

IALC Peace Fellowship Report
26 January – 10 February 2010

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When Will Fragmentation Per Se Increase/Decrease Biodiversity?
A Species-Area Relationship Approach

General Overview

Receiving the IALC Wayne Owens Peace Fellowship allowed me an experience that contributed greatly to my understanding of patterns of biodiversity in space and time. This experience would not be gained without the support of the International Arid Land Consortium. I've visited the University of Arizona, at Tucson, Arizona for two weeks at the end of January, 2010. During my stay I was honored to work and exchange ideas with Dr. Michael L. Rosenzweig. Beside the scientific work (summarized below) Dr. Rosenzweig and his wife, Carole, treated me with much appreciated kindness and hospitality. I stayed at the boundary of the Tumamoc-Hill Desert Laboratory, a reserve owned by the University of Arizona and one of the most beautiful places I have ever seen – giant Saguaros scattered around, along with amazing native flora and fauna. The Tumamoc-Hill Desert Laboratory is one of the world's oldest permanent study-plots of long term vegetation dynamics, and I was honored to work at one of the cradle-places of modern ecology. I would like to thank Lynda Klasky, the program coordinator of the Desert Laboratory, for her kind help and support. In addition, I've joined several meetings of a graduate-students' course on reconciliation ecology, given by Dr. Rosenzweig. The course thrives to establish a connection between ecology and architecture students that co-work on a reconciliation project - this was an inspiring challenge and an optimistic moment in an era of human destruction of the natural environment.

In addition to my work with Dr. Rosenzweig, I also had a chance to meet Dr. Goggy Davidowitz (Department of Ecology and Evolutionary Biology, University of Arizona). Dr. Davidowitz shared with me some of his many insights on the ecological consequences of body-size regulation of insects and we had very interesting discussions on the interaction between physiological ecology and landscape ecology. Finally, I also met Dr. Brian McGill (School of Natural Resources, University of Arizona), whose important comments and suggestions on my PhD thesis plans were priceless.

I wish to send my deepest thanks to Dr. Jim Chamie, the Managing Director of the International Arid Lands Consortium, and to all members of the IALC for this opportunity. Receiving the IALC Peace Fellowship resulted with a fruitful experience, both scientifically and personally, that will contribute greatly to my abilities as a young scientist. Final thanks are given to my advisor in Israel, Dr. Yaron Ziv who encouraged me to apply for the IALC Peace Fellowship and provided important scientific and personal support throughout the way.

Abstract

Fragmentation usually couples two separate processes, the loss of area and the decrease in the connectivity of the remaining patches. The well established pattern of species-area relationships (SPAR) clearly show that a loss of area will result with a decrease in biodiversity. However, the effect of fragmentation per se on biodiversity is less clear. In the literature, fragmentation per se has been shown to increase, decrease or not affect biodiversity. In the work I've done with Dr. Rosenzweig, we explored the affect of fragmentation per se on biodiversity of spiders in the fragmented landscapes of Southern Judea Lowlands (SJL), Israel. SJL lies in the transition zone between the Mediterranean ecosystem in the north, and the arid Negev desert in the south. Over a short gradient of 30 km, mean annual precipitation drops from 450 mm/y to 250 mm/y. At the Landscape scale, SJL is an agro-ecosystem with patches of different area embedded inside an agricultural matrix. We used a data-set comprising of more than 15,000 spider individuals from 200 species or morpho-species. The spiders were sampled in three 4x3.2 km landscapes along the sharp climatic gradient. In each landscape, I've sampled 12 patches of different area and a continuous area. For each landscape, we estimated the number of species in each patch using accumulation curves. We conducted a linear regression of $\log(\text{species})$ against $\log(\text{area})$ and extrapolated the SPAR to the combined total area of all 12 patches. We estimated the number of species in all 12 patches together, and explored if the value lay above, below or on the line of the regression. Additional analysis was conducted to separate the affect of fragmentation per se from area by selecting all combination of patches whose total area lies in a small range ($\pm 5\%$) around the area of a focal patch. We did it separately for different fragmentation levels (number of patches whose area is combined), ranging from 2 till 9. We calculated the mean Fisher's alpha for different fragmentation levels and compared the value to the Fisher's alpha of the focal patches. We found that in all three landscapes, the estimated number of species in all 12 patches lay above the expected species diversity of the SPAR. We also found that in SJL, an increase in Fisher's alpha correlates with an increase in the fragmentation levels. We suggest that in SJL, the turnover of species between patches overcompensates for the reduced number of species in each patch due to area loss. Finally, we developed a simple, SPAR-based-theory that may explain the contradicting affect of fragmentation per se on biodiversity.

Introduction

The fragmentation of natural habitats by human-related land-uses is one of the most concerning threats to biodiversity worldwide. Fragmentation usually couples two separate processes, the loss of area and the decrease in the connectivity of the remaining patches. The well established pattern of species-area relationships (SPAR) clearly show that a loss of area will result with a decrease in biodiversity. However, the effect of fragmentation per se on biodiversity is less clear. In the literature, fragmentation per se has been shown to increase, decrease or not affect biodiversity.

Exploring the effect of fragmentation per se is also relevant to the long lasting single large or several small (SLOSS) dilemma in reserve planning. When a certain, finite area is available for reserve, the spatial distribution of the area may affect the number of species which the reserve will harbor. If policy makers wish to protect as many species as possible, they have to optimize the distribution of the finite area in space. Each strategy has its pros and cons. If a single larger patch is conserved, there is no change in connectivity. In addition, a single large reserve minimizes edge effects. However, if all the area is continuous there is a risk that a large-scale disturbance or catastrophes will result with the extinction of a large proportion of biodiversity. On the other hand, several small patches may spread the risk over a larger area, thereby decreasing the probability of landscape-scale extinctions. Yet, the population in each remaining patch is small, resulting with high rates of local extinctions and fast species turnover rates in time. Exploring the effect of fragmentation per se on biodiversity both theoretically and empirically may aid policy makers in decision making. In the work I've done with Dr. Rosenzweig, we explored the effect of fragmentation per se on biodiversity of spiders in the fragmented landscapes of Southern Judea Lowlands, Israel. We asked whether fragmentation per se will increase, decrease or not affect biodiversity and tried to develop a theory that will predict the effect of fragmentation per se on biodiversity.

Methods

Study Site

Southern Judea Lowlands (SJL) lies at the transition zone between the Mediterranean ecosystem in the north of Israel and the Arid Negev desert in the south. Over a short north/south gradient of 30 km, mean annual precipitation drops from 450 mm/y to 250 mm/y and the percent cover of perennial vegetation drops from 55% of natural area in the north to 30% in the south. At the landscape scale, SJL is a fragmented agro-ecosystem with remnant natural patches embedded inside an agricultural matrix. At the patch scale, the remnant natural patches differ one from the other in their area, shape and internal heterogeneity. Finally, at the local scale, several microhabitats (hereafter, MH) are present, differing one from the other in their structure, microclimate, spider community structure and arthropod (prey) community structure.

Sampling

Three 3.2×4 km² landscapes were identified along the climatic gradient of SJL – Galon (north), Lachish and Dvir (south). In each landscape, 12 patches of different area and shape were sampled along with a large, continuous area. Samples were taken from 9 different a-priori defined microhabitats using a D-VAC (portable vacuum machine). Each sample was 0.5×0.5 m² and contained one uniform MH. A total of 742 samples were taken and the sampling intensity increased with patch area. All spiders were identified to the lowest possible taxonomic level. If identification to the taxonomic species was not possible, we used morpho-species. A total of 15,407 spiders were sampled, representing 32 families and 200 species or morpho-species.

Analysis

To separate the effect on biodiversity of fragmentation per se from the effect of area loss, we used two analysis methods. We generalized the analysis that was developed by Dr. Rosenzweig and the 2005 recipient of the IALV Peace Fellowship, Gal Yaacobi (see Yaacobi et al. 2007). In the first method we built the species area curves and extrapolated it to the total area of all patches combined. We then compared the observed and estimated number of species in all patches to the expected one according to the SPAR. The second method relies on calculating the Fisher's alpha index of diversity for the patches and for different combination of patches, while controlling for total area. A separate analysis was conducted in each of the three landscapes.

Species Area Relationship

For each patch we estimated the number of species, using accumulation curves of the samples. We used presence/absence data on each sample, and estimated the number of species in the entire patch using the F5 estimator developed by Dr. Rosenzweig and colleagues (Rosenzweig et al. 2003). F5 estimates the number of species using the equation:

$$S_{obs} = S^{1-N^{-f(N)}}, \text{ where: } f(N) = qN^q,$$

with **S_{obs}**- the number of species observed, **S**- the estimation for the total number of species, **N**- the number of individuals (or incidences for presence/absence data) and **q**- a scaling coefficient. We used the ws2m software (Turner et al. 2003) for this analysis. After repeating the procedure for each patch, we conducted a linear regression of the log of the estimated number of species against the log of patch area. We extrapolated the regression equation to the total area of all 12 patches combined and to the area of the continuous area. We used a similar accumulation method on all 12 patches together (i.e., we used all the samples taken on all the 12 patches as if they were taken from one patch) and for the continuous area. We also noted the observed number of species in all 12 patches combined and in the continuous area.

Fisher's Alpha Index of diversity

In each landscape, we listed all the possible combination of patches for fragmentation levels of 2-12. We define a fragmentation level as the number of patches to which a focal patch is divided to. That is, a fragmentation level of 4 indicates that a focal patch is divided to 4 patches. For each focal patch, we selected all the combinations whose total area is more or less similar to the area of the focal patch. We used a threshold of $\pm 5\%$ of the area of the focal patch. For each such combination we calculated the Fisher's alpha diversity index. We also calculated the Fisher's alpha of each patch (fragmentation level 1) and of the continuous area. Since more combination that lies within the 5% range were found for the larger patches, we calculated the weighted mean (\pm standard error) of Fisher's alpha for fragmentation level 1. We then calculated the mean Fisher's alpha for fragmentation levels 2, 3, 4, 5, 6, 7 and 8 (in Galon also 9), for which combination that meet the 5% threshold criteria were found. We compared the Fisher's alpha between different levels of fragmentation.

Results

We report here the results of only two landscapes – Dvir and Lachish. In Dvir and Lachish all the patches have a more or less similar structure – they are all moderate slope hills whose rocky structure was too hard for modern agriculture. However, in Galon, two groups of patches were sampled. The first group is similar to the patches sampled in the two other landscapes. The second groups are depression patches that probably form due to soil erosion and are distinct in all terms (structure, topology, MH heterogeneity, species diversity and abundance) from all other patches. Most of the depression patches have small area. The SPAR of Galon that includes the depression patches is non-significant in a log-log space, with a slope of $z=0.24$ and $R^2=0.18$. The SPAR without the depression patches is significant, with a slope of $z=0.13$ and $R^2=0.5$. Many combinations for the second line of analysis (Fisher's alpha) include the depression patches, thereby adding a bias to the estimate; therefore we decided not to report them here. However, we note that the qualitative results observed in Galon were similar to those of Dvir and Lachish.

Species Area Relationship

The species area curves of Dvir and Lachish were statistically significant with $p=0.017$ and $p=0.031$, respectively (figure 1). In both landscapes, the estimated number of species in the continuous area lay very close to the extrapolated regression line. The number of observed species in the 12 patches lay very close to the extrapolated regression line in Dvir and above the line in Lachish. The estimated number of species in the 12 patches lay considerably above the extrapolated regression line in both landscapes. The z value of the species area curve (the slope in the log-log space) was 0.23 in Dvir and 0.16 in Lachish. That is, in Lachish the slope is similar to values known in the literature for mainland systems (0.1-0.2). However, the z value of Dvir is at upper boundary of mainland systems slopes and below the values usually observed for true Islands curves (0.25-0.35)

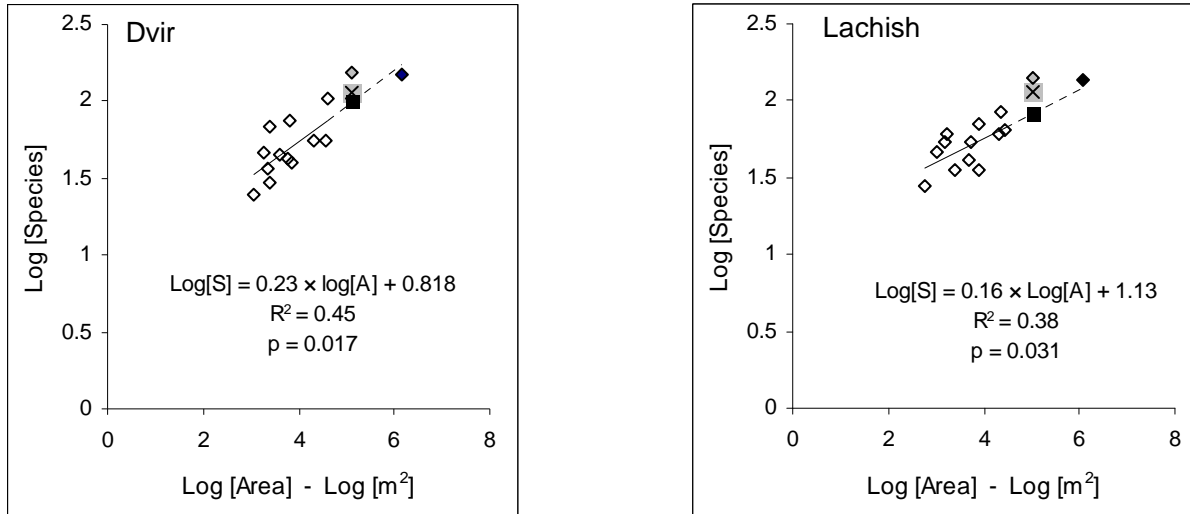


Figure 1: Species area curves for Dvir and Lachish. Open diamonds represent the estimated number of species in the patches. Filled square is the expected number of species according to the regression equation in an area that equal in size to the total area of the 12 patches. X is the actual number of species observed in all 12 patches and grey filled diamond is the estimated number of species for the 12 patches. Filled diamond is the estimated number of species in the continuous area.

Fisher's Alpha Index of diversity

The total number of combinations from each fragmentation level that were used in the analysis is given in table 1. In both Dvir and Lachish, mean Fisher's alpha increases with an increase in the fragmentation level (figure 2). In Dvir, no increase relative to fragmentation level 1 was observed for fragmentation level 2 and 3. However, a linear increase is observed from fragmentation level 4 to 8. In Lachish, an increase in mean Fisher's alpha was observed right from the fragmentation level of 2. In the two landscapes, the mean Fisher's alpha does not reach the observed value in the continuous area. A similar pattern of increased mean Fisher's alpha with increased fragmentation level is observed when exploring each focal patch separately. However, the trend is weaker when the focal patches become smaller.

Table 1: The number of combinations whose total area equals the area of any focal patch, for each fragmentation level and in each landscape. Fisher's alpha values were calculated for each combination.

Fragmentation level	2	3	4	5	6	7	8	Total
Dvir	15	23	36	111	99	25	2	311
Lachish	17	40	44	46	45	14	2	208

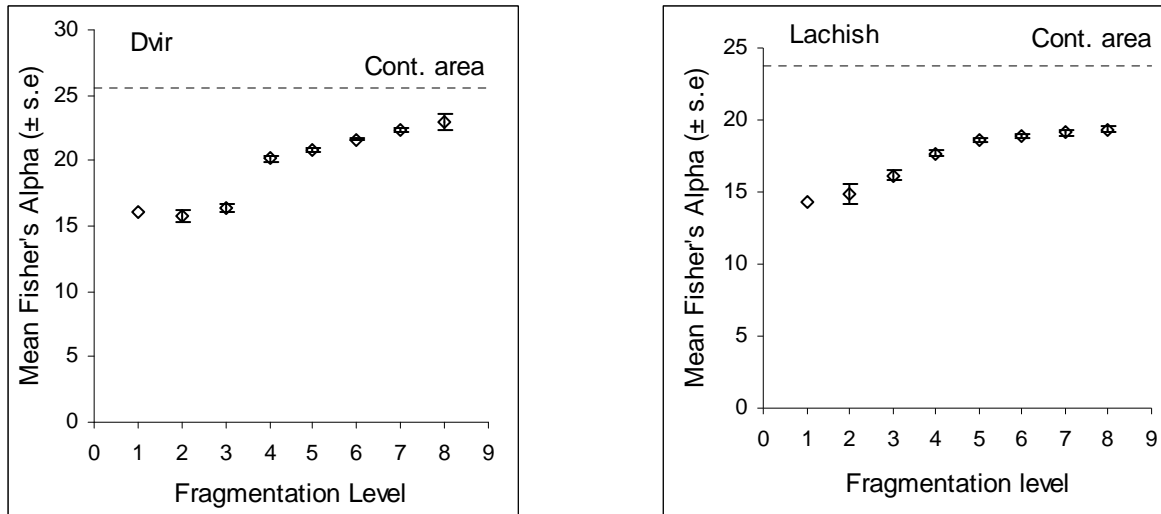


Figure 2: Mean (\pm s.e) Fisher's alpha index of diversity for different fragmentation levels in Dvir and Lachish. The values for fragmentation level 1 are the weighted mean of the fisher's alpha value of the original patches. Weights were according to the total number of combinations found for any specific focal patch. Fragmentation level is the number of patches whose total area equals the area of a focal patch. The dashed horizontal line is the Fisher's alpha value of the continuous area. Note the increase in values with increased fragmentation level.

Discussion

In this report we addressed the question- what is the affect of fragmentation per se on biodiversity of spiders in Southern Judea Lowlands? The answer according to the two analyses we have done is that in SJL and for spiders, fragmentation per se increases biodiversity. The analysis according to the species area curves (figure 1) decouples the effect of loss of area from the effect of fragmentation per se by yielding an expected value of biodiversity for a continuous piece of natural habitat that equals in area to the combined total area of all 12 patches. This analysis revealed that the estimated number of species in all 12 patches is higher than the expected one according to the SPAR. The analysis according to the mean Fisher's alpha decouples loss of area from fragmentation per se by selecting combination of patches whose total area equals the area of a focal patch, and comparing the Fisher's alpha values. The use of fisher's alpha also controls for sampling bias. The analysis of the fisher's alpha values for different fragmentation levels reveals that fragmentation per se increases spiders' biodiversity in SJL (figure 2). The similar results obtained by two separate and different analyses straighten the conclusion that in SJL, fragmentation increases spider biodiversity. Why is this so and what does it mean?

We hypothesize that the affect of fragmentation per se on biodiversity is a balance between two processes. The first process is the reduction in number of species per patch when the patch is smaller. This process is a straightforward conclusion from one of the most consistent patterns in nature – the species area relationship. However, when combining several small patches, the total number of species that is found is dependent upon the turn-over of species between the patches. When a different community is found in each

patch, the total number of species will over-compensate for the reduced number of species in each patch and fragmentation will positively affect biodiversity. When a similar community is found in all patches, the turnover of species will be low, and fragmentation per se will negatively affect biodiversity. This hypothesis may explain the different affect of fragmentation per se on biodiversity in different species and taxa (see figure 17.3 in: Rosenzweig 2005). Below we develop a theory that may explain and predict the affect of fragmentation per se on biodiversity.

So, is fragmentation per se a desired situation when it increases biodiversity? We believe that the answer is no for several reasons. Firstly and most important, in natural systems fragmentation per se is not separated from loss of area. Natural patches become fragmented not by moving in the landscapes, but by loss of area due to human development. The loss of area will eventually cause extinction of species.

Secondly, the increased biodiversity states nothing on the identity of the species. Fragmentation will probably affect negatively species whose dispersal abilities are lower and whose original population sizes were lower. Therefore, the risk of extinction due to fragmentation per se is not randomly distributed among species. If we wish to conserve biodiversity, we need to focus on the species that are most likely to suffer from the modification of the landscape, i.e. from fragmentation and area loss. That is, even though fragmentation increases diversity in SJL, it may cause changes in community structure that are not visible in the commonly used species diversity indices.

Thirdly, the turnover of species between patches is a result of local extinctions and balancing colonization. When the patches become smaller, the extinction rates increase due to population size related stochastic events. However, the smaller population sizes also mean that fewer individuals disperse. Therefore, the probability that a species that became locally extinct will be substituted by another species that colonize the patch is reduced. That is, over longer time spans, fragmentation per se will decrease diversity even in systems which currently seem to be positively affected by it.

A SPAR based theory for the affect of fragmentation per se on biodiversity

We developed a simple theory that may explain and predict the circumstances in which fragmentation per se will increase, decrease or not affect biodiversity. We start with the known power equation of the species area relationship:

$$\text{Eq.1- } S_A = cA^z$$

Where, **c** and **z** are the scaling coefficients, **S_A** is the number of species in the area **A** and **A** is the area of the focal patch. We define the fragmentation level – **FL** – as the number of equal-area fragmented patches (FP) to which the focal patch is divided to. **FL** is an integer starting from 1. The area of each of the fragmented patches is **A/FL**. Therefore, the expected number of species in each of the fragmented patches (**S_{FP}**) can be estimated from the SPAR (Eq.1) as:

Eq.2 - $S_{FP} = c (A/FL)^z = cA^z / FL^z$

The total number of species that are found in all the fragmented patches together (S_{FPTobs}) has a maximum and minimum values that can be estimated from the SPAR. The maximal number of species that can be found in all the fragmented patches together occurs when there is **no** overlap in species identity between patches. Therefore, the maximal number of species in all the fragmented patches equals:

Eq.3 - $S_{FPTmax} = FL \times cA^z / FL^z = FL^{1-z} cA^z$

Interestingly, the value of eq. 3 is also the total number of species incidences that are found in all the fragmented patches together. The minimal number of species occurs when there is a **complete** overlap in species identity between the fragmented patches. Therefore the minimal number of species equals the value of eq. 2 above.

The observed S_{FPT} can lie anywhere between the maximal and minimal values above. We define q_{obs} as the proportion of deviation from the maximal number of species, S_{FPTmax} (eq. 3). Therefore, the observed number of species in all the fragmented patches together (S_{FPTobs}) equals: $q_{obs} \times FL^{1-z} cA^z$. and:

Eq.4 - $S_{FPTmin} = cA^z / FL^z \leq q_{obs} \times FL^{1-z} cA^z \leq FL^{1-z} cA^z = S_{FPTmax}$

So, q_{obs} lies in the range: $1/FL \leq q \leq 1$. We define the threshold q (q_T) as the value of q_{obs} in which the total number of species in all the fragmented patches (S_{FPTobs} , eq.4) will equal the number of species in the focal patch (S_A , eq.1):

Eq.5 - $S_{FPTobs} = S_A$
 $q_T \times FL^{1-z} cA^z = cA^z$
 $q_T = 1/FL^{1-z} = FL^{z-1}$

Note, that the threshold q is independent of the area of the focal patch and of one of the scaling coefficient (c) of the SPAR. However, the threshold q is dependent upon the slope of the spar in the log-log space (z) and the fragmentation level (FL). Figure 3 illustrate the change in q_T for different values of z and for different fragmentation levels (FL). For a given z value, q_T decreases with FL , and for a given FL , q_T increases with z . When q_{obs} will be higher than the threshold q (q_T), the biodiversity in the set of fragmented patches will be higher than the biodiversity in the focal patch. When q_{obs} will be lower than the threshold q (q_T), the biodiversity in the set of fragmented patches will be lower than the biodiversity in the focal patch.

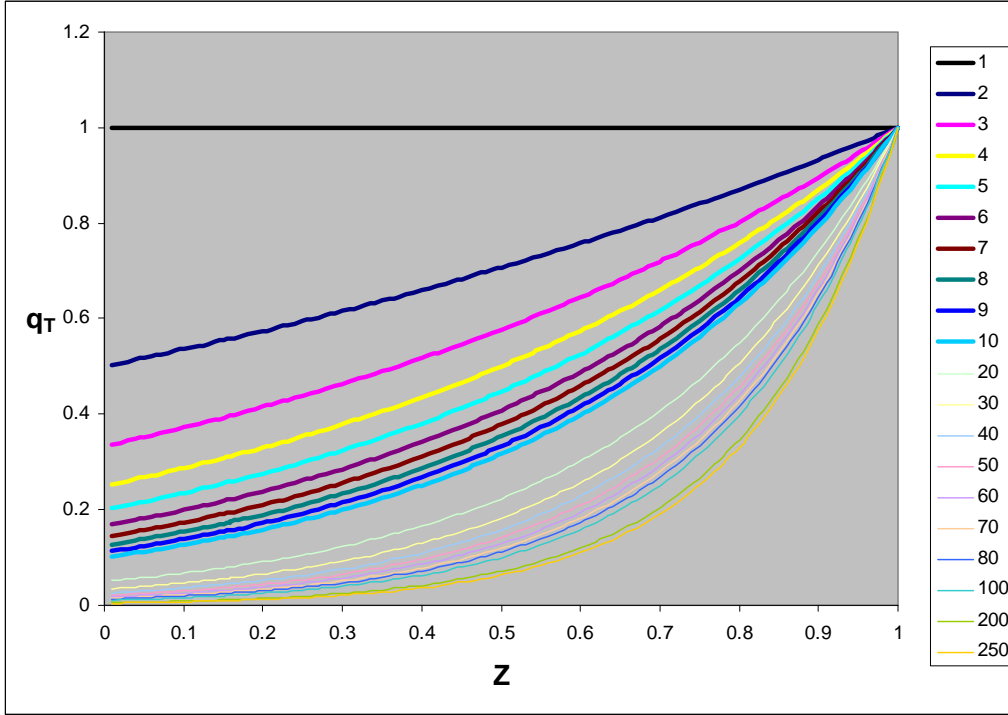


Figure 3: The change in threshold q with z (slope of the SPAR in a log-log space), for different fragmentation levels (FL). Values according to eq.5. Each series is for a different fragmentation level (1-250 patches). For a given z , threshold q decrease with FL and for a given FL, threshold q increase with z .

The observed value of q (q_{obs}) can be easily estimated from data as the ratio between the total number of species that are found on all the fragmented patches and the total number of incidences (occurrence of a species in a patch). However, a mathematically identical but a more informative representation comes from Incidence Frequency Curves (IFC). IFC summarize the distribution of occurrences between the fragmented patches. IFC are calculated from the species-patches matrix. Each species can occur in 1, 2, 3 ... FL patches. The number of patches in which a species occurs is his incidence value. IFC summarize the proportion of species that occur on 1 patch, 2 patches and so on until FL patches. The species to total incidence ratio (q_{obs}) can be calculated from the IFC according to:

$$\text{Eq. 6 - } q_{obs} = \sum_{i=1}^{FL} \frac{p_i \times (FL^{1-z} \times c \times A^z)}{i}$$

Where, p_i is the proportion of species that occurred on i patches, and the term within the parentheses is the total number of incidences (eq.3). The value of q_{obs} will change with a change in the IFC. When the IFC will be skewed toward incidences of $i=1$ (fig 4a) q_{obs} will be highest. When IFC will have a more uniform distribution, q_{obs} will have moderate (fig 4b). When q_{obs} will be skewed toward incidences of $i=FL$, q_{obs} will be lowest (fig 4c).

IFC are expected to change with patch area. When the patch is very small, a large proportion of the patch is edge habitat (the edge to core ratio is large). Most species in the edge area are species that thrive in the

matrix. Therefore, the overlap of species between patches will be high. That is, the IFC will be skewed toward **FL** and the q_{obs} will be relatively low.

When the patch becomes larger (but still relatively small), the edge to core ratio decreases, and the proportion of edge species in each patch decreases as well. Therefore, most of the species are species whose main habitat occurs in the natural area. The IFC is expected to exhibit a larger skew toward incidences of 1, for several reasons. Firstly, each patch has only a small proportion of the species pool. If species are randomly selected from the species pool, the probability that similar species will be found in many patches is reduced. Second, the population of all species becomes smaller, resulting with a high turnover of species in time (fast extinction rates). Since the populations of the more dominant species are also small, they also become locally extinct relatively fast. Therefore, competitive exclusions are rare and the community is not structured by hierarchical competitive dynamics, resulting with higher turnover of species between patches. At this stage the q_{obs} is expected to increase with patch area.

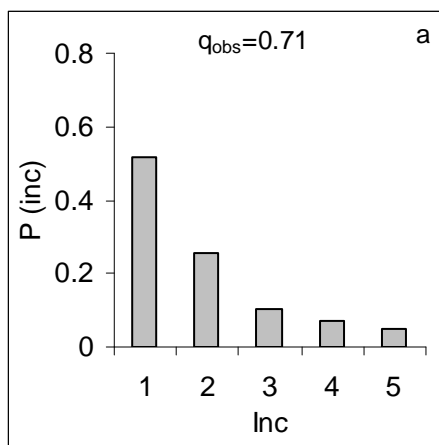
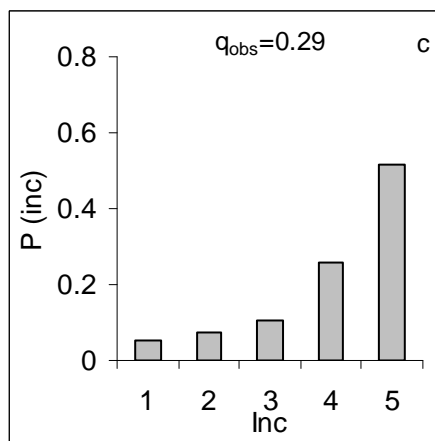
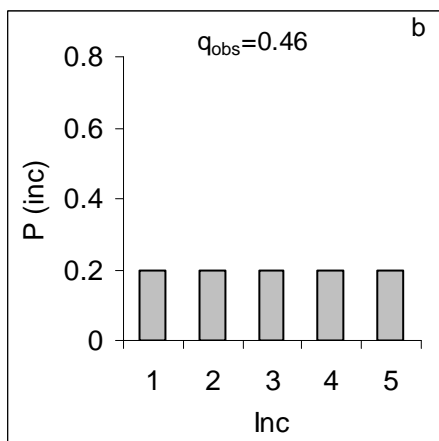


Figure 4: Examples of three different Incidence Frequency Curves for a fragmentation level of 5. Value on the abscissa is the number of patches in which a species was found. Value on the ordinate is the proportion of species found for each incidence value. **a)** – IFC skewed toward incidences of 1. **b)** – IFC with uniform distribution. **c)** – IFC skewed toward incidences of **FL** (5 in this example). q_{obs} values for each IFC are given.



When the patches further increase in area, the IFC is expected to shift again toward incidences of **FL** and the q_{obs} is expected to decrease with area. The proportion of species from the species pool in each patch

increases, and therefore the overlap between patches in species identity increases. In addition, populations of the dominant species become larger (i.e. stochastic extinction rate of the dominant species is reduced), resulting with a community that is more structured by hierarchical competitive dynamics.

Combining all the expected trends of IFC and q_{obs} with area, we expect that the q_{obs} will show a unimodal trend with patch area (See figure 5). Since for a given fragmentation level, the threshold q is independent of area (eq. 5), the q_{obs} can intercept the q_T in two points, represented by two areas, **Amin** and **Amax**. In the area below **Amin**, q_{obs} is lower than q_T and the species diversity in all the fragmented patches will be lower than the biodiversity in one focal patch (figure 5). In the range between **Amin** and **Amax**, the q_{obs} is larger than q_T , and the species diversity in the set of fragmented patches is expected to be higher than the biodiversity in a focal patch (figure 5). Finally, above **Amax**, q_{obs} is again lower than q_T and the species diversity in all the fragmented patches is again expected to be lower than the biodiversity in one focal patch (figure 5). The SPAR of the fragments is expected to have a concave shape around the SPAR of the focal patches in a log-log space. Interestingly, if the values of q_{obs} for different fragmentation levels are similar, the theory predicts that the range for which fragmentation per se will increase biodiversity (between **Amin** and **Amax**) is expected to increase, since for a given z value, q_T decreases with an increase in fragmentation level (figure 3).

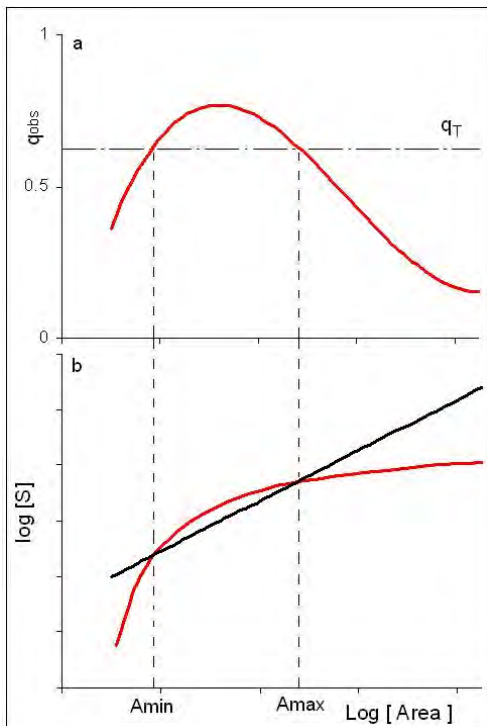


Figure 5: The change in (a) q_{obs} and (b) \log (species) with \log (area). The q_{obs} has a unimodal trend with \log (area) and crosses the threshold q (horizontal dashed line in a) in two points. The points have areas of **Amin** and **Amax**. Below **Amin**, q_{obs} is lower than q_T and the SPAR of the fragments (red line, b) lies below the SPAR of the focal patches (black line, b). Between **Amin** and **Amax**, q_{obs} is above q_T , and the SPAR of the fragments is above the SPAR of the focal patches. Above **Amax**, q_{obs} is again below q_T , and the SPAR of the fragments is below the SPAR of the focal patches.

To summarize, the results above indicate that for the spiders in SJL, fragmentation per se increases biodiversity. The theoretic model suggests a possible mechanism that may explain the results – a balance between patch area and turnover of species between patches. Indeed, some preliminary analysis reveals that for most of the combinations used, the q_{obs} is above the q_T . The model developed here may provide an applicable tool to assess the affect of fragmentation per se on biodiversity. This tool may be applied relatively easy from sampled data. It only requires the fragmentation level, the slope of the SPAR in log-log space (z), the number of species in a set of patches and the number of incidences in the same set of patches. Using only these four variables, researchers can estimate the possible affect of fragmentation per se on biodiversity- increase, decrease or not-affect biodiversity. Additional analyses that aim to explore some of the predictions of the model are currently underway. I again wish to thank the IALC Peace Fellowship for the opportunity to collaborate with Dr. Rosenzweig.

Acknowledgments

I would like to send my sincere gratitude to the International Arid Land consortium for the opportunity to work with Dr. Rosenzweig on the data-set I've sampled in my Master's thesis. I also wish to thank Dr. Rosenzweig and his wife Carole for the wonderful two weeks I spent in Tucson, Arizona. Special thanks are given to my advisor, Dr. Yaron Ziv, who encouraged me to apply for the IALC Peace Fellowship, guided me prior to my travel and gave important remarks once I've returned.

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