

Notes from Tuesday 8 December 2015

Reasons to modify R :

- * Asymmetry: e.g. most plants can self-pollinate; all bees are obligate nectar feeders. Method: $R_{bees} \text{ beta}(10, 0.8)$; $R_{plants} \text{ beta}(0.1, 1)$
- * Bimodal: $R_{plants} \text{ beta}(0.2, 0.2)$
- (hard) Taxon specific information (e.g. wasps eat meat)
- * R determined by individual species' interaction degree and strength distribution (correlated or not, depending on the system)
- * Shuffle R for each iteration/extinction event
- (hard) allow for host-switching: internal (new links arise) vs external (R compensates as interactions dissolve)
- Species ID matters (Memmot) *JO: not sure what this meant*

Background

Vieira and Almeida-Neto (2014) proposed a stochastic coextinction model to simulate extinction cascades with more complexity than previous models. One major finding contrary to existing (topological coextinction) models (TCM) was that the likelihood and severity (degree; “the number of extinction episodes, with each episode involving one or more species, summed across both tropic levels”) of a cascade increases with network connectance in mutualistic networks. Their model (1) picked species at random for the primary extinction event, and (2) incorporated information about the species' dependence on the interaction, R , but drew this value randomly from a uniform distribution, independent of other properties of the species, and applied the same value to all species. Importantly, they showed that R chosen from either low, medium, or high values has substantial impact on the outcome of the extinction cascade (probability of a cascade, mean number of extinctions, proportion spp lost). However, we know that not all species are equally prone to extinction, and the dependence of a species on an interaction network can covary with other properties of the species. We build upon their model by modifying the parameter R , with the goal of making coextinction

simulations more realistic by incorporating information from ecological networks and conducting simulations on both empirical and simulated datasets. We report how the covariation between species' network traits (e.g. degree, strength, specialization) and their dependence on a network R impacts co-extinction cascades. Further, we assess differences in network structure and species' traits before and after extinction cascades. Further, we test our model on simulated networks generated according to parameters that people seem to think are important properties of mutualistic networks.

What are the properties of all of the species; esp - are there differences between the primary extinction and secondary extinction. Is there similarity in network traits of species that never go extinct?

Previous studies made the following assumptions:

1. Coextinction requires the loss of all partners
2. Interaction strengths do not matter (i.e. a species survives as long as at least one partner survives, even if it only weakly interacts with that partner)
3. Variation in how much a species depend on their partners was ignored. For example, plants' ability to self-pollinate is ignored.

Thus, Vieira and Almeida-Neto proposed a model that

1. incorporates variation in dependences
2. relaxes the assumption that coextinction requires the loss of all interaction partners

Under the proposed model the dependence of species on the interactions controls the likelihood of extinction cascades and thus highly connected networks are more susceptible to cascades. The model is more realistic since it considers the possibility of compensatory effects.

Their model:

Let:

d_{ij} is the population-level strength of the interaction.

R_i is assumed constant for each species and reflects the intrinsic demographic dependence of species i on the mutualism in question

$P_{ij} = R_i d_{ij}$ is the probability of species i going extinct following the extinction of a mutualistic partner species j .

Simulations proceed by removing one species at a given trophic level, and removing species from the other set according to P . d_{ij} are recalculated after each extinction

Possible Directions

1. MP originally stated that Vieira and Almeida-Neto consider only a single value of R for the entire network; however, JO believes each species has a different R . Note that each species has ONE R , not a different R for each of the possible partners. MP: This is unrealistic. Different species depend on the interaction with different degrees. This R could also be seen as the participation of the species in a particular network. For instance, if we are studying a frugivory network species that eat insects, but are also included in the network will have smaller R than strict frugivores. Similarly, a species that feed on fruits that we are considering but also on other fruits that, for some reason, are not included in this particular network, has smaller R . Thus, the R parameter is what defines the boundaries of the network. It would be interesting to perform simulation where R obeys a probability distributions. How different R distributions changes the size and shape of extinction cascades? Are there critical points given by the parameters of these distributions?
2. The authors only explored mutualisms. It would be interesting to test whether their conclusions hold for other interaction types.
3. One of the possibilities we discussed was testing the effects of extinction on multilayered networks. This would be the obvious step after step 1. We could start from the simple scenario with 2 interaction types (e.g. mutualism, herbivory) and then explore other combinations. An empirical system that we could play with are defensive mutualisms for which MP believes Cecilia might have suitable data.
4. Since the model was designed with mutualisms in mind, one extinction can only have negative effects over the partners. However when we think on antagonisms (competition, predation, parasitism), extinctions

may favor other species. Since the model is probabilistic, we could also have, Q , which is the probability of density increase after an extinction. P could also change if antagonists increased enough in abundance. we should discuss the feasibility of adding this to the model while keeping it simple.

What we've done

1. Generalized the model so each species has an R value
2. R values are sampled from a probability distribution
3. Exploring how extinctions cascades respond to R distributions with different shapes

Done

- Generalized the model so each species has an R value
- R values are sampled from a probability distribution

Next steps/TODO

- We are currently exploring how extinctions cascades respond to R distributions with different shapes
- play with the R codes in the Supporting information and try to devise an alternate model encompassing option 4 above (extension to antagonisms)
- think how we can generalize this to antagonist interactions. In antagonistic interactions the loss of a prey species may have a demographic impact on the predator, but the loss of the predator can have a positive impact on the prey - We need to discuss how to generalize the same model to include these possibilities
- First test - How including variable R values (species dependence on interactions) across species change the original results? Use the same network, same r_{low} , same r_{up} , one set of simulations with one R value (as in Vieira and Almeida-Neto 2015), second set of simulation with several R values

- Second test - How different distributions of Rvalues (different ways in which species depend on the mutualism) change the probability of cascades and the number of coextinctions? We could choose uniform, normal and exponential, and few parameter combinations for each (3?)
- Third test - Does network topology affect the consequence of multiple Rvalues? Perform a series of tests with networks with different topologies
- for all tests besides looking at the number of coextinctions and coextinctions degree we could examine how topology changed

More thoughts ...

From meeting 20150818 (MP+JO):

$$P_{ij} = R_{ij}d_{ij}, \text{ if } i \text{ is a predator}$$

Probability that i increases in density is given by: $Q_{ij} = R_{ij}d_{ji}$, if i is a prey species

if the density increases we could have one iteration step where interaction frequencies are changed by some factor - assuming that population density affects interaction frequencies

- A. response of model output to probabilistic values of R
- B. behavior of model on non-mutualistic interactions
- C. merge multiple networks using multi-layer network approach (perhaps very difficult)