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## 1 INTRODUCTION

Process that maintains species diversity, species richness and species distribution are one of the central questions in ecology. There are dozens of theories proposed to explain distribution patterns of the species (e.g. Hutchison's hyper-volume concept (1957), Mc-Arthur 's Broken stick model, Janzen-Connel effects, Chesson's lottery model (1981), Connells intermediate disturbance hypothesis, and Hubbell's neutral theory (Hubbell, 2001)). Spatial distribution of tree species associated with several factors (e.g. habitat heterogeneity, dispersal limitation and tree interactions). Species composition is different with respect to high elevation areas, mid elevation areas, and low elevation. Limited dispersal ability of species delay competitive exclusion not allowing superior species to reach all the favorable sites. May be facilitation and competition of species determine species distribution of species. However, facilitation in tropical forest is rare. Competition is often found at small spatial scales. Many processes operate at different spatial scales. Detail analysis of spatial distribution can reveal processes that operate at different spatial scale (Condit *et al.* 2000; Wiegand and Moloney 2004; He and Legendre 2002; Seidler and Plotkin 2006; Wiegand *et al.* 2007; Shen *et al.* 2009). In this study attempt is made to

understand the spatial distribution of species using Clarke-Evans test, Ripley's K-function, L-function, and Pair-Correlation function.

## 2 METHODOLOGY

**Clarke-Evans Test:** Clark-Evans index may be the simplest spatial measurement, used to analyze the spatial distribution of species. It measures the mean distance to its  $n^{\text{th}}$  nearest neighbor. Observed  $n^{\text{th}}$  nearest neighbor distance is compared with expected distance under random displacement of species. Simulation with different distribution can be used for thorough understanding spatial arrangement from 1m to 100 meters. The Clark and Evans (1954) aggregation index in R is a crude measure of clustering or dispersion of a spatial pattern. It measures the mean  $n^{\text{th}}$  nearest neighbour distance in the pattern to that expected for a homogeneous Poisson point process.  $R > 1$  suggests dispersion, while  $R < 1$  indicates clustering (Baddeley, *et al.* 2015).

**Homogeneous Poisson Processes.:** In a homogenous Poisson process in which the

points are independently scattered and the intensity  $\lambda$  of the process is constant (Fig. 1a).

**Ripley's K-function:** Ripley's K function is widely used to examine spatial point patterns. Ripley K function is better than the Clarke-Evans test because it accounts spatial arrangement of all the individuals up to a certain distance (Dixon 2001). Here we used univariate Ripley's K-function. Ripley K function indicates average number of points within distance of a randomly chosen point (Fig. 1a). However, Ripley's K function is little bit difficult to interpret and L-function is also used.

**L-function:** It is a transformed form of the Ripley's K-function given by,

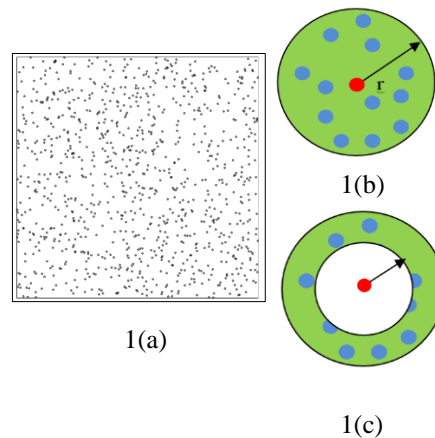
$$L_{\text{hom}}(r) = \sqrt{\frac{K_{\text{hom}}(r)}{\pi}}$$

Both of them suffer with memory effect (i.e. small scale aggregation or dispersion bring forward and mimic spatial clustering or dispersion at large spatial scales). We used pair-correlation function or O-ring statistic (Wiegand and Moloney 2004) or Omega function (Condit et al. 2002) which identifies spatial distribution at a given scale (Fig. 1c). Our null model is a homogeneous Poisson process. If observed distribution is above the homogenous Poisson process it shows clustering whereas below shows dispersion

**Data:** We used data from fully mapped 25-ha forest plot in *Sinharaja* Sri Lanka. In this forest all the species which are greater than or equal to 1cm at diameter of breast height were measured. Individuals were identified to species. Tree locations were given. In this forest plot nearly 200,000 individuals (approximately 220 species) were identified. In this analysis we exclude singleton species.

**Statistical data analysis:** All the analysis

was performed using statistical software R (R Core Team, 2017). We used the package "spatstat" in R to perform Clarke-Even's test, Ripley's K-function, L-function, and pair-correlation function (Baddeley and Turner, 2000).



**Figure 1:** (a) Homogeneous Poisson process, (b) Ripley's K-function (c) Pair-correlation function

### 3 RESULTS AND DISCUSSION

Following results were found. According to Clarke-Evan's test 179 species were clustered. Only few shows disperse pattern.

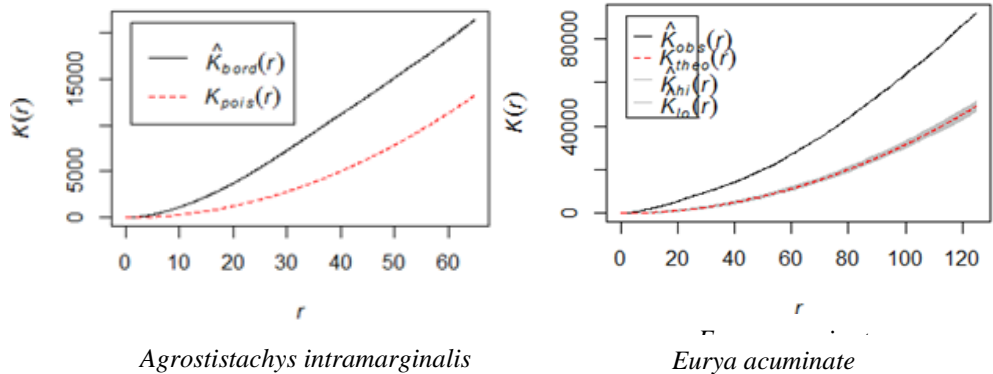
**Table 1.** Spatial structure of number species: Clarke-Evan's test

Spatial Pattern	No. of Species
Cluster	179
Random	31
Disperse	10

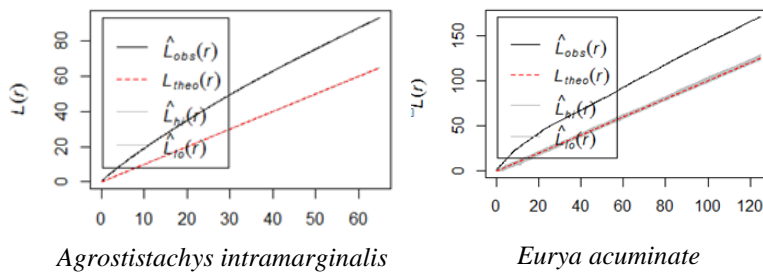
Ripley's K-function was performed for all the species. Few results were shown in Fig. 2. Most of them show clustering even up to 100 meters (red dotted line corresponds to the homogeneous Poisson process, gray area indicates the confidence bounds, and the black line indicates the observed pattern).

We have seen that for highly abundant species, simulation envelope becomes narrow. Pair Correlation function

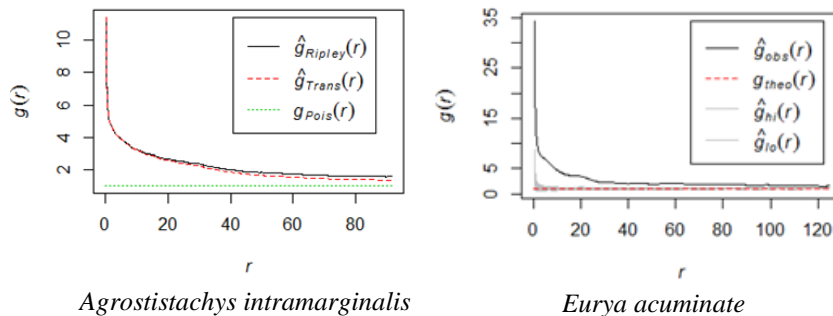
indicates drastic fall of clustering at large scale. It shows strong clustering at small scales (Fig. 4).



**Figure 1:** Ripley's K-function for some selected species in the 25-ha Sinharaja forest plot



**Figure 2:** L-function for some selected species in the 25-ha Sinharaja forest plot



**Figure 3:** Pair-correlation -function for some selected species in the 25-ha Sinharaja

## 4 CONCLUSIONS AND RECOMMENDATIONS

However, this study has some limitations. Our statistics are first order statistic and most of the clustering is due to species habitat association or dispersal limitation (e.g. see Condit *et al.*, 2002). It is necessary to remove the effect due to habitat association and dispersal limitation to see whether any tree-tree interaction is exist (second order statistic). For example Shen *et al.* (2009), Wang *et al.* (2011) and Lin *et al.* (2012) simulated Homogenous/Inhomogeneous Poisson process and Thomas Cluster process to calculate species richness. This method can be modified little and use in a Pair-Correlation function context or one can use neighborhood approach used by Wiegand *et al.* (2007) or Pattern reconstruction (Wiegand *et al.*, 2013) to remove interaction at medium to large scales. In future we hope to extend this study along the above mentioned path to disentangle the effect at different spatial scales.

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