

Temporal changes in the spatial distribution of carabid beetles around arable field-woodlot boundaries

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Supplementary material:

Figures S1 – S4

R Script

Figure S1 - Aerial photograph of the study area. This figure is not covered by the CC BY licence. [Source: www.mapy.cz< <http://www.mapy.cz>>]. All rights reserved, used with permission. Drawings were added in Photoshop 5.0 software.

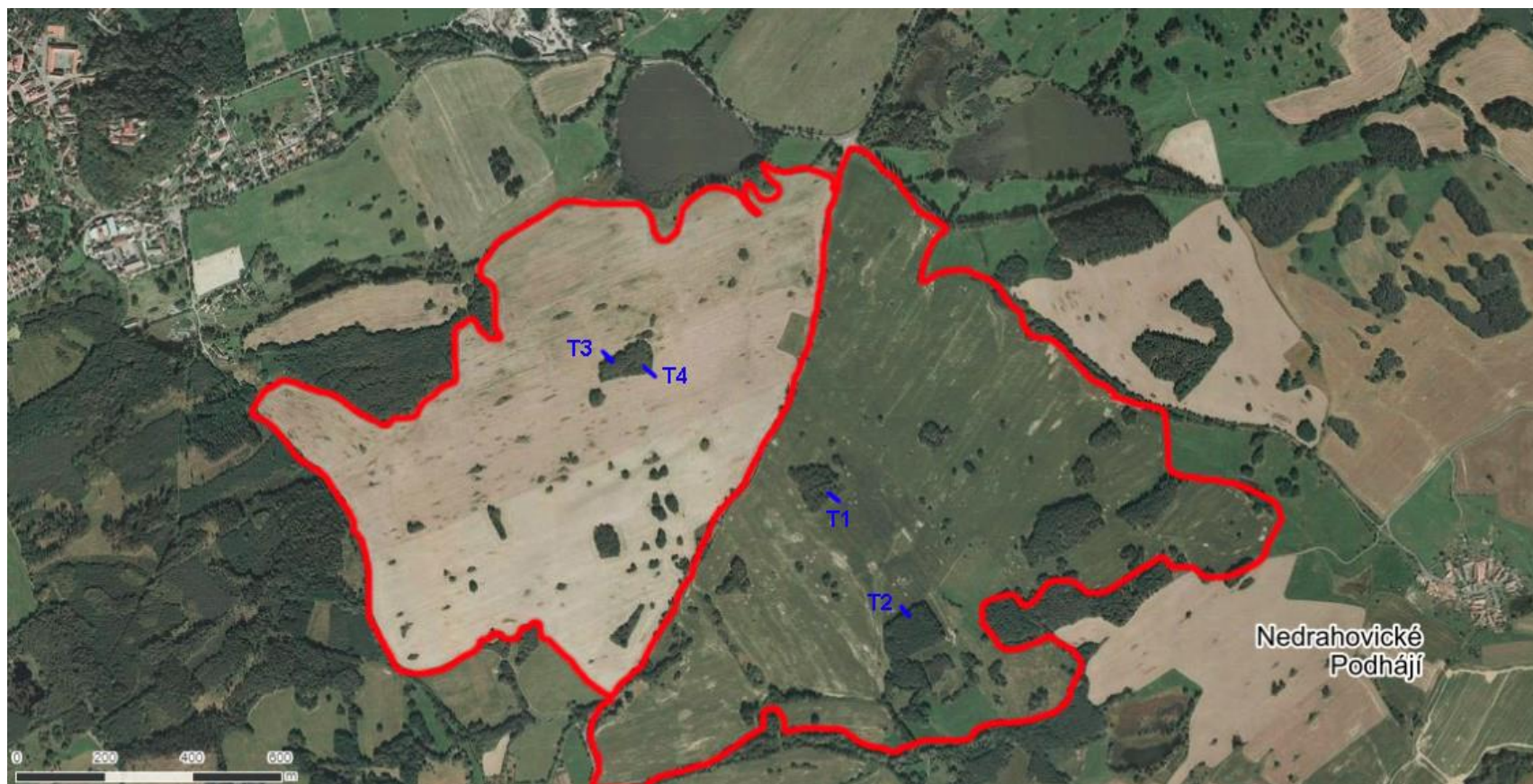


Figure S2 - Comparison of carabid abundance (activity-density) between woodlot and arable field interiors

```
> m<-glmmPQL(N~Period*Position, random =~ 1|Transect, family=quasipoisson, data=dat)
```

```
> anova.lme(m, test="F")
```

	numDF	denDF	F-value	p-value
(Intercept)	1	21	621.4771	<.0001
Period	3	21	10.1275	0.0002
Position	1	21	16.0571	0.0006
Period:Position	3	21	0.3696	0.7757

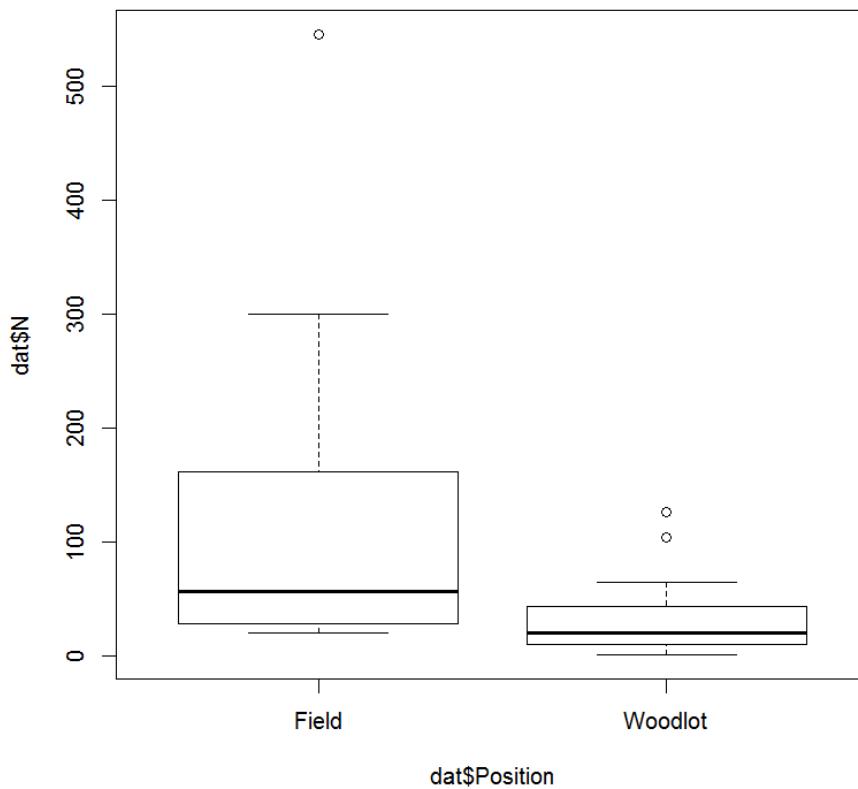


Figure S3 - Temporal shifts in species composition of carabid assemblages originating from various sampling sites (positions on transects)

For the purpose of visualisation of temporal shifts in carabid assemblages originating from particular distances, unconstrained unimodal analysis DCA was performed. Samples were classified according to the position on a transect (-20 m = yellow, -10 m = orange, -3 m = red, 0 m = brown, 3 m = light green, 10 m = medium green, 20 m = dark green) within resulting ordination diagram and these originating from the same transect were connected by lines to highlight temporal changes of respective carabid assemblages.

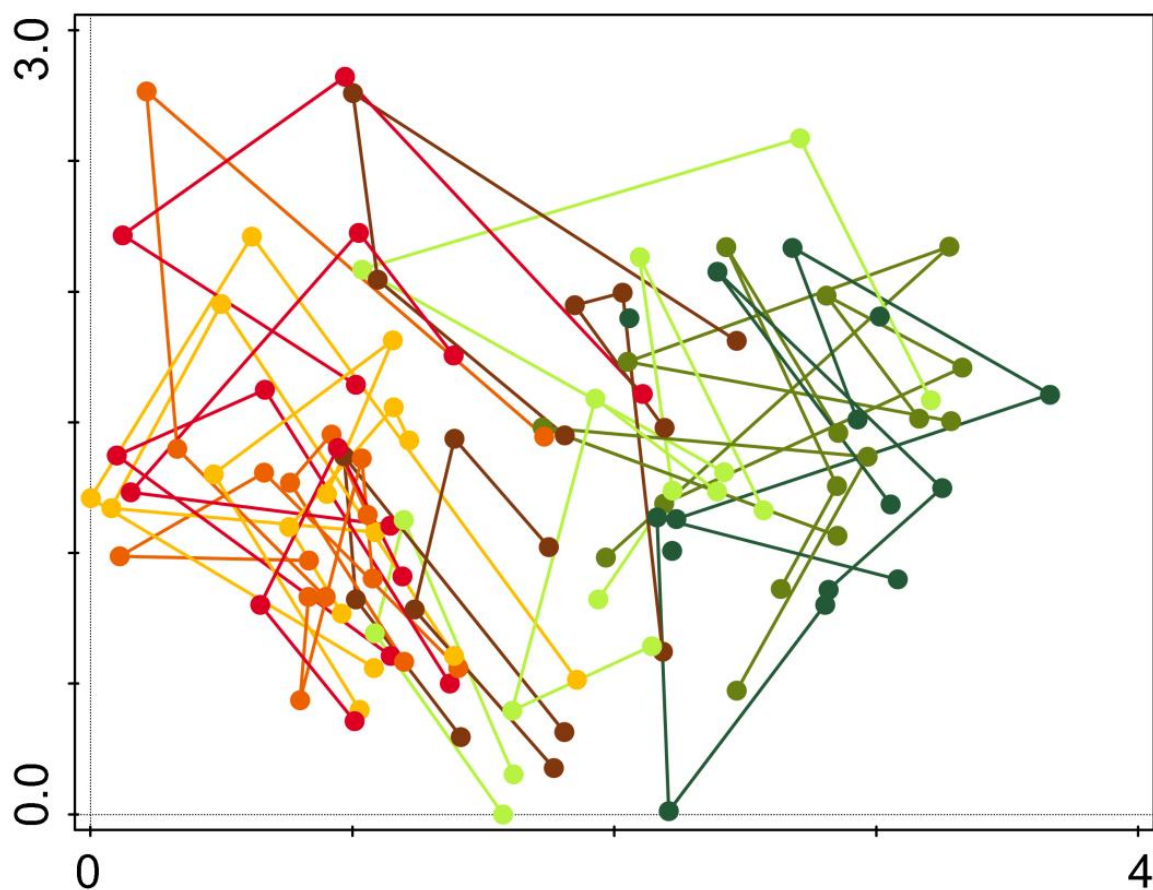
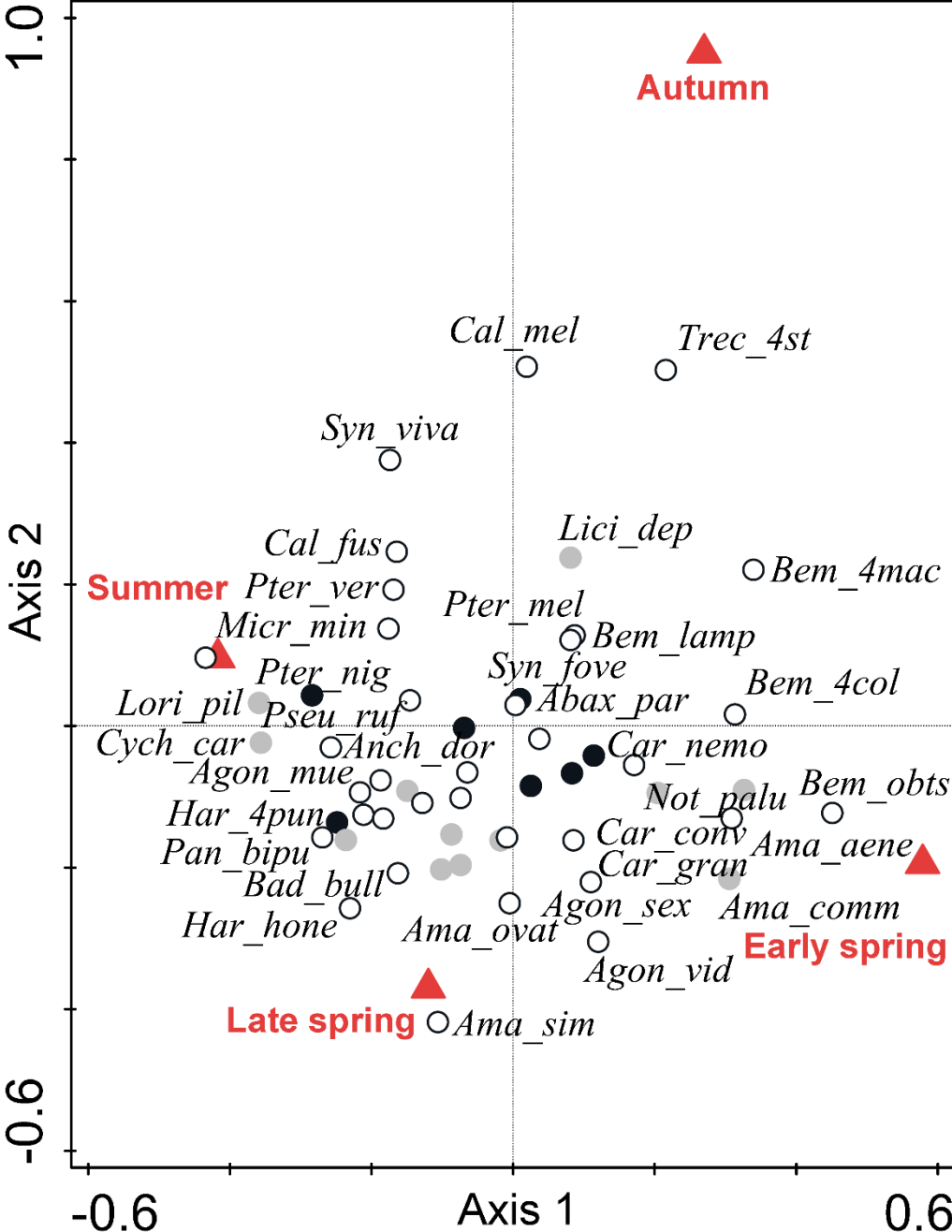


Figure S4 - Net effect of time on species composition of carabid assemblages



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R script

```
### Supplementary material to the manuscript#
### Temporal changes in the spatial distribution of carabid beetles
around arable field-woodlot boundaries -----
### code written by Martin Macek martin.macek@ibot.cas.cz

#code written and used under R 3.2.5 version
library(eHOF) #using eHOF version 1.7

carabid <- read.table("carabid.csv",sep=";",head=T) #read data from file
str(carabid) #check table structure

#carabid activity
#compares spatial structure of activity of carabid beetles (using
relative numbers - e.g. actual number of individuals at given sample
divided by transect total at given sampling period)

month.sel <- c(7,10,4,5) # select sampling periods for pairwise
comparison
bootnr <- 499 #set number of permutations
x <- unique(head.sp$Distance)
set.seed(324)
types <- c("I","II","III","IV","V")

#relative activity
variables <- c("std.count","o.count","f.count","g.count") #select
variable of interest: relative activity
var.names <- c("All carabids","Open habitat species","Forest
species","Habitat generalists")

#relative diversity
variables <- c("total.prop","open.prop","for.prop","gen.prop") #select
variable of interest: relative diversity
var.names <- c("All carabids","Open habitat species","Forest
species","Habitat generalists")

#prepare multiple-plot window
widths <- rep(1,length(variables))
widths[1] <- 1.1 # make first column 10% wider
heights <- rep(1,length(month.sel))
heights[length(month.sel)] <- 1.1 # make last row 10% wider

#pdf("relative_activity.pdf",8,8) #inicialize pdf device (relative
activity)
pdf("relative_diversity.pdf",8,8) #inicialize pdf device (relative
diversity)

layout(mat=matrix(data =
1:(length(variables)*length(month.sel)),nrow=length(variables),ncol=4,byr
ow=T),widths=widths,heights=heights)

for(j in 1:length(variables)){
  variable <- variables[j]
```

```

set.seed(324)
for(k in 1:4){
  pair <- month.sel[-k] #rest of the year to be compared with
selected month
  hof.pred <- matrix(data= NA, nrow = length(-20:20), ncol = bootnr)
#create matrix to store bootstrapped values
  for(i in 1:bootnr){subs <- c(sample(which(carabid$Distance == x[1]
& carabid$Month %in% pair),12,replace=T), #sample values with
replacement for each transect position
                                sample(which(carabid$Distance == x[2]
& carabid$Month %in% pair),12,replace=T),
                                sample(which(carabid$Distance == x[3]
& carabid$Month %in% pair),12,replace=T),
                                sample(which(carabid$Distance == x[4]
& carabid$Month %in% pair),12,replace=T),
                                sample(which(carabid$Distance == x[5]
& carabid$Month %in% pair),12,replace=T),
                                sample(which(carabid$Distance == x[6]
& carabid$Month %in% pair),12,replace=T),
                                sample(which(carabid$Distance == x[7]
& carabid$Month %in% pair),12,replace=T))
  occ <- carabid[subs,variable] #permuted relative activity values
  grad <- carabid[subs,"Distance"] #transect positions of permuted
samples
  hof.rnd <- HOF(occ,grad,family = gaussian,boot= NULL,selectMethod =
"IC.weight", modeltypes=types,M=1,lim=100,test="Dev") #HOF model
  hof.pred[,i] <-
predict(hof.rnd,model=pick.model(hof.rnd,test="Dev",modeltypes
=types),newdata = c(-20:20)) #store prediction from model to matrix
}

  occ.obs.yr <- carabid[carabid$Month %in% pair,variable] #permuted
relative activity values
  grad.yr <- carabid[carabid$Month %in% pair,"Distance"] #transect
positions of permuted samples
  hof.yr <- HOF(occ.obs.yr,grad.yr,family = gaussian,boot=
NULL,selectMethod = "IC.weight", modeltypes=types,M=1,lim=100,test="Dev")
#HOF model
  hof.pred.yr <-
predict(hof.rnd,model=pick.model(hof.rnd,test="Dev",modeltypes
=types),newdata = c(-20:20)) #store prediction from model to matrix

  pair.2 <- month.sel[k] #month selected for comparison, same as
previos
  hof.pred.2 <- matrix(data= NA, nrow = length(-20:20), ncol =
bootnr)
  for(i in 1:bootnr){subs.2 <- c(sample(which(carabid$Distance ==
x[1] & carabid$Month %in% pair.2),4,replace=T), #sample values with
replacement for each transect position
                                sample(which(carabid$Distance ==
x[2] & carabid$Month %in% pair.2),4,replace=T),
                                sample(which(carabid$Distance ==
x[3] & carabid$Month %in% pair.2),4,replace=T),
                                sample(which(carabid$Distance ==
x[4] & carabid$Month %in% pair.2),4,replace=T),

```

```

                                sample(which(carabid$Distance ==
x[5] & carabid$Month %in% pair.2),4,replace=T),
                                sample(which(carabid$Distance ==
x[6] & carabid$Month %in% pair.2),4,replace=T),
                                sample(which(carabid$Distance ==
x[7] & carabid$Month %in% pair.2),4,replace=T))
    occ.2 <- carabid[subs.2,variable]
    grad.2 <- carabid[subs.2,"Distance"]
    hof.rnd.2 <- HOF(occ.2,grad.2,family = gaussian,boot=
NULL,selectMethod = "IC.weight", modeltypes=types,M=1,lim=100,test="Dev")
    hof.pred.2[,i] <-
predict(hof.rnd.2,model=pick.model(hof.rnd.2,test="Dev",modeltypes
=types),newdata = c(-20:20))
}

#HOF for original data
occ.obs <- carabid[which(carabid$Month == pair.2),variable]
grad.obs <- carabid[which(carabid$Month == pair.2),"Distance"]
hof.obs <- HOF(occ.obs,grad.obs,family = gaussian,boot=
NULL,selectMethod = "IC.weight", modeltypes=types,M=1,lim=100,test="Dev")
hof.obs.pred <-
predict(hof.rnd.2,model=pick.model(hof.rnd.2,test="Dev",modeltypes
=types),newdata = c(-20:20))

#plot results
if(k == 1) par(mar=c(3,4.5,0.5,0.5)) # make space for labels in
first column
if(k > 1) par(mar=c(3,3,0.5,0.5))
if(k == 1 & j == 4) par(mar=c(4.5,4.5,0.5,0.5)) # make space for
labels in first column of last row
if(k > 1 & j == 4) par(mar=c(4.5,3,0.5,0.5)) # make space for
labels in last row

ylim <- max(carabid[,variable]) #set ylim for a row using maximum
observed value of variable
plot(seq(-20,20,1),
apply(hof.pred,1,quantile,0.5),ylim=c(0,ylim),type="n",xlab=NA,ylab=NA,ma
in=NA,cex.axis=1.1)
grid(lty=3,col="gray60")
#text(-20,ylim*0.9,c(month.sel)[k],cex=1.2,pos=4) code by months
text(-20,ylim*0.9,LETTERS[(j-1)*length(month.sel) +
k],cex=1.2,pos=4) #code by letters
if(k == 1) mtext(var.names[j],2,3,cex=1.1) #y axis labels

polygon(c(-20:20,20:-20),
c(apply(hof.pred,1,quantile,0.025),rev(apply(hof.pred,1,quantile,0.975)))
,col="#00000030",border=NA)
lines(-20:20, apply(hof.pred,1,median),lwd=2,lty=2) #median of
bootstrapped model predictions
#lines(-20:20, hof.pred.yr,lwd=2,lty=2) #observed model prediction

polygon(c(-20:20,20:-20),
c(apply(hof.pred.2,1,quantile,0.025),rev(apply(hof.pred.2,1,quantile,0.97
5))),col="#AD111160",border=NA)
lines(-20:20, apply(hof.pred.2,1,median),lwd=2,lty=1,col=2) #median
of bootstrapped model predictions
#lines(-20:20,hof.obs.pred,lwd=2,lty=1,col=2) #original data fit

```



```
        if(k == 3 & j == length(variables)) mtext("Distance from arable  
field-woodlot boundary (m)",1,3,cex=1.2,adj=1)  
    }  
}  
dev.off()
```