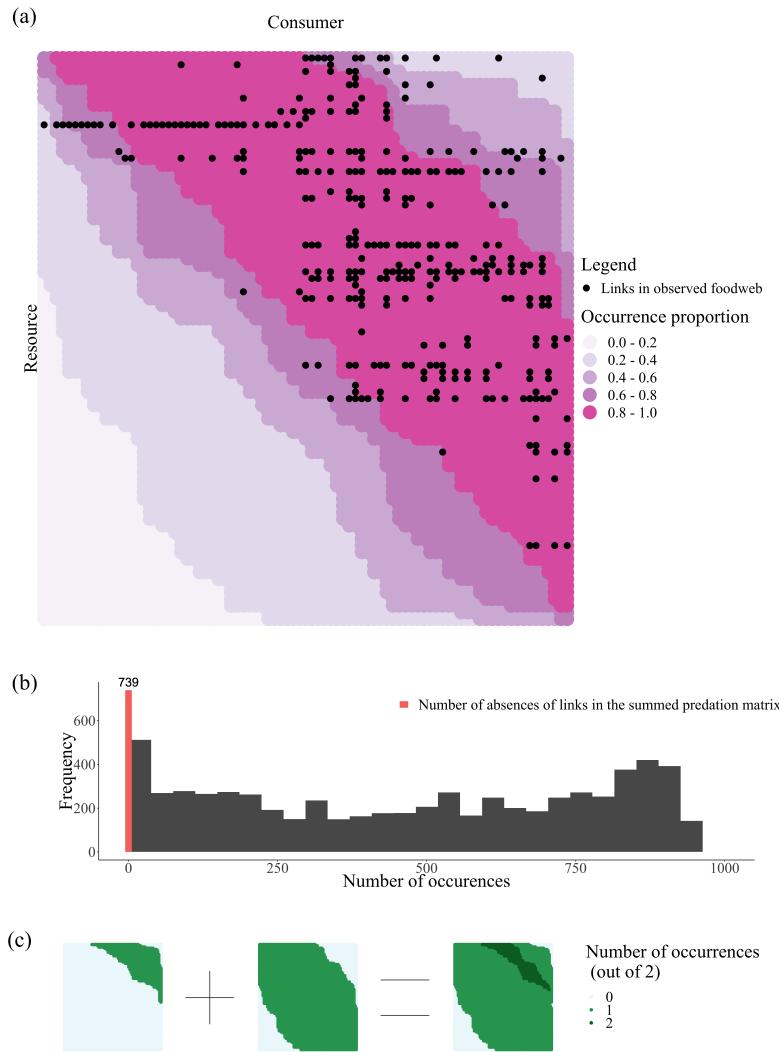


Figure S13: Ythan

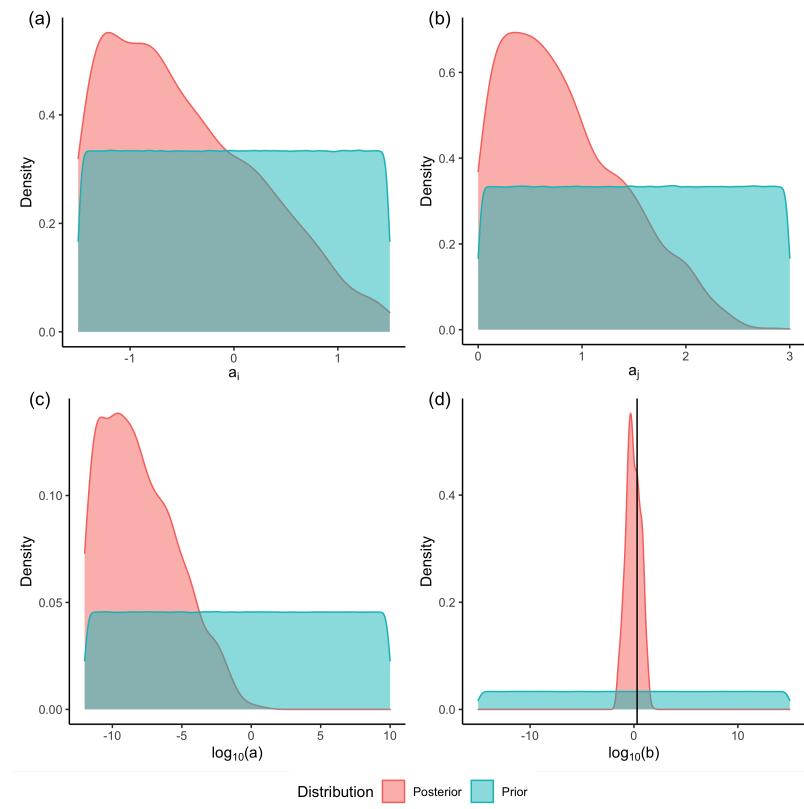


Figure S14: Benguela Pelagic

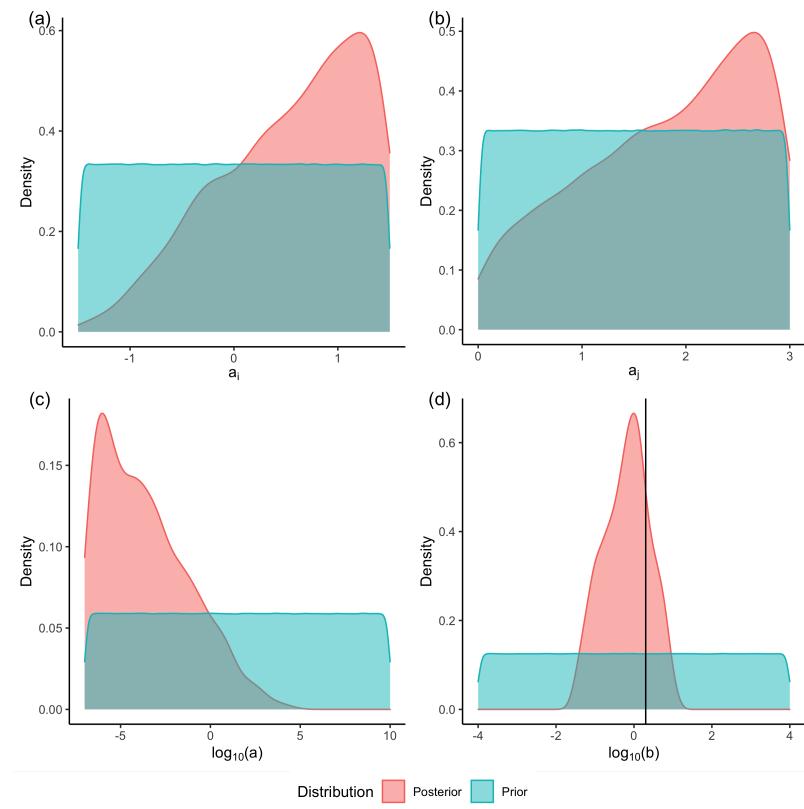


Figure S15: Broadstone Stream (taxonomic aggregation)

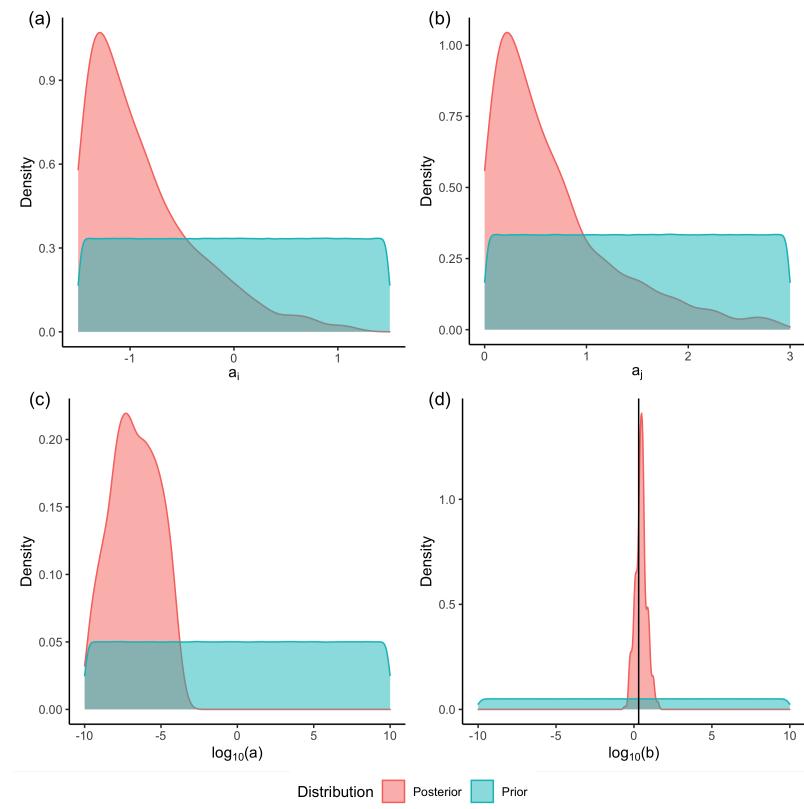


Figure S16: Broadstone Stream (size aggregation)

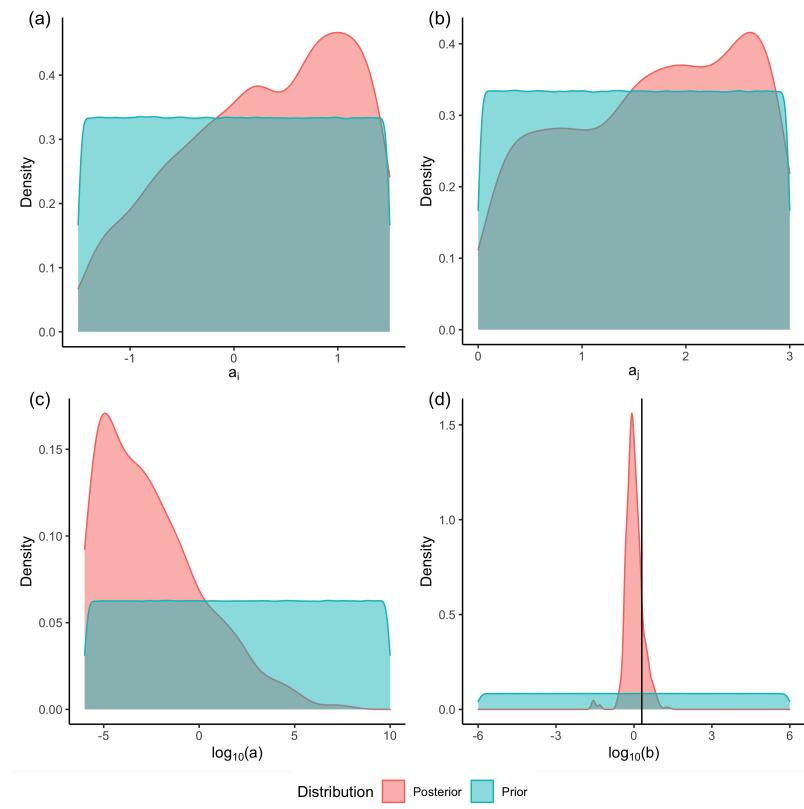


Figure S17: Broom

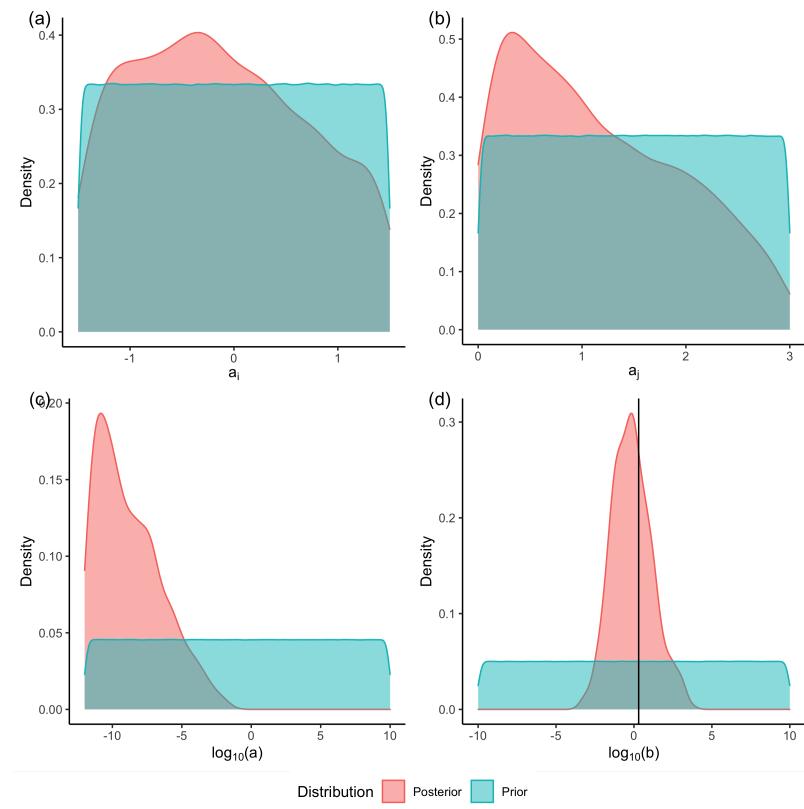


Figure S18: Capinteria

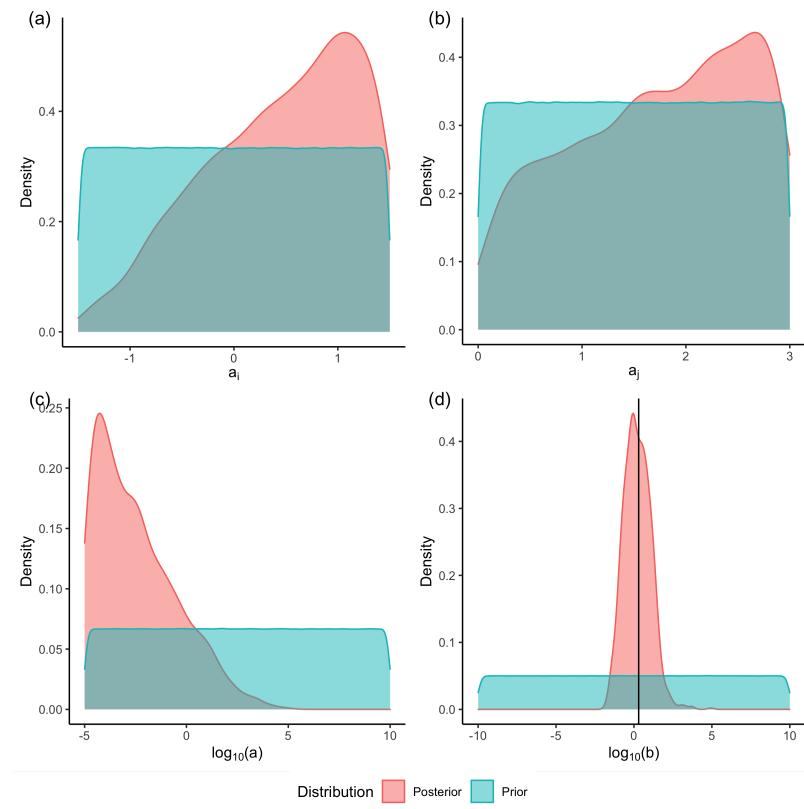


Figure S19: Caricaie Lakes

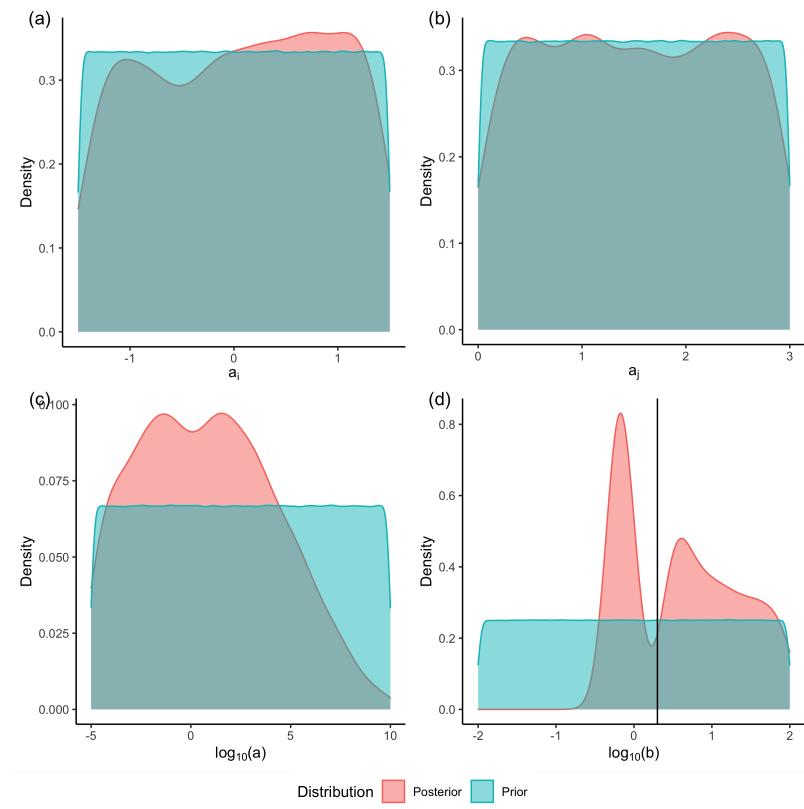


Figure S20: Grasslands

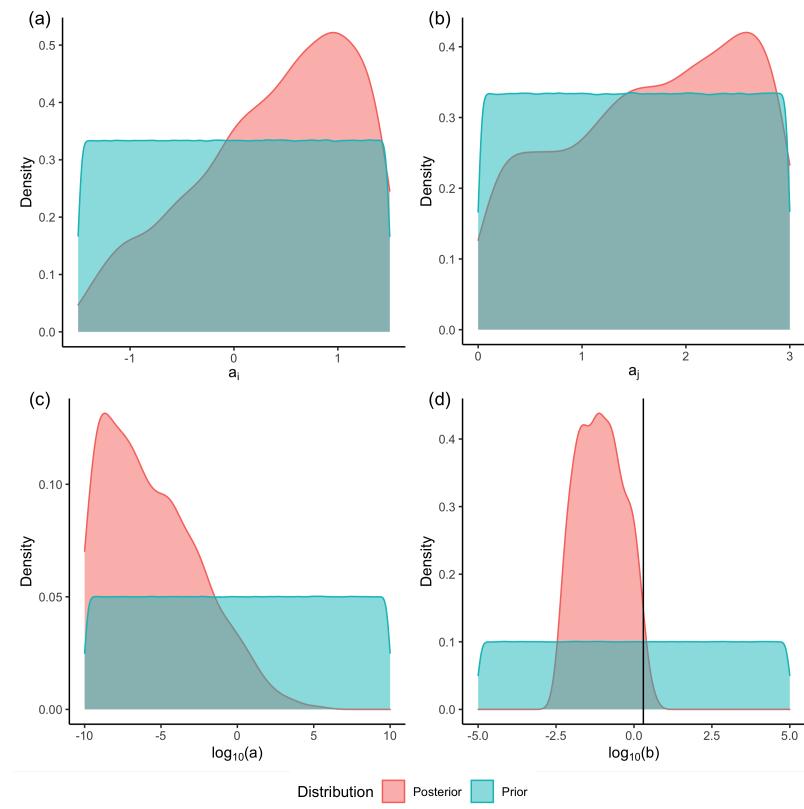


Figure S21: Mill Stream

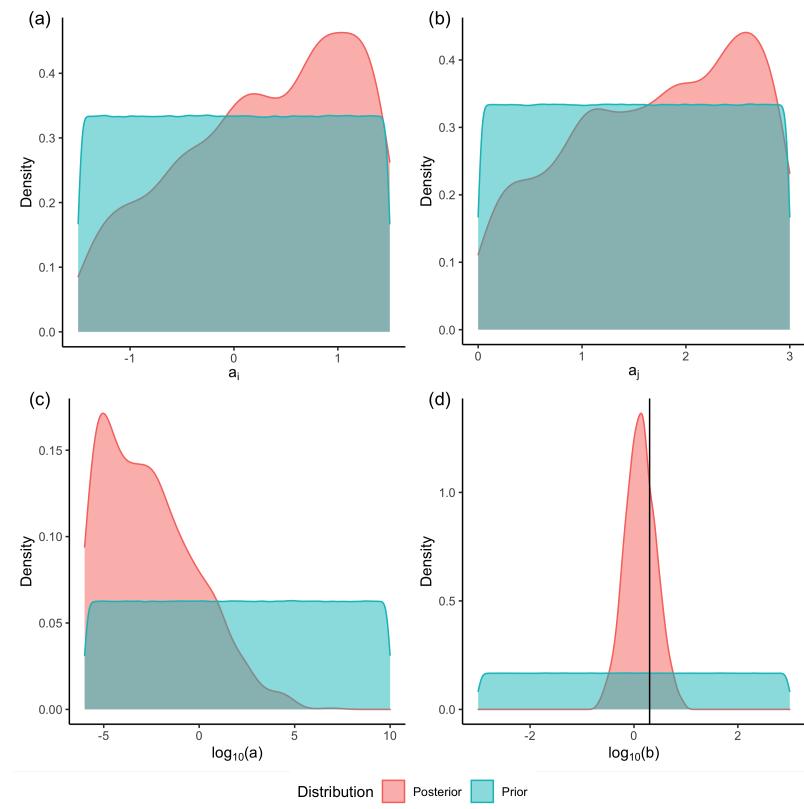


Figure S22: Skipwith Pond

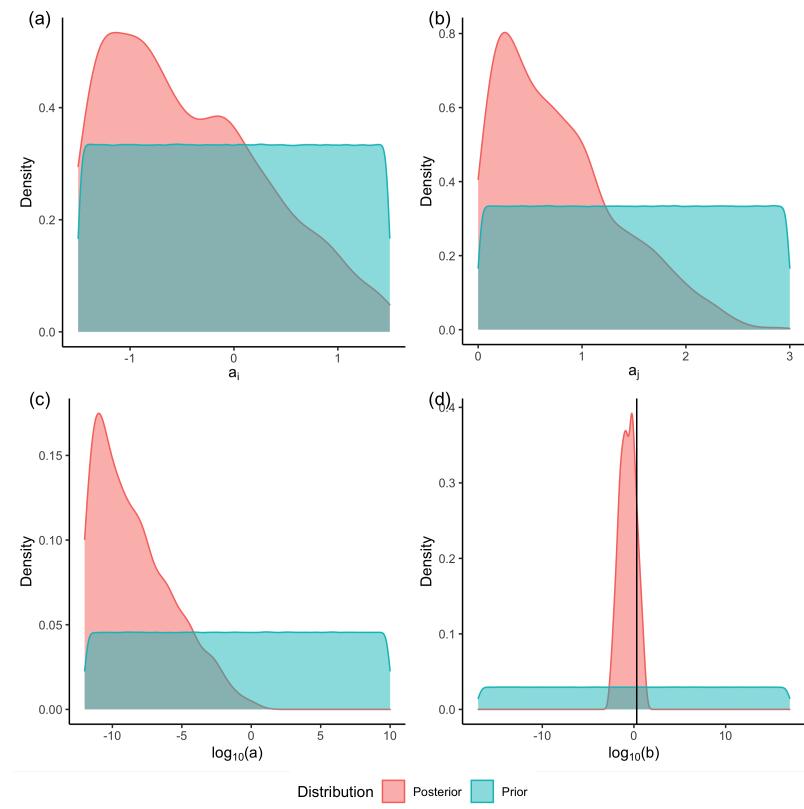


Figure S23: Small Reef

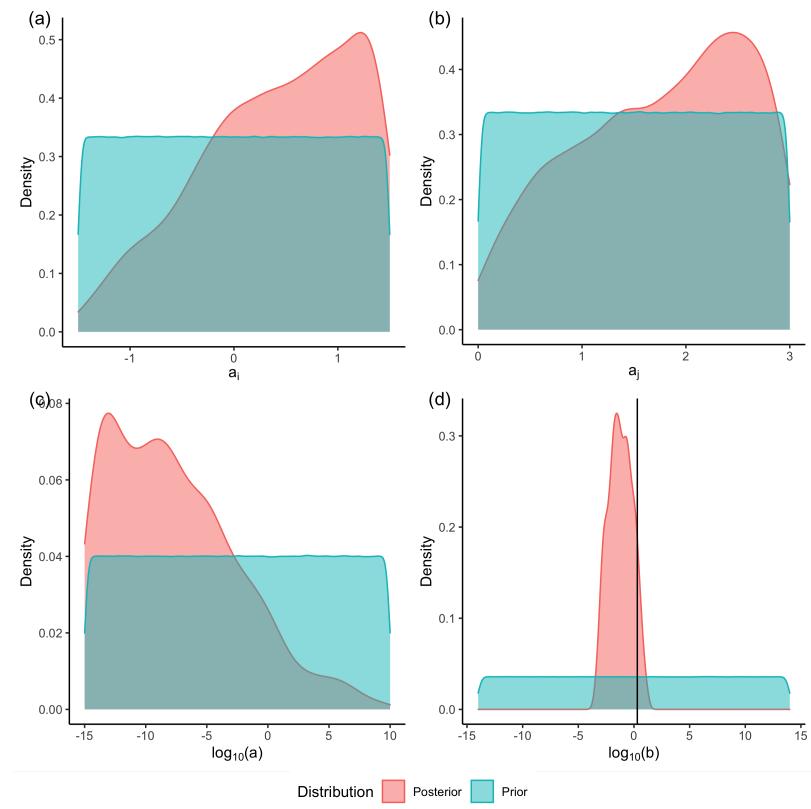


Figure S24: Tuesday Lake

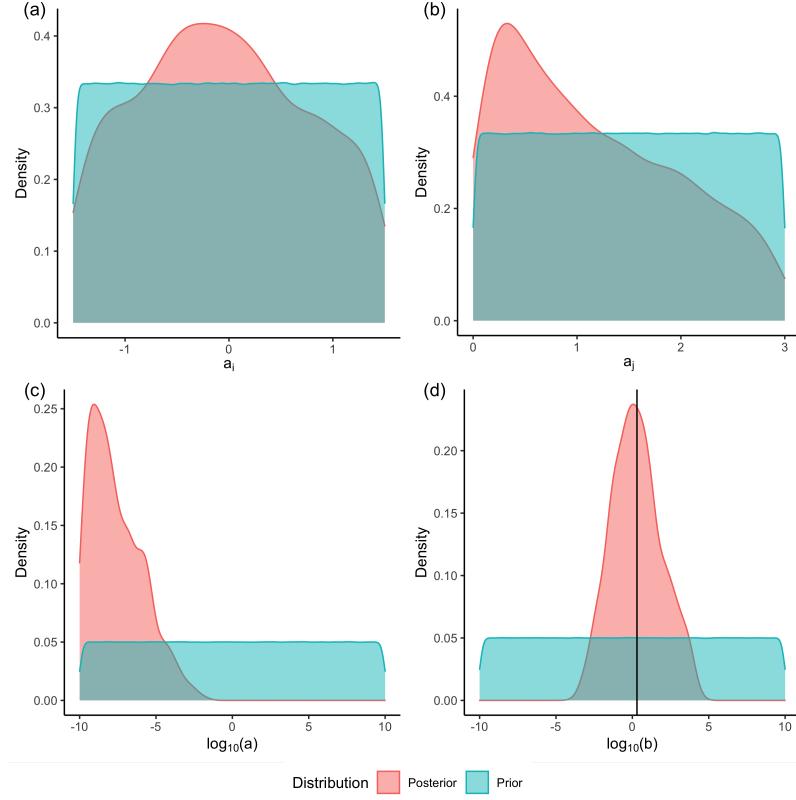


Figure S25: Ythan

## 87 4 Comparison between methods

88 We found consistent results among all three ABC methods (Fig. S27). The marginal posteriors of the ADBM  
 89 parameters estimated using the three ABC methods for the Benguela Pelagic food web were quite similar in  
 90 Fig. S26. In terms of simplicity, rejection ABC was the easiest to implement and resulted in similar results  
 91 as the MCMC ABC and SMC ABC. To achieve similar number of accepted parameter values, MCMC ABC  
 92 required a higher number of simulations, as MCMC ABC resulted in correlated parameter values and needed  
 93 to be thinned. MCMC ABC was the most time consuming method. The SMC ABC method helped us to  
 94 understand how the parameter distribution converged in response to the decrease in tolerance.

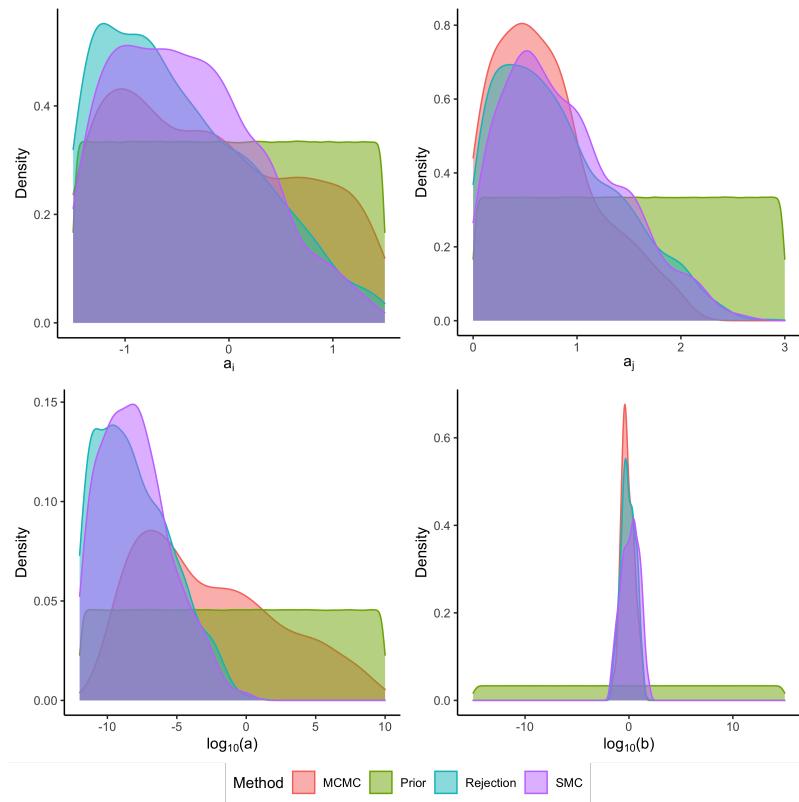


Figure S26: Marginal posterior distributions of the ADBM parameters estimated from rejection ABC, MCMC ABC and SMC ABC for Benguela Pelagic food web.

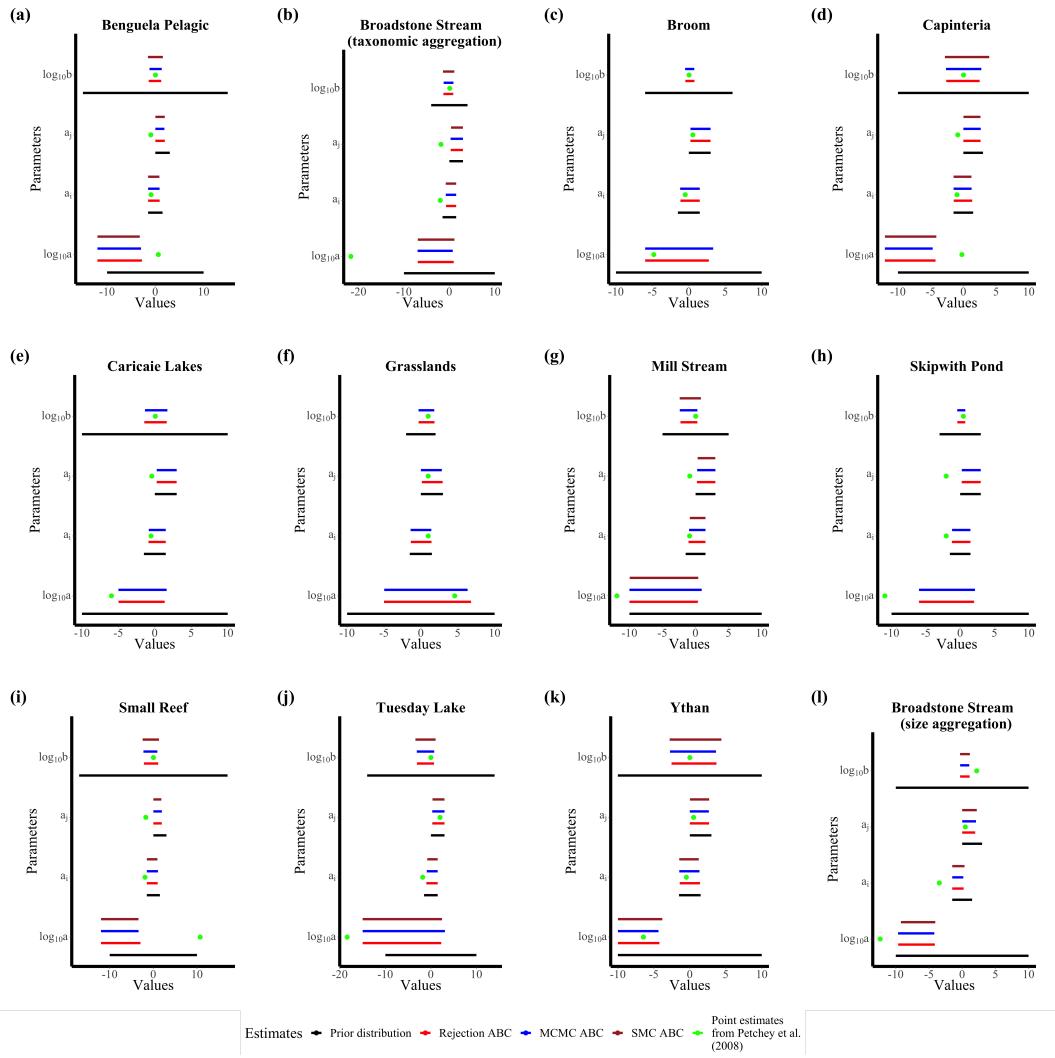


Figure S27: The 95% credible intervals of marginal posterior distributions of the ADBM parameters estimated from rejection ABC, MCMC ABC and SMC ABC for 12 food webs.

## 95 5 Model parameters

96 In the ADBM, the contingency model of optimal foraging predicts the diet  $k$  of each consumer  $j$  that  
 97 maximises rate of energy intake given below:

$$98 \quad \frac{\sum_{i=1}^k \lambda_{ij} E_i}{1 + \sum_{i=1}^k \lambda_{ij} H_{ij}}$$

$$99 \quad \frac{\sum_{i=1}^k A_{ij} N_i E_i}{1 + \sum_{i=1}^k A_{ij} N_i H_{ij}}$$

$$100 \quad \frac{\sum_{i=1}^k a M_i^{a_i} M_j^{a_j} n M_i^{n_i} e M_i}{1 + \sum_{i=1}^k a M_i^{a_i} M_j^{a_j} n M_i^{n_i} \frac{h}{b - \frac{M_i}{M_j}}}$$

$$101 \quad \frac{\sum_{i=1}^k n a e M_i^{a_i + n_i + 1} M_j^{a_j}}{1 + \sum_{i=1}^k n a h M_i^{a_i + n_i} M_j^{a_j} \frac{1}{b - \frac{M_i}{M_j}}}$$

102 Since, the maximum of the above expression is affected by the product  $nah$ , estimating all the three parameters  
 103 would be redundant, which would result in strong correlation. Therefore, it is sufficient to estimate any single  
 104 parameter from  $nah$ , so we estimated only  $a$ . We set  $n = 1$  and  $h = 1$ . Also, parameter  $e$  does not affect the  
 105 value of  $k$  at which the above expression has a maximum, so value of  $e$  can be arbitrary.

## 106 6 Prior selection of a

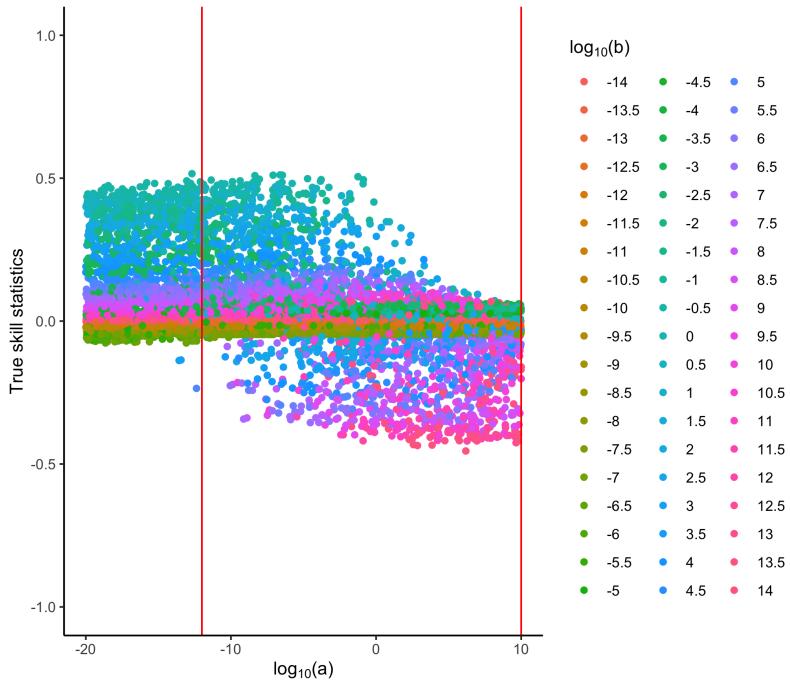


Figure S28: True skill statistics between the observed and predicted food web for Benguela Pelagic food web plotted against the attack rate scaling parameter  $a$  which is in log scale. The red lines represent the boundaries for the prior range of  $\log_{10}(a)$ .

## 107 7 Parameter correlations

108 A few of the parameters were strongly correlated (Fig. S29). E.g., 0.71 correlation coefficients between  $a$  and  
 109  $a_i$  in Broadstone stream (size aggregation) food web. However, 98% of parameter pairs showed less than

110 0.5 correlation coefficient and 82% were less than 0.25. The highest correlation, 0.71 was due to somewhat  
 111 redundant effects of the two parameters ( $a$  and  $a_i$ ) on connectance, which is a mathematical feature of the  
 112 model rather than anything of great biological significance.

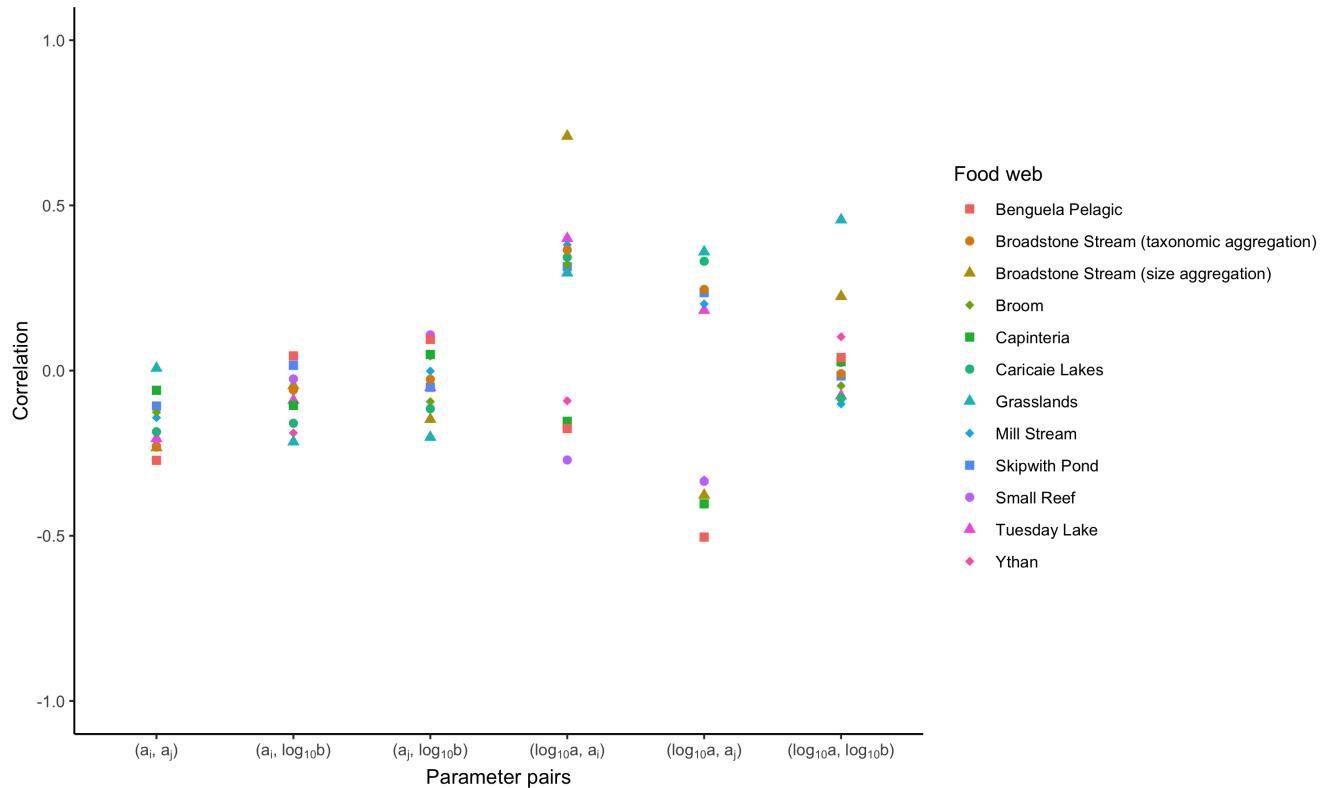


Figure S29: Correlations between parameter pairs of ADBM for 12 food webs.

## 113 8 Principal Component Analysis on structural properties

Table 1: Variance in structural properties explained by the first three principal components and correlation between connectance and first principal component.

Food web	Principal Component I	Principal Component II	Principal Component III	Correlation(PCI, Connectance)
Benguela Pelagic	0.66	0.20	0.07	-0.96
Broadstone Stream (taxonomic aggregation)	0.73	0.12	0.10	0.94
Broom	0.54	0.19	0.11	-0.89
Capinteria	0.65	0.13	0.10	0.92
Caricaie Lakes	0.59	0.18	0.10	0.85
Grasslands	0.57	0.20	0.10	0.74
Mill Stream	0.59	0.18	0.12	0.94
Skipwith Pond	0.61	0.19	0.11	0.89
Small Reef	0.67	0.11	0.09	0.95
Tuesday Lake	0.70	0.12	0.08	0.97
Ythan	0.64	0.18	0.08	0.86
Broadstone Stream (size aggregation)	0.47	0.25	0.17	0.60
Average	0.62	0.17	0.10	0.88

114 **9 Summary table of linear regression between average standard-**  
115 **ized error and true skill statistic from Figs S30 and S31**

116 **9.1 Benguela Pelagic**

```
117 ##
118 ## Call:
119 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)
120 ##
121 ## Residuals:
122 ##      Min       1Q   Median       3Q      Max
123 ## -0.07694 -0.02674 -0.01177  0.03389  0.07406
124 ##
125 ## Coefficients:
126 ##             Estimate Std. Error t value Pr(>|t|)
127 ## (Intercept)  0.32936   0.02082   15.82   <2e-16 ***
128 ## TSS        -0.50035   0.04517  -11.08   <2e-16 ***
129 ## ---
130 ## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
131 ##
132 ## Residual standard error: 0.03708 on 998 degrees of freedom
133 ## Multiple R-squared:  0.1095, Adjusted R-squared:  0.1086
134 ## F-statistic: 122.7 on 1 and 998 DF,  p-value: < 2.2e-16
```

135 **9.2 Broadstone Stream (taxonomic aggregation)**

```
136 ##
137 ## Call:
138 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)
139 ##
140 ## Residuals:
141 ##      Min       1Q   Median       3Q      Max
142 ## -0.042217 -0.007716  0.000558  0.006924  0.027255
```

```

143  ##
144  ## Coefficients:
145  ##             Estimate Std. Error t value Pr(>|t|)
146  ## (Intercept)  0.34058    0.00334 101.97  <2e-16 ***
147  ## TSS        -0.36439    0.01151 -31.65  <2e-16 ***
148  ## ---
149  ## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
150  ##
151  ## Residual standard error: 0.01135 on 998 degrees of freedom
152  ## Multiple R-squared:  0.5009, Adjusted R-squared:  0.5004
153  ## F-statistic: 1001 on 1 and 998 DF, p-value: < 2.2e-16

```

### 154 9.3 Broadstone Stream (size aggregation)

```

155  ##
156  ## Call:
157  ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)
158  ##
159  ## Residuals:
160  ##      Min       1Q   Median       3Q      Max
161  ## -15.4077  -4.2887   0.1484   4.7925  13.4487
162  ##
163  ## Coefficients:
164  ##             Estimate Std. Error t value Pr(>|t|)
165  ## (Intercept)  73.714     5.097   14.46  <2e-16 ***
166  ## TSS        -83.629     7.283  -11.48  <2e-16 ***
167  ## ---
168  ## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
169  ##
170  ## Residual standard error: 5.828 on 998 degrees of freedom
171  ## Multiple R-squared:  0.1167, Adjusted R-squared:  0.1158
172  ## F-statistic: 131.9 on 1 and 998 DF, p-value: < 2.2e-16

```

173 **9.4 Broom**

```
174 ##  
175 ## Call:  
176 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)  
177 ##  
178 ## Residuals:  
179 ##      Min       1Q   Median      3Q      Max  
180 ## -0.244483 -0.03674  0.01409  0.044485  0.08370  
181 ##  
182 ## Coefficients:  
183 ##             Estimate Std. Error t value Pr(>|t|)  
184 ## (Intercept)  0.437254  0.005208  83.97 < 2e-16 ***  
185 ## TSS        -0.152599  0.020292  -7.52 1.22e-13 ***  
186 ## ---  
187 ## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
188 ##  
189 ## Residual standard error: 0.05713 on 998 degrees of freedom  
190 ## Multiple R-squared:  0.05363,    Adjusted R-squared:  0.05268  
191 ## F-statistic: 56.55 on 1 and 998 DF,  p-value: 1.218e-13
```

192 **9.5 Capinteria**

```
193 ##  
194 ## Call:  
195 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)  
196 ##  
197 ## Residuals:  
198 ##      Min       1Q   Median      3Q      Max  
199 ## -0.21149 -0.07455  0.04157  0.07726  0.13695  
200 ##  
201 ## Coefficients:  
202 ##             Estimate Std. Error t value Pr(>|t|)
```

```

203 ## (Intercept) 0.36582    0.01153  31.729 < 2e-16 ***
204 ## TSS          -0.13714    0.02796  -4.906 1.09e-06 ***
205 ##
206 ## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
207 ##
208 ## Residual standard error: 0.09871 on 998 degrees of freedom
209 ## Multiple R-squared:  0.02354,   Adjusted R-squared:  0.02257
210 ## F-statistic: 24.06 on 1 and 998 DF,  p-value: 1.087e-06

```

## 211 9.6 Caricaie Lakes

```

212 ##
213 ## Call:
214 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)
215 ##
216 ## Residuals:
217 ##      Min       1Q     Median      3Q      Max
218 ## -0.22367 -0.04988  0.02288  0.06424  0.10604
219 ##
220 ## Coefficients:
221 ##             Estimate Std. Error t value Pr(>|t|)
222 ## (Intercept) 0.34378    0.00892 38.541 < 2e-16 ***
223 ## TSS         0.28148    0.04888  5.758 1.13e-08 ***
224 ##
225 ## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
226 ##
227 ## Residual standard error: 0.07685 on 998 degrees of freedom
228 ## Multiple R-squared:  0.03216,   Adjusted R-squared:  0.03119
229 ## F-statistic: 33.16 on 1 and 998 DF,  p-value: 1.131e-08

```

## 230 9.7 Grasslands

```
231 ##
```

```

232 ## Call:
233 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)
234 ##
235 ## Residuals:
236 ##      Min       1Q   Median      3Q      Max
237 ## -0.113414 -0.045792  0.001642  0.041063  0.181017
238 ##
239 ## Coefficients:
240 ##             Estimate Std. Error t value Pr(>|t|)
241 ## (Intercept) 0.190539  0.007333 25.982 < 2e-16 ***
242 ## TSS         0.373534  0.056238  6.642 5.08e-11 ***
243 ## ---
244 ## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
245 ##
246 ## Residual standard error: 0.05478 on 998 degrees of freedom
247 ## Multiple R-squared:  0.04233,    Adjusted R-squared:  0.04137
248 ## F-statistic: 44.12 on 1 and 998 DF,  p-value: 5.076e-11

```

## 249 9.8 Mill Stream

```

250 ##
251 ## Call:
252 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)
253 ##
254 ## Residuals:
255 ##      Min       1Q   Median      3Q      Max
256 ## -0.31085 -0.06180 -0.03214  0.11952  0.15870
257 ##
258 ## Coefficients:
259 ##             Estimate Std. Error t value Pr(>|t|)
260 ## (Intercept) 0.49738   0.01835  27.10 <2e-16 ***
261 ## TSS        -0.42983   0.02642 -16.27 <2e-16 ***
262 ## ---

```

```

263 ## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
264 ##
265 ## Residual standard error: 0.1155 on 998 degrees of freedom
266 ## Multiple R-squared: 0.2096, Adjusted R-squared: 0.2088
267 ## F-statistic: 264.6 on 1 and 998 DF, p-value: < 2.2e-16

```

## 268 9.9 Small Reef

```

269 ##
270 ## Call:
271 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)
272 ##
273 ## Residuals:
274 ##      Min       1Q   Median       3Q      Max
275 ## -0.142108 -0.058311  0.006842  0.057750  0.090019
276 ##
277 ## Coefficients:
278 ##             Estimate Std. Error t value Pr(>|t|)
279 ## (Intercept) 0.24598    0.01060 23.202  <2e-16 ***
280 ## TSS        -0.02566    0.02490 -1.031    0.303
281 ## ---
282 ## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
283 ##
284 ## Residual standard error: 0.06266 on 998 degrees of freedom
285 ## Multiple R-squared: 0.001063, Adjusted R-squared: 6.213e-05
286 ## F-statistic: 1.062 on 1 and 998 DF, p-value: 0.303

```

## 287 9.10 Tuesday Lake

```

288 ##
289 ## Call:
290 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)
291 ##

```

```

292 ## Residuals:
293 ##      Min       1Q   Median      3Q      Max
294 ## -0.22724 -0.05970  0.02208  0.07776  0.10697
295 ##
296 ## Coefficients:
297 ##              Estimate Std. Error t value Pr(>|t|)
298 ## (Intercept) 0.44743   0.01961   22.82 <2e-16 ***
299 ## TSS        -0.38757   0.03284  -11.80 <2e-16 ***
300 ##
301 ## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
302 ##
303 ## Residual standard error: 0.08694 on 998 degrees of freedom
304 ## Multiple R-squared:  0.1225, Adjusted R-squared:  0.1216
305 ## F-statistic: 139.3 on 1 and 998 DF,  p-value: < 2.2e-16

```

## 306 9.11 Ythan

```

307 ##
308 ## Call:
309 ## lm(formula = mean_err ~ TSS, data = mean_err_TSS)
310 ##
311 ## Residuals:
312 ##      Min       1Q   Median      3Q      Max
313 ## -15.4077 -4.2887  0.1484  4.7925 13.4487
314 ##
315 ## Coefficients:
316 ##              Estimate Std. Error t value Pr(>|t|)
317 ## (Intercept) 73.714     5.097   14.46 <2e-16 ***
318 ## TSS        -83.629     7.283  -11.48 <2e-16 ***
319 ##
320 ## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
321 ##
322 ## Residual standard error: 5.828 on 998 degrees of freedom

```

```

323 ## Multiple R-squared:  0.1167, Adjusted R-squared:  0.1158
324 ## F-statistic: 131.9 on 1 and 998 DF,  p-value: < 2.2e-16

```

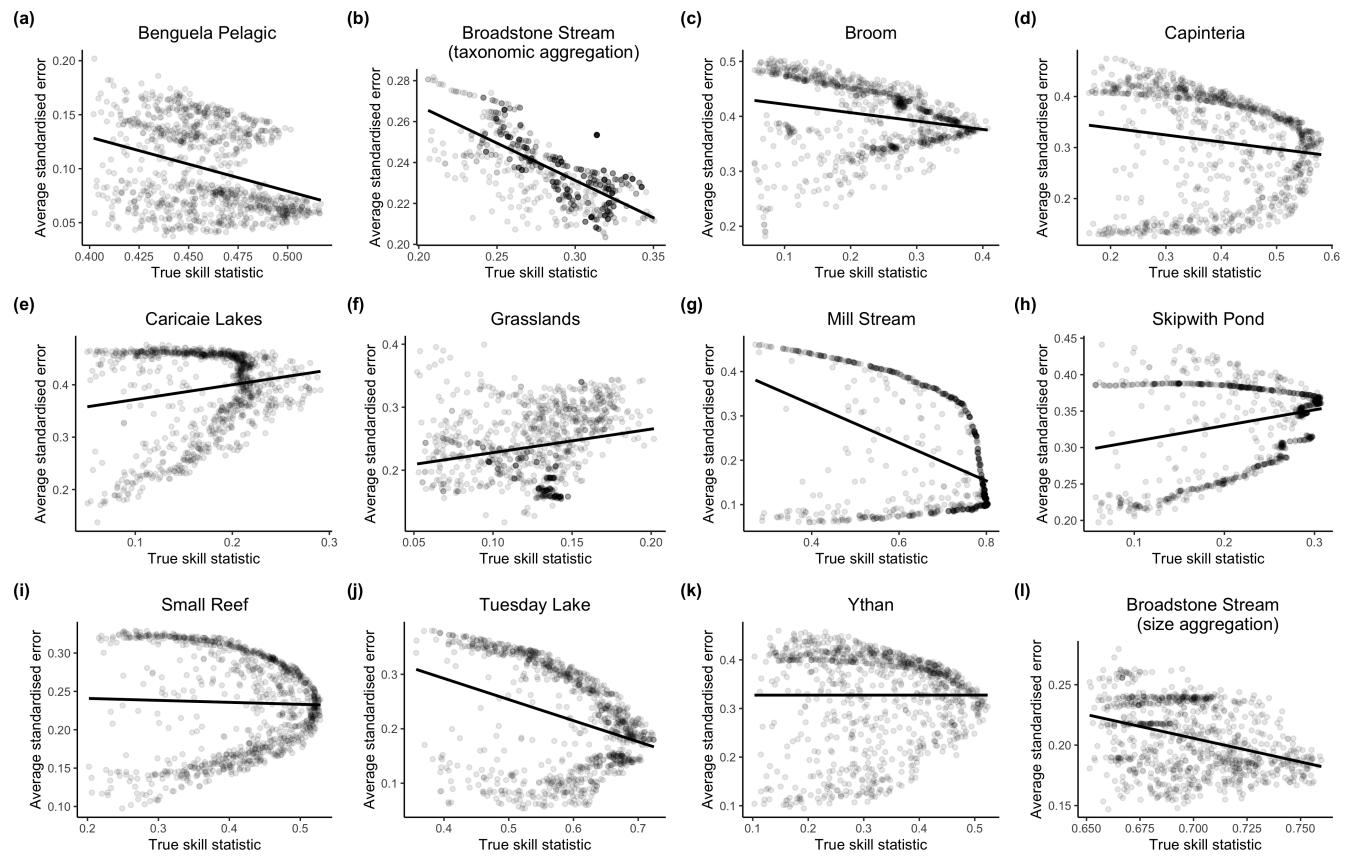


Figure S30: The mean standardised error of the food web properties predicted from the ADBM parameterised using rejection ABC plotted against the true skill statistic for each food webs. The solid lines are linear regressions (details in SI-S9).

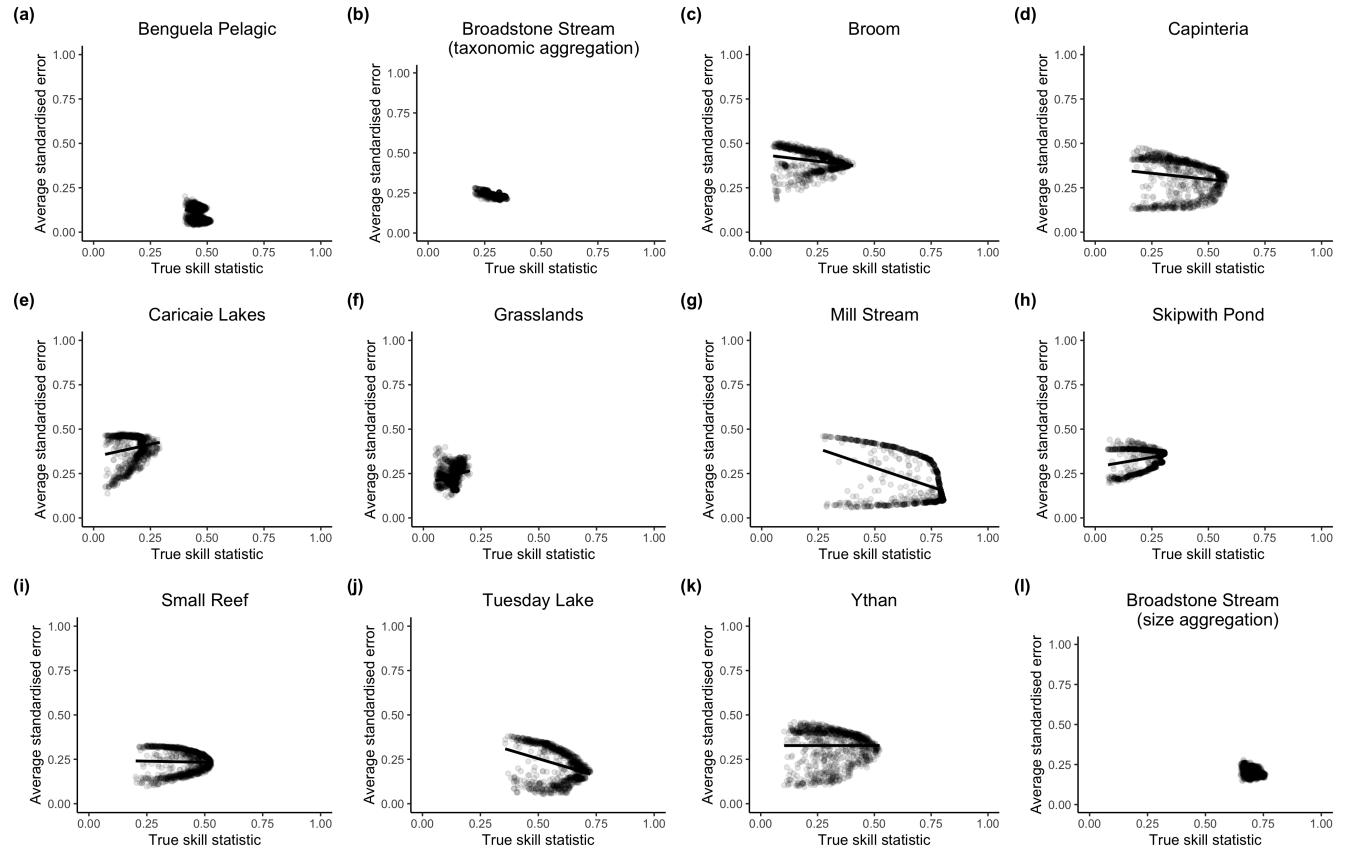


Figure S31: The mean standardised error of the food web properties predicted from the ADBM parameterised using rejection ABC plotted against the true skill statistic for each food webs. The solid lines are linear regressions (details in SI-S9). The limits of the horizontal and vertical axes have been set between 0 and 1.

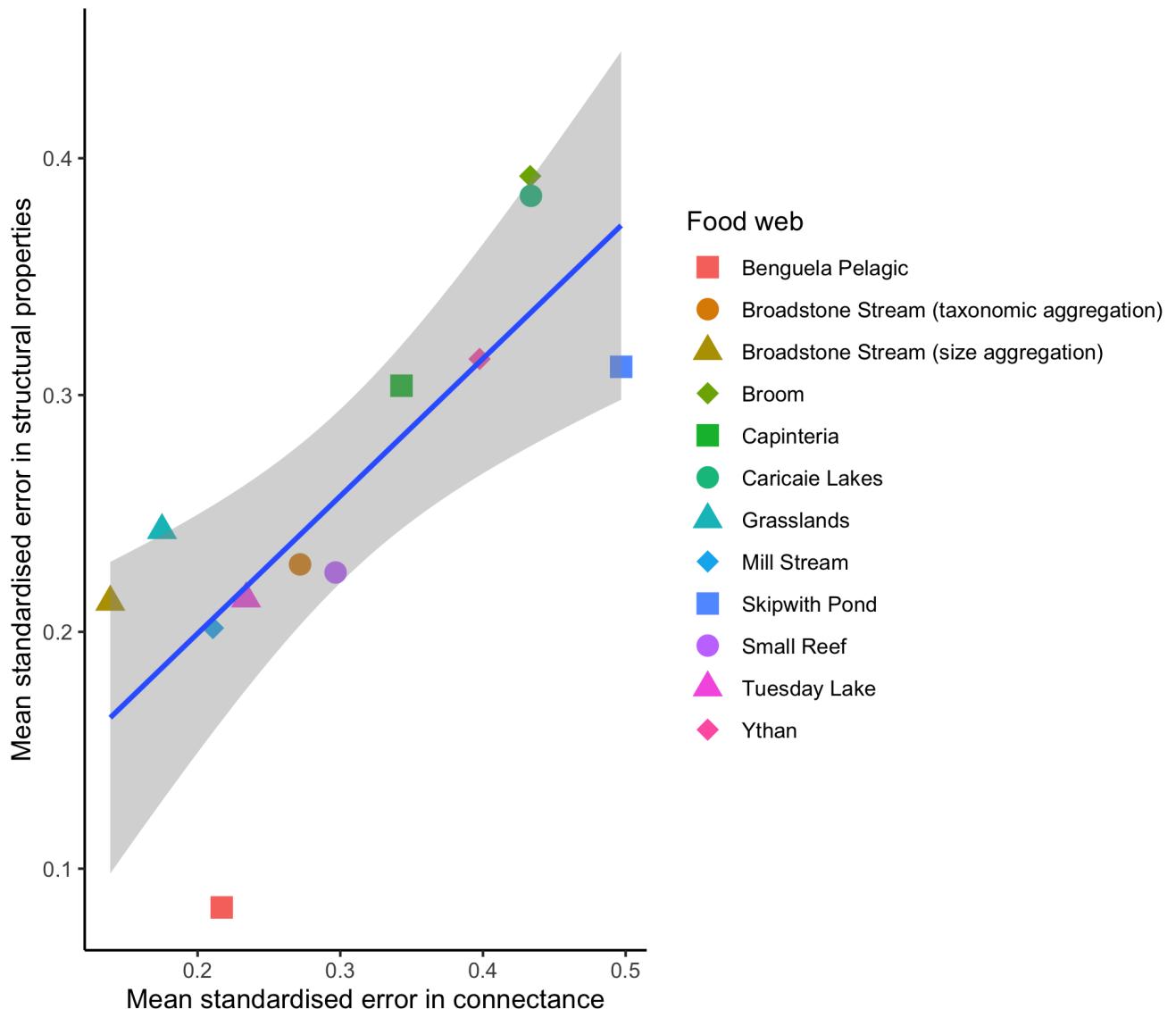


Figure S32: The mean standardised error in structural properties of food web versus mean standardised error in connectance. Solid blue line is linear regression ( $t = 3.911$ ,  $df = 10$ ,  $P = 0.0029$ )

## 325 References

- 326 Gelman, Andrew, and Donald B. Rubin. 1992. "Inference from Iterative Simulation Using Multiple Sequences." *Statistical Science* 7 (4): 457–72. <https://doi.org/10.1214/ss/1177011136>.
- 327 Marjoram, P., J. Molitor, V. Plagnol, and S. Tavare. 2003. "Markov Chain Monte Carlo Without Likelihoods." *Proceedings of the National Academy of Sciences* 100 (26): 15324–28. <https://doi.org/10.1073/pnas.03068>

330 99100.