Supplementary Information

**Bridging ecology and conservation: from ecological networks to ecosystem function**

Eric Harvey1,2, Isabelle Gounand1,2, Colette Ward3 and Florian Altermatt1,2

**Corresponding Author:** [eric.harvey@eawag.ch](mailto:eric.harvey@eawag.ch)

**Affiliations:**

1Department of Evolutionary Biology and Environmental Studies, University of Zurich,

Winterthurerstrasse 190, CH-8057 Zürich, Switzerland.

2Eawag: Swiss Federal Institute of Aquatic Science and Technology, Department of Aquatic Ecology, Überlandstrasse 133, CH-8600 Dübendorf, Switzerland

3 National Center for Ecological Analysis and Synthesis, University of California, Santa Barbara 735 State Street, Suite 300, Santa Barbara, CA, USA 93101-5504

**Table of Contents**

Appendix 1: Practical assessment of species interactions and their effect on the stability of ecological networks 3

Step 1: Network structural stability 3

*Definition of the stability metric* 3

*General principle of the analysis* 4

*Parameterization of the community matrix* 4

*Minimal data required: the adjacency matrix* 5

*Steps by steps of how to use the script “keystone\_interactions.R”* 5

Step 2: Number of extinctions 6

Literature cited 8

# Appendix 1: Practical assessment of species interactions and their effect on the stability of ecological networks

We propose a simple two-step procedure to identify the interactions of interest for conservation of ecological networks: First, rank each pairwise species interaction according to its effect on network structural stability when removed. Second, calculate the number of extinctions following the removal of each interaction. The information provided by this analysis allows targeting of interactions that are important to preserve whole network structure and to avoid extinctions. This approach can be done *in silico* based on a minimal set of information, and can guide decision-making.

## Step 1: Network structural stability

### *Definition of the stability metric*

**Structural stability** measures the contribution of network topology (i.e. the distribution of interaction links between species) to the stability of local dynamics (Fox 2006). Specifically, it can be calculated by either the real part of the community matrix dominant eigenvalue, which corresponds to the resilience of the web to a small perturbation (e.g. May 1972, Fox 2006), or by the minimum intraspecific competition necessary for the system to be stable (e.g. Neutel et al. 2002, 2007, Sauve et al. 2016). Both metrics are considered equivalent, however for simplicity we used the latter, following Sauve et al. (2016). Therefore, to calculate network stability our provided R script calls functions written by Sauve et al. (2016), which can be downloaded from their online supplementary information: http://onlinelibrary.wiley.com/doi/10.1890/15-0132/full. They provide a justification of this stability metric in their Appendix A. This metric was initially developed by Neutel et al. (2002), and is equivalent to that used by Allesina and Tang (2012) and Tang et al. (2014). The smaller the metric value, the more resilient is the network.

### *General principle of the analysis*

(see our provided R script “keystone\_interactions.R”)

We calculate the initial structural stability of the network when all interactions are present (henceforth ‘**initial stability’**), and compare this initial value to the structural stability when one interaction at a time is removed (henceforth ‘**secondary stability’**). We repeat the procedure for each interaction and rank interactions according to differences between initial and secondary stability (see *Steps by steps of how to use the script “keystone\_interactions.R”* section below for more details). We thereby identify the interactions most important to the stability of an interacting community.

### *Parameterization of the community matrix*

The community matrix is the Jacobian matrix of a community model at equilibrium, where each element *Jij* quantifies the effect that species *j* has on species *i* growth rate (e.g. if species *i* eats species *j*, *Jij>0* and *Jji<0*). Therefore, the calculation of structural stability generally implies that we know the strength of interactions between species. However, because quantitative interaction strength is difficult to collect and rarely available, we propose to use the statistical alternative developed by Tang et al. (2014) and Sauve et al (2016), which permits estimation of structural stability from qualitative information. This procedure consists of randomly drawing interaction strengths many times for the same network topology (given by the adjacency matrix: community matrix with species in rows consumer species in columns), calculating each time the structural stability. We obtain a distribution of values for the stability metric from which we can extract a central measure (here, the median) of stability associated with the given topology. In our script, interaction strengths are randomly drawn from normal distributions with mean µ=1 and sd=0.1, following Sauve et al. (2016). If some quantitative information is known to allow the derivation of a more precise shape of the distribution of interactions strengths, this can be directly implemented to improve the calculation of the stability criteria (see Tang et al. 2014).

### *Minimal data required: the adjacency matrix*

The minimum information required is a 0/1 adjacency matrix M of size S x S (S, the total number of species) where 1 reports a link between two species (0 is the absence of such a link). In the case of a food web (antagonistic interactions), as in our example, if species *i* eats species *j*, *Mij* = 1 and *Mji* = 0. Our script uses functions of Sauve et al. (2016), which also allow integration of bi-directional interactions (such as mutualisms; plant-pollinator in their study). In the adjacency matrix, bi-directional interactions must be reported as *Mij* = *Mji*=1.

### *Steps by steps of how to use the script “keystone\_interactions.R”*

To use the script, you must provide the adjacency matrix with the names of species specified as in the .csv file example (“adjacency\_matrix\_foodweb.csv”). The script then executes the following operations:

* Calculating the initial stability:
  + A seed is set, in order to get the same parameterization sets when removing interactions.
  + Calculation of the structural stability for 10,000 parameterizations of interaction strengths; the parameterization is done by the function “jacobian\_binary()” and the calculation of the stability by the function “stability()”, both from the script of Sauve et al. (2016)
  + We took the median of the resulting stability metric distribution as global estimation of structural stability of the network.
* Calculating secondary stability.

For each interaction:

* + We set the interaction to 0 in the adjacency matrix
  + We recalculate the structural stability for the same 10,000 parameterizations used to calculate initial stability.
  + As stated above, the stability difference is calculated as (initial stability) – (median of secondary stability)
* Ranking the interactions based on the stability difference and plot them.

Because structural stability increases with decreasing values of our stability metric, a positive stability difference means that the removal of the interaction induces a gain in structural stability while a negative stability difference corresponds to a loss of structural stability.

Note 1: the stability metric used works only if there are no cannibalistic interactions (only 0 on the diagonal of the adjacency matrix M). When cannibalism is present the real part of the dominant eigenvalue (resilience) should be used as the stability metric.

Note 2: the ranking becomes less variable (to different seeds) when the number of parameterization sets increases. In our example 10,000 parameterizations leads to quite stable ranking among clusters of interactions with similar effects on stability. However within clusters with very similar effects, interaction ranks may shift depending on the seed used. This variability is avoided if data on interaction strengths are provided.

## Step 2: Number of extinctions

In the structural stability metrics we did not take into account potential extinction, because it is necessary to keep the same size of community matrix to compare stability criteria. However, the removal of one interaction could lead to the extinction of specialist species (those feeding on one resource), and possibly to secondary extinctions if these specialists are resources for other hyper-specialists. We therefore propose to combine the above structural stability criterion with the total number of extinctions following the removal of an interaction (robustness), to identify keystone interactions. The second part of our script thus calculates the robustness of the web to removal interactions. For this you must provide the list of basal species, that is species which do not need a resource species to persist (i.e. primary producers) in the same order as the adjacency matrix, and include the names of the species as in the example .csv file “basal\_species\_foodweb.csv”.

# Literature cited

Allesina, S., and S. Tang. 2012. Stability criteria for complex ecosystems. Nature 483:205-208.

Fox, J. W. 2006. Current food web models cannot explain the overall topological structure of observed food webs. Oikos 115:97–109.

May, R. M. 1972. Will a large complex system be stable? Nature 238:413–414.

Neutel, A. M., J. A. P. Heesterbeek, and P. C. de Ruiter. 2002. Stability in real food webs: weak links in long loops. Science 296:1120–1123.

Neutel, A.-M., J. A. P. Heesterbeek, J. van de Koppel, G. Hoenderboom, A. Vos, C. Kaldeway, F. Berendse, and P. C. de Ruiter. 2007. Reconciling complexity with stability in naturally assembling food webs. Nature 449:599–602.

Sauve , A. M.C., Thébault, E., Pocock, M.J.O. and Fontaine C. 2016. How plants connect pollination and herbivory networks and their contribution to community stability. Ecology (in press, available online).

Tang, S., Pawar, S. and Allesina, S. 2014. Correlation between interaction strengths drives stability in large ecological networks. Ecology Letters 17:1094-1100.