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LANSING WOODS

S-114.4202 Special Course in Computational Engineering II

February 12, 2012

1 Data description

It's an important question in forest ecology whether certain tree species are spatially associated with each other and how they respond to competition. The Lansing Woods dataset [3] contains the location and botanical classification of 2251 trees. The data was collected in Lansing Woods, Clinton County, Michigan USA by D.J. Gerrard in 1969 from a square area of 282×282 metres.

The dataset is available in the *R* package *spatstat* [5, 1]. It's a categorically marked dataset, where the mark can have one of the values

- blackoak
 - *Quercus velutina*
 - known associates: whiteoak, redoak, hickory, maple
- redoak
 - *Quercus rubra*
 - known associates: whiteoak, blackoak
- whiteoak
 - *Quercus alba*
 - known associates: whiteoak, redoak
- hickory
 - *Carya*
 - known associates:
- maple
 - *Acer*
 - known associates:
- misc

Look
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The interesting questions will be:

- do the associations known *a priori* show in the data
- do some species avoid some other species
- clustering behavior inside and between the species

The dataset is plotted in figure 1.

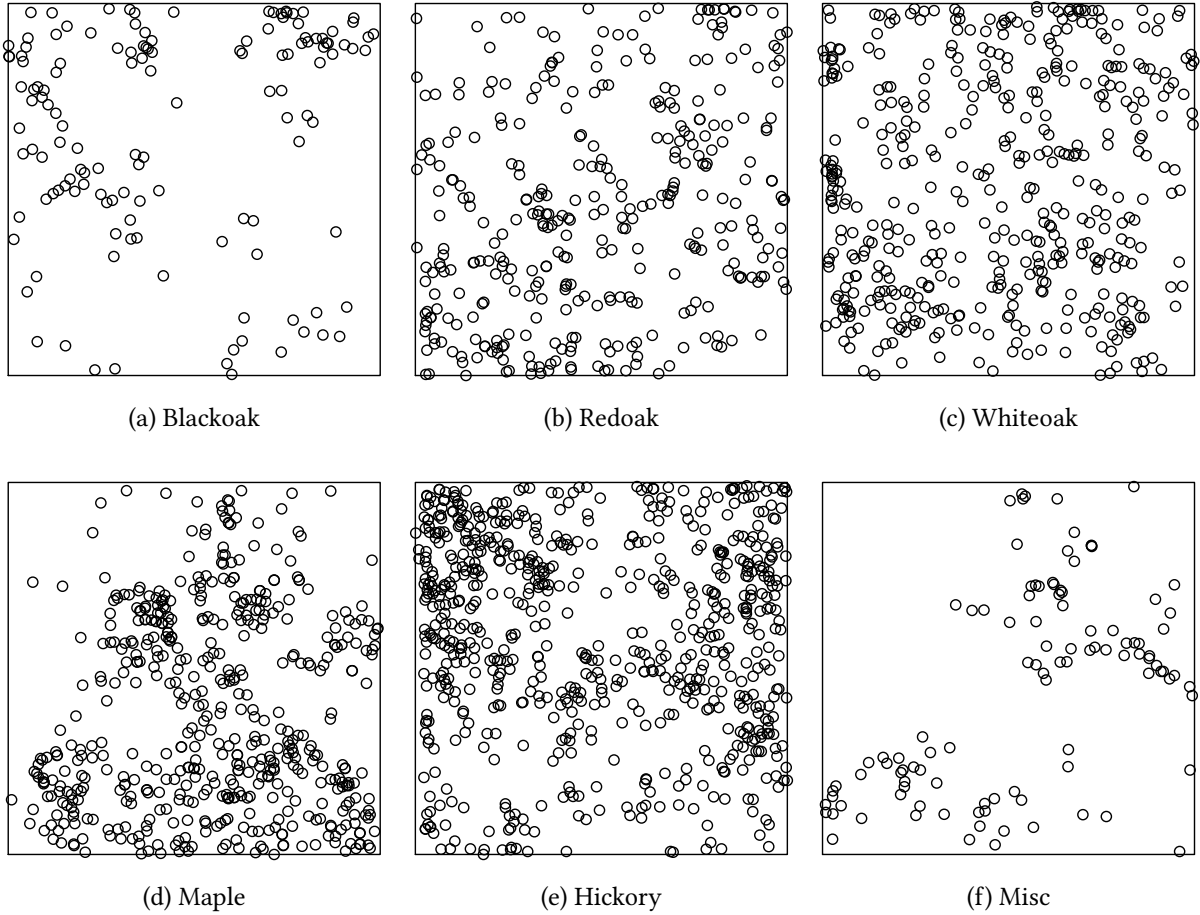


Figure 1: The Lansing Woods dataset

2 Preprocessing

The different oaks, namely the black, the white and the redoaks seem to display rather homogenous intensities judging from the point patterns. Taking into account the prior information, that these oaks tend associate with each other, it seems reasonable to combine the different oaks into a single category. Also since there is no information regarding the constitution of the “misc” category, it is discarded from further analysis. The point patterns resulting from these preprocessing steps are displayed in figure 2.

3 Intensity analysis

It’s obvious just by looking at figure 1 that the intensity profiles exhibit significant interspecies variability. For example oaks seems to have almost homogenous intensity whereas maples displays a much more inhomogenous pattern. A Gaussian kernel smoothed intensity estimate is displayed in figure 3, where

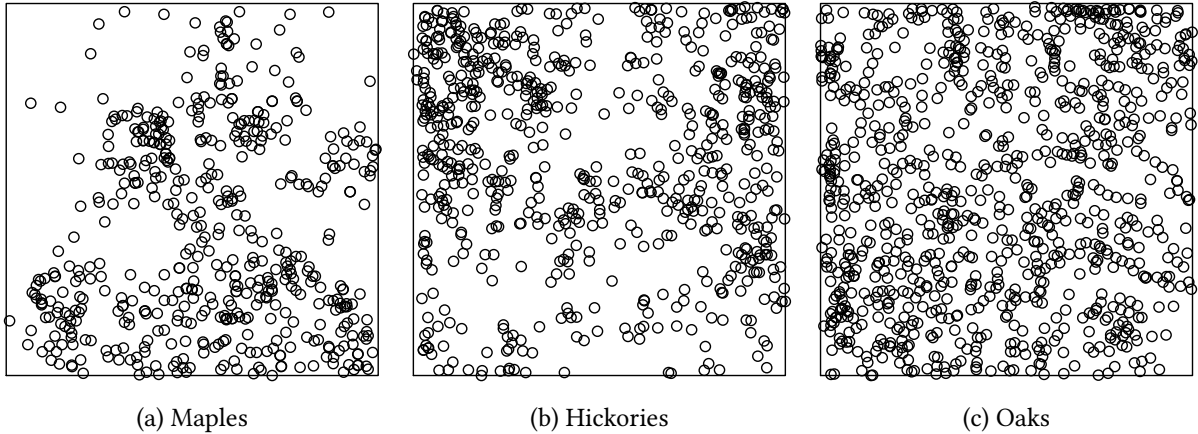


Figure 2: The dataset after preprocessing

the intensities are comparable between species.

The most striking conclusion from figure 3 is that the patterns for hickories and maples are almost complementary. The intensity of the oaks varies somewhat, but it seems that there are some oaks pretty much everywhere in the window.

More conclusions can be drawn by plotting some combined point patterns. In figure 4 there are all the trees plotted together, then the oaks and finally the maples and the hickories combined. Indeed, it seems that when plotted in these combinations, it would be reasonable to assume constant intensities. We can already come to the following conclusions

- discarding the marks, the intensity of trees is homogenous
- oaks are independent of other species
- hickories and maples show strong segregation

4 Marking model

5 Interaction analysis

Next we will attempt to characterize the interactions within a single species and amongst different species.

5.1 Intra-species interaction

I have plotted the inhomogenous L-functions $[4][2]$ for the maples and hickories and the ordinary L-function for the oaks. These are displayed in figure 5.

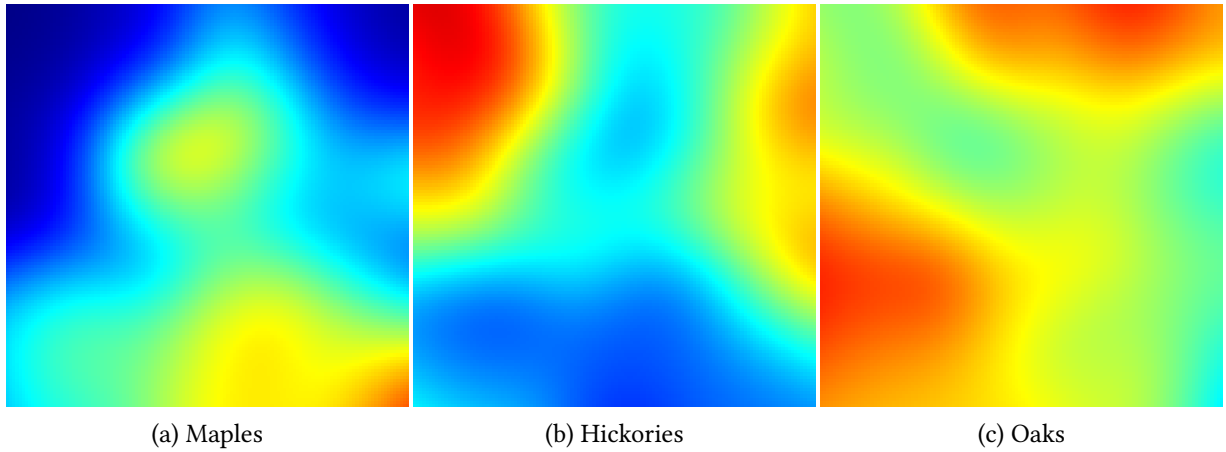


Figure 3: Gaussian Kernel smoothed intensity estimates

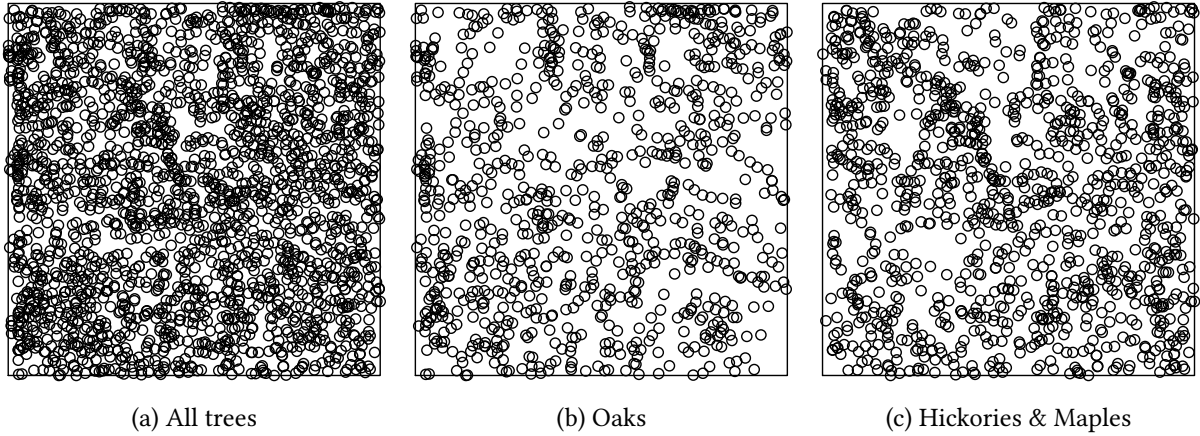


Figure 4: Point patterns with different combinations of the marks in the dataset. The patterns display homogenous intensity.

5.2 Inter-species interaction

The interspecies interaction was quantified by using the two different summary statistics: the *partial pair correlation function* (PPCF) and the *mark connection function*. These can both be interpreted as displaying the probability, that there is a point of species i an r distance away from a point of species j . The plots have been made for all the pairings i, j from the three species, resulting in 6 different plots (pairings of type i, i are also included). The PPCF is displayed in figure 6b and the mark-connection function in figure 6a. As can be seen, both of them show quite similar results.

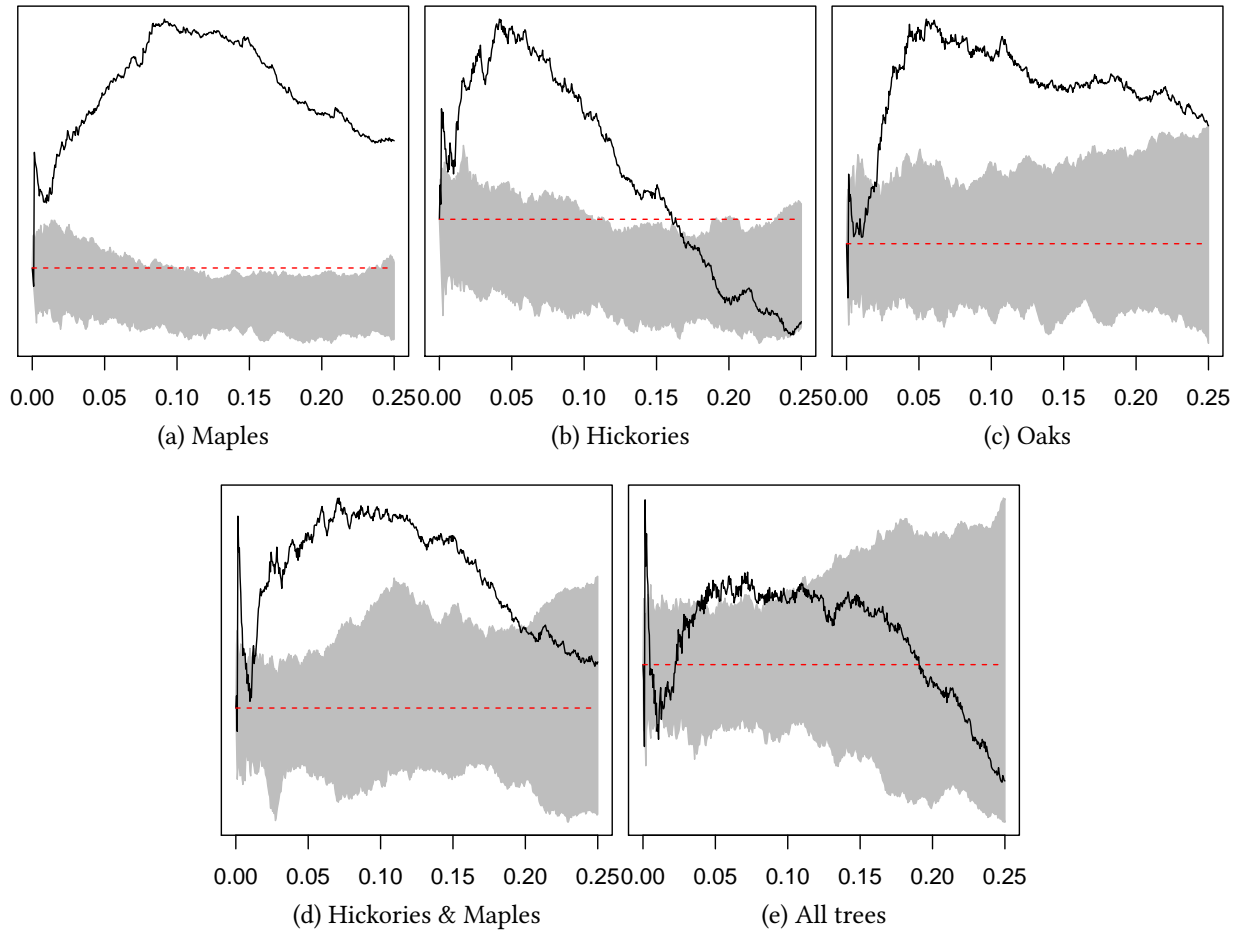
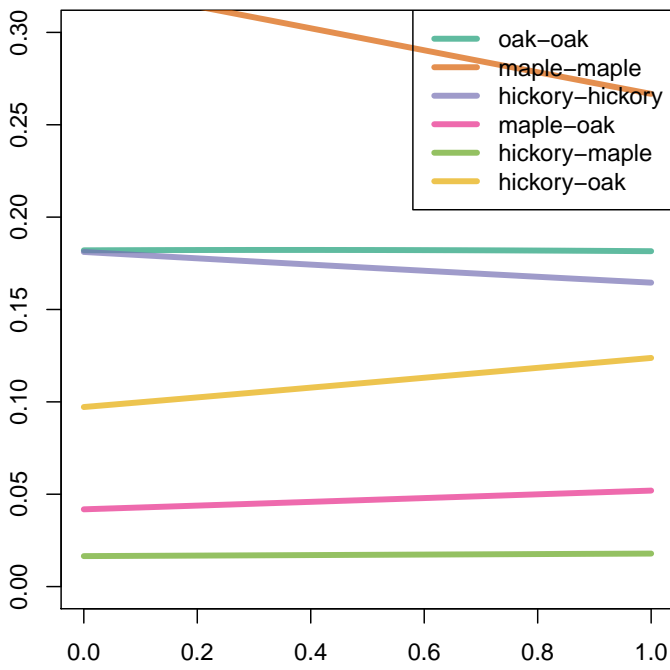
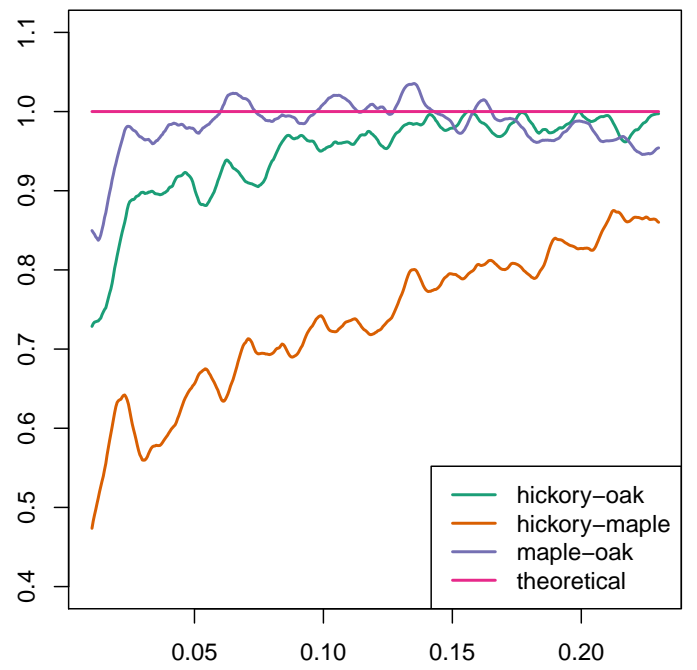


Figure 5: Besag's L-function for the different species. For maples and hickories the inhomogenous version was used. In all of the figures there are the envelopes after 20 monte carlo tests assuming complete spatial randomness.



(a) Mark-connection function



(b) PPCF

Figure 6: The mark-connection function and the partial pair-correlation function that measure intra- and interspecies interactions.

6 Methods

7 Results

8 Conclusion

References

- [1] Adrian Baddeley and Rolf Turner. “Spatstat: an R package for analyzing spatial point patterns”. In: *Journal of Statistical Software* 12.6 (2005). ISSN 1548-7660, pp. 1–42. URL: www.jstatsoft.org (cit. on p. 1).
- [2] A.E. Gelfand, P. Diggle, and P. Guttorm. *Handbook of spatial statistics*. Chapman & Hall/CRC handbooks of modern statistical methods. Taylor & Francis Group, 2010. ISBN: 9781420072877. URL: <http://books.google.fi/books?id=Xf4leslPDz5C> (cit. on p. 3).
- [3] D.J. Gerrard. “Competition quotient: a new measure of the competition affecting individual forest trees”. In: *Research Bulletin 20, Agricultural Experiment Station* (1969) (cit. on p. 1).
- [4] J. Illian. *Statistical analysis and modelling of spatial point patterns*. Statistics in practice. John Wiley, 2008. ISBN: 9780470014912. URL: http://books.google.fi/books?id=_U6BER2stYsC (cit. on p. 3).
- [5] R Development Core Team. *R: A Language and Environment for Statistical Computing*. ISBN 3-900051-07-0. R Foundation for Statistical Computing. Vienna, Austria, 2011. URL: <http://www.R-project.org/> (cit. on p. 1).

R code

```
# Lansing wood data analysis

exportFigs <- 1
displayFigs <- 0
interaction <- 0
speciesinteraction <- 1
intensity <- 0
dimyx <- ifelse(exportFigs,c(500,500),c(100,100))

require("spatstat");
require("RColorBrewer")
#require("playwith");
data(lansing)
lansingm <- lansing

#unitname(lansingm) <- c("metre", "metres", round(924/3.2808399))
unitname(lansingm) <- list("metre", "metres", 1)
ft2m <- round(lansing$window$units$multiplier/3.2808399)
lansingm <- affine(lansingm, diag(c(ft2m, ft2m)))

jet.colors <-
  colorRampPalette(c("#00007F", "blue", "#007FFF", "cyan",
                    "#7FFF7F", "yellow", "#FF7F00", "red", "#7F0000"))

mar_lab <- c(2.5, 2.5, 1.5, 1.0)
mar_tight <- c(0.1, 0.1, 0.1, 0.1)
myplot <- function(..., width=6, height=6, mar=mar_lab, file=FALSE, nodevoff=FALSE)
{
  if(displayFigs) {
    quartz()
    par(mar=mar)
    p <- plot(...)
    if(!exportFigs) {
      return(p)
    }
  }
  if(exportFigs && file != FALSE) {
    pdf(file=file, width=width, height=height)
    par(mar=mar)
    p <- plot(...)
    if(!nodevoff) {
      dev.off()
    }
    return(p)
  }
}

listplot <- function(k, v, file=FALSE, formula=FALSE, ...) {
  if(formula != FALSE) {
    return(myplot(v, formula, file=sprintf(file, k), ...))
  } else {
    return(myplot(v, file=sprintf(file, k), ...))
  }
}
```

```

    }
  }

sigma <- bw.relrisk(lansing);

nlansing <- lansingm[lansingm$marks!="misc"];
levels(nlansing$marks) <- c("oak", "hickory", "maple", NA, "oak", "oak")

hm <- lansingm[lansingm$marks=="maple" | lansingm$marks=="hickory"];
levels(hm$marks) <- c(NA, "hickory", "maple", NA, NA, NA)

oaks <- lansing[grepl("oak", lansing$marks)]
levels(oaks$marks) <- c("blackoak", NA, NA, NA, "redoak", "whiteoak")

oakhm <- nlansing
levels(oakhm$marks) <- c("oak", "hm", "hm")

bw <- bw.diggle(nlansing)

if(intensity) {
  dens1 <- density(split(nlansing),
    sigma=2.5*sigma,
    dimyx=dimyx)

  rl=relrisk(nlansing, sigma=2.5*sigma)

  # smoothed intensities
  mapplot(listplot, names(rl), rl,
    MoreArgs=list(
      zlim = c(0, 0.7),
      col=jet.colors(512),
      main="",
      mar=mar_tight,
      ribbon=FALSE,
      file="intensity_relative_%.pdf",
      width=3,
      height=3
    ))

  # original point patterns
  mapplot(listplot, names(split(lansing)), split(lansing),
    MoreArgs=list(
      main="",
      mar=mar_tight,
      file="lansing_%.pdf",
      width=3,
      height=3
    ))

  # combined point patterns
  mapplot(listplot, list("oaks", "hm", "all"), list(oaks, hm, lansing),
    MoreArgs=list(
      use.marks=FALSE,
      pch=21,
      main=""
    ))

```

```

        mar=mar_tight,
        file="lansing_%s_combined.pdf",
        width=3,
        height=3
    ))
}

if(interaction) {

  patrn <- c(split(nlansing),list(hm=hm,all=nlansing))
  Ls <- mapply(envelope,patrn,list(Lest,Linhom,Linhom,Lest,Lest),
    MoreArgs=list(
      nsim=99,
      correction="Ripley",
      normpower=2,
      sigma=2.5*sigma
    ),SIMPLIFY=FALSE)
  mapply(listplot,names(patrn),Ls,
    MoreArgs=list(
      main="",
      formula=".~r~r",
      file="l_%s.pdf",
      legend=FALSE,
      width=3,
      height=3,
      mar=c(2.0,0.3,0.1,0.3),
      yaxt="n"
    ))
}

if(speciesinteraction) {

  # mark connection functions, pairwise
  bw <- 2*bw.stoyan(nlansing)
  i <- c("hickory","hickory","maple","hickory","maple","oak")
  j <- c("oak","maple","oak","hickory","maple","oak")
  markcs <- mapply(
    markconnect,
    rep(list(nlansing),length(i)),
    i,
    j,
    MoreArgs=list(
      r=seq.int(0,1,1/500),
      correction="Ripley",
      bw=bw,
      normalise=FALSE
    ),SIMPLIFY=FALSE)
  markc <- markcs[[1]]
  markc <- markc[,c("r","iso")]
  for(m in markcs[2:length(markcs)]) {
    markc <- cbind(markc,m[,c("r","iso")])
  }
  col <- sapply(brewer.pal(length(markc)-1,"Dark2"),function(c) {
    return(paste(c,as.hexmode(round(0.7*255)),sep=''))
  },USE.NAMES=FALSE)

```

```

v <- myplot(
  markc,
  legend=FALSE,
  col=col,
  lty=1,
  lwd=4,
  ylab="mark-connection",
  main="",
  file="markc.pdf", nodevoff=TRUE,
  xlim=c(0,1),
  ylim=c(0,0.3),
  width=5,
  height=5)
legend('topright',
  mapply(function(i,j){
    return(sprintf("%s-%s",i,j))
  }, rev(i), rev(j)),
  col=col,
  lwd=4,
  lty=v$lty)
if(exportFigs) {
  dev.off()
}

# pair correlation functions, pairwise
# pcfs <- mapply(
#   pcfcross,
#   list(nlansing, nlansing, nlansing),
#   list("hickory", "hickory", "maple"),
#   list("oak", "maple", "oak"),
#   MoreArgs=list(
#     correction="Ripley",
#     bw=bw
#   ), SIMPLIFY=FALSE)
# pcf <- pcfs[[1]]
# for(m in pcfs[2:3]) {
#   pcf <- cbind(pcf, m[, cbind("r", "iso")])
# }

# vv <- myplot(
#   pcf,
#   legend=FALSE,
#   col=col,
#   lty=1,
#   lwd=2,
#   ylab="pcf",
#   main="",
#   ylim=c(0.4, 1.1),
#   xlim=c(0.01, 0.23),
#   file="pcf.pdf", nodevoff=TRUE, width=5,
#   height=5)

# legend('bottomright',
#   c('hickory-oak', 'hickory-maple', 'maple-oak', 'theoretical'),

```

```
# col=col,  
# lwd=2,  
# lty=vv$lty)  
  
# if(exportFigs) {  
#   dev.off()  
# }  
}
```