

Scientific reports for short and exchange visit grants

Title of the proposed research project: Development of size-based approaches to analyze the robustness of ecological communities

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Purpose of the visit

To visit Mark Emmerson's Biodiversity research group at University College Cork, Ireland, to discuss and exchange ideas on size-based approaches to (i) estimating interaction strengths, (ii) parameterize food webs models and (iii) subsequently analyze their robustness to disturbances. The ultimate goal of this is to develop an understanding of how size structure (distribution of body sizes) within food webs affects various aspects of the robustness of ecological communities and how the contribution of individual species to community robustness (the keystone status of species) are affected by perturbations to the structure of ecological communities (in particular species extinctions and invasions). Among other things this will increase our understanding of how size-biased species extinctions (or invasion of alien species) could be expected to affect the structure and function of ecosystems.

Description of the work carried out during the visit

During the visit we started to explore whether species contributions to community robustness are context dependent. That is, when the structure of a food web is altered (e.g. by changing the number of species) does the keystone status of species change? We used a set of 100 locally stable food webs with 50 species in each to explore this question. During my stay in Cork, we set up a program to look at how different traits (body size, generality, vulnerability, trophic position and connectedness) of the identified keystone species in the 100 food webs change as the structure of the food webs in which they are embedded in change (see figure 1), i.e. species were removed according to different extinction sequences. The extinction sequences used were, from the highest value to the lowest, body size, trophic position, connectedness, generality, vulnerability and numerical abundance.

Short description of the program:

Basically, what the program does is that it identify the keystone species in the initial ecological community, then, species is removed following different extinction sequences and between every species deletion the traits of the keystone species in the new configuration of the food web is obtained. Each time one species were lost following the extinction sequence numerical simulations using Lotka-Volterra dynamics with type 1 functional response were used to search for a new local stable configuration. During the numerical simulations species could go secondary extinct but as the remaining species stabilized near equilibrium we checked for local stability and if reached the keystone species in the remaining community were identified. Keystone species was estimated in four different ways: 1) The species that affected community resilience most when being perturbed, i.e. when there is a small change in the intrinsic growth rate of the species 2)

the species that affected community structure most (i.e. the equilibrium abundances of all the other species in the food web) when being perturbed 3) the species corresponding to the maximum value in the left eigenvector of the Jacobian matrix and 4) the species corresponding to the maximum value in the right eigenvector of the Jacobian matrix (see Berg et al 2010, O’Gorman et al 2010).

Before I left Cork we had time to finish the simulations and preliminary results were obtained.

Description of the main results obtained

We are now in the process of analyzing the results. The results will show 1: How the traits of the keystone species change as the system becomes degraded (see figure 1) 2: The risk of food web collapse associated with the different extinction sequences and 3: Consistency over the four different approaches to identify keystone species, that is, do the traits of the keystone species change in a similar way or in a different way depending on how the keystone species were identified?

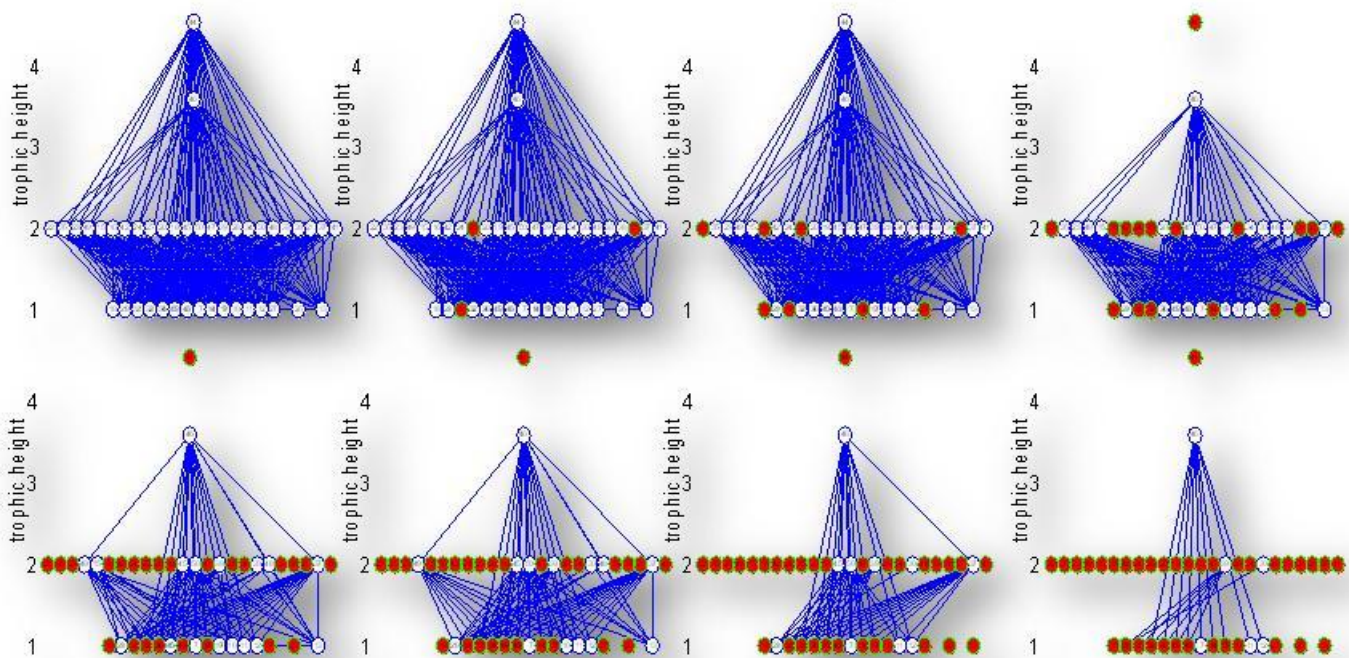


Figure 1. The breakdown of an ecological community. The initial community contains 50 species and in each new configuration of the food web, resulting after a primary species deletion and the secondary extinctions that take place due to that primary extinction, the traits of the keystone species is obtained. This allows us to study whether traits of the keystone species change as the structure of the community change.

Future collaboration with host institution (if applicable)

We will continue our collaboration with Mark Emmerson's research group and during my stay in Cork we started to plan for one more upcoming project. This project will result in a review article considered for publication in TREE. In this review, we will address similarities and differences between population sensitivity analysis and community sensitivity analysis and clarify and sort out the information given by for example the left and right eigenvectors in the model used in these approaches.

Projected publications/articles resulting or to result from the grant (ESF must be acknowledged in publications resulting from the grantee's work in relation with the grant).

1. Sofia Berg, Alexander Pimenov, Catherine Bridget Palmer Mark Emmerson and Tomas Jonsson, Extinction drivers – how do traits of most important species vary under different extinction scenarios?
2. Catherine Bridget Palmer, Alexander Pimenov, Sofia Berg, Tomas Jonsson and Mark Emmerson, Traits of the most important species - are those traits consistent for different ways of estimate keystone species?

Literature cited

Berg S., M. Christianou, T. Jonsson & B. Ebenman (2010) Using sensitivity analysis to identify keystone species and keystone links in size-based food webs. *Oikos* in press

O'Gorman, E. J. , U. Jacob, T. Jonsson & M. C. Emmerson (2010) Interaction strength, food web topology and the relative importance of species in food webs. *Journal of Animal Ecology* 79:682-692