**2. Method**

General methodology (quasi sign stability)

**2.1 Model**

One of the benefits of using quasi sign-stability to determine the stability of food webs is that we do not need to explicitly define a model structure. Rather, the elements of the Jacobian matrix can be sampled from an underlying distribution that can be based on the predictions from a general model.

We assumed a general predator dependent functional response (Abrams & Ginzburg, 2000) where there is mutual interference among consumers. This means that the functional response is dependent on both the prey and predator densities, rather than only on prey density (as in prey-dependent). On the spectrum of interference between prey-dependence (no interference) and ratio-dependence (complete interference where the functional response is dependent on the number of prey per predator) our assumed predator-dependent functional response is not as extreme as, but is closer to, ratio-dependence (Arditi & Ginzburg 2012).

Given “hungry” predators a ratio-dependent functional response is approximately linear and the dynamics of the system are donor-controlled (Arditi & Ginzburg 2012). In a donor-controlled system the mortality imposed by predation is independent of predator abundance (when abundance is high) in this idealized example. Predator abundance will therefore have no impact on prey abundance. The linear approximation of the ratio-dependent system away from saturation as a donor-controlled model can be considered similar to the way in which Lotka-Volterra equations represent a linear approximation of Hollings’ nonlinear model.

The sign matrix of a donor-controlled system is triangular, with positive values on one side of the diagonal and zeros on the other side. As May (1973) noted, a triangular matrix would imply qualitative stability, thus in this ideal scenario any number of trophic levels will create a stable structure, the same as in a purely linear food chain. With the assumption of a predator-dependent functional response that lies close to, but not at the ratio-dependent end of the spectrum in our numerical simulations we relaxed the conditions of a perfect donor-control model. Rather than assuming that predators have no impact on their prey we substituted small values relative to the impact of prey on predators.

**2.2 Web Construction**

*2.2.1 Toy model*

To illuminate our hypothesis we start with a simple example of webs with two to six species arranged in a chain. These webs are characterized by universal omnivory, where each species consumes from all levels below its own, making the chain more web-like (**Figure 2**). Each web was then converted into a signed matrix, with (+/-) assigned to each predator prey link and a (-) assigned to the diagonal, indicating negative density dependence. Due to our use of universal omnivory, the sign matrices consist of positives on the upper triangle of the matrix, and negatives on the lower triangle.

*2.2.2 Robustness of assumptions*

Random ten-species webs were generated with varying levels of connectance. To ensure that we were sampling webs with all possible chain lengths the construction of each random web was started with a chain of two to ten species (one to nine links). Then, depending on the connectance, any remaining links were randomly assigned among species. For example, a ten species food web with a connectance (links per species squared) of 0.14 has 14 links. Thus a random web initiated with a ten species chain would have five more links randomly distributed, while a random web initiated with a five species chain would have nine more links distributed among the species. Each web was constrained such that each species either consumed another species directly, or was consumed itself (i.e. no unconnected nodes).

We chose not to use models of food webs such as the cascade, niche, or nested hierarchy because they tend to reproduce the properties of empirical food webs based on a set of phenomenological rules. To test why some food webs persist and others do not a model that produces realistic food webs would not be useful, as they would likely include whatever properties allow them to persist in nature by chance. A thorough exploration of the parameter space of potential food web configurations would need to include webs that cannot exist in nature, which is why a random model is more useful to test our hypotheses.

**2.3 Simulations**