Simple rules yield complex food webs

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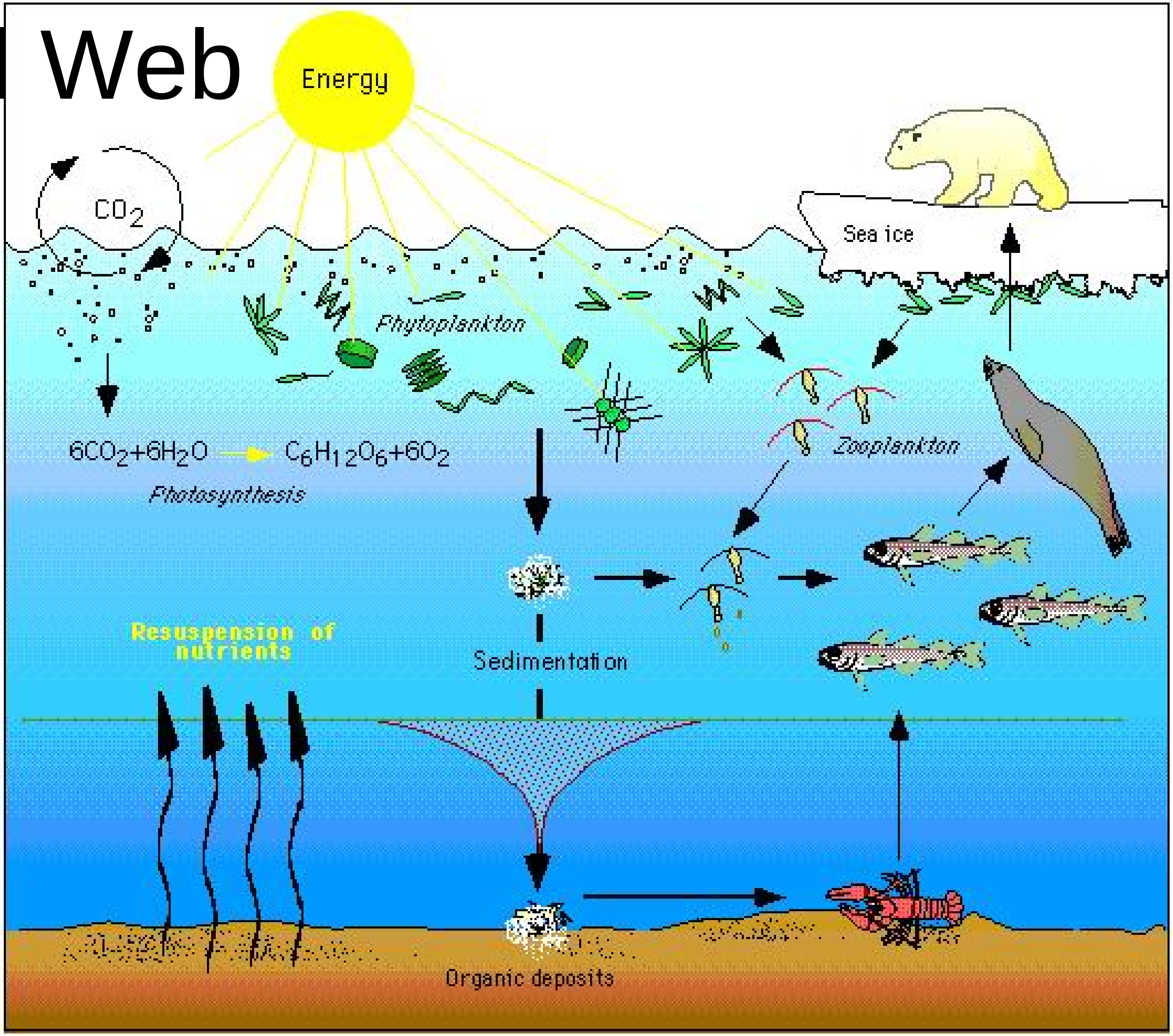
Food Web



Drawn by Christopher Krembs

Food Web Model

- Individual (species) models
  - Uniform/Classified
  - How many parameters involved

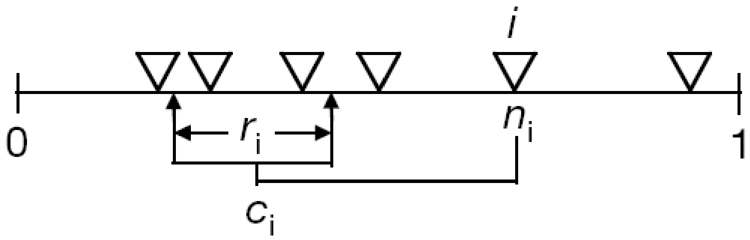
Previous Model

- Random model
  - any link among ***S*** species occurs with the same probability (*P*) equal to **C** of the empirical web
  - Global connections

Previous Model – Cont’d

- Cascade model
  - assigns each species a random value drawn uniformly from the interval [0,1] and each species has probability $P = 2\boldsymbol{CS}/(\boldsymbol{S} - 1)$ of consuming only species with values less than its own.
  - Good explanation for trophic levels
  - underestimates interspecific trophic similarity
  - overestimates food-chain length and number in larger webs

New Model



- Each of ***S*** species (for example, ***S*** = 6, each shown as an inverted triangle) is assigned a 'niche value' parameter (n_i) drawn uniformly from the interval [0,1]. Species ***i*** consumes all species falling in a range (r_i) that is placed by uniformly drawing the centre of the range (c_i) from [r_i/2, n_i]. This permits looping and cannibalism by allowing up to half of r_i to include values n_i.

How to evaluate the model

- Compare with actual food webs
- Compare with other model
- In this paper
    - 7 actual empirical food webs
    - 12 parameters

7 actual empirical food webs

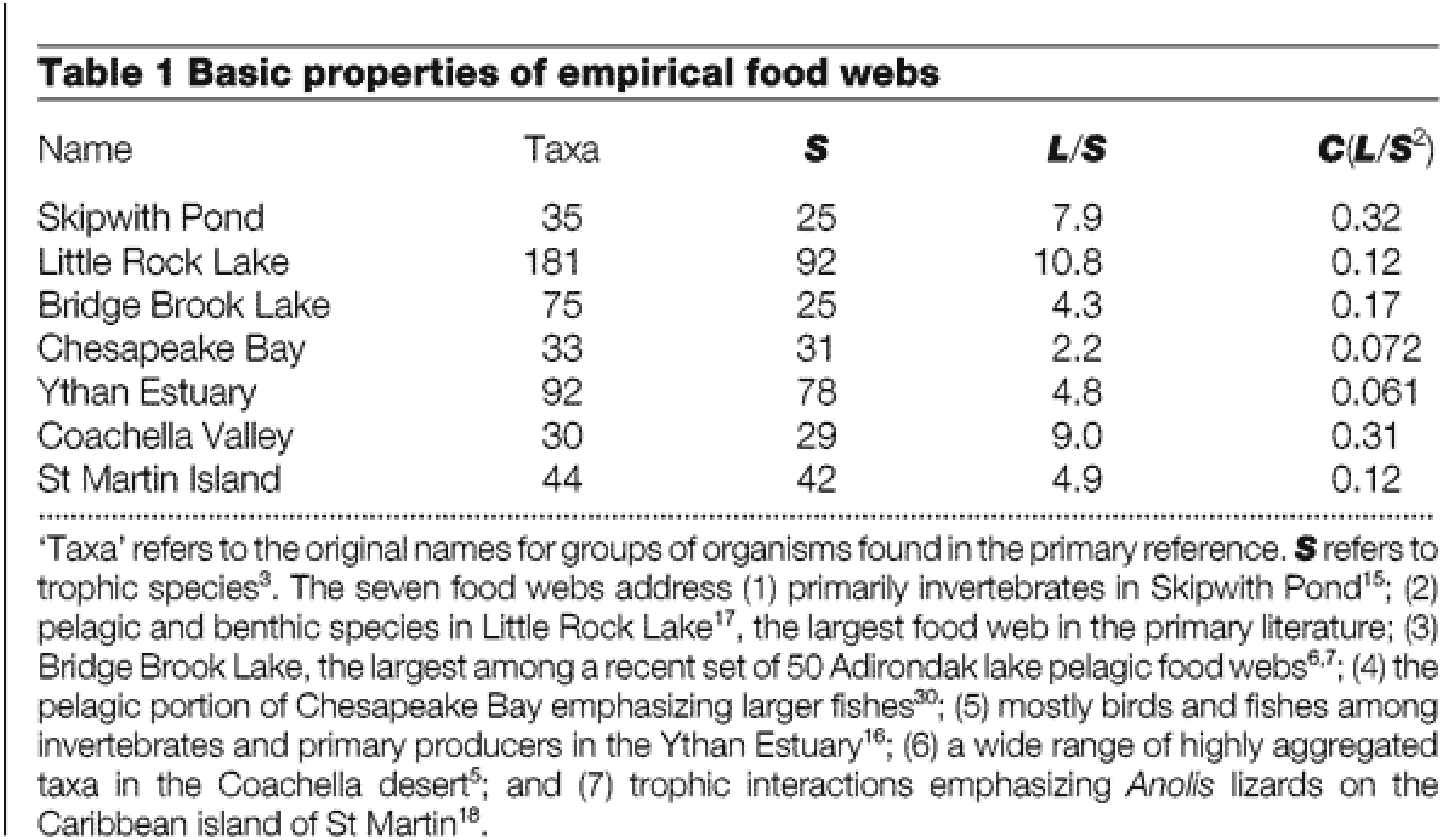


Table 1 Basic properties of empirical food webs

Name	Taxa	S	L/S	$C (L/S^2)$
Skipwith Pond	35	25	7.9	0.32
Little Rock Lake	181	92	10.8	0.12
Bridge Brook Lake	75	25	4.3	0.17
Chesapeake Bay	33	31	2.2	0.072
Ythan Estuary	92	78	4.8	0.061
Coachella Valley	30	29	9.0	0.31
St Martin Island	44	42	4.9	0.12

'Taxa' refers to the original names for groups of organisms found in the primary reference. S refers to trophic species[3]. The seven food webs address (1) primarily invertebrates in Skipwith Pond[15]; (2) pelagic and benthic species in Little Rock Lake[17], the largest food web in the primary literature; (3) Bridge Brook Lake, the largest among a recent set of 50 Adirondak lake pelagic food webs[6,7]; (4) the pelagic portion of Chesapeake Bay emphasizing larger fishes[30]; (5) mostly birds and fishes among invertebrates and primary producers in the Ythan Estuary[16]; (6) a wide range of highly aggregated taxa in the Coachella desert[5]; and (7) trophic interactions emphasizing *Anolis* lizards on the Caribbean island of St Martin[18].

12 parameters

- (i–iii) Species:
  - the fractions of top (***T***, species with no predators),
  - intermediate (***I***, species with both predators and prey)
  - basal (***B***, species with no prey) species.
- (iv, v) The standard deviations (s.d.) of generality (*GenSD*) and vulnerability (*VulSD*) quantify the respective variability of species' normalized prey (*Gi*) and predator (*Vi*) counts:

12 parameters – Cont’d

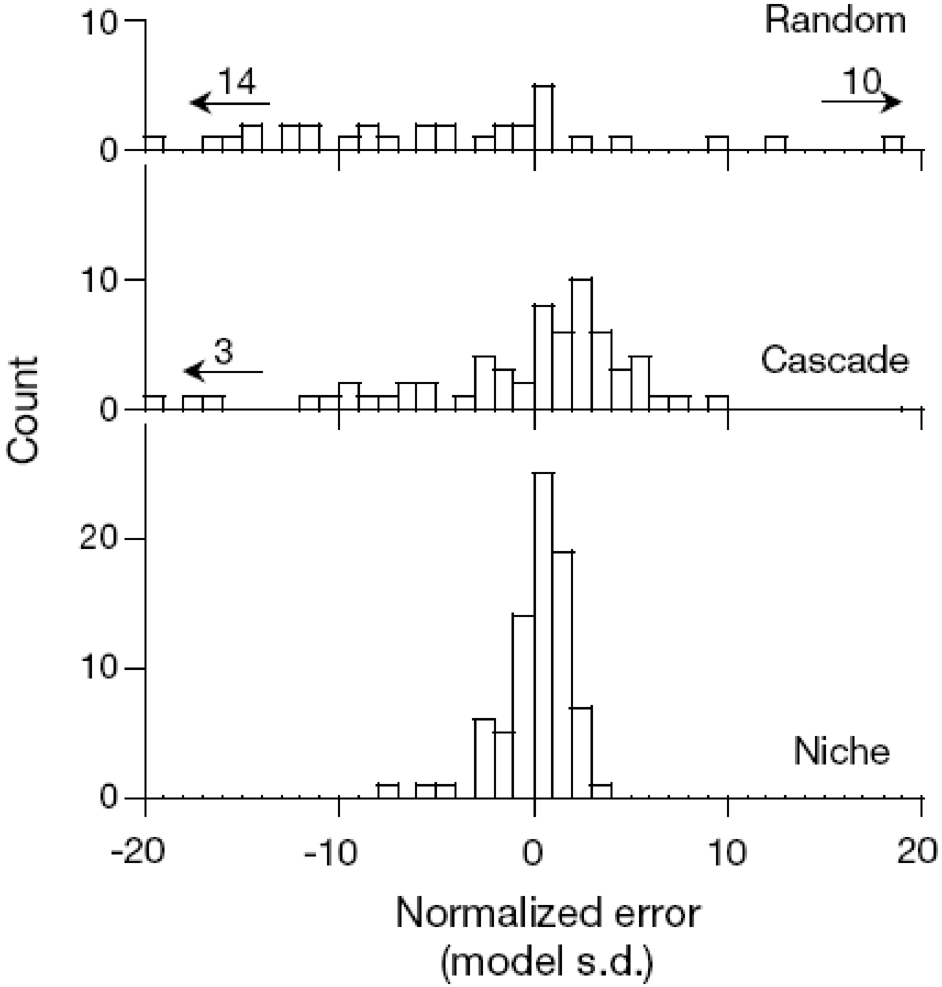
- (vi) Trophic similarity (of a pair of species (***s****ij*))
  - the number of predators and prey shared in common divided by the pair's total number of predators and prey
- (vii–ix) A food chain path:
  - *ChnLg:* The mean
  - *ChnSD:* s.d. of food chain lengths
  - *ChnNo:* the log of the number of food chains are measured.

12 parameters – Cont’d

- (x) *Cannib*
  - The fraction of species that are cannibals
- (xi) *Loop*
  - the fraction of species involved in longer 'loops', which are food chains that include the same species twice
- (xii) Omnivory
  - fraction of species that consume two or more species and have food chains of different lengths.

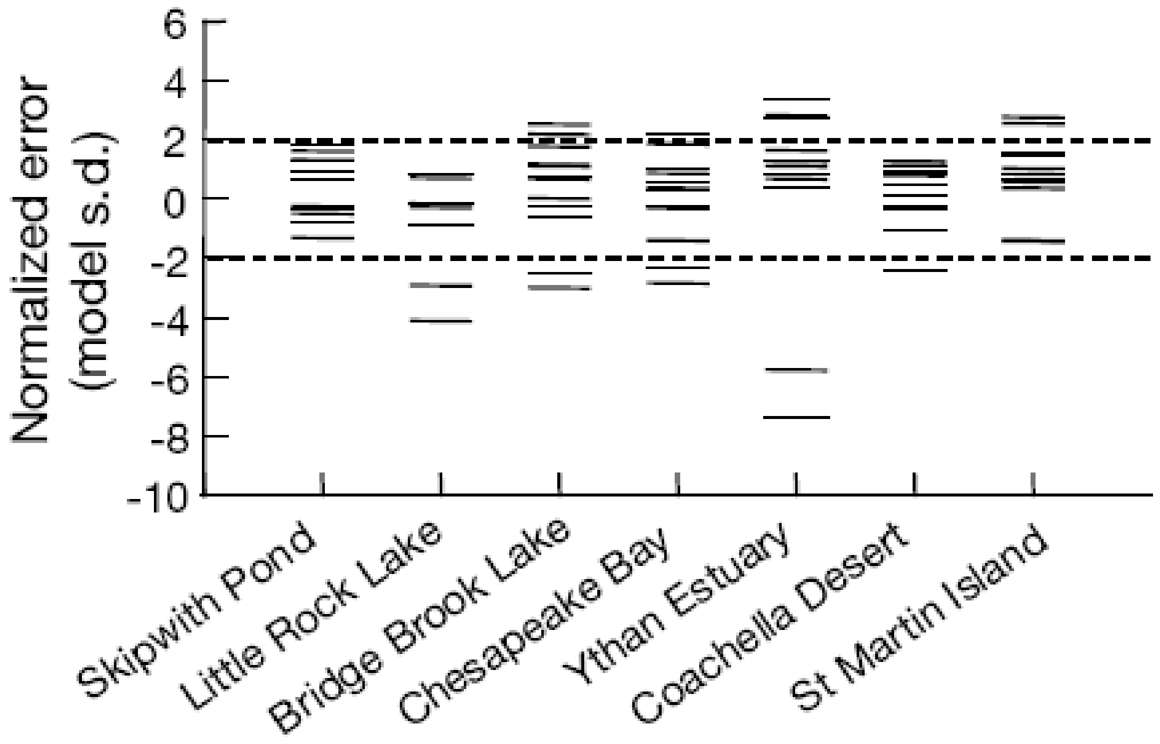
Model Evaluation (I)

- Distribution of normalized errors between empirical data and models



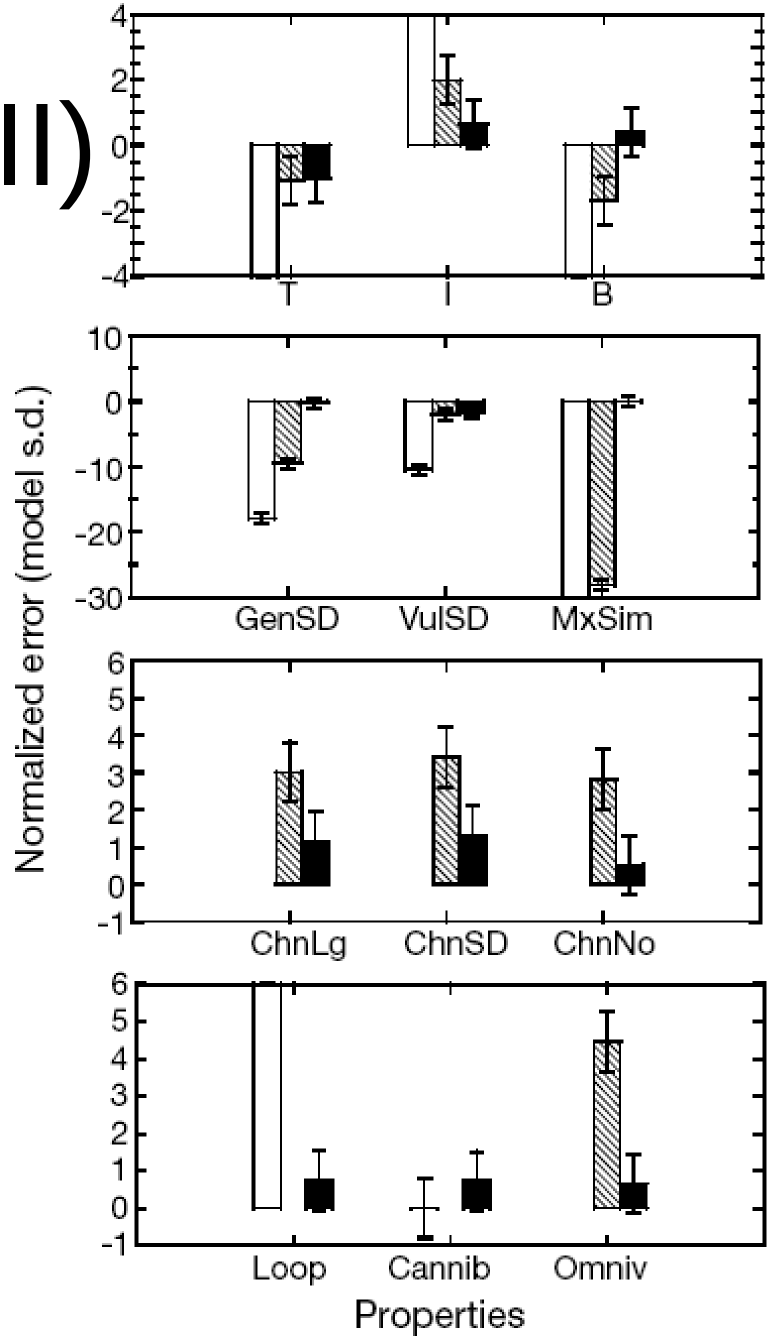
Model Evaluation (II)

- The niche model's normalized errors for each property of each food web



Model Evaluation (III)

- Mean normalized error of each property for each model averaged across the seven food webs



Conclusion

- The new model fits the actual data well
- facilitates a relaxed hierarchy of trophic interactions among species ordered in one dimension
- provides a benchmark for evaluating food webs
- provides structural framework to studies of link-strength distributions in a larger system

Summary

- Simple and Beautiful Model for Food Web
- Good fit with the actual data
- Clear result analysis

End
Thank you