Classifying Forest Stands According to Spatial Species Mingling

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Work report 493 2018
Master thesis in Forest Sciences 30 hp A2E
Forest Sciences – Masters Program

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ISSN: 1401–1204
ISRN: SLU–SRG–AR–493–SE

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Master thesis in Forest Sciences at the Department of Forest Resource Management, 30 credits, EX0835, A2E
Forest Sciences – Masters Program
Supervisor: Arne Pommerening, SLU, Dept. of Forest Resource Management, resource analysis
Examiner: Erik Wilhelmsson, SLU, Dept. of Forest Resource Management, forest planning

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Swedish University of Agricultural Sciences
Department of Forest Resource Management
Publication: Umeå
Publication Year: 2018

ISSN 1401–1204
ISRN SLU–SRG–AR–493–SE

Abstract

Legislature and international treaties increasingly underline the importance of biodiversity and sustainability, hence the need for accurate measurements, regarding the aforementioned concepts. Biodiversity is a comprehensive term, which can be very difficult/costly to measure directly. Therefore, surrogate measures can be used to quantify different aspects of biodiversity. An indicator closely linked to biodiversity in forest ecosystems is forest structure.

To quantify different aspects of forest structure metrices from the field of *point process statistics* can be used. In this study we introduce the new function $J(\bar{r})$ and evaluate its ability to describe species mingling in forest stands. This is done by incorporating data from 20 fully inventoried stands from different parts of the world. Producing curves from $J(\bar{r})$ and from the mark mingling function, $\nu(r)$ which is arguably the most similar established function. The curves are classified in groups based on characteristics. This is done separately for each function to be able to investigate how the groups differ between $J(\bar{r})$ and $\nu(r)$ and to see what new information $J(\bar{r})$ could provide, additional to $\nu(r)$.

This study suggests that the new function of $J(\bar{r})$ provides additional information to the mark mingling function, mostly related to $J(\bar{r})$ being based on the nearest neighbour (NN) concept and thus providing more information on local neighbourhoods. This research also points to the value of $J(\bar{r})$ being potentially more suitable to use on smaller plots, such as those commonly used in forest inventories.

Keywords: Quantitative ecology, forest biometrics, forest structure, biodiversity function, species mingling.

Sammanfattning

I lagstiftning och internationella fördrag betonas vikten av biodiversitet och hållbarhet, vilket medför ett behov av att kunna utföra korrekta mätningar och övervaka utvecklingen, relaterat till förenämnda begrepp. Biodiversitet är en övergripande term, som kan vara väldigt svår och dyr att mäta i sin helhet. Istället för att mäta biodiversitet direkt, kan man genomföra andra mätningar, vars resultat korrelerar med biologisk mångfald. I skogsekosystem är beståndsstrukturen ofta nära kopplad till biodiversitet. Genom att använda sig av mätetal från forskningsområdet *point process statistics* är det möjligt att kvantifiera olika aspekter av beståndsstruktur.

I denna studie introduceras $J(\bar{r})$, en ny funktion som är baserad på ett existerande mätetal. $J(\bar{r})$ testas angående hur väl funktionen kan beskriva trädindividers spatiala fördelning i bestånd, med avseende på arttillhörighet. För att åstadkomma detta används data från 20 totalinventerade bestånd, från olika delar av världen. Kurvor från bestånden produceras med den nya funktionen $J(\bar{r})$, och mark mingling-funktionen, $\nu(r)$, som antas vara den mest likartade av existerande funktioner. Kurvorna delas därefter in i grupper baserat på egenskaper, detta görs separat för de enskilda funktionerna, med syftet att undersöka hur de resulterade grupperna skiljer sig åt, för $J(\bar{r})$ och $\nu(r)$, och för att kunna avgöra vilken ny information som $J(\bar{r})$ kan tillföra.

Denna studie antyder att den nya funktionen $J(\bar{r})$ genererar delvis skiljaktig information jämfört med $\nu(r)$, framförallt relaterat till att $J(\bar{r})$ utgår från varje specifikt träd och jämför arttillhörighet med de närmaste träden i beståndet. $J(\bar{r})$ kan potentiellt vara lämpligare att använda på små provytor, vilka vanligen används i skogliga inventeringar.

Nyckelord: Kvantitativ ekologi, biodiversitetsfunktion, beståndsstruktur, skogliga mätetal.

Preface

I would like to take the opportunity and mention a few individuals, who have helped me with this study. First and foremost, I would like to thank my wise and hardworking supervisor, Professor Arne Pommerening, who except from being an excellent supervisor, has taught me plenty, partly through many intriguing discussions. Whenever I came knocking on the door to his office, he always dropped whatever work currently occupying his desk, regardless of his busy schedule, to provide me with insight and guide me in the right direction with the thesis. I would also like to thank Dr. Zhao Zhonghua and Dr. Hongxiang Wang, from the Research Institute of Forestry, CAF, Beijing, for providing data from China and helping me to interpret the results. Thanks to Jonas Bohlin for the picture on the title page. I would finally like to express gratitude to my friends and fellow students, for the support, and great atmosphere shared during the time we spent writing our individual theses.

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1 Introduction

1.1 Sustainability and policy

The term sustainability related to timber resources is old and implies meeting the needs of today without compromising the needs of the future (Sands, 2005). During the United Nations conference, in Rio 1992, the term sustainability in forestry was defined to include economic, social, ecological, cultural and spiritual values (DESA, 1992). The European Union's forest strategy, is as well focused on multiple uses of forest resources in a sustainable manner, where the forests are to be managed in a way that maintains among other things, its biodiversity, productivity and the potential to fulfil economical, ecological, social functions (European Commission, 2013). In Rio 1992, 150 countries signed the "Convention on Biological Diversity" (CBD), and Since then, more countries have signed. The Convention's three main goals are: (1) The conservation of biodiversity. (2) Sustainable use of the components of biodiversity and (3) sharing the benefits arising from the commercial and other utilization of genetic resources in a fair and equitable way (CBD Secretariat, 2000; United Nations, 1992). Legislature and international treaties do increasingly underline the importance of biodiversity and sustainability related to environmental, economic and social values. Ecosystem based management is required by the CBD, implying that the ecosystem is used for economic and social gains, while sustaining and enhancing the environmental state (Laurila-Pant *et al.*, 2015; CBD Secretariat, 2000; United Nations, 1992).

1.2 Complexity in measuring biodiversity

Biodiversity can be defined and measured in multiple ways. A widely used definition for biodiversity is : "The variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part: This includes diversity within species, between species and of ecosystems" (United Nations, 1992). This definition is included in policies and adopted by many countries, it is also used in the Convention on Biological Diversity (Mace *et al.*, 2012; United Nations, 1992). To be able to preserve biodiversity, it is important to quantify biodiversity. Biodiversity is a comprehensive term, which can be difficult/costly to measure directly. Therefore, surrogate measures are used to quantify different aspects of biodiversity (Gao *et al.*, 2014; Boutin *et al.*, 2009). A central aspect of biodiversity is the number of species or species richness. However, species richness is in itself not sufficient to reflect all the aspects of biodiversity and is difficult to measure objectively (Fleishman *et al.*, 2006).

For conservation and forest management it is important to include spatial and compositional attributes in the forest to be able to represent important features such as function and resilience (Mace *et al.*, 2012; Fleishman *et al.*, 2006). An indicator closely linked to biodiversity in forest ecosystems is forest structure (Boutin *et al.*, 2009; Lindenmayer *et al.*, 2000). Information regarding forest structure is of fundamental importance to forest management and forest planning. The same measurements which are important in silviculture can also provide useful information related to ecology and conservation, e.g. by indicating whether a certain forest is of any value as habitat for certain organisms (Kimmins, 2004).

1.3 Defining forest structure and relevant indices

Forest structure is a combination of the spatial dispersal of tree locations, spatial mingling of tree species and spatial variation in tree dimensions, both horizontally and vertically (Aguirre *et al.*, 2003; Pommerening, 2002). Forests with dissimilar structure can have different traits in terms of economy, ecology and social values. Indices and functions describing different types of forest structure can show the existing structure in relation to some baseline structure, which is often connected to the concept of spatial randomness (Illian *et al.*, 2008).

There are many indices and functions from the field of point process statistics, which can be used to quantify forest structure. One group within these quantities are based on the nearest-neighbour (NN) concept, comparing a given tree with the closest neighbouring trees. Some of the indices only process and generate information regarding tree locations, for example, *the aggregation index* (Clark & Evans, 1954) and *the uniform angle/contagion index* (Gadow *et al.*, 1998). There are also indices that include, not only the locations, but also additional tree attributes, generally referred to as "marks". A mark is a qualitative or quantitative attribute connected to a specific tree, for example; species or diameter (Pommerening *et al.*, 2011; Illian *et al.*, 2008). An example of such an index is the mingling index.

The mingling index ($M_i^{(k)}$) is a single-tree mingling index derived from Pielou's coefficient of segregation (Gadow, 1993; Pielou, 1977). The index gives the proportion of neighbouring trees that are of a species different to the subject tree among the k nearest neighbours. When investigating mingling in a whole forest stand, all M_i values are added up and then divided by the number of trees (Pommerening, 2002). Usually a correction for spatial edge bias applies, such as the NN1 edge correction from (Pommerening & Stoyan, 2006). From these calculations the population mingling index $\bar{M}$ is obtained, belonging to a group of indices often referred to as neighbour summary statistics (NNSS). $M_i^{(k)}$ is defined as

$$M_i^{(k)} = \frac{1}{k}\sum_{j=1}^{k} \mathbf{1}\left(\text{species}_i \neq \text{species}_j\right) \tag{1}$$

When calculating $M_i^{(k)}$, the number of nearest neighbours k is usually set to 3 or 4 denoting the same fixed number of neighbouring trees used in the calculations for every tree. According to Lewandowski and Pommerening (1997), expected mingling (implying independent species marks), EM, is independent of the number of neighbours, k, and can be calculated as

$$\mathbf{E}M = \sum_{i=1}^{s} \frac{N_i\left(N - N_i\right)}{N\left(N-1\right)} \tag{2}$$

with s, the number of species, N, the total number of trees in the observation window and N_i, the number of trees of species i.

In analogy to Pielou's segregation index, $\bar{M}^{(k)}$ and EM can be combined in an index J (Eq. 3), expressing the relationship between observed species mingling and completely random species mingling. Pommerening and Uria-Diez (2017) refer to the index as species segregation index.

$$J = 1 - \frac{\overline{M}^{(k)}}{\mathbf{E}M} \tag{3}$$

Consequently, $J = 0$, if the species are independently or randomly dispersed. $J = 1$, if the nearest neighbours and an observed tree always share the same species (attraction of the same species). If all neighbours always have a neighbour of a different species from that of a tree under study, $J = -1$ (attraction of different species or segregation) (Pommerening & Uria-Diez, 2017).

Further techniques of quantifying aspects of forest structure include so-called second-order characteristics. These are functions that incorporate the distance variable r, to calculate correlations between all pairs of trees that occur around distance r. These can be useful when data from sufficiently large observation windows are available with at least 150 trees (Pommerening *et al.*, 2011; Pommerening & Stoyan, 2006)., since they can show point interactions occurring on at longer distances. An example of a second-order function that describes species mingling is the *mark mingling function*, $\nu(r)$, (Pommerening *et al.*, 2011; Illian *et al.*, 2008) (will be described in detail in eq. 6 in chapter 2.2.1), which is a variation of the *mark correlation function* (see for example Illian *et al.* (2008)). These indices produce information on how marks interact, if they are completely independent, inhibit or attract each other (Pommerening, 2002).

1.4 Objectives

The objective of this study is to investigate what new information the $J(\bar{r})$ function provides on the mingling patterns in forest stands as opposed to existing second-order functions, specifically in relation to the *mark mingling function* $\nu(r)$.

2 Material and methods

2.1 Data

Detailed data from 20 fully mapped forest stands have been used to test the performance of the two competitive functions. Most of the included forest stands are located in different regions in China and Europe. There is also one stand situated in Mexico and another in South Africa. The combination of forest data, provides a diverse group concerning climatic zones and multiple other traits, which is ideal for exploring and testing the new function $J(\bar{r})$. Some of the forest sites included in this project exhibited a complex forest structure and are challenges to the functions included in this study. This makes the data very suitable (Hui & Pommerening, 2014). Data from the Chinese stands included in this study have been published in other papers before, for example in Yuanfa *et al.* (2012), but not in the context of this study. Stands from outside of China were included as contrasts and known references and have also been published in other studies before (see for example Pommerening *et al.* (2011) and Pommerening and Uria-Diez (2017)).

As part of the surveying work, every tree in the forest stand has been given a unique number for identification. Relevant information, such as tree species, stem diameter at 1.3 meters *(dbh)* and stem-centre coordinates were gathered during fieldwork. For a better understanding of the individual stands and their species mingling patterns, each stand map was plotted for visualization (Figures 1-5). The circular symbols denote tree locations and their diameter were scaled according to stem diameter. The different colours represent tree species. Values for stems ha^{-1}, stand basal area (Figure 6) and species richness (Figure 7) were plotted to make it easier to compare the stands to each other regarding the same variables.

For the purpose of this study, a letter combination of one, two or three letters have been assigned to the stands for easier identification. The letter combination is related to each stand's origin. In the case where there are multiple stands from the same region, each individual stand was given a further letter to allow identification of stands within each region. For example, if there were four stands within a region, each stand was given a letter in consecutive order, e.g. a, b, c and d.

2.1.1 Chinese stands

2.1.1.1 Xiaolongshan, Gansu, China

The Xiaolongshan Forest is located in the warm temperate-subtropical transitional zone of the north-facing slopes of the Qinling Mountain Range. Two plots from the Xiaolongshan Forest have been used. The first plot is referred to as XSa, this stand has to a large extent been shaped by natural processes. However, management has been performed to diversify stand structure. The forest of XSa is dominated by *Pinus tabulaeformis* plantations mixed with naturally regenerated *Quercus acuteserrata*, *Tilia paucicostata* Maxim., *Crataegus kansuensis* Wilson. and *Pyrus xerophila* Yü.

The second plot is referred to as XSb. This forest has been left unmanaged and is only shaped by natural processes. XSb is a mixed pine-oak forest, mainly composed of *Quercus aliena var. acuteserrata* Maxim., *Quercus liaotungensis* Koidz., *Pinus armandii* Franch., *Pinus tabulaeformis Carr.*, *Pobulus davidiana* Dode., *Rhus verniciflus* Stokes. and *Kalopanax septemlobus* Koidz.

Measures characterising the plots in the Xiaolongshan Forest can be found in Table 1, plots are denoted by XSa and XSb.

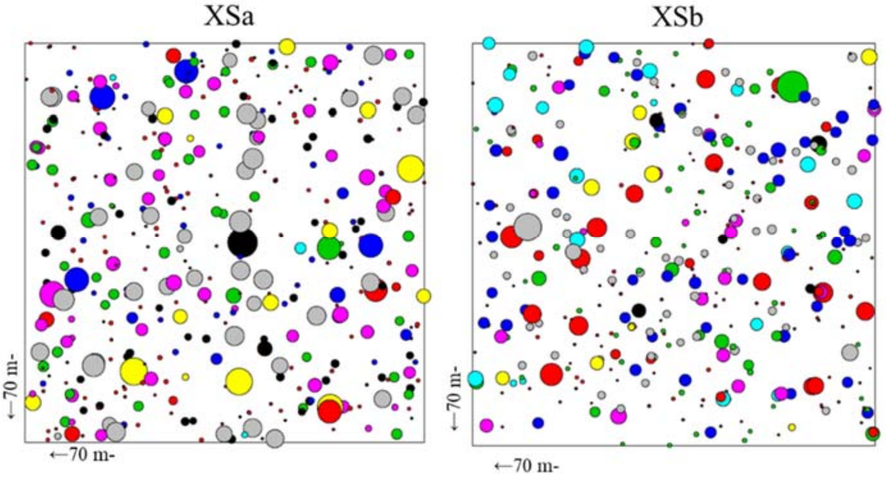

Figure 1. *Plotted stands from Xiaolongshan. The circles represent tree locations and their diameter were scaled according to stem diameter. The different colours represent tree species.*

2.1.1.2 Jiulongshan, Beijing, China

The Jiulongshan Forest is located in the western suburbs of Beijing. This is a warm-temperate broadleaved deciduous forest with planted pine species as the main tree species. One stand is dominated by planted *Platycladus orientalis* (*L.*) *Franco.* and is mixed with some naturally regenerated species such as *Quercus variabilis* Blume., *Broussonetia papyrifera* (L.) Vent., *Ailanthus altissima* (Mill.) Swingle, *Prunus davidiana* Carr. and *Gleditsia sinensis* Lam. The other is a mixed forest stand planted with *Pinus tabuliformis* and *Larix gmelinii* (Rupr.) Rupr var. *principis-rupprechtii* as the main species.

Detailed information on two plots from Jiulongshan can be found in Table 1. In this thesis, I refer to these stands as JSa and JSb.

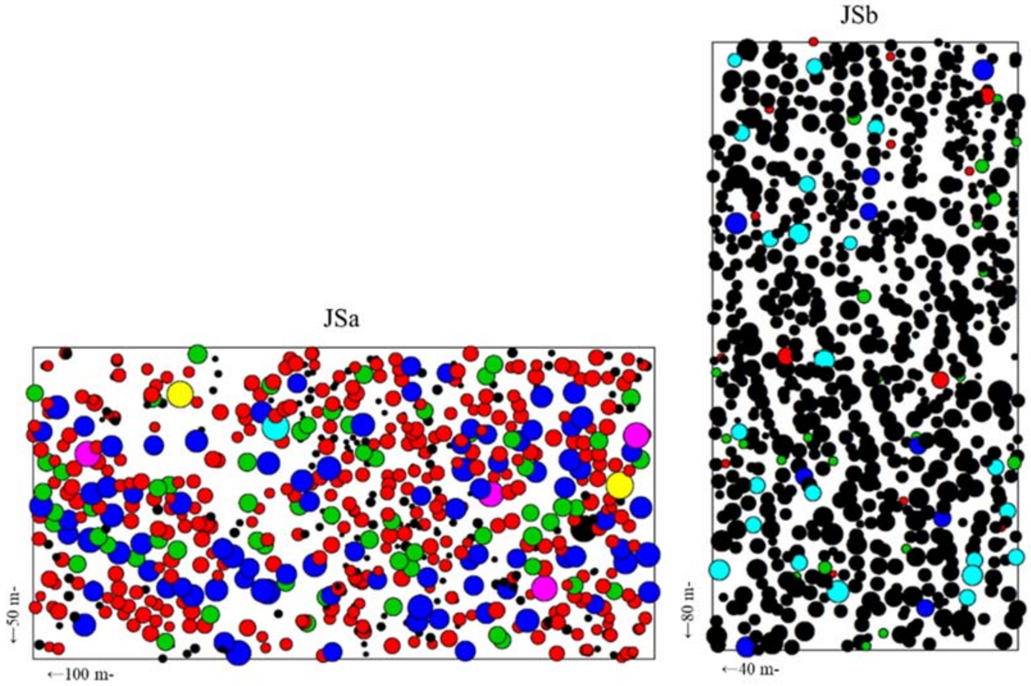

Figure 2. *Plotted stands from Jiulongshan. The circles represent tree locations and their diameter were scaled according to stem diameter. The different colours represent tree species.*

2.1.1.3 Jiaohe, Jilin, China

The vegetation type in the Jiaohe forest region is that of a typical temperate mixed forest, including coniferous and broad-leaved trees. The main tree species are *Fraxinus mandshurica* Rupr., *Pinus koraiensis* Sieb et Zucc., *Juglans mandshurica* Maxim., *Carpinus cordata* Bl. and *Abies holophylla* Maxim. Historically this region belonged to the trial forest farm of Jilin Forestry College and forest management ceased 60 years ago. The current tree distribution patterns can be regarded as the result of natural processes. The forest plots in this region are highly mixed and have a tightly closed canopy with around 20 tree species.

Six plots from Jiaohe are included. The plots were selected to reflect the main characteristics of natural Korean pine broadleaved forests. Relevant variables for each stand are shown in Table 1. The six individual plots from Jiaohe have been assigned to the following letter combinations for identification: Ja, Jb, Jc, Jd, Je and Jf.

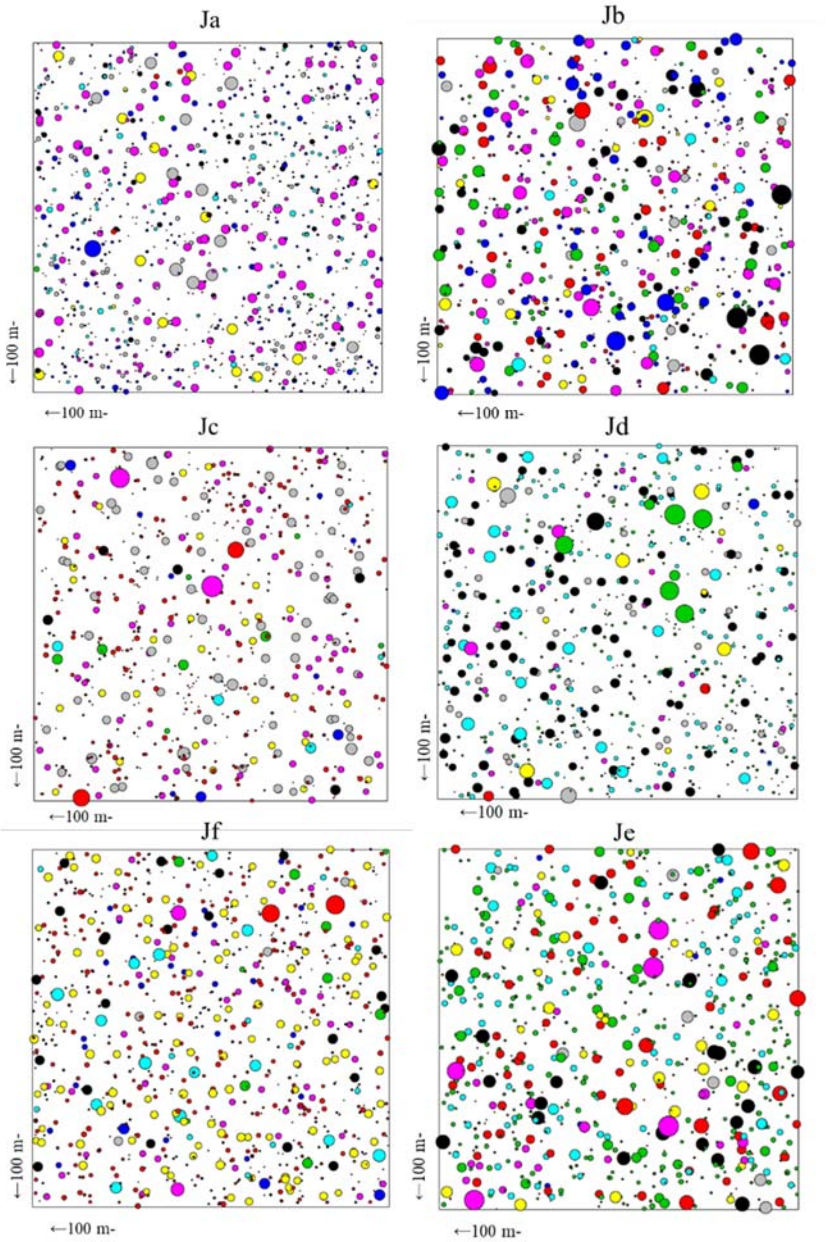

Figure 3. *Plotted stands from Jiaohe. The circles represent tree locations and their diameter were scaled according to stem diameter. The different colours represent tree species.*

2.1.2 Stands from outside China

The following descriptions for stands located outside China were modified from Pommerening and Uria-Diez (2017). Relevant quantitative information from the stands from outside China for these forest stands is presented in Table 1. These stands have been assigned to abbreviations presented here in the order of stand descriptions below: M, W, Bi, B, K, R, P, S, Z and D.

Manderscheid is a temperate, deciduous forest located in the West German state Rhineland-Palatinate. Tree species within the plot are sessile oak (*Quercus petraea* Matt.) and beech (*Fagus sylvatica* L.). This stand has been managed to produce high quality oak. Beech is a by-product whilst improving the quality of oak timber (Pommerening & Uria-Diez, 2017). The species seem randomly dispersed in relation to each other.

The Walsdorf data are from a management demonstration site in the German state of Rhineland-Palatinate. The two main species favoured in forest management are beech (*Fagus sylvatica* L.) and Norway spruce (*Picea abies* (L.) KARST.) (Pommerening & Uria-Diez, 2017; Gadow *et al.*, 2012).

The Bialowieza forest stretches from eastern Poland across the border to western Belorussia. Data are taken from outside the strict reserve of the Polish part of Bialowieza National Park. The overstorey consists of pedunculate oak (*Quercus robur* L.) mingled with (*Pinus sylvestris* L.) and an understorey of Norway spruce (*Picea abies* (L.) KARST.), hornbeam (*Carpinus betulus* L.) and silver birch (*Betula pendula* ROTH) (Pommerening & Uria-Diez, 2017). The stand is managed according to the principles of continuous cover forestry (Pommerening & Murphy, 2004). The species appear to occur in clusters.

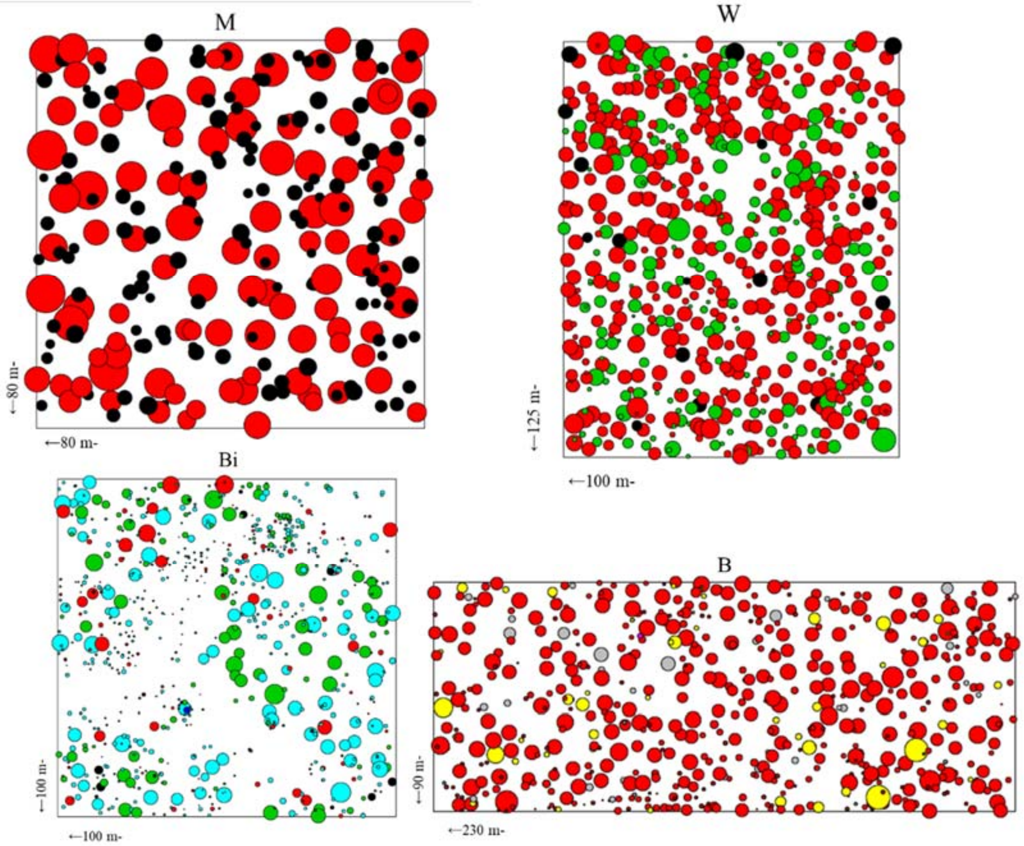

Figure 4. *Plotted stands from Manderscheid, Walsdorf, Bialowieza and Bovenden. The circles represent tree locations and their diameter were scaled according to stem diameter. The different colours represent tree species.*

Bovenden is located in the German state of Lower Saxony, close to the city of Göttingen in the Göttinger Wald. This stand is dominated by beech (*Fagus sylvatica* L.). Other species include ash (*Fraxinus excelsior* L.) and sycamore (*Acer pseudoplatanus* L.). The stand is managed with the goal of producing high quality timber. Beech is very dominant.

In South Africa, located in the in the Afromantane research forest, within the Diepwalle State Forest is the Knysna plot. Named after the nearby coastal town of Knysna. The plot has not been managed since 1954. Three of the most common species include ironwood (*Olea capensis* L. subsp. *macrocarpa*), Kamassi (*Gonioma kamassi* E. MEY.) and real yellowwood (*Podocarpus latifolius* (THUNB.) R. BR. ex MIRB.).

The Rosalia plot is a part of the experimental forest of the University of Natural Resources and Life Sciences, Vienna. Located in the mountain ridge of Rosalia on the border of two Austrian states, Lower Austria and Burgenland. The plot is dominated by beech (*Fagus sylvatica* L.) and Norway spruce (*Picea abies* (L.) KARST.). The management follows the principles of continuous cover forestry (Pommerening & Murphy, 2004).

The stand Pen yr Allt Ganol in Wales (UK) is situated in Gwydyr Forest within in the Snowdonia National Park. The stand is mature with an overstorey of Scots pine (*Pinus sylvestris* L.) and Sitka spruce (*Picea sitchensis* (BONG.) CARR.). There is a well-developed understorey containing mostly broadleaves of native species and birch (*Betula* ssp.). Forest management stopped a few decades ago.

The Södderich data originate from a stand in the Södderich Forest close to the city of Göttingen, Germany. Södderich is a part of Göttinger Wald. The forest stand is dominated by three tree species, beech (*Fagus sylvatica* L.), ash (*Fraxinus excelsior* L.) and sycamore (*Acer* pseudoplatanus L.). As in Bovenden, forest management is aimed at favouring ash and sycamore (so-called noble hardwoods because they fetch higher timber prices than beech).

Zarand, a research plot located in the Western Carpathians of Romania belongs to the forest reserve of Runcu-Grosi. The site remained to a large extent unaffected by human activities and consists of oak (*Quercus petraea* MATT.) and beech (*Fagus sylvatica* L.).

The forest region of Durango State is located in the northern part of Mexico. The plot is referred to as Durango in this study and can be found in the high range of the Sierra Madre Occidental. It is managed by the local community, mainly performing selective cuttings, generating an income important for the region. The most frequent species are *Quercus sideroxyla* BONPL., *Pinus durangensis* MARTÍNEZ, Arbutus spp. and *Quercus crassifolia* BONPL.

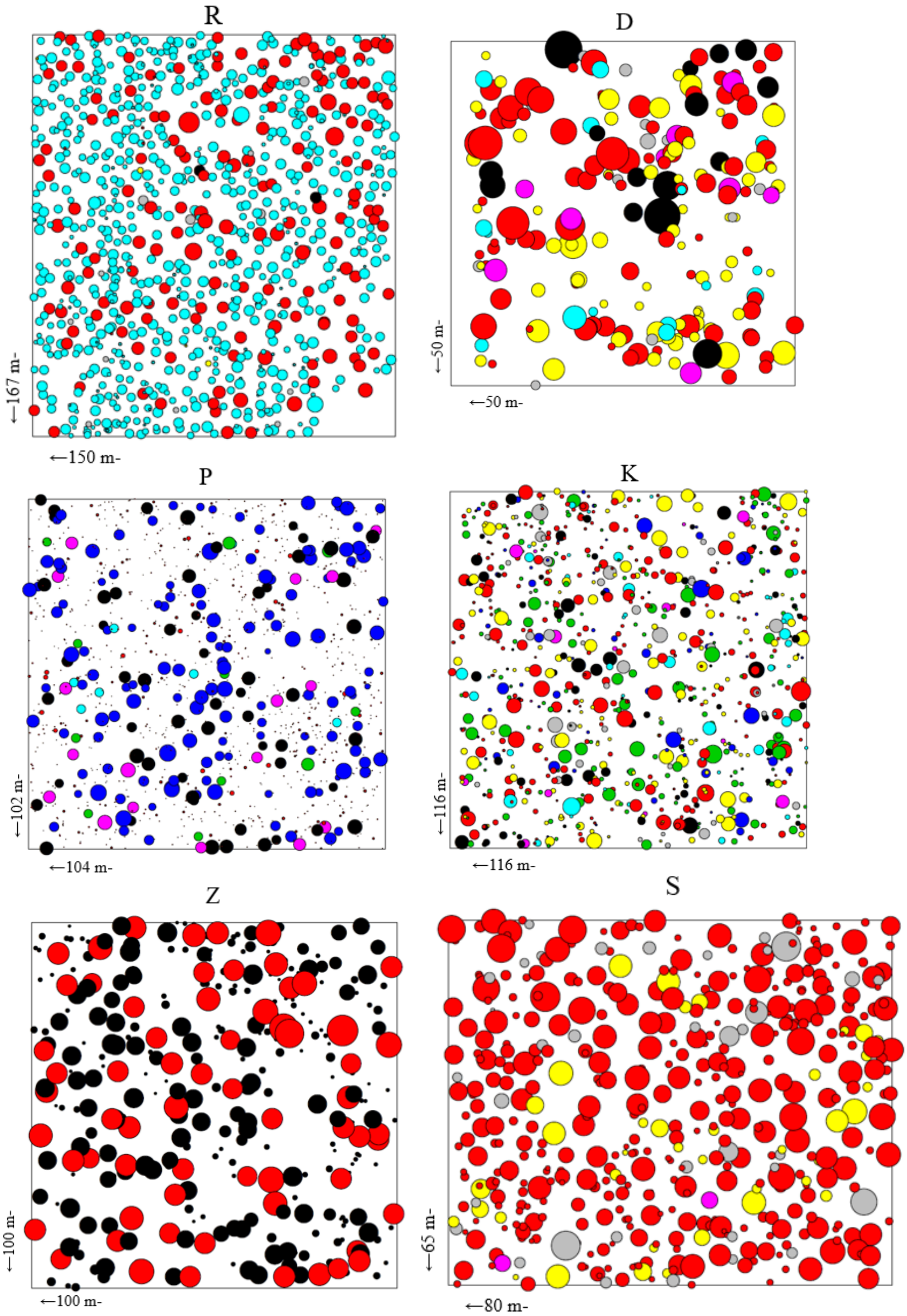

Figure 5. *Plotted stands from Knysna, Rosalia, Pen yr Allt Ganol, Södderich, Zarand and Durango. The circles represent tree locations and their diameter were scaled according to stem diameter. The different colours represent tree species.*

Table 1. *Key information for each of the forest stands to show plot characteristics.*

Forest stand	Number of species	Stems ha^{-1} (most abundant species)	Stand basal area (most abundant species)	Mean dbh [cm]	Mingling index $\bar{M}^{(4)}$	Species segregation index *J*(*4*)
Manderscheid (M)	2	381.3 (254.7, 126.6)	29 (11.6, 17.1)	28	0.428	0.039
Walsdorf (W)	3	503.0 (346.9, 143.4, 12.7)	35 (18.9, 15.1, 1.0)	28	0.231	0.479
Bialowieza (Bi)	5	764.0 (439.0, 219.0, 85.0, 17.0, 4.0)	35 (16.1, 3.2, 14.6, 0.1, 0.9)	19	0.463	0.196
Bovenden (Bo)	5	293.4 (263.2, 17.5 11.2, 1.0, 0.5)	29 (22.5, 4.6, 2.1, 0.1, 0.01)	32	0.216	-0.134
Xiaolongshan (XSa)	33	861.2 (216.3, 130.6, 93.9, 81.6, 73.5)	28 (13.9, 1.0, 1.8, 4.6, 0.3)	16	0.805	0.096
Xiaolongshan (XSb)	35	736.7 (163.3, 144.9, 73.5, 67.3, 63.3)	25 (8.5, 2.7, 4.0, 1.8, 0.8)	17	0.777	0.140
Jiulongshan (JSa)	13	1312.4 (390.2, 359.2, 330.0, 124.2 58.2)	25 (11.0, 7.7, 3.1, 1.5, 1.3)	14	0.470	0.454
Jiulongshan (JSb)	8	2331.3 (2034.4, 140.6, 59.4, 53.1, 25.0)	20 (18.6, 0.8, 0.5, 0.2, 0.1)	10	0.196	0.162
Jiaohe (Ja)	20	1185.0 (297.0, 228.0, 116.0, 93.0, 70.0)	31 (2.4, 4.7, 1.8, 4.3, 2.6)	15	0.777	0.107
Jiaohe (Jb)	19	666.0 (134.0, 121.0, 98.0, 95.0, 47.0)	30 (3.9, 8.6, 1.1, 1.0, 2.7)	18	0.826	0.076
Jiaohe (Jc)	22	749.0 (149.0, 112.0, 105.0, 88.0, 67.0)	28 (1.8, 1.4, 3.6, 6.0, 3.4)	18	0.770	0.133

Jiaohe (Jd)	19	815.0 (136.0, 107.0, 99.0, 84.0, 82.0)	28 (7.8, 0.7, 1.9, 2.4, 1.6)	16	0.803	0.107
Jiaohe (Je)	22	826.0 (147.0, 122.0, 118.0, 103.0 67.0)	29 (2.5, 2.5, 8.0, 2.5, 4.6)	18	0.838	0.061
Jiaohe (Jf)	18	968.0 (162.0, 154.0, 146.0, 134.0 125.0)	29 (2.5, 2.0, 7.5, 7.3, 2.5)	16	0.804	0.084
Zarand (Z)	2	354.5 (209.1, 145.5)	43 (36.9, 5.7)	33	0.448	0.145
Rosalia (R)	7	359.4 (178.3, 171.1, 4.4, 2.8, 2.4)	36 (20.8, 14.4, 0.4, 0.2, 0.2)	34	0.452	0.116
Södderich (S)	7	899.7 (703.0, 111.0, 77.9, 5.8, 1.9)	25 (16.0, 5.1, 3.0, 0.5, 0.4)	17	0.306	0.286
Pen yr Allt Ganol (P)	11	1121.8 (281.9, 278.1, 243.2, 102.8 80.1)	34 (12.1, 8.8, 1.1, 0.7, 0.3)	12	0.578	0.039
Knysna (K)	20	593.0 (165.7, 114.4, 92.9, 52.0, 32.0)	33 (16.0, 7.0, 2.1, 1.5, 1.3)	22	0.828	0.078
Durango (D)	12	844.0 (208.0, 192.0, 164.0, 116.0, 48.0)	21 (5.3, 5.1, 2.9, 2.9, 1.6)	16	0.737	0.192

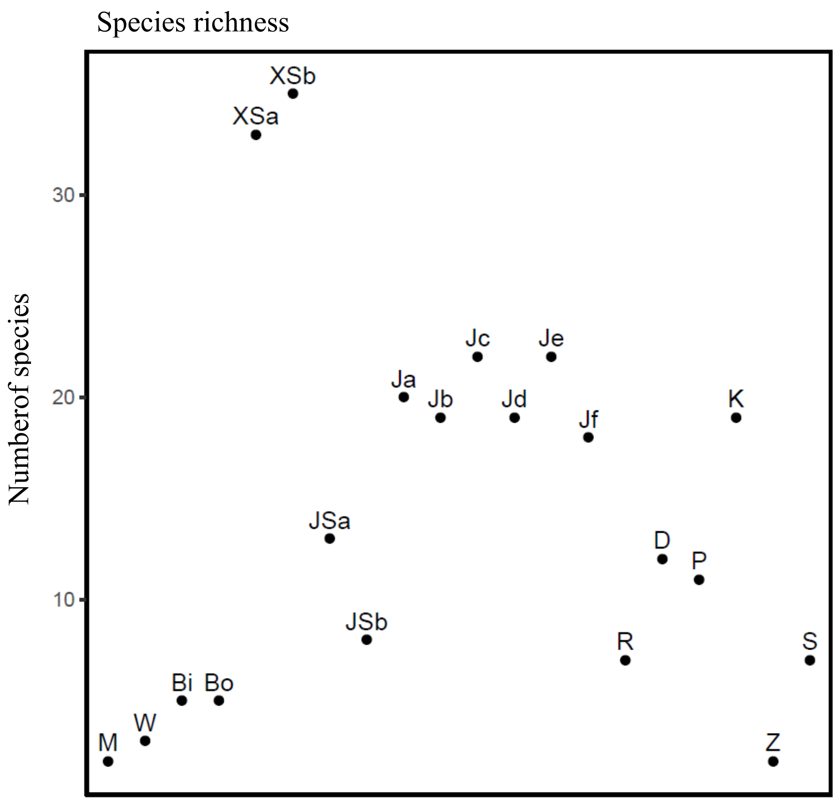

Figure 6. *Number of species present in the individual stands.*

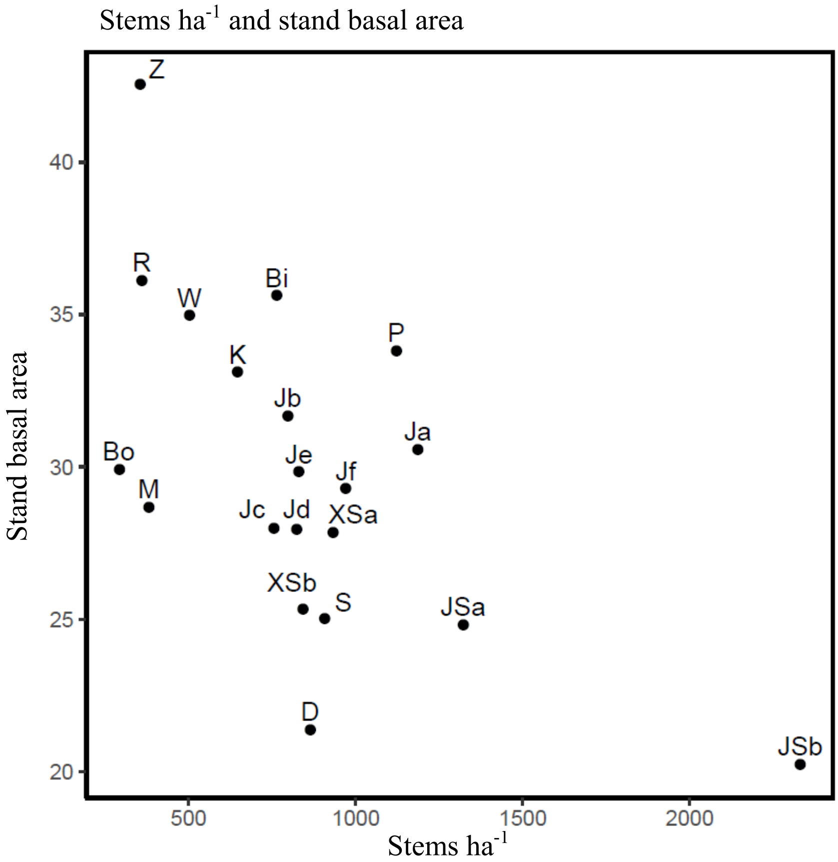

Figure 7. *Stand basal area plotted against the number of stems per hectare, each stand is represented by the respective stand id.*

2.2 Methods

As previously described, $\bar{M}$ can be calculated once you have the single tree index $M_i^{(k)}$ for all trees in a stand. By doing so the single tree indices have been aggregated to an index describing forest structure at stand level. More information can potentially be gained by transforming stand-level index $\bar{M}^{(k)}$ to a continuous function dependent on k, i.e. $\bar{M}(k)$. However, it is more informative to form this function based on J, to create the function $J(k)$ (Eq.4). Similar attempts have been made, estimating mingling distributions with continuous functions, see for example Pommerening *et al.* (2011) and Hui and Pommerening (2014).

$$\mathrm{J}(k) = 1 - \frac{\bar{M}^{(k)}}{EM} \tag{4}$$

The continuous function $J(k)$ can be standardised for easing comparisons between different forest stands. For each k, there is a mean distance $\bar{r}$ in each stand group of k nearest neighbours, which allows the estimation of the continuous function $J(\bar{r})$ (Figure 8).

$$\mathrm{J}(\bar{r}) = 1 - \frac{\bar{M}^{(k)}(r)}{EM} \tag{5}$$

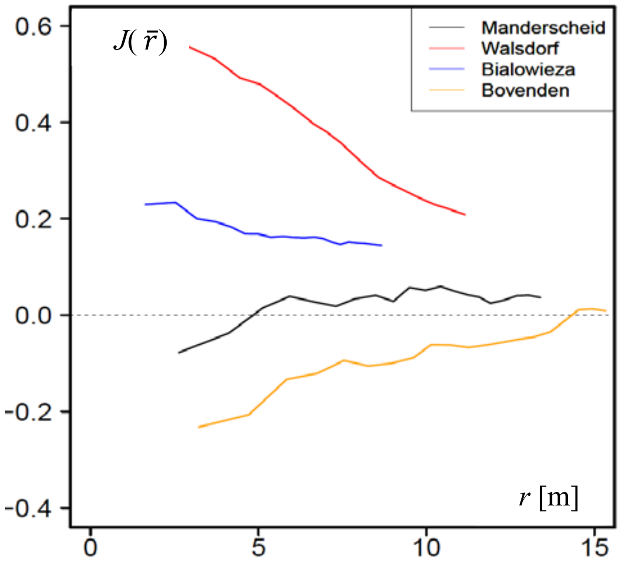

Figure 8. *Continuous function $J(\bar{r})$ applied to a selection four quite different forest stands. In Walsdorf and Bialowieza, the interspecies relationship exhibits a strong tendency towards species segregation. In Manderscheid, the trees show almost a random dispersal of species, whilst in Bovenden, the tree species are attracted to each other.*

For $J(\bar{r})$, stands show characteristics of intra-species attraction if $J(\bar{r})$ is positive. Negative values for $J(\bar{r})$ is evidence of the opposite, i.e. interspecies attraction occurs within the stand. These characteristics of intra- vs interspecies attraction is relative to the completely random spatial dispersal of species given the species abundances of a particular forest. Curves further away from zero are increasingly unlikely to have independent species marks. The values for $J(\bar{r})$ generally approach zero as k and $\bar{r}$ increase, but they do this in different ways, i.e. there are average slopes involved which characterise each forest stand additionally. In Figure 1, four stands are included providing examples of $J(\bar{r})$ curves with dissimilar characteristics. Information on the stands in terms of species mingling can be found in different aspects of a $J(\bar{r})$ curve. Traits for each curve, such as linearity, slope, intercept, length might provide useful information about the stands.

For the purpose of this study the number of nearest neighbours k was set to include all integer values for k between 1-10. Correction for spatial edge bias was made for the $J(\bar{r})$ curves with the flexible NN1 buffer method (Pommerening & Stoyan, 2006). The edge bias correction exclude trees from the calculations where the k nearest neighbours are further away from the subject tree than the edge of the study sites (Pommerening *et al.*, 2011).

To obtain the variables of average slope and intercept we approximated the curves with a linear equation (Andrilli & Hecker, 2010), running through the first and the final values for each curve. Average slope is the same as the gradient of the straight line. Intercept is the value of the linear equation where it intersects the y-axis.

Among the established second-order characteristics, the mark mingling function, defined in Eq. 6 (Pommerening *et al.*, 2011) is arguable closest in concept to $J(\bar{r})$ (Figure 9). x_1 and x_2 represent individual points (trees) for which $m(\cdot)$ are their respective marks (species). W represents the observation window and k_h stands for the Epanechnikov kernel function. $A(W_{x_1} \cap W_{x_2})$ is the area of intersection of W_{x_1} and W_{x_2}, see Illian et al. (2008, p. 481f. and p. 188). The test function t included in the mark mingling function (Eq. 7) is very similar to the mingling index (Eq. 1), which $J(\bar{r})$ is based upon. Mark mingling curves have been produced for the stands included in this study and compared to the performance of the $J(\bar{r})$ curves.

$$\hat{\nu}(r) = \frac{1}{\mathbf{E}M} \sum\nolimits^{\neq}_{x_1, x_2 \in W} \frac{\mathbf{1}(m(x_1) \neq m(x_2))\, k_h(\|x_1 - x_2\| - r)}{2\pi r A(W_{x_1} \cap W_{x_2})} \tag{6}$$

$$t(m_1, m_2) = 1(m_1 \neq m_2) \tag{7}$$

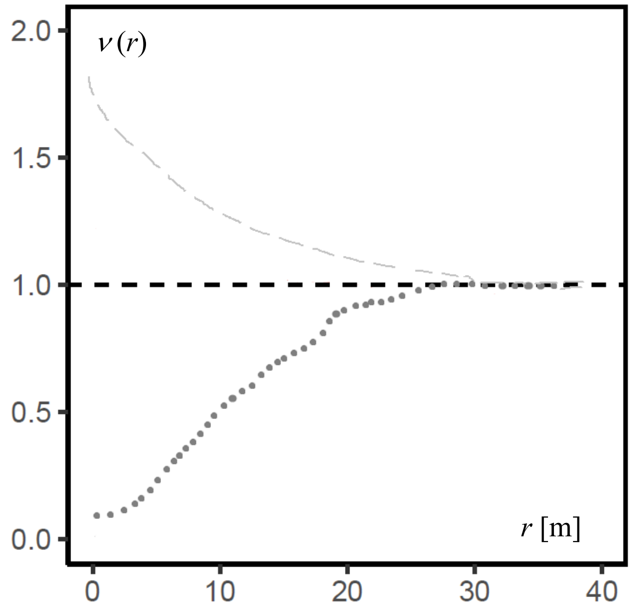

Figure 9. *Schematic example (modified figure from Pommerening et al. (2011)) of two possible outputs from the mark mingling function. The thin, dashed curve indicates interspecies attraction, whilst the dotted curve represents intraspecies attraction. At r equal to circa 30 the interacting range have reached its maximum extent for both curves and beyond this point species are randomly distributed (Pommerening et al., 2011).*

2.2.2 Cluster analysis

A cluster analysis was performed for both functions in this project, as described in Illian *et al.* (2008). The classification of forest stands was done according to spatial species mingling as a strategy for evaluating $J(\bar{r})$: The better $J(\bar{r})$ classifies forest stands in terms of species mingling in the cluster analysis compared to the mark mingling function, the more informative $J(\bar{r})$ is.

The general intention of a cluster analysis is to bring out hidden features in the data and assign objects to groups based on similarities. Hierarchical methods initially cluster individual objects into lower level groups. The lower level groups are then combined to form clusters of a higher ranking (Borcard *et al.*, 2018). When performing a cluster analysis in this study, the curves act as the objects and are combined at multiple levels of similarity to form groups. After a number of initial experiments, the *Canberra distance* (Lance & Williams, 1967) was used to compute the distances between the different curves of $J(\bar{r})$. *The* method for the cluster analysis was finally settled on the *Wards minimum distance method* (Everitt *et al.*, 2011).

The variables included for classifying the curves of $J(\bar{r})$ were slope, intercept and the sum of squares of deviations from linearity (SSDL) (Liu *et al.*, 2009). To obtain the variables of average slope and intercept we approximated the curves with a linear equation (Andrilli & Hecker, 2010), running through the first and the final-values for each curve. The slope parameter of this linear model corresponds with the average slope of $J(\bar{r})$. The intercept is the value of the linear equation indicating where the line crosses the y-axis. The third variable of SSDL (as described by Liu *et al.* (2009)) can be calculated by fitting the $J(\bar{r})$ -curves to the best fitting nonlinear polynomial and then comparing the difference between the nonlinear curve and a simple straight line. From these calculations, one value for each curve is obtained, describing how far from linearity the specific $J(\bar{r})$ -curve is. For the mark mingling curves, the value of $\nu(r)$ for each distance r was directly included in the calculations with a step width of 1 for r ranging from 1 to 35.

Curves of $J(\bar{r})$ and $\nu(r)$ were calculated for each of the 20 stands included in this thesis. The curves were visually assessed and subjectively pre-assigned to groups based on the perceived characteristics of each curves. A cluster analysis was then performed for each of the two functions with the intention of reducing subjectivity in the method and to include hidden features of the curves. Interesting patterns of the curves for each respective function were compared.

The calculations and figures for this report was performed and produced using R and RStudio (R Core Team, 2017) including programming code both in R and C^{++}. Most of the code was provided by the supervisor (Prof. Arne Pommerening), while extensions were written by the author.

3 Results

3.1 $J(\bar{r})$ function

As expected, from a diverse collection of stands, curves exhibiting a wide range of characteristics have been obtained (Figure 10). The curves differ in several ways, such as length, average slope and how much they deviate from linearity. Most importantly the curves differ in terms of their relative location in the graph indicating aggregation or segregation of heterospecific trees. This can be measured by the intercept of the linear trend lines used to estimate average slope. It is intriguing that most stands have $J(\bar{r})$-curves starting with a positive value, and remaining positive for their entire range of the curve. The curves related to M and Bo are deviating a lot from the patterns of the majority, starting with negative values for $J(\bar{r})$, approaching a Poisson distribution from the side of interspecies attraction. The mingling pattern of Bo with its strong attraction of heterospecific trees is particularly rare and stand out from all other forest stands. The curves of stands W and JSa have higher values for $J(\bar{r})$ than all the other stands, for the whole range of the curves.

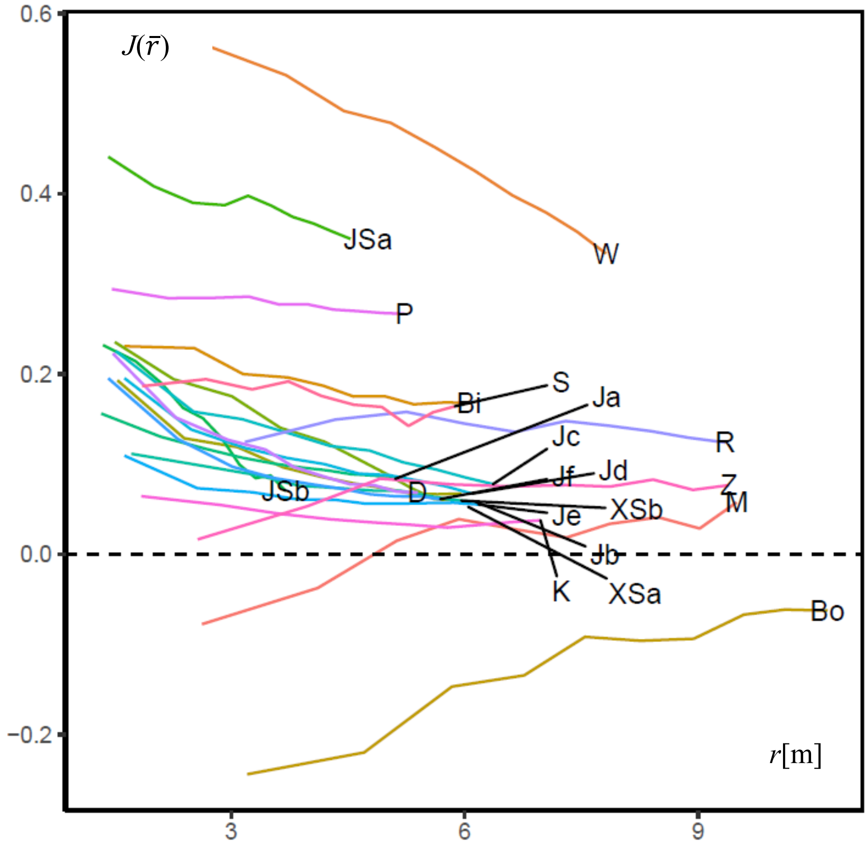

Figure 10. *$J(\bar{r})$, for all 20 forest stands included in this thesis. The curves have been labelled using the respective abbreviations, see Table 1.*

Based on visual interpretation, the curves have been allocated to four groups (Figure 11). The first group includes four stands, namely Bo, M and Z, sharing similar lengths and exhibiting convex shapes. The average slope is similar for Bo, M and Z, starting with a steeper value that decreases as $\bar{r}$ increases. The $J(\bar{r})$ curves Bo and M are the only two curves in this study that are present below the reference line running through zero and indicates complete spatial randomness, displaying interspecies attraction. The curve of Bo has a negative value for $J(\bar{r})$ in the entire range of $\bar{r}$, whilst the curve related to M is only negative for small $\bar{r}$, i.e. in the immediate surroundings of every tree. The second group includes stands D, Ja, Jb, Jc, Jd, Je, Jf, K and XSa. Most of the mingling curves in this group are in close proximity to each other and have similar values in terms of average slope and intercept of the linear trend line. Most of the curves of this group even seem to form parallel trajectories. They all start at about the same distance for $\bar{r}$ and between 0.05 and just above 0.2 for $J(\bar{r})$. The mingling curves of this groups (perhaps with the exception of K) seem less linear than the curves of other groups, approaching random species dispersal with decreasing slope. The curves in group three are Bi, S, R and P, displaying characteristics of linearity with a low average slope value. The curves of Bi, S and P are short in relation to most curves in the other groups, because tree density is high in these forests. The fourth and final group is represented by the stands W, XSb, JSa and JSb. The curves are similar to those of the third group. appearing linear but unlike the curves of group three, these $J(\bar{r})$ curves share the trait of having steeper negative slopes. This is also the group, where the highest values for $J(\bar{r})$ can be found in W.

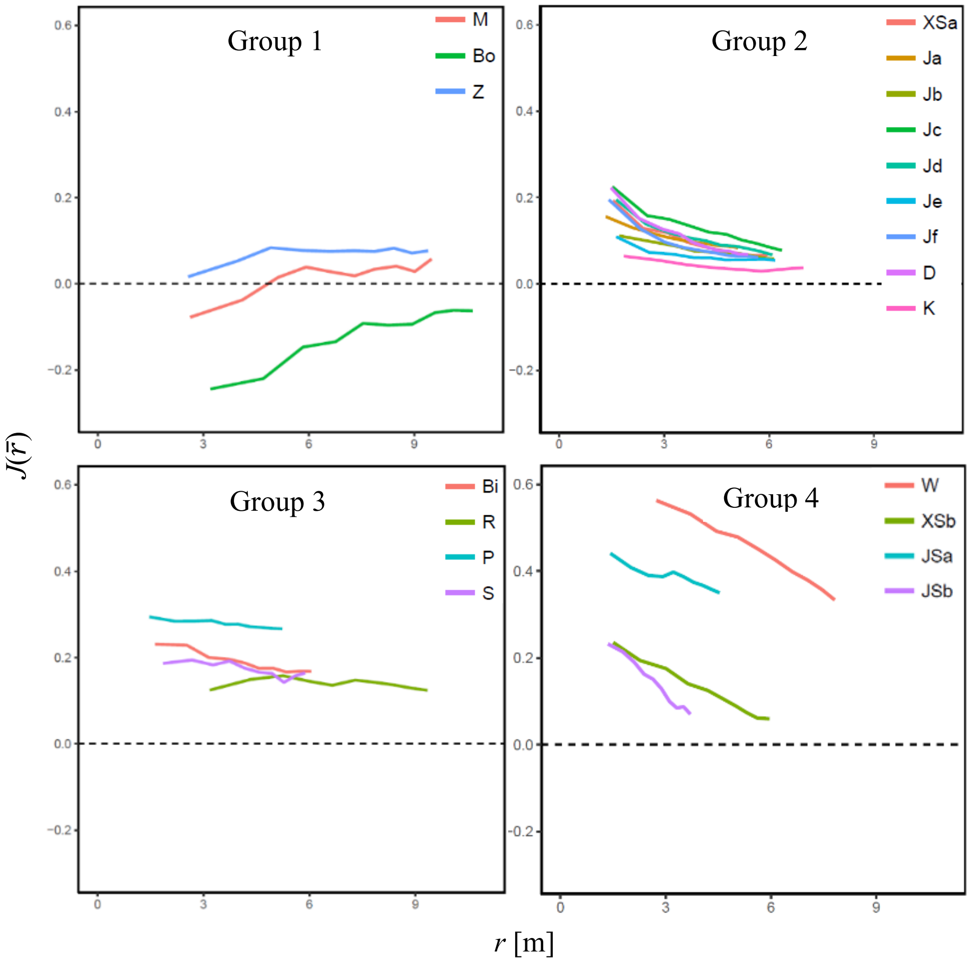

Figure 11. *Curves of $J(\bar{r})$, presented in four groups, suggested based on characteristics. Curves are identified with respective abbreviation*, see Table 1.

3.2 Mark mingling function

Similar to the curves of $J(\bar{r})$, the curves of $\nu(r)$ also exhibit a range of different characteristics (Figure 12). However, they are somewhat less differentiated than the curves of $J(\bar{r})$. Most of the curves start with a value of less than one for $\nu(r)$, thus showing a tendency for trees of the same species to aggregate. These curves of the mark mingling function initially have a steeper slope that levels off as $\nu(r)$ approaches random dispersal of species ($\nu(r)$ approaching one). There are a few stands for which the respective curves deviate from this pattern, for example M, R and JSb. It is interesting that Bo, M and W are outliers within the mark-mingling curves which correspond well with those of $J(\bar{r})$. The mark-mingling curves differ from each other in multiple aspects, for example in the initial value for $\nu(r)$, average slope, (non)linearity and general shape of each curve. In contrast to the function of $J(\bar{r})$, the range for all $\nu(r)$-curves are the same, i.e. 0 to 35 meters, since this was a setting when using of the function is this thesis.

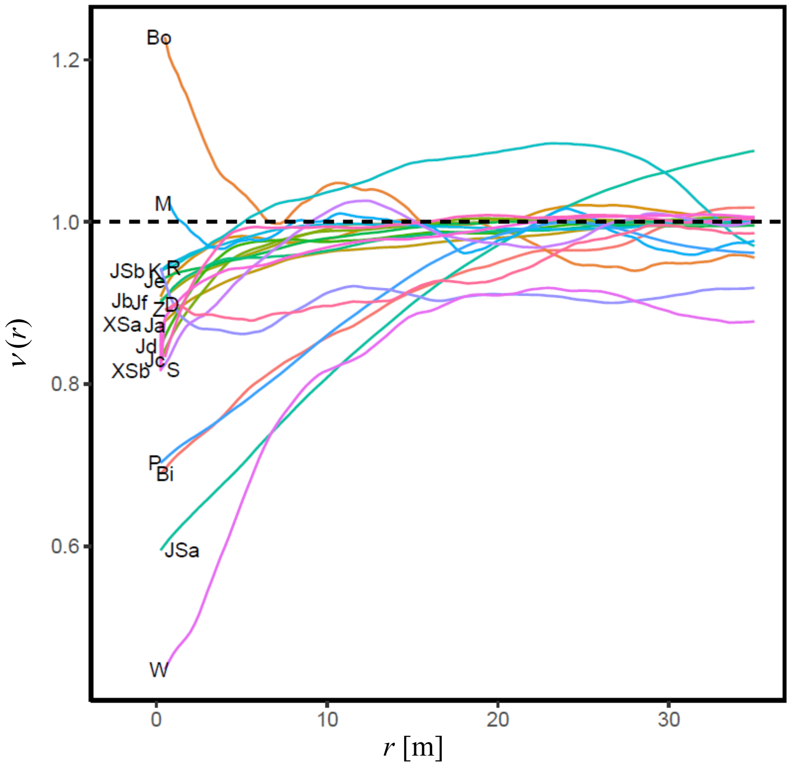

Figure 12. *Mark mingling curves of all stands together.* The curves have been labelled using the aforementioned abbreviations, see Table 1.

Four groups of stands have been identified by visually interpreting the curves (Figure 13.). Group one is made up by the stands Bi, P, JSa and W. These curves all start with relatively low values for $\nu(r)$, between circa 0.4 and 0.7. As r increases, the value for $\nu(r)$ increasingly deviates from linearity. The second group consist of the stands Ja, Jb, Jc, Jd, Je, Jf, XSa, XSb, K, S and D. This appears to be to be the most homogenous group, with curves that all start with a value for $\nu(r)$ at around 0.8-0.9. The curves then rapidly approach random distributions of species, and from that point on remain almost exactly on the dashed line representing

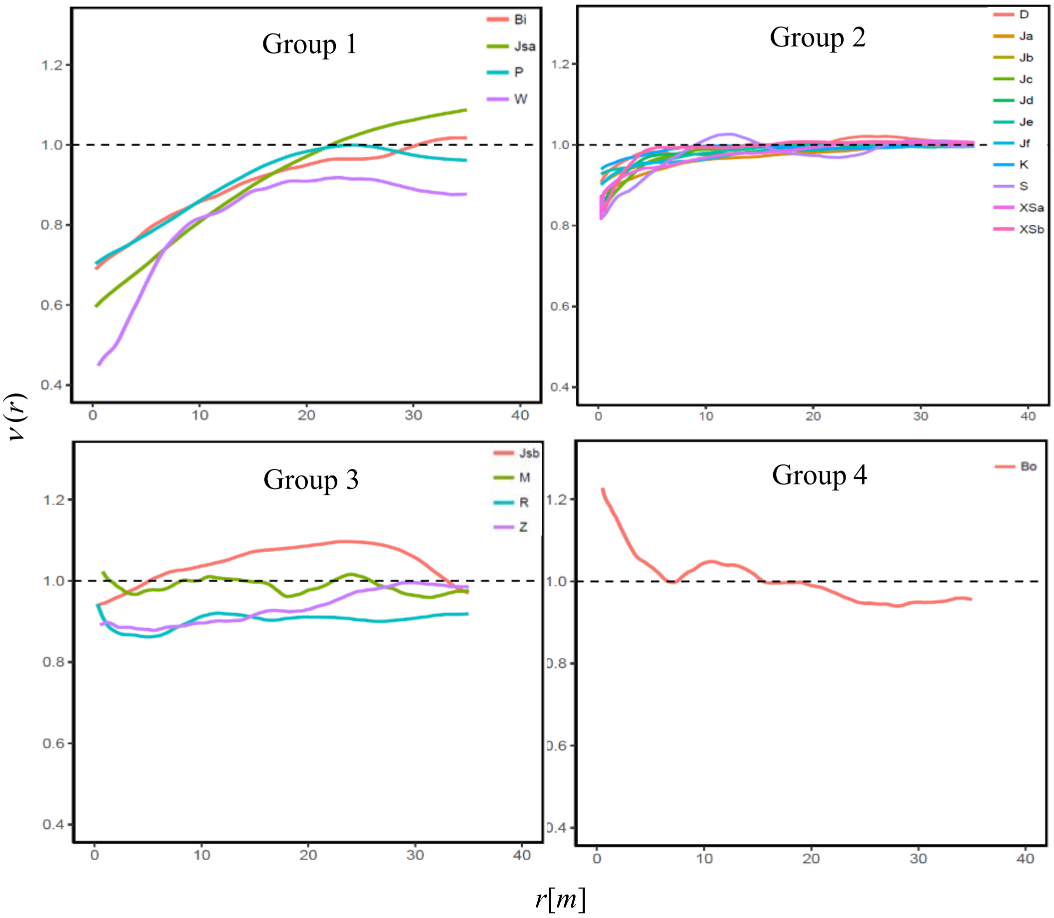

Figure 13. *Curves of the mark mingling function,* $\nu(r)$*, separated into four groups. The groups are suggested based on visual interpretation and each group include stands with similar traits. The curves have been labelled using the aforementioned abbreviations, see Table 1.*

$\nu(r) = 1$. The stands of Z, R, M and JSb represent a third group with curves near 1, sharing the common characteristic of having an average slope near 0. M is very close to complete spatial species randomness throughout the range of r. JSb stands out within this group, with a concave shaped curve that start and end with a value for $\nu(r)$ equal to less than one. In the fourth and final group I placed the curve of Bo. The shape of this curve does not resemble any of the other curves, starting with a very high value for $\nu(r)$, at slightly over 1.2. From the initial high value, the curve immediately starts to drop and gradually approaches $\nu(r)$=1, reaching complete spatial randomness at $r \approx 7$m. The curve then makes a small concave bump above $\nu(r)$=1 and then stay close to the dashed line of $\nu(r)$=1.

3.3 Cluster analysis

Two cluster analyses were performed, separately for $J(\bar{r})$ and the mark mingling function $\nu(r)$, resulting in four groups. As suspected, the resulting groups are dissimilar for $J(\bar{r})$ and $\nu(r)$, classifying the stands very differently, depending on which one of the two functions is included in the cluster analysis.

Concerning $J(\bar{r})$, the first of the four groups differ the most from the rest of the groups, diverging from the other groups on the highest rank (Figure 14). This group contain curves from the three stands Bo, M and Z. The second group is the largest, including seven curves from the stands D, Jc, Jd, Jf, R, P and XSa. The curves from the corresponding stands of JSa, JSb, W and XSb make up a third group. $J(\bar{r})$ curves from the remaining six stands off, Jb, Je, Bi, K and S make up the fourth and final group.

The groups of $\nu(r)$ are more difficult to interpret, since clusters at multiple hierarchal levels are being paired together (Figure 15). All stands from the Chinese regions of Jiaohe and Xiaolongshan are grouped together with the stands of Bo, D, K, M, and JSb. The second group contain a single curve from the stand of W. The stands of R and Z form the third group. The fourth and final group includes the stands JSa, Bi and P. The first group is notably larger than the other three groups.

The clusters/groups formed diverge more between the functions in the cluster analysis than for the suggested groups. For $J(\bar{r})$, two of the suggested groups match the first and the third group from the cluster analysis. However, the remaining groups from the suggested groups and the cluster analysis are rather different from each other. Regarding the groups for the mark mingling function $\nu(r)$, the first group from the cluster analysis contain fourteen stands relating to the second group for the suggested groups, surprisingly merged with the only curve of group four, Bo and the curves of JSb and M. However, the curves for Bo and JSb stand out within the first group, being the most divergent curves, see Figure 15. From the cluster analysis a new group including a single curve is obtained but unlike in the suggested groups this group contain the curve for W, present in the lower part of the graph. The third and fourth group from the cluster analysis are similar to respectively the first and fourth of the suggested groups but with fewer included curves, which were instead assigned to other groups in the cluster analysis.

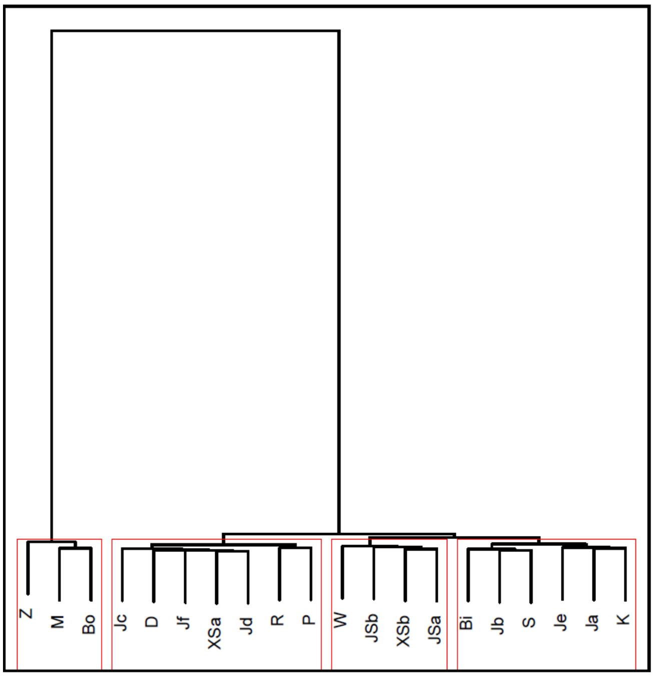

Figure 14. *Cluster analysis based on the* $J(\bar{r})$*-curves. Curves refereed to with respective abbreviation, see Table 1. The red lines show groups with similar characteristics. The groups are numbered 1-4 in consecutive order from left to right.*

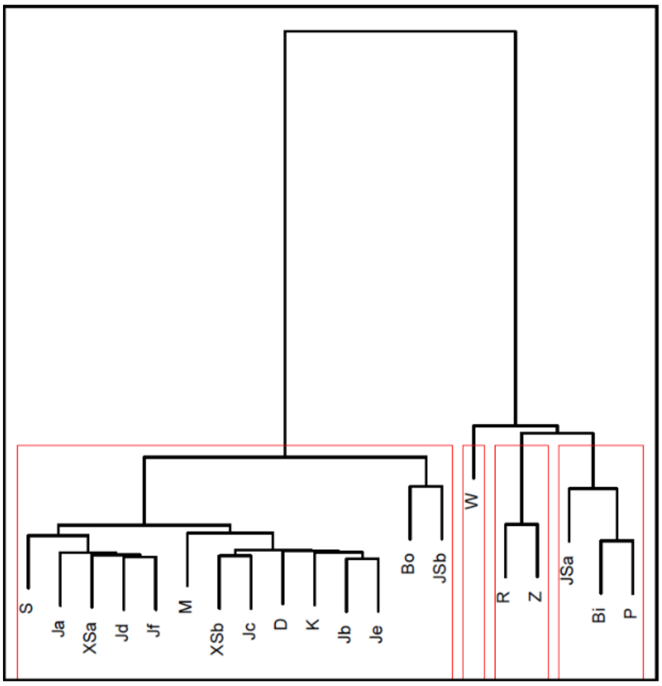

Figure 15. *Cluster analysis for* $\nu(r)$*-curves. For the meaning of the abbreviations, see Table 1. The group are separated into groups with red boundary lines. The groups are numbered 1-4 in successive order from left to right.*

4 Discussion

4.1 The curves of $J(\bar{r})$ and $\nu(r)$

Since the concept of the two functions $J(\bar{r})$ and $\nu(r)$ are fundamentally different, it was natural to expect differences in the shapes of the curves and the way how they discriminate between different spatial species mingling patterns.

Since $J(\bar{r})$ is based on the nearest neighbours of individual trees, it can be observed that the length of each curve contains information on tree density in the corresponding stand (Figure 10 and Table 1). The curves of $J(\bar{r})$ can be compared with the same number of closest neighbours for every stand. All curves of $\nu(r)$ are present in the same range between r = 0-35 m, which is useful when investigating and comparing mingling patterns between stands on absolute distances for r.

The curves of $J(\bar{r})$ include the same information as the species segregation index (Pommerening and Uria-Diez, 2017) but for the whole range of the included nearest neighbours k ($k = 1, \ldots, 10$ in this study). This can be useful, since the species segregation index can show similar values for two stands for a certain k and when k is set to another value, the same stands might differ significantly. In addition, it is likely that each forest stand has an optimal k, which is difficult to determine and is again different for other stands (Pommerening, 2006).

Even if the functions generate similar results, it might be easier to understand and perform the calculations for $J(\bar{r})$ than for $\nu(r)$ (compare Eq. 5 and Eq. 6), particularly in forest practice.

Some of the curves of $J(\bar{r})$ and $\nu(r)$ do not approach complete species randomness in the observed range. For $J(\bar{r})$ this means that the end of the interaction range has not yet been reached. In the case of the mark mingling function this is most likely due to inhomogeneities in the spatial patterns.

4.2 Suggested groups of and cluster analysis

The first suggested group of $J(\bar{r})$ is identical to the first group from the cluster analysis, consisting of stands from Europe with very low tree density. M and Bo are heavily managed whilst Z is shaped by natural processes. They share the traits of having low species richness and being dominated by beech, which is a shade tolerant secondary tree species. The managed forests have lower values for $J(\bar{r})$ but similarly shaped curves, perhaps explained by the dominance of beech.

In the second suggested group with curves from nine stands, the forest structure have been shaped by natural processes or by low impact forestry. All stands have a very high species richness with no single dominant species in terms of stems ha^{-1} (Table 1). As can be observed, all the stands from Jiaohe have been assigned to this group. The stands from the second and third suggested groups are spread between the second and the fourth group obtained from the cluster analysis. The curves from the third suggested group are mostly from stands managed with low impact forestry.

The fourth suggested group and the third group from the cluster analysis are identical. Including curves with steep slopes that appear linear. The value for $J(\bar{r})$ decreases relatively fast, thus indicating a relatively short interaction range. Mostly so for the curve of JSb which is at least partly due to its very high value for stems ha^{-1} (Figure 7).

The first suggested group for $\nu(r)$ and the fourth group from the cluster analysis start with relatively low values for $\nu(r)$ and then gradually approach spatial randomness. It seems as if the stands exhibit spatial heterogeneity, which may explain why they do not seem to approach random dispersal of species as k and $\bar{r}$ increases.

In the second suggested group, most stands have too a large degree been shaped by natural processes or low impact forestry. They share the traits of having high species richness and not being dominated by one or a couple species. The stand of S deviates in terms of all traits mentioned for this group but also in the shape of its curve. All the curves from this group and three additional curves are placed in the first group from the cluster analysis. The number of groups were decided to four for the cluster analysis of $\nu(r)$, for easier comparison with the others. However, additional groups would have divided the very large first group which would have been interesting.

The third suggested group includes the stands of M, R and Z that all have low number of stems ha^{-1} and relatively few species. The stand of JSb also belong to this group with the highest number of stems ha^{-1} and include thirteen species. Besides the outlier stand of JSb, the other three stands are all stands with a large proportion of beech. This group relates to the third group from the cluster analysis which only includes the curves from R and Z.

The stand of Bo, making up the fourth suggested group, the shape of this curve is most likely due to the forest management within the stand.

One reasonable alternative for the suggested groups would have been to place the stands of Bo, M and Z in the same group. They all start with a negative slope that then levels off relatively quickly and then follow a similar pattern, however, the initial slope is much more pronounced in the curve of Bo which is why it was assigned to its own group.

Although clearly different, the suggested groups for the two functions are more similar than the groups obtained in the cluster analysis, especially if the alternative group mentioned in the paragraph above were considered. The curves of $J(\bar{r})$ seem to vary more between the stands, one clear example of more variation for $J(\bar{r})$ is that the stands can vary in length. Even if stands were assigned differently for the two functions, it seemed when doing the subjective classification that both functions managed to produce distinguishable curves for the stands formed by natural processes or by low impact forestry, with high species richness and no single dominating species. These curves were allocated to group two for the suggested groups of each function. Showing characteristics of being non-linear and starting at 0.05-0.2 for $J(\bar{r})$ and 0.8-0.95 for $\nu(r)$. Unanimously approaching random distribution of species.

Not surprisingly, since the functions are fundamentally different, the groups created by the cluster analysis differed considerably between the two functions, producing four rather different groups of curves for each function. Part of this difference in clustering is because different variables from each function were included in the cluster analysis. Results better for comparison could potentially have been generated if the included variables for $\nu(r)$ were more similar to those used when performing the cluster analysis for the $J(\bar{r})$-function.

The cluster analysis for $J(\bar{r})$ groups the curves for M, Bo and Z together. Seemingly, these curves are similar to each other but deviate from other curves, which might suggest that the clustering method used for $J(\bar{r})$ was more useful and/or that the curves of $J(\bar{r})$ include information more descriptive when classifying forest stands based on species mingling patterns.

4.3 Reflections and future studies

The data used in this study is from fully mapped stands and therefore ideal for evaluating and comparing the performance of indices and functions. Due to progress in surveying and computer technology, data with such a high level of detail are increasingly available. However, forest inventories at local, regional and national scale are often based on small sample plots. For example, the Swedish National Forest Inventory use circular sample plots with a radius of 10 meters (Fridman *et al.*, 2014). The data from these plots are sufficient for the function of $J(\bar{r})$, provided $k < 6$.

Second-order functions including $\nu(r)$ seem to need at least 150 trees to obtain dependable results (Pommerening *et al.*, 2011; Pommerening & Stoyan, 2006). The data from most forest inventories is therefore not compatible with the mark mingling function. The function of $J(\bar{r})$ does not have the same demands and can be used in smaller plots when keeping the value for k relatively low. However, problems may arise when correcting for edge biases within a small plot. One method to avoid edge bias is to perform plus-sampling (Stoyan & Stoyan, 1994), where additional measurements are performed to include the closest neighbouring trees outside the research or inventory plot. However, this requires that $\max(k)$ is fixed and will not be changed later.

An alternative approach when testing these functions could be to use simulated data to compensate for missing off-plot neighbours (Pommerening & Stoyan, 2008). Such data could complement the point patterns observed in small observation windows.

The transformations of the mark mingling index via the species segregation index to $J(\bar{r})$ could also be done with similar indices describing other aspects of forest structure, such as stem-diameter differentiation or the uniform angle index (Pommerening, 2002). With a combination of multiple curves describing different aspects of biodiversity it may be possible to achieve a more complete quantitative description of forest structure.

Another interesting idea is to combine functions such as $J(\bar{r})$ and $\nu(r)$ with data generated from remote sensing techniques and apply the functions on individual pixels.

4.4 Conclusion

This study suggests that the new function of $J(\bar{r})$ provides information additional to the information provided by the mark mingling function. $J(\bar{r})$ is based on the nearest neighbour concept, thus providing more information on local neighbouring trees. This research also pointed to the potential value of $J(\bar{r})$ for smaller research and inventory plots, such as those commonly used in forest inventories. Further research is needed to complement this initial impression of the differences between $J(\bar{r})$ and $\nu(r)$. This relates to environmental policy, with the need to quantify biodiversity and monitor our sustainability or lack thereof.

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