

# Beta diversity in space and time



# $\beta$ diversity

Please run these lines now!

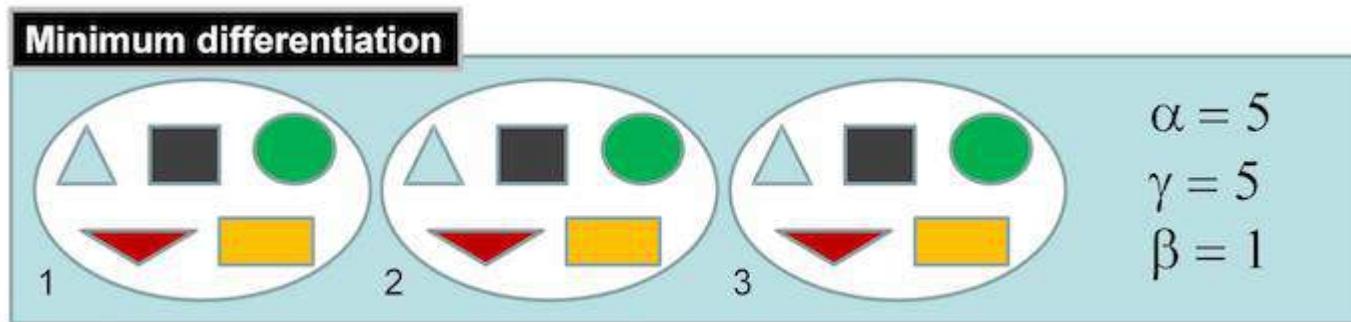
```
library(adklakedata)
zoops <- adk_data('crustacean')
pH <- adk_data('chem')
```

Other packages to load/install if you haven't done so yet)

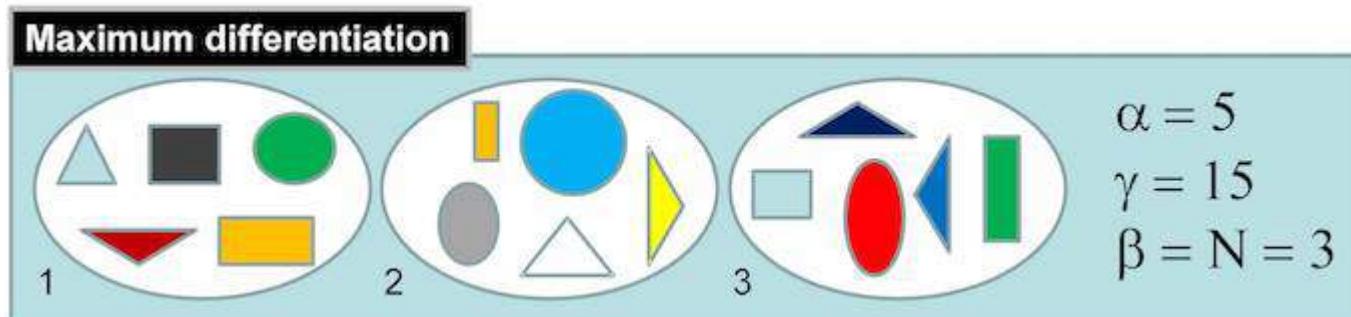
```
library(RCurl)
library(vegan)
library(gclus)
library(RColorBrewer)
library(ade4)
library(adespatial)
library(dplyr)
library(tidyr)
library(magrittr)
library(ggplot2)
```

# $\beta$ diversity

- Defined by R.H. Whittaker in 1960 as gamma / mean(alpha)
- Low  $\beta$  diversity



- High  $\beta$  diversity



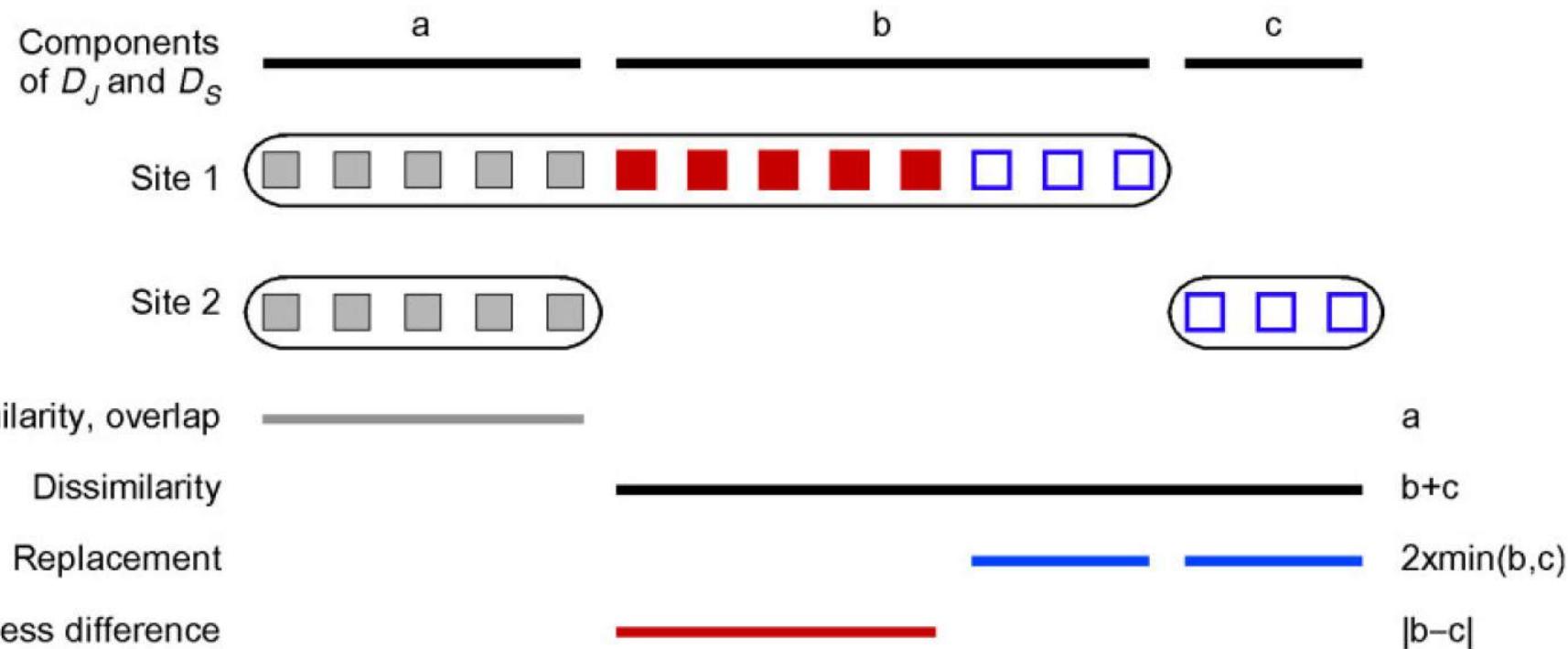
# $\beta$ diversity

- Key driver of metacommunity dynamics
- Affected by human disturbances (e.g. biotic homogenization). Important conservation target.
- Beta diversity among pairs of sites: dissimilarity indices (Jaccard, Sørensen, Bray-Curtis). Abundance or incidence based.
- Anderson *et al.* (2011) Navigating the multiple meanings of  $\beta$  diversity: a roadmap for the practicing ecologist. *Ecology Letters* **14**:19-28.
- [https://methodsblog.wordpress.com/2015/05/27/beta\\_diversity/](https://methodsblog.wordpress.com/2015/05/27/beta_diversity/)

# $\beta$ diversity

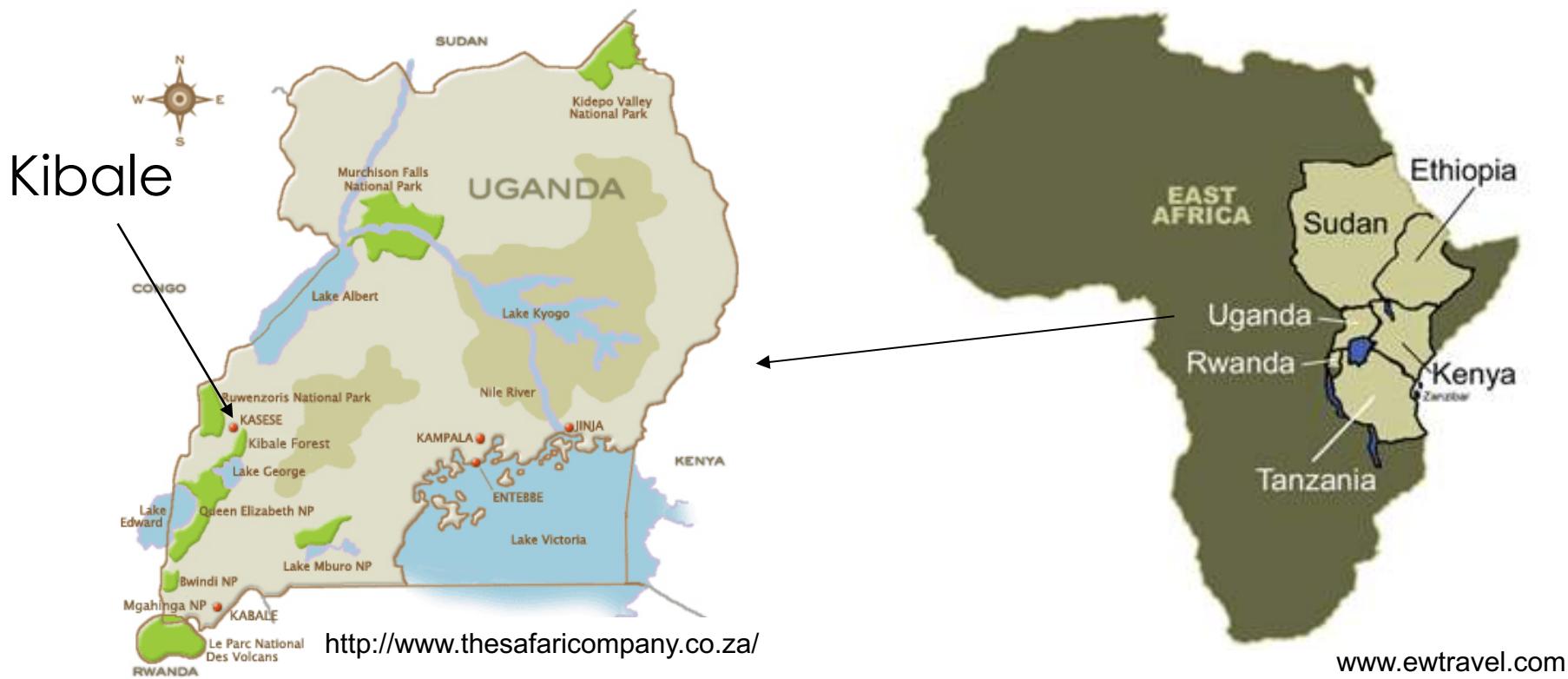
## Components of beta diversity

**total dissimilarity = replacement + richness differences**



# Example1: Kibale Forest (spatial $\beta D$ )

Park in the 'Eastern Afromontane biodiversity hotspot'.  
Does deforestation influence stream  $\beta$  diversity?



# Example1: Kibale Forest (spatial $\beta D$ )



Kibale

# Example1: Kibale Forest (spatial $\beta D$ )



# Example1: Kibale Forest (spatial $\beta D$ )

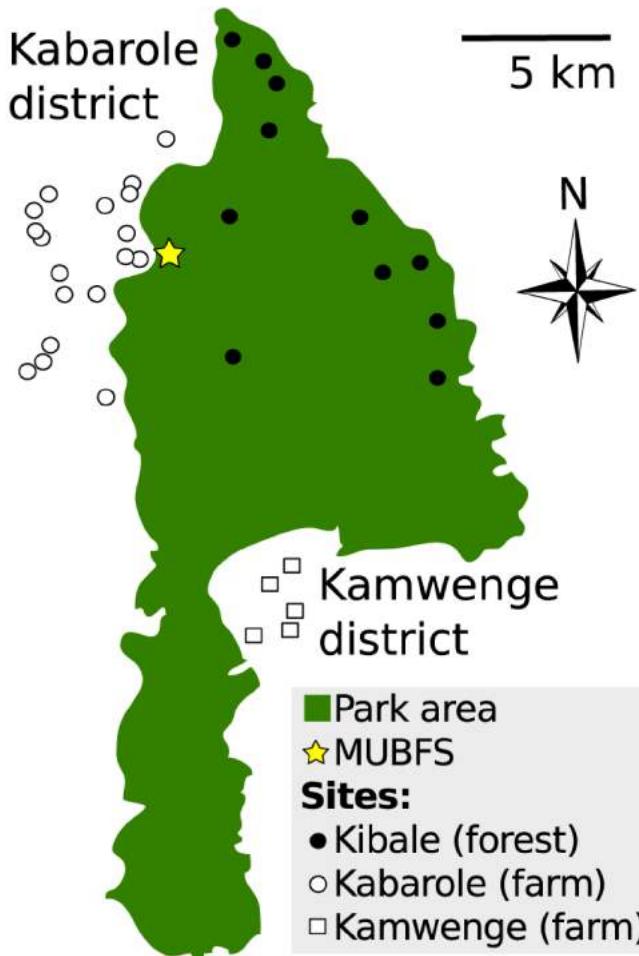


# Example1: Kibale Forest (spatial $\beta D$ )



# Example1: Kibale Forest (spatial $\beta D$ )

Environmental and community data from 11 forested streams and 23 agricultural streams.



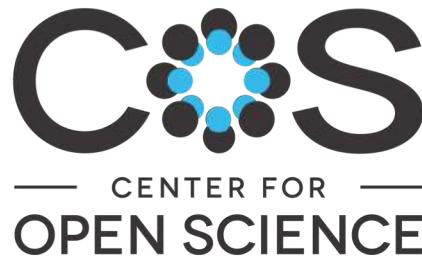
# Example1: Kibale Forest (spatial $\beta D$ )

## Getting the dataset from Github

```
kib <- read.csv(text =  
getURL("https://raw.githubusercontent.com/VFugere/Q  
CBS_betadiv/master/kibale_inverts.csv"), header=T)
```

## Getting the dataset from OSF

```
devtools::install_github('chartgerink/osfr')  
library(osfr)  
osfr::download_files('zc6xt', '/Users/Vincent/Desktop/')  
kib <- read.csv('/Users/Vincent/Desktop/kibale_inverts.csv',  
header=T)
```



# Example1: Kibale Forest (spatial $\beta D$ )

Fixing some issues:

```
colnames(kib) [1] <- 'site.code'  
kib$land.use <- relevel(kib$land.use, 'park')
```

Have a look at the data:

```
head(kib)  
str(kib)
```

Will model community composition (columns  
aeshnidae:veliidae) ~ land.use. Useful matrices:

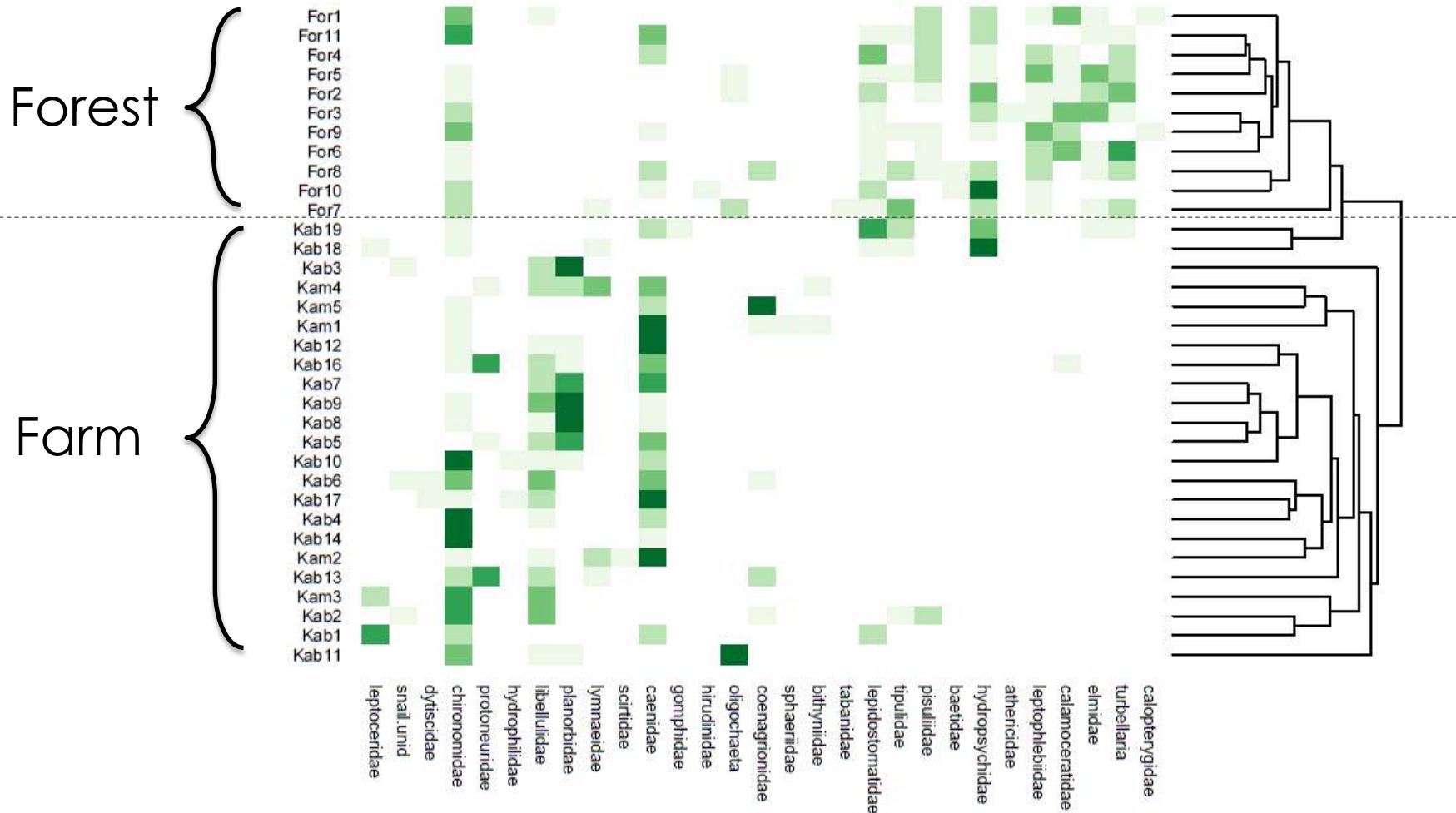
```
spe <- kib[,-c(1:3)]  
row.names(spe) <- kib$site.code  
site <- kib[,2:3]  
rownames(site) <- kib[,1]
```

# Example1: Kibale Forest (spatial $\beta D$ )

## 'Classic' community composition analysis

```
spe.dis <- vegdist(log1p(spe), method='bray') #Bray-Curtis  
  
spe.dis.UPGMA <- hclust(spe.dis, method="average")  
spe.dis.o <- reorder.hclust(spe.dis.UPGMA, spe.dis)  
dend <- as.dendrogram(spe.dis.o)  
com.tx <- apply(t(spe),1,sum) #common taxa for heat map plot  
spe.com <- spe[,which(com.tx > 20)]  
or <- vegemite(spe.com, spe.dis.o,scale='log')  
heatmap(t(spe.com[or$species]), Rowv=NA, Colv=dend, cexRow=0.5,  
cexCol=0.5, col=c('white', brewer.pal(5,"Greens"))),  
scale="column", revC = T, margin=c(4.5,8))
```

# Example1: Kibale Forest (spatial $\beta D$ )



adonis(spe.dis ~ land.use, data=site, permutations=1000)

# Example1: Kibale Forest (spatial $\beta D$ )

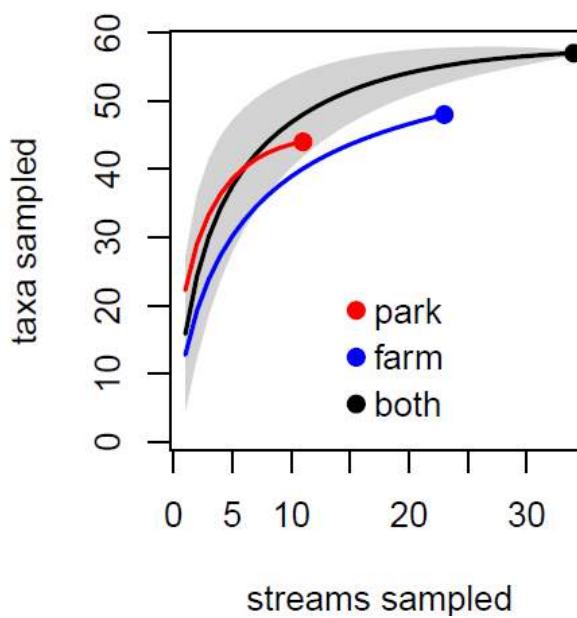
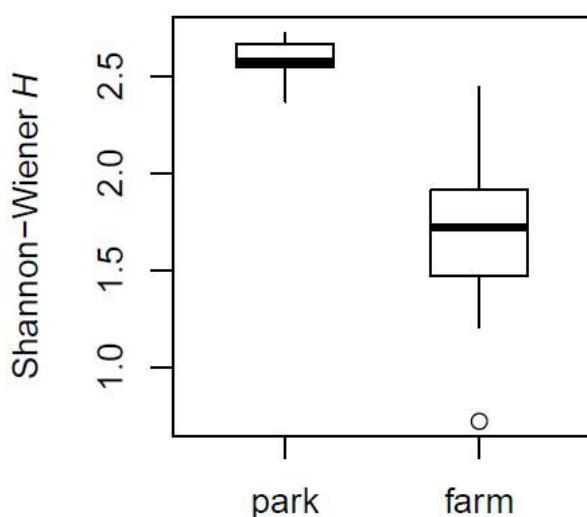
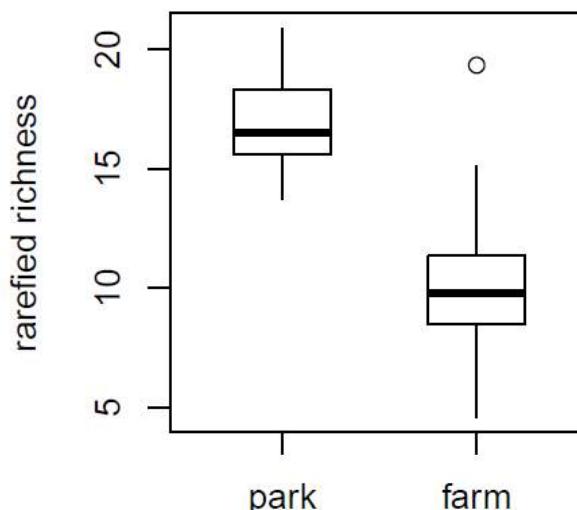
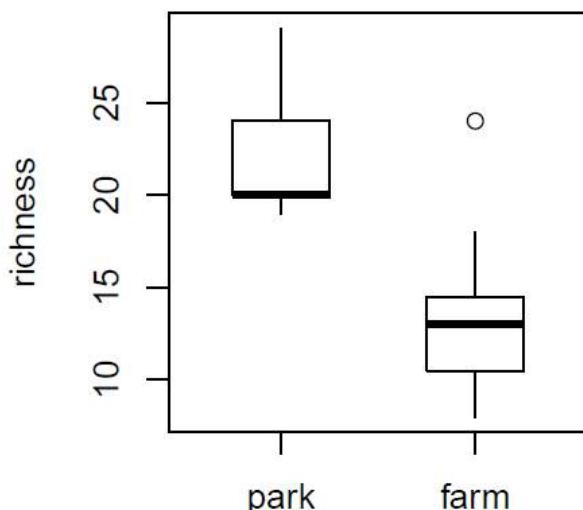
## Alpha diversity

```
div <- site[,1:2]
div$abund <- apply(spe,MARGIN=1,FUN=sum)
div$richness <- specnumber(spe)
div$r.richness <- rarefy(spe,min(div$abund))
div$shannon <- diversity(spe, index='shannon')
```

## Some boxplots then spec accum curves:

```
plot(specaccum(spe), xlab = "streams sampled", ylab = "taxa
sampled", ci.type='polygon', ci.col='light gray', ci.lty=0,
lwd=2)
plot(specaccum(spe[which(div$land.use == 'park'),]), add=TRUE,
ci=0, lwd=2, col='red')
plot(specaccum(spe[which(div$land.use == 'farm'),]), add=TRUE,
ci=0, lwd=2, col='blue')
points(x=c(34,11,23),y=c(57,44,48),pch=16,col=c(1,2,4),cex=1.2)
legend('bottom', legend = c('park','farm','both'), bty='n',
pt.cex=1.2, pch=16, col=c('red','blue','black'))
```

# Example1: Kibale Forest (spatial $\beta D$ )



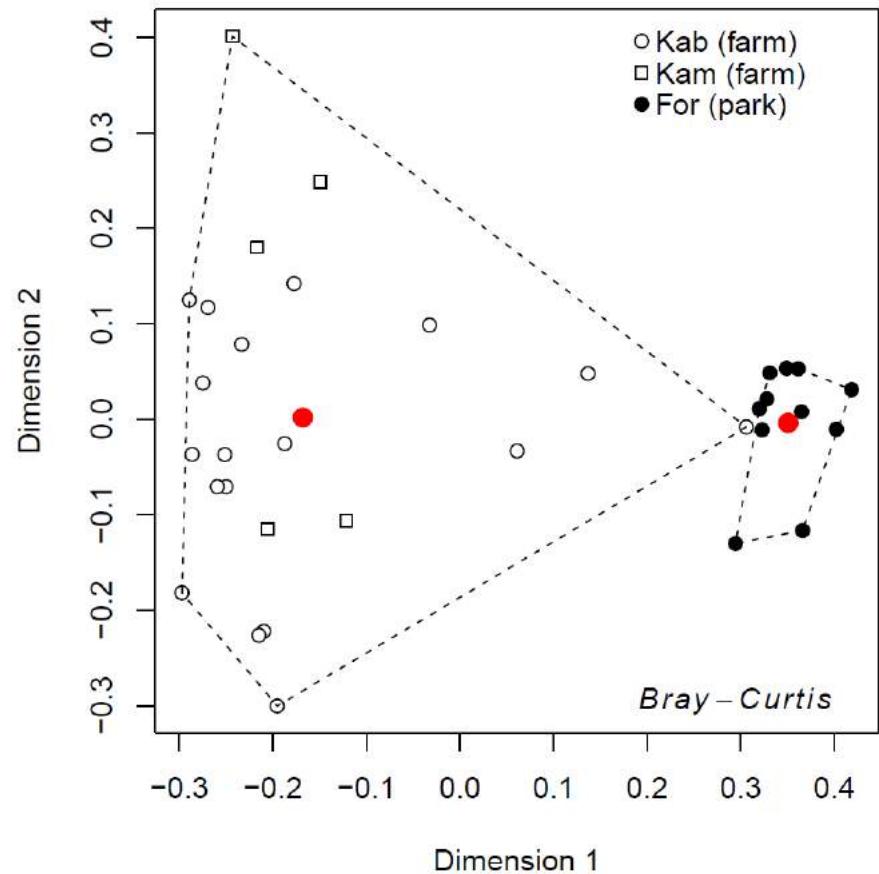
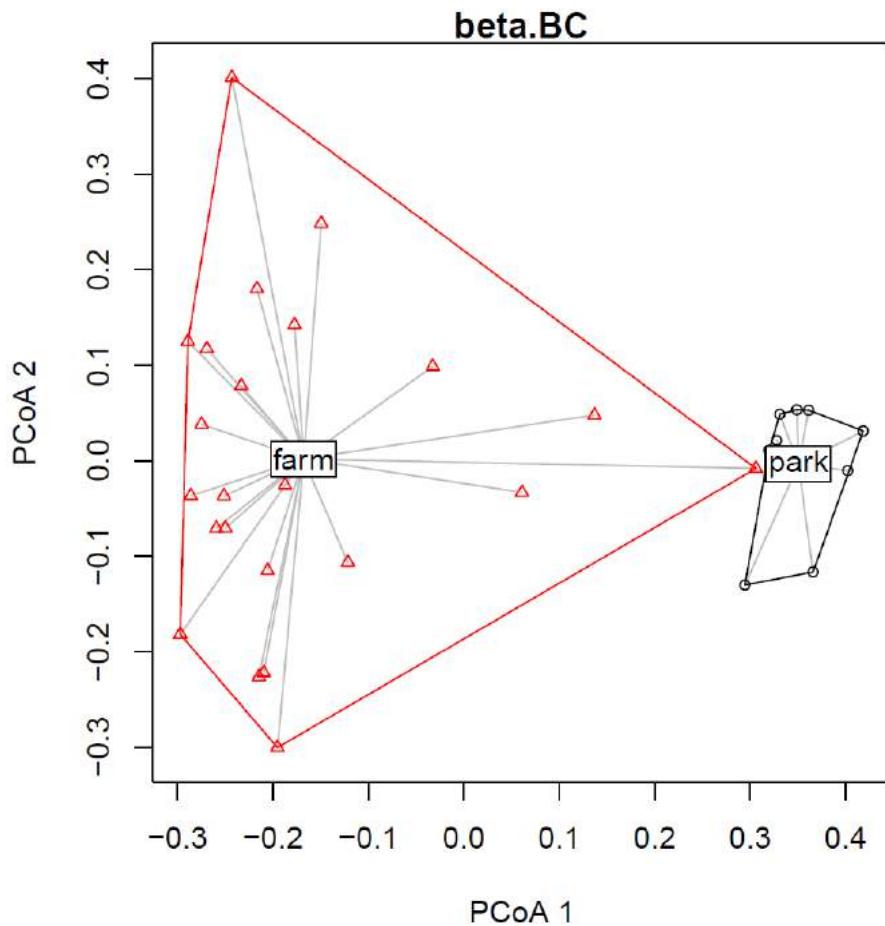
# Example1: Kibale Forest (spatial $\beta D$ )

```
#beta diversity, at last
```

```
beta.BC <- betadisper(spe.dis, site$land.use, type = 'centroid')
```

```
plot(beta.BC) #ugly
```

```
mybetadivplot(beta.BC)
```



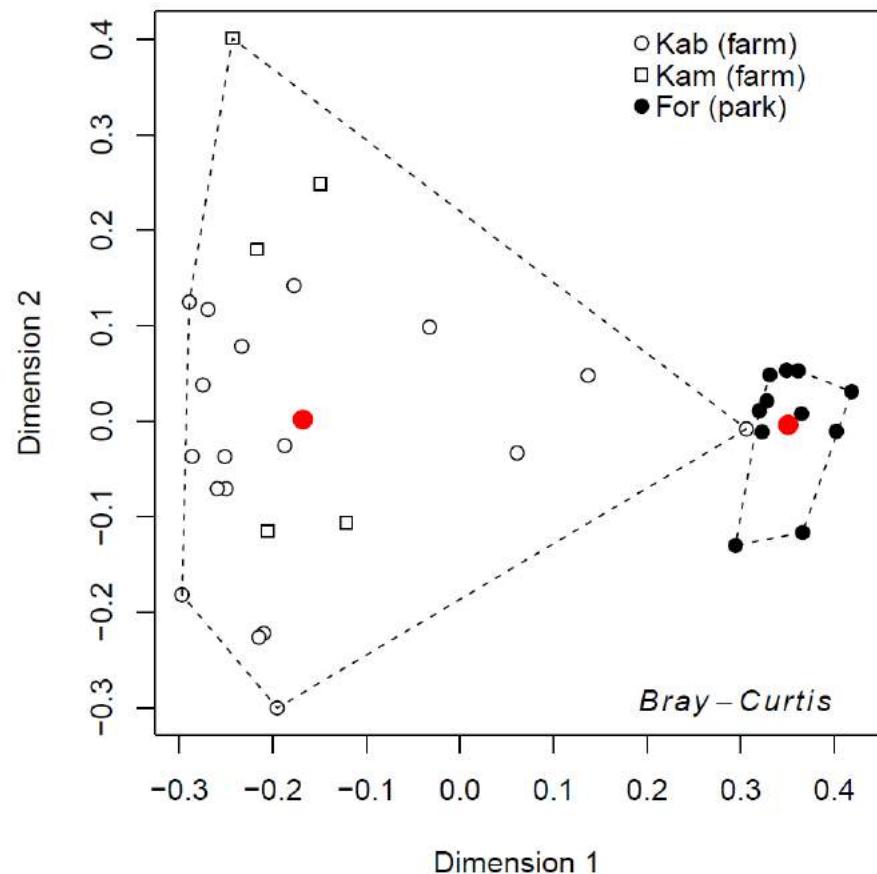
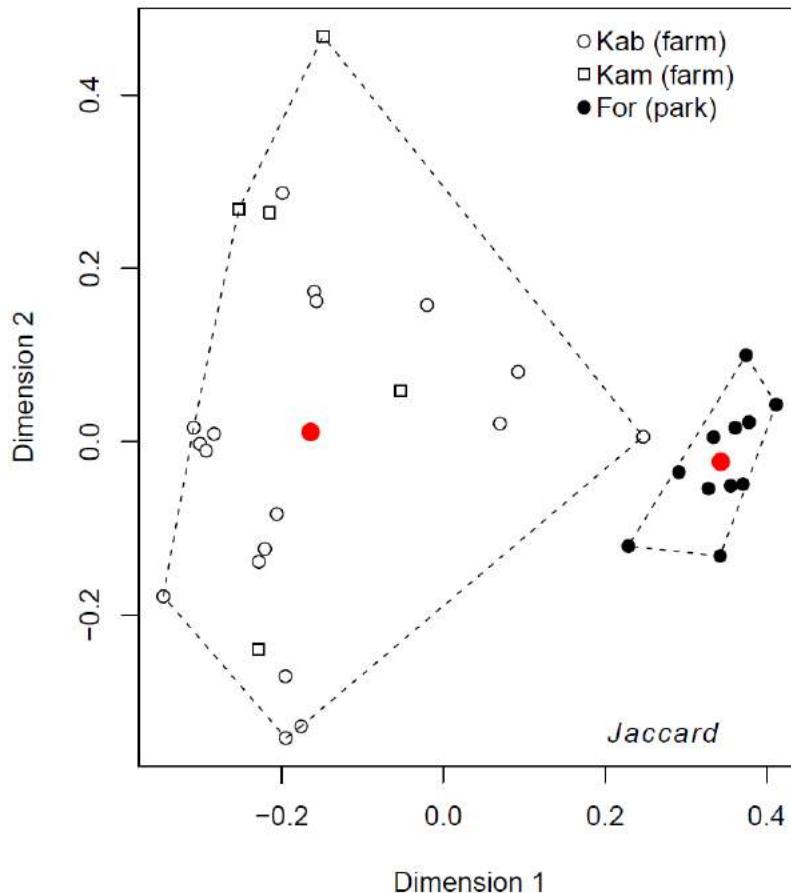
# Example1: Kibale Forest (spatial $\beta D$ )

```
#with incidence-based index instead
```

```
dist.jac <- vegdist(spe, method='jaccard', binary=T)
```

```
beta.jac <- betadisper(dist.jac, site$land.use, type='centroid')
```

```
mybetadivplot(beta.jac)
```



# Example1: Kibale Forest (spatial $\beta D$ )

```
permute test(beta.jac)
```

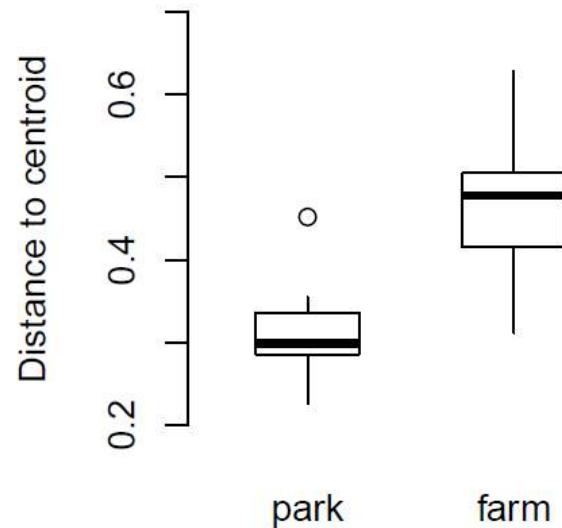
```
> permute test(beta.jac)

Permutation test for homogeneity of multivariate dispersions
Permutation: free
Number of permutations: 999

Response: Distances
      Df  Sum Sq  Mean Sq      F N.Perm Pr(>F)
Groups     1 0.16536 0.165361 32.538    999  0.001 ***
Residuals 32 0.16263 0.005082
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
```

```
boxplot(beta.jac$distances ~ site$land.use,
        ylab="Distance to centroid", whisklty=1,
        boxwex=0.5, staplelw=1, frame.plot=F,
        xaxt='n', ylim=c(.2,.7))

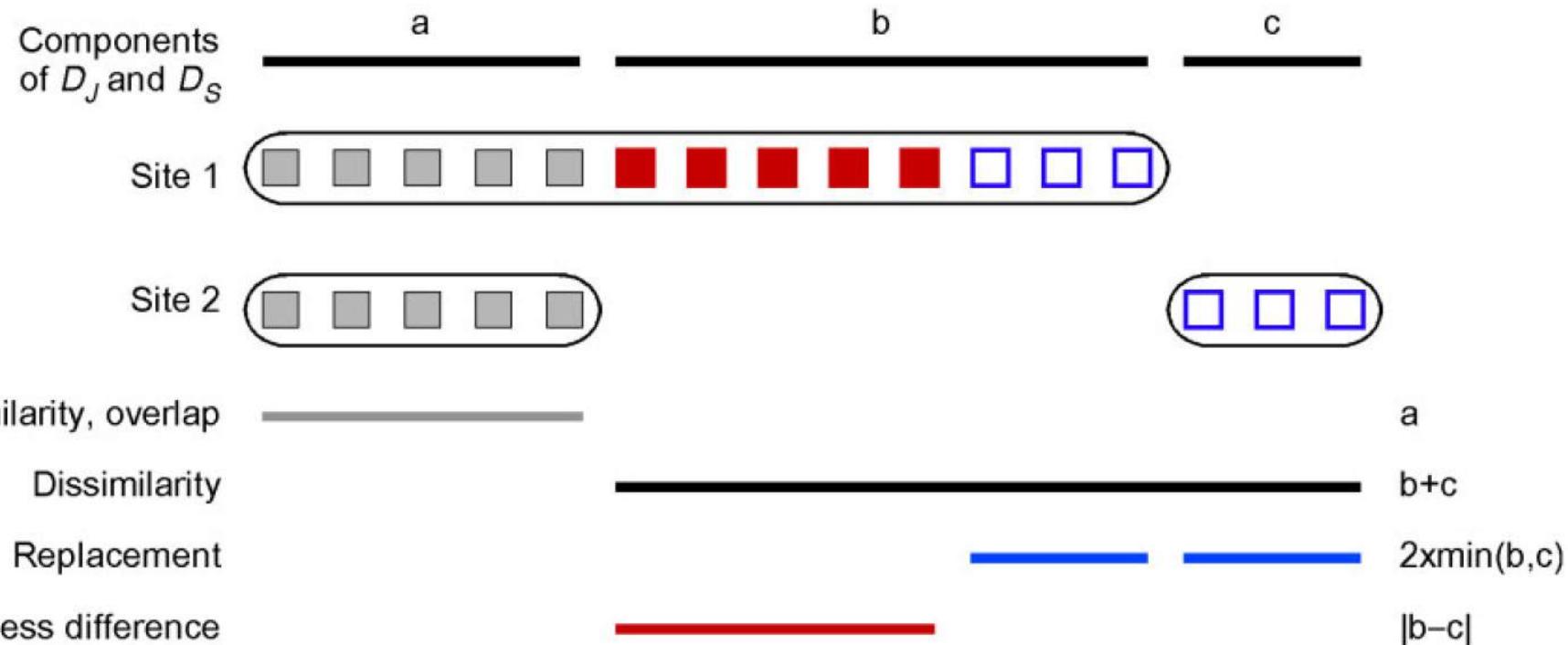
axis(1, at=c(1,2), labels=c('park','farm'),
     tick=F)
```



# Example1: Kibale Forest (spatial $\beta D$ )

But is it due to nestedness or actual turnover?

**total dissimilarity = replacement + richness differences**



# Example1: Kibale Forest (spatial $\beta D$ )

But is it due to nestedness or actual turnover? Partitioning total dissimilarity into replacement and richness diff:

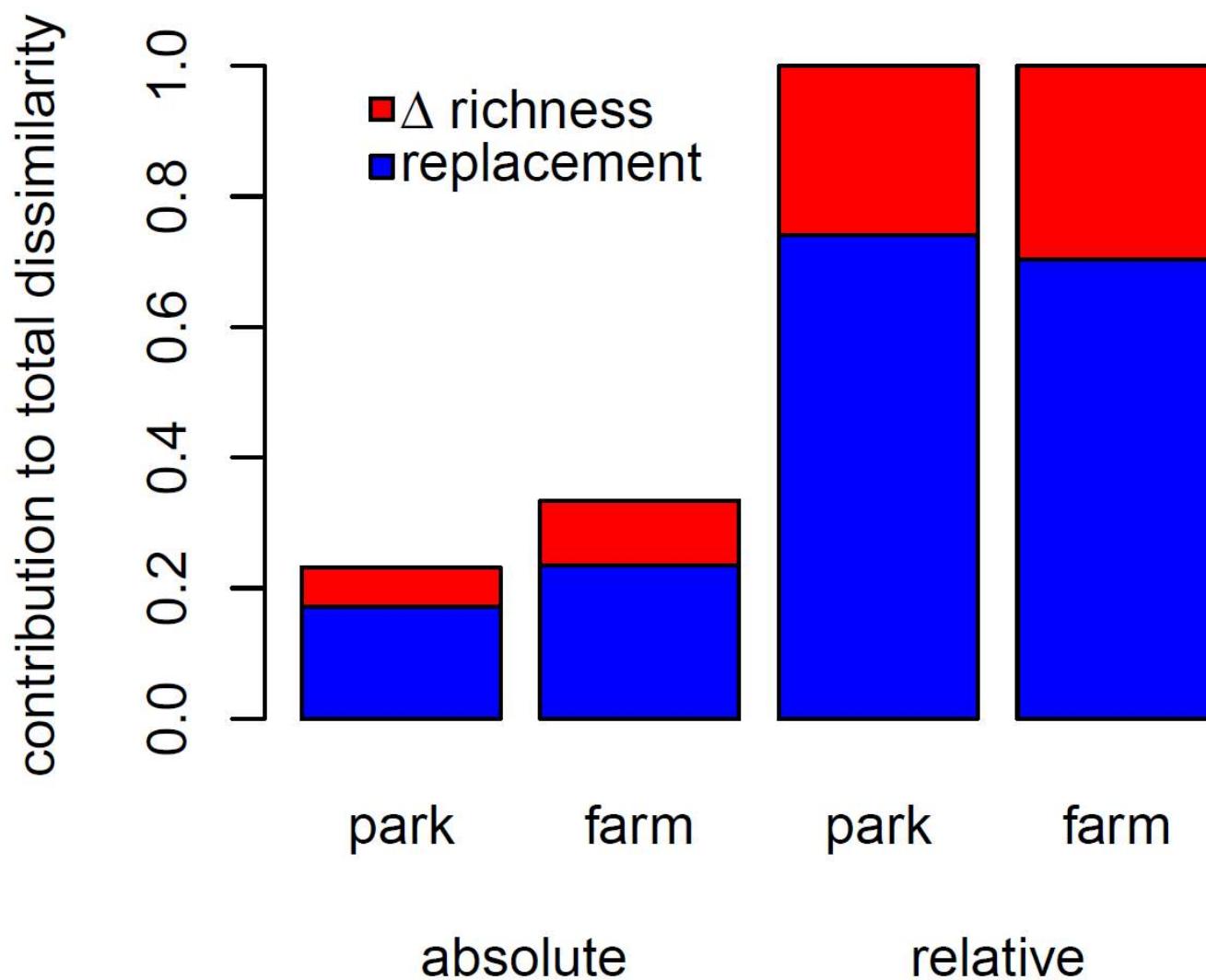
```
park.jac <- beta.div.comp(spe[site$land.use == 'park', ],  
    coef='J', quant=F)  
farm.jac <- beta.div.comp(spe[site$land.use == 'farm', ],  
    coef='J', quant=F)  
park.jac
```

The screenshot shows an R console window with the following output:

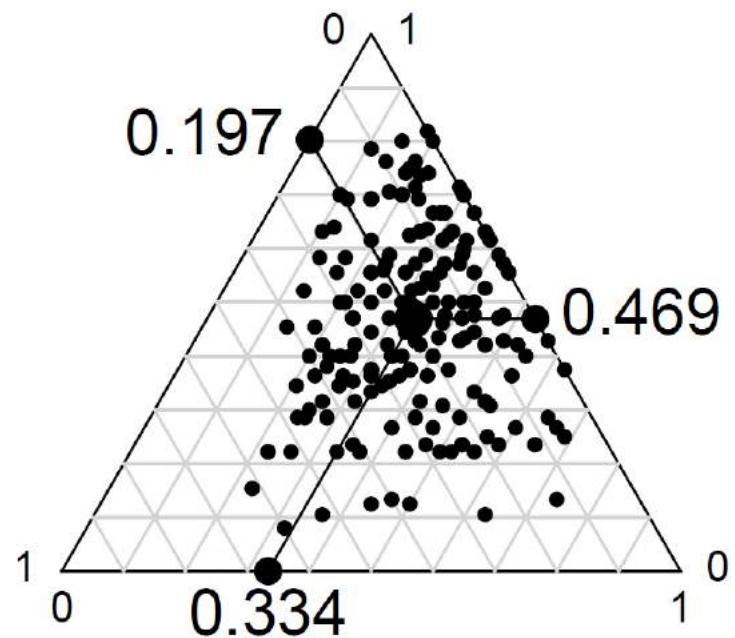
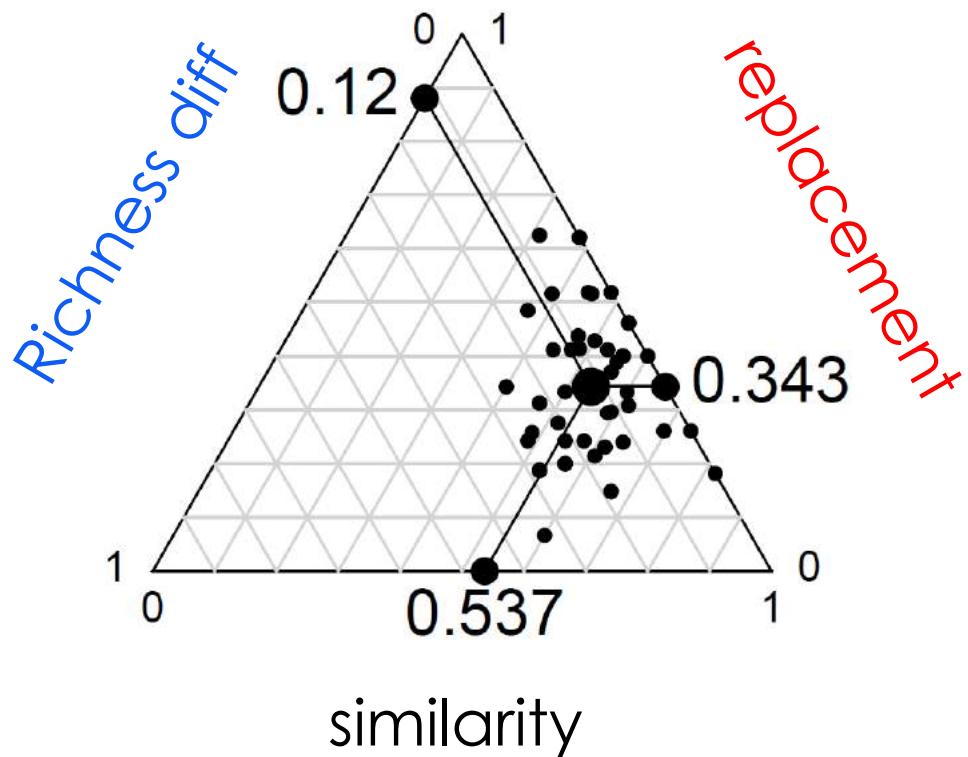
```
Console ~/ ↗  
For9  
For10  
For11 0.25806452  
  
$D  
For1 For2 For3 For4 For5 For6 For7 For8 For9 For10  
For2 0.4545455  
For3 0.5312500 0.4117647  
For4 0.5483871 0.4242424 0.4000000  
For5 0.3846154 0.4687500 0.3928571 0.4642857  
For6 0.4444444 0.4687500 0.3333333 0.4074074 0.4000000  
For7 0.6875000 0.6000000 0.6363636 0.6129032 0.5185185 0.6206897  
For8 0.4444444 0.5151515 0.5000000 0.5172414 0.2608696 0.4615385 0.4615385  
For9 0.5000000 0.4687500 0.3333333 0.4642857 0.4000000 0.1818182 0.6206897 0.4615385  
For10 0.5588235 0.4444444 0.4705882 0.5294118 0.4333333 0.5312500 0.4333333 0.4333333 0.5312500  
For11 0.3600000 0.4000000 0.4827586 0.3846154 0.3043478 0.4400000 0.5555556 0.4400000 0.4400000 0.5161290  
  
$part  
BDtotal Repl RichDif Repl/BDtotal RichDif/BDtotal  
0.2317362 0.1715647 0.0601715 0.7403448 0.2596552  
  
$Note
```

\*If used abundance-based index, would change 'quant' to TRUE.  
Would then get replacement vs. abundance differences

# Example1: Kibale Forest (spatial $\beta D$ )



# Example1: Kibale Forest (spatial $\beta D$ )



# Example1: Kibale Forest (spatial $\beta D$ )

Example used the ‘Podani’(and Schmera) partitioning method. Alternative is ‘Baselga’ method/indices, either using `beta.div.comp()` or package ‘betapart’



János Podani & Dénes Schmera



**Methods in Ecology and Evolution** PART OF ECOLOGICAL SOCIETY

APPLICATION |  Free Access

## betapart: an R package for the study of beta diversity

Andrés Baselga , C. David L. Orme

First published: 18 June 2012 | <https://doi.org/10.1111/j.2041-210X.2012.00224.x> | Cited by: 232

Correspondence site: <http://www.respond2articles.com/MEE/>

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Andres Baselga

# Example1: Kibale Forest (spatial $\beta D$ )

Example used the ‘Podani’(and Schmera) partitioning method. Alternative is ‘Baselga’ method/indices, either using `beta.div.comp()` or package ‘betapart’



## Global Ecology and Biogeography

A Journal of  
Macroecology

Macroecological Methods | Free Access

### Interpreting the replacement and richness difference components of beta diversity

Pierre Legendre

First published: 16 July 2014 | <https://doi.org/10.1111/geb.12207> | Cited by: 119

Editor: José Alexandre Diniz-Filho

SECTIONS

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41 pp. of supp mat (!) explain the various Baselga/Podani indices at length

# Example 2: Adirondack lakes (temporal $\beta D$ )

```
library(adklakedata)
zoops <- adk_data('crustacean')
pH <- adk_data('chem')
```

# SCIENTIFIC DATA

OPEN

**Data Descriptor: Long-term dataset on aquatic responses to concurrent climate change and recovery from acidification**

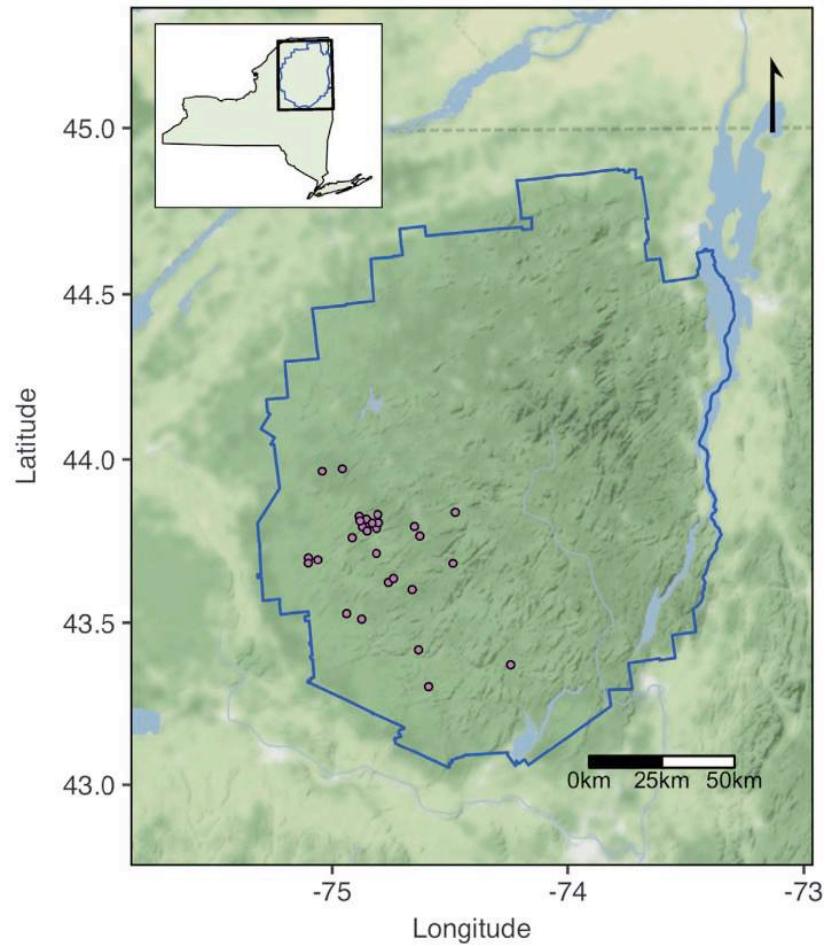
Received: 15 December 2017

Accepted: 22 February 2018

Published: 10 April 2018

Taylor H. Leach *et al.*<sup>#</sup>

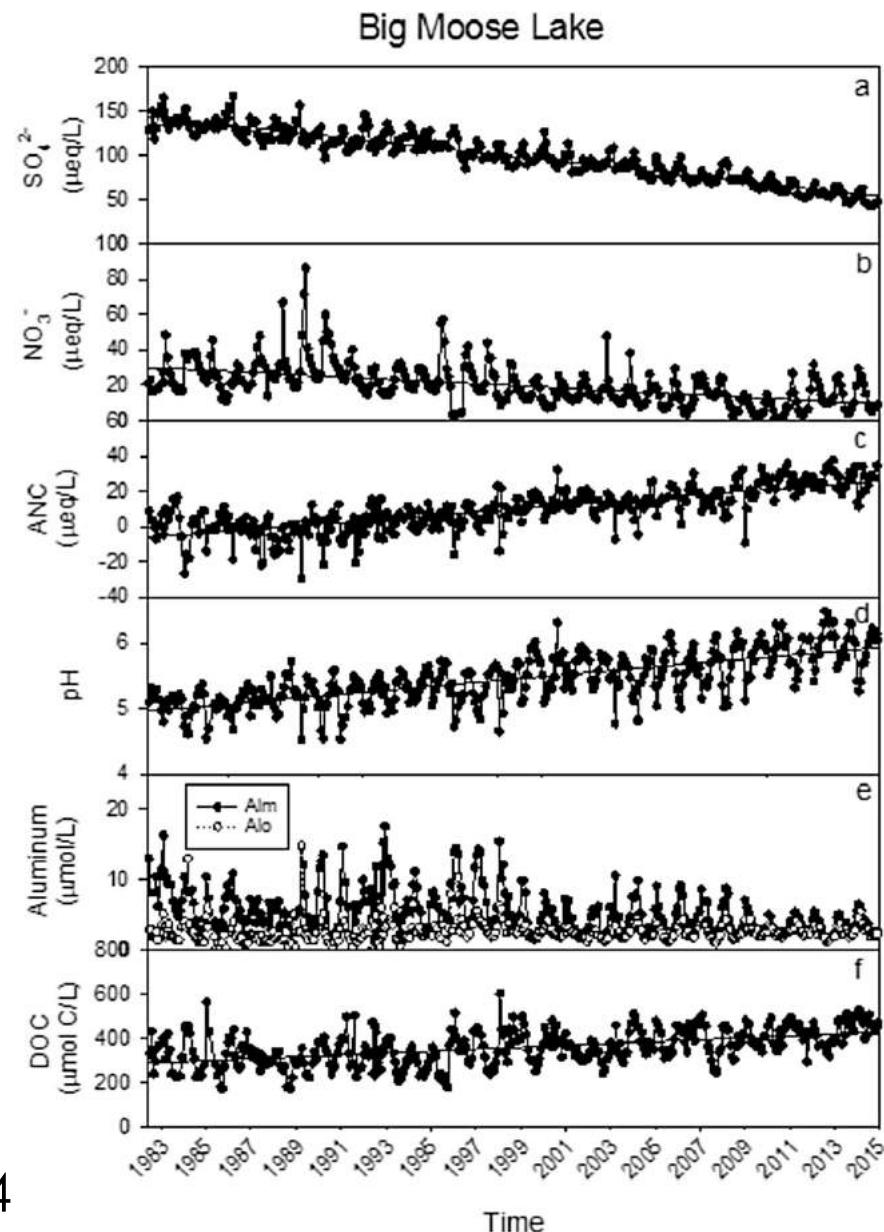
## Example 2: Adirondack lakes (temporal $\beta D$ )



# Example 2: Adirondack lakes (temporal $\beta D$ )



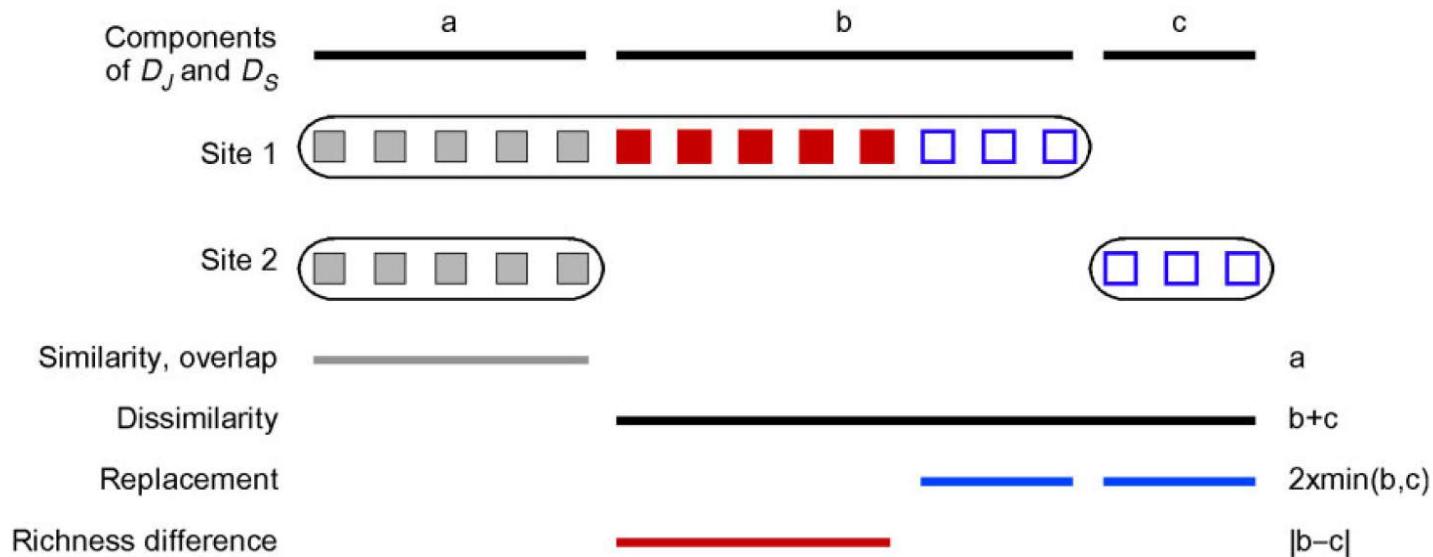
With ongoing recovery from acidification, have crustacean communities changed?



# Example 2: Adirondack lakes (temporal $\beta D$ )

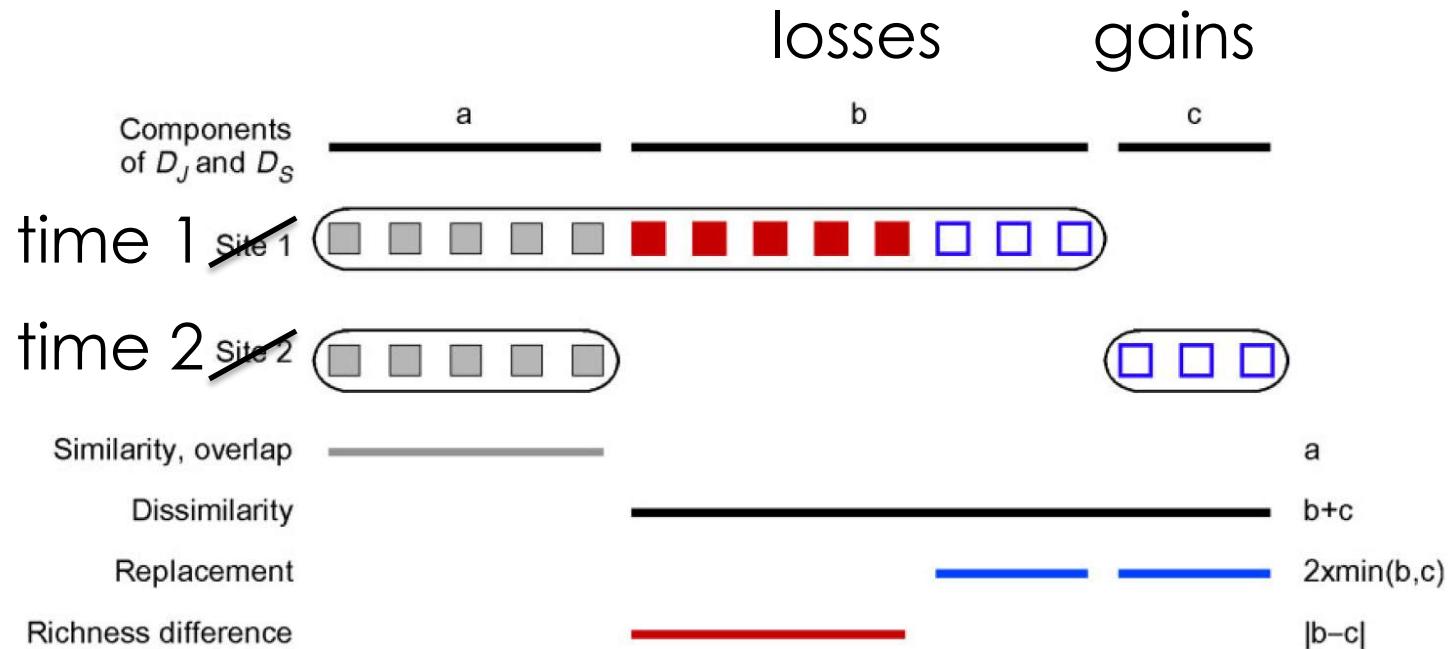


**total dissimilarity = replacement + richness differences**



**Temporal beta index (TBI) =  $D = B + C$**

# Example 2: Adirondack lakes (temporal $\beta D$ )



**Temporal beta index (TBI) =  $D = B + C$**

# Example 2: Adirondack lakes (temporal $\beta D$ )

Global Ecology  
and Biogeography

A Journal of  
Macroecology

Research Paper

## Diatom diversity patterns over the past c. 150 years across the conterminous United States of America: Identifying mechanisms behind beta diversity

Amanda K. Winegardner , Pierre Legendre, Beatrix E. Beisner, Irene Gregory-Eaves, Fabien Leprieur

First published: 4 October 2017 | <https://doi.org/10.1111/geb.12640>

Funding information FRQNT Équipe grant; NSERC PGS-D; McGill International Travel Grant; Q ... [More](#) ▾



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TOOLS



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<http://adn.biol.umontreal.ca/~numerical ecology/Rcode/>

```
TBIfunc <-  
getURL("https://raw.githubusercontent.com/VFugere/QCBS_beta

/master/TBI.R", ssl.verifyPeer = FALSE)  
  
eval(parse(text = TBIfunc))


```

## Appendix S3!

# Example 2: Adirondack lakes (temporal $\beta D$ )

```
zoops$Sp <- paste0(zoops$Genus, '.', zoops$Species) %>% as.factor  
zoops %<>%  
  select(-PERMANENT_ID, -date, -(month:ug_WWperind), -mgWW.l) %>%  
  group_by(lake.name, year, Sp) %>%  
  summarize(density = mean(org.l)) %>%  
  spread(Sp, density)
```

only 50% of lakes have data up to 2012. Others stop at 2006

```
with(zoops, table(lake.name, year))  
table <- with(zoops, table(lake.name, year))  
names(table[table[,18] == 1,18]) -> lakes2kp  
zoops %<>% filter(lake.name %in% lakes2kp)
```

Adding pH:

```
pH %<>% select(lake.name, year, pH) %>%  
  group_by(lake.name, year) %>%  
  summarize(pH = mean(pH))  
zoops <- left_join(zoops, pH, by = c('lake.name', 'year')) %>%  
  select(lake.name, year, pH, everything()) %>%  
  as.data.frame
```

# Example 2: Adirondack lakes (temporal $\beta$ D)

To use TBI() function, need a community matrix for time1 and time2

```
com.y1 <- zoops %>% filter(year == 1994) %>%
  select(Aglaodiaptomus.leptpus:unknown.unknown) %>% as.matrix
com.y2 <- zoops %>% filter(year == 2012) %>%
  select(Aglaodiaptomus.leptpus:unknown.unknown) %>% as.matrix
```

Run also the code to set up a receiving matrix, and then we use TBI() based on presence/absence (Jaccard) dissimilarity

```
TBI.res <- TBI(com.y1, com.y2, method="jaccard", pa.tr=T, save.BC=T)

TBI.res$TBI #Jaccard dissimilarities among time points
TBI.res$BC #number of taxa lost (B) and gained (C)
TBI.res$BCD.mat #relative contributions of gains and losses
```

# Example 2: Adirondack lakes (temporal $\beta D$ )

```
Console ~/ →
> TBI.res
$TBI
 [1] 0.5000000 0.5714286 0.8181818 0.6363636 0.2857143 0.5000000 0.5454545 0.5000000 0.5000000 0.1428571
[11] 0.2727273 0.2857143 0.4285714 0.2000000

$p.TBI
 [1] 0.43 0.24 0.01 0.15 0.88 0.55 0.25 0.40 0.42 0.99 0.83 0.86 0.59 0.94

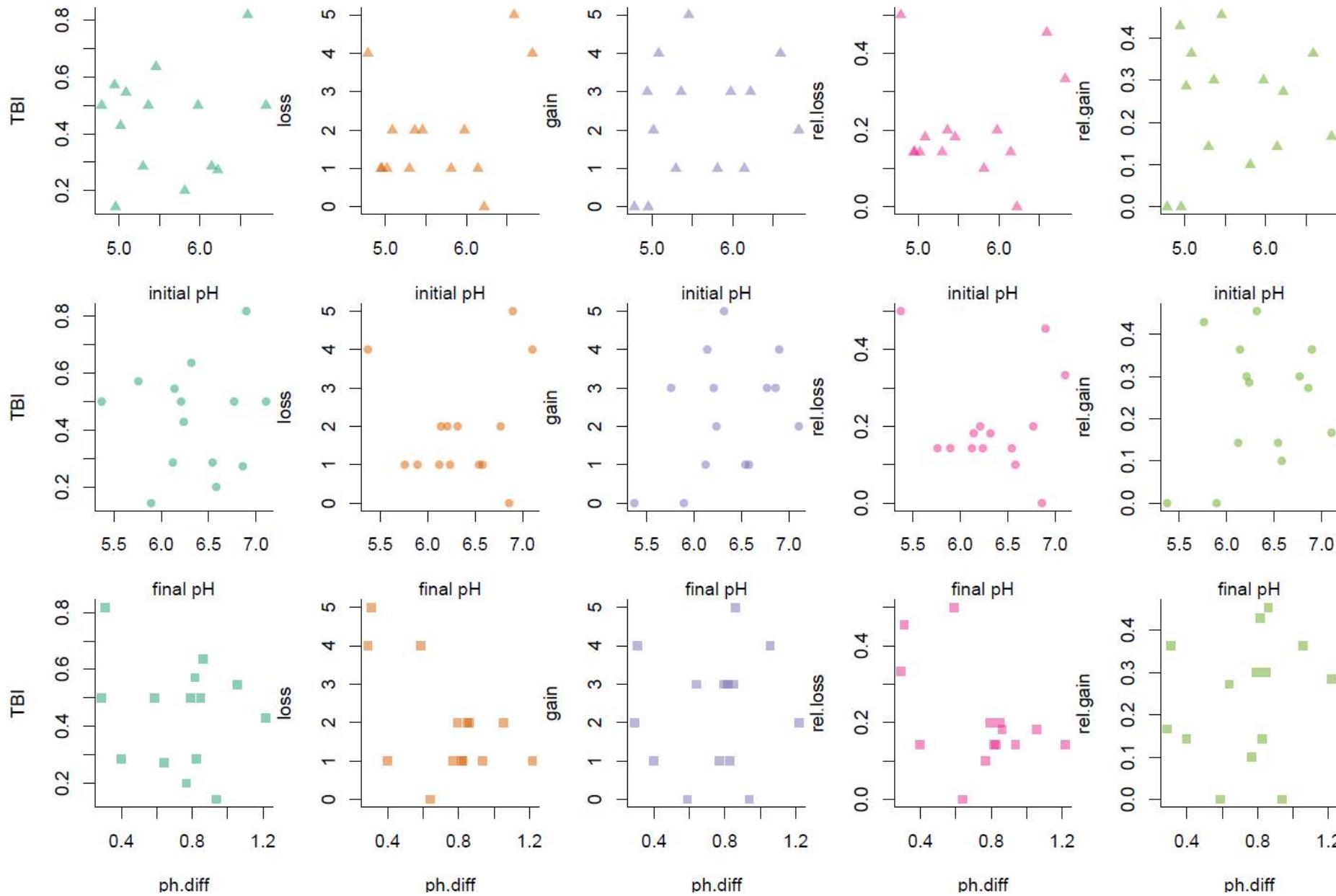
$p.adj
 [1] 1.00 1.00 0.14 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00

$BCD.mat
      B/(A+B+C) C/(A+B+C) D=(B+C)/(A+B+C) Change
Site.1 0.2000000 0.3000000 0.5000000 +
Site.2 0.1428571 0.4285714 0.5714286 +
Site.3 0.4545455 0.3636364 0.8181818 -
Site.4 0.1818182 0.4545455 0.6363636 +
Site.5 0.1428571 0.1428571 0.2857143 +
Site.6 0.5000000 0.0000000 0.5000000 -
Site.7 0.1818182 0.3636364 0.5454545 +
Site.8 0.2000000 0.3000000 0.5000000 +
Site.9 0.3333333 0.1666667 0.5000000 -
Site.10 0.1428571 0.0000000 0.1428571 -
Site.11 0.0000000 0.2727273 0.2727273 +
Site.12 0.1428571 0.1428571 0.2857143 +
Site.13 0.1428571 0.2857143 0.4285714 +
Site.14 0.1000000 0.1000000 0.2000000 +

$BCD.summary
mean(B/den) mean(C/den) mean(D) B/(B+C) C/(B+C) Change
 0.2047001   0.2372294  0.4419295  0.4631962  0.5368038    +

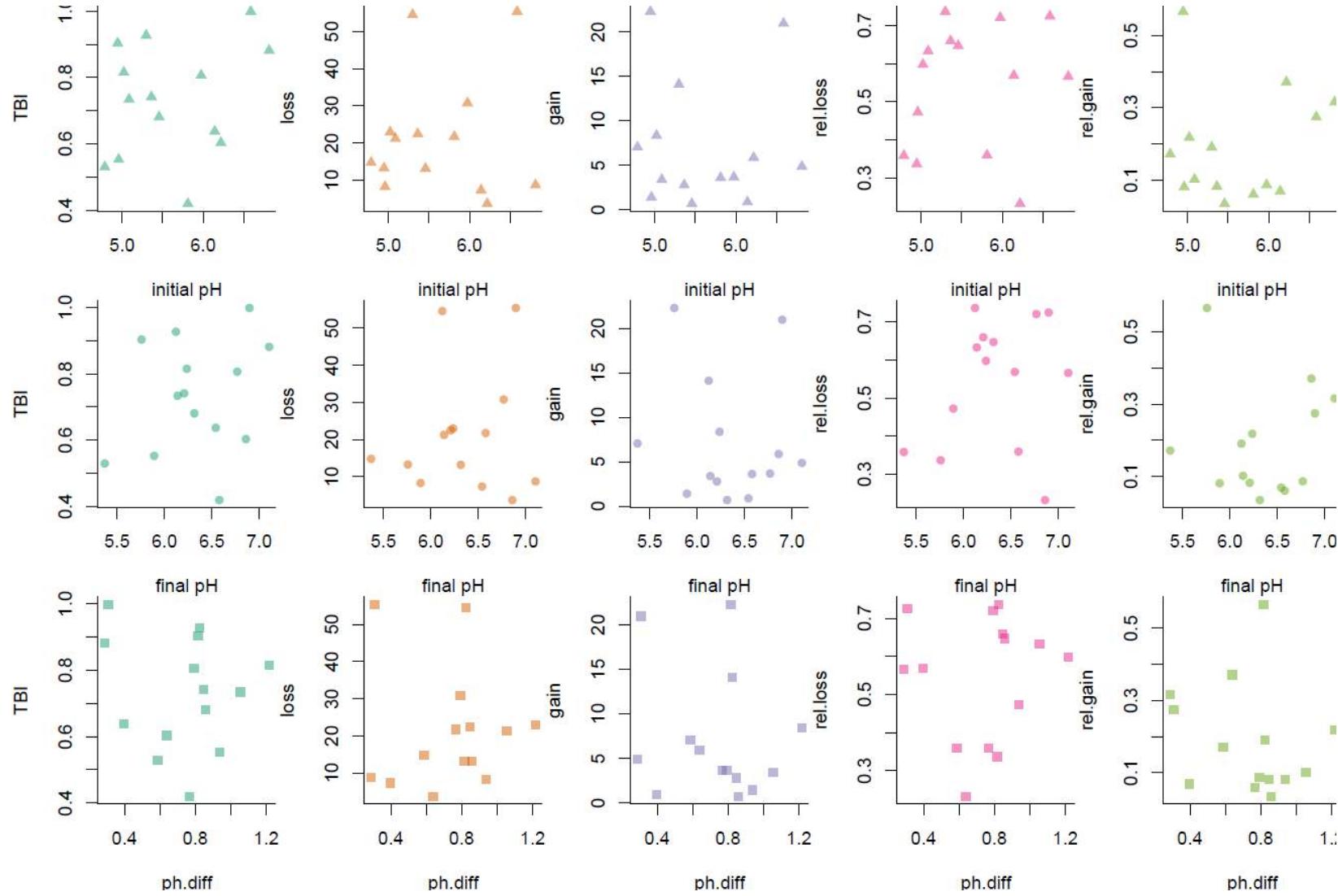
$BC
      B C
Site.1 2 3
Site.2 1 3
Site.3 5 4
Site.4 2 5
Site.5 1 1
Site.6 4 0
Site.7 2 4
Site.8 2 3
Site.9 4 2
Site.10 1 0
Site.11 0 3
Site.12 1 1
Site.13 1 2
Site.14 1 1
```

# Example 2: Adirondack lakes (temporal $\beta D$ )



# Example 2: Adirondack lakes (temporal $\beta D$ )

```
TBI.res <- TBI(com.y1, com.y2, method="ruzicka", pa.tr=F, save.BC=T)
```



# Example 2: Adirondack lakes (temporal $\beta$ D)

Research Paper

Diatom diversity patterns over the past c. 150 years across the conterminous United States of America: Identifying mechanisms behind beta diversity

Amanda K. Winegardner ✉, Pierre Legendre, Beatrix E. Beisner, Irene Gregory-Eaves, Fabien Leprieur

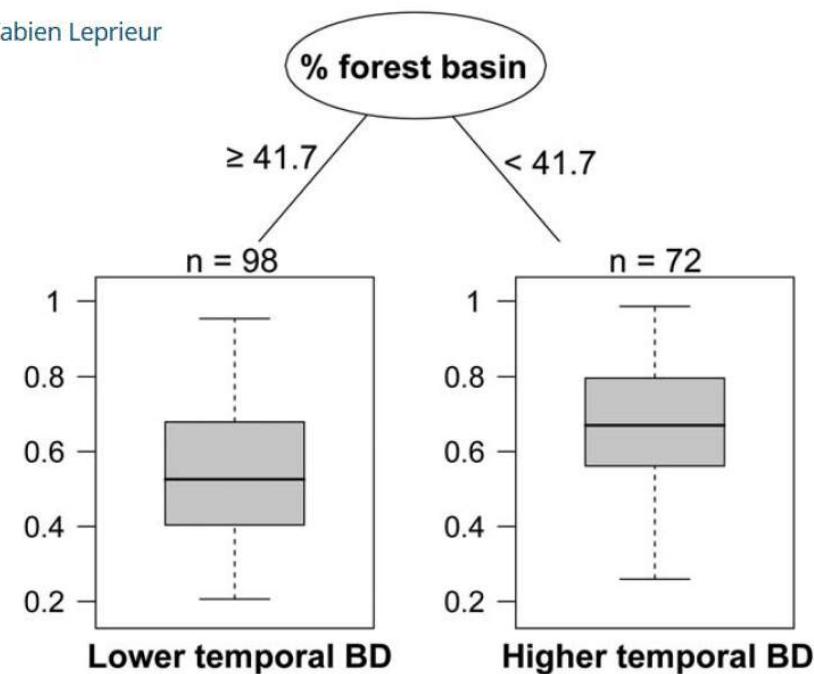
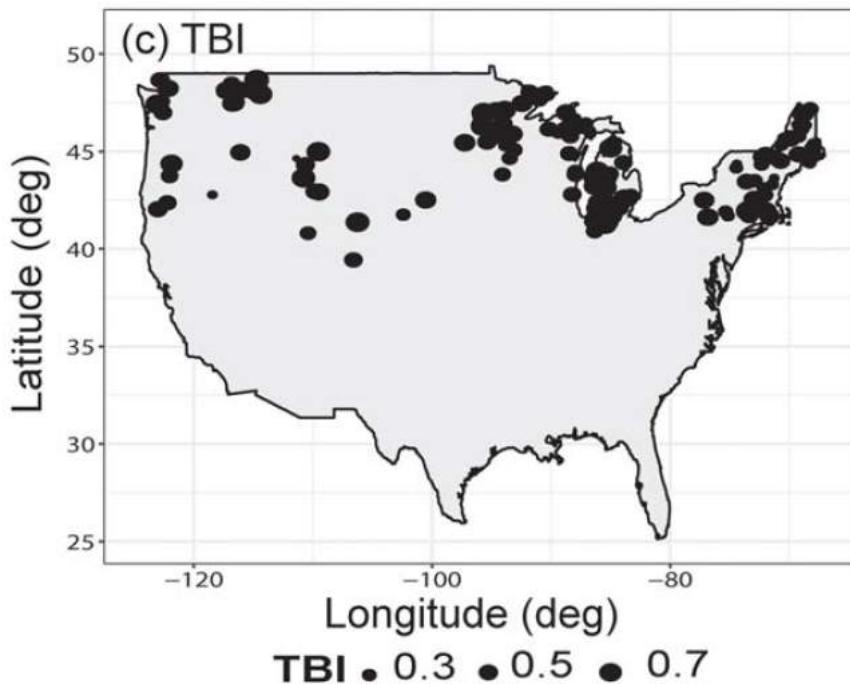


FIGURE 5 Univariate regression tree of total temporal beta diversity explained by the percentage of forest in each basin ( $n = 169$ ; genus level). The  $R^2_{\text{adj}} = .36$

# Example 2: Adirondack lakes (temporal $\beta D$ )

DOI: 10.1111/geb.12690

RESEARCH PAPER

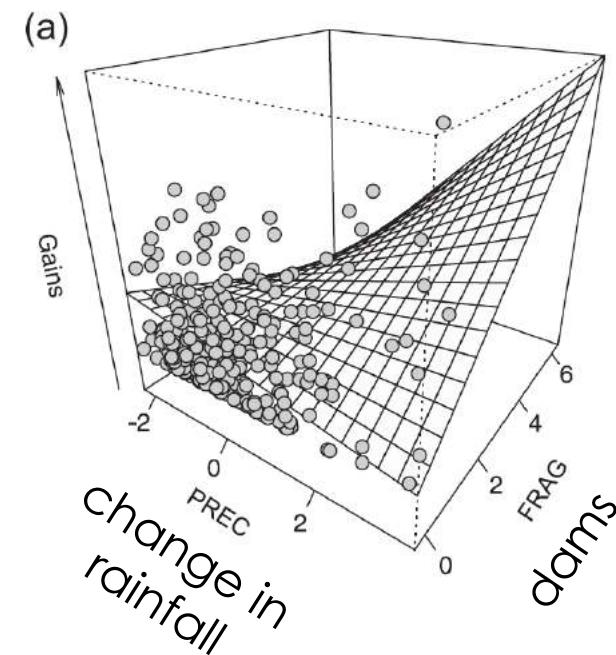
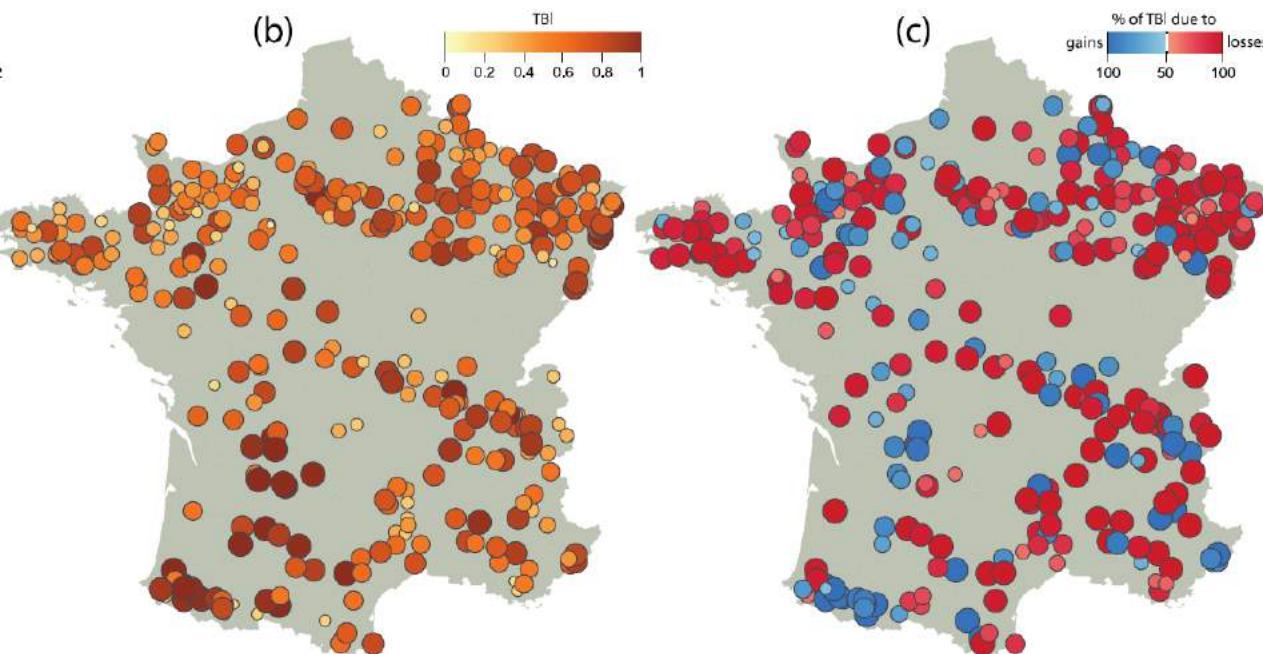
WILEY

Global Ecology  
and Biogeography

A Journal of  
Macroecology

Concomitant impacts of climate change, fragmentation and non-native species have led to reorganization of fish communities since the 1980s

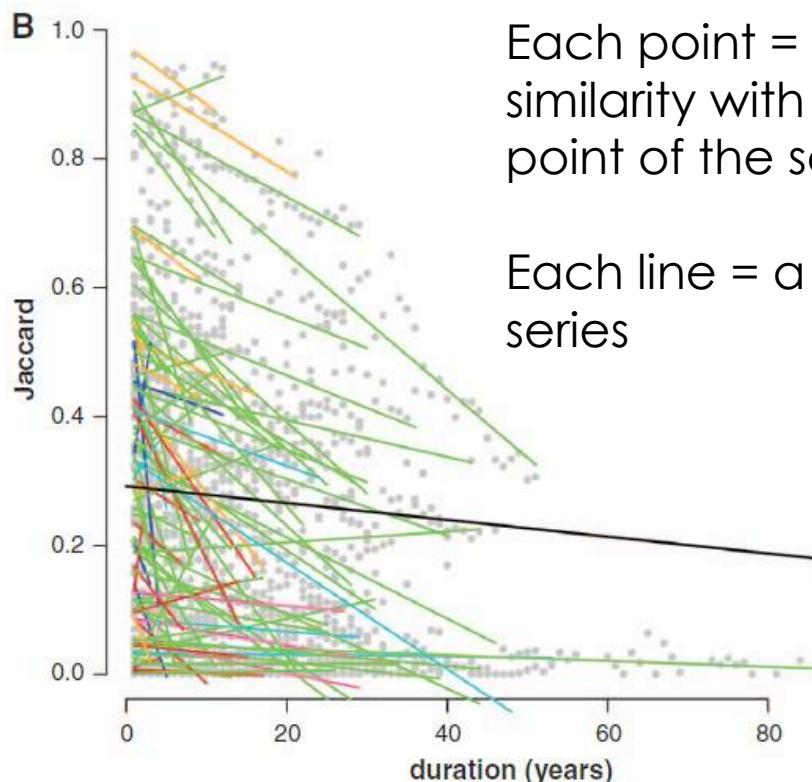
Lucie Kuczynski<sup>1</sup> | Pierre Legendre<sup>2</sup> | Gaël Grenouillet<sup>1,3</sup>



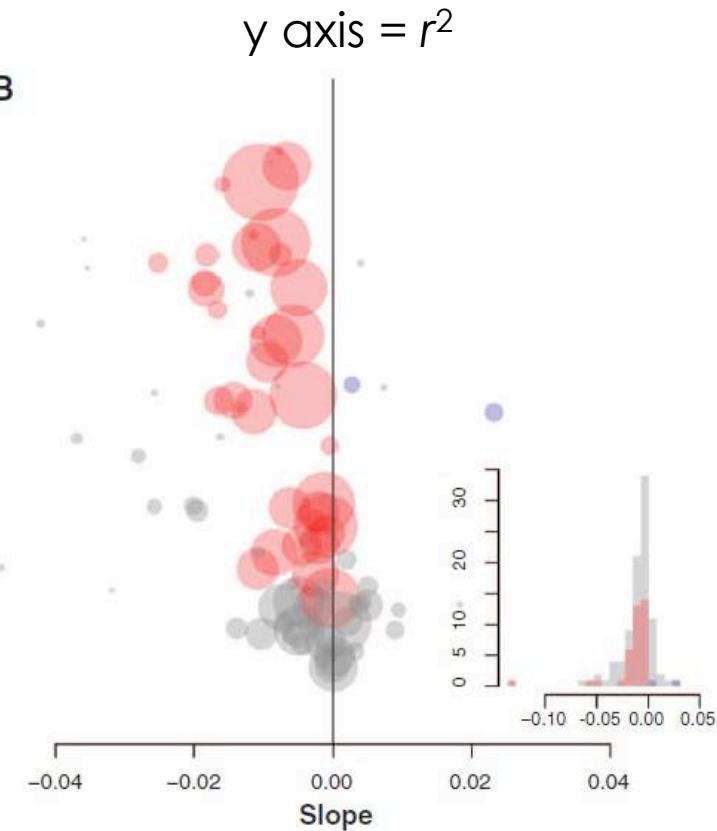
# Example 2: Adirondack lakes (temporal $\beta$ D)

## Assemblage Time Series Reveal Biodiversity Change but Not Systematic Loss

Maria Dornelas,<sup>1,\*</sup> Nicholas J. Gotelli,<sup>2</sup> Brian McGill,<sup>3</sup> Hideyasu Shimadzu,<sup>1,4</sup> Faye Moyes,<sup>1</sup> Caya Sievers,<sup>1</sup> Anne E. Magurran<sup>1</sup>



Mean slope of -0.01 means 1% change in composition per year (global average temporal beta diversity)



# Example 3: Qc reservoirs (visualizing $\beta D$ )



Katrine Turgeon

<http://katrineturgeonresearch.weebly.com/>



**Canadian Journal of Fisheries and Aquatic Sciences**  
Journal canadien des sciences halieutiques et aquatiques

**Boreal river impoundments caused nearshore fish  
community assemblage shifts but little change in diversity:  
A multi-scale analysis**

(Accepted)

Works at Hydro-Québec as a research scientist.

Just accepted a TT position at UQO (starting in September)... if you are interested to work on reservoir ecology and their food web stability, contact her! ;)

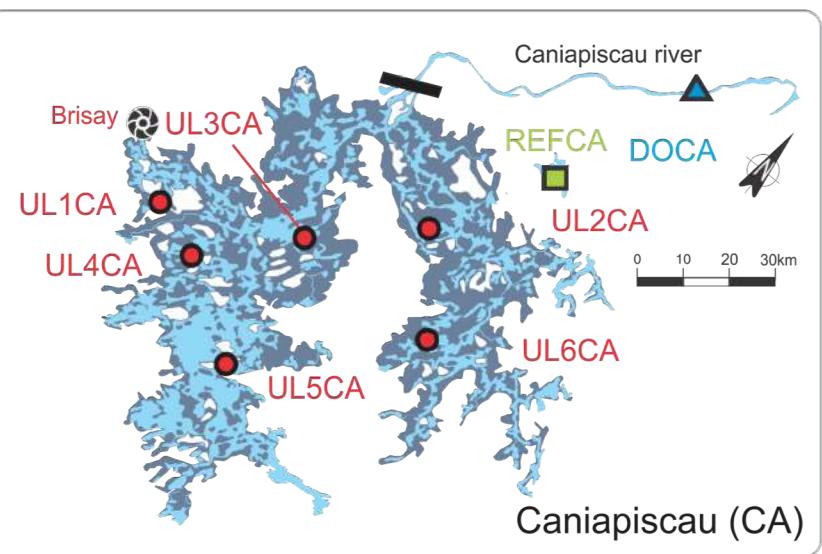
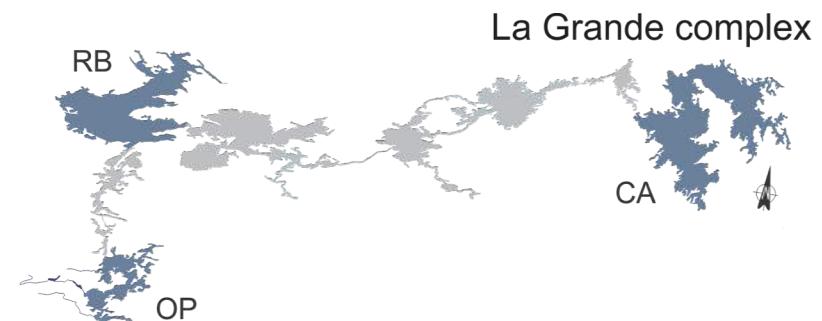
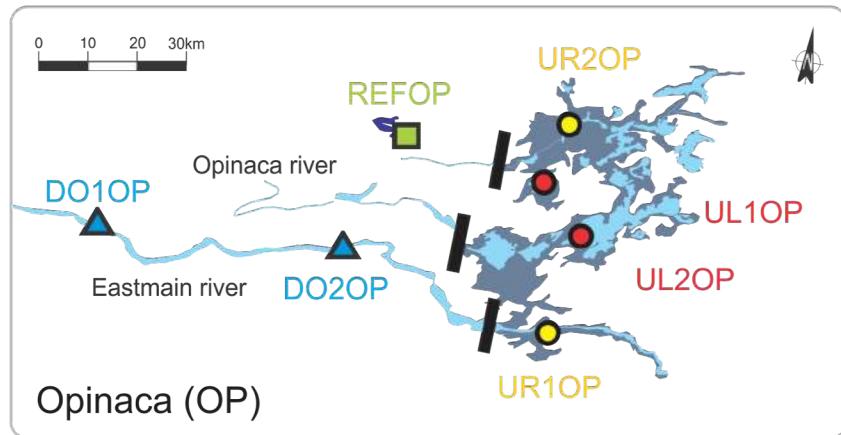
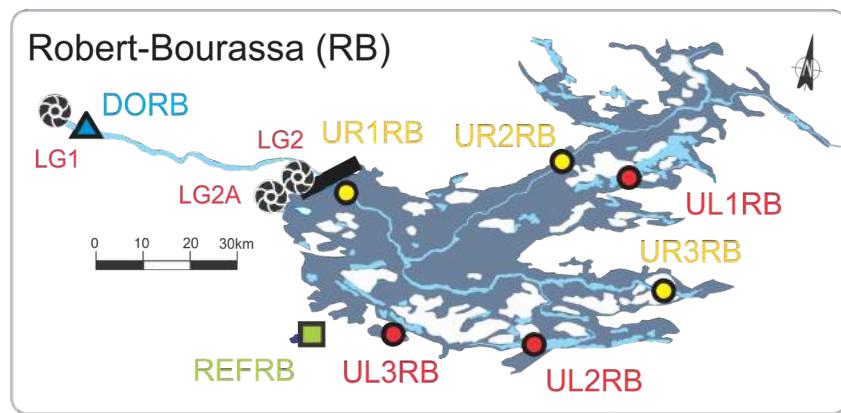
# Example 3: Qc reservoirs (visualizing $\beta D$ )



How do fish community respond to  
river impoundment in Northern  
Québec (boreal region) ?

# Example 3: Qc reservoirs (visualizing $\beta D$ )

Extremely rich dataset!!! Many impacted stations (upstream and downstream of the dam) before and after impoundment, and some reference lakes



# Example 3: Qc reservoirs (visualizing $\beta D$ )

First, let's explore what is going on with gamma diversity at the complex level...

```
LG_Y_I<-LG_Y[LG_Y$I_R=="I",c(2,8:40)] # SUBSET OF IMPACTED STATIONS  
LG_Y_R<-LG_Y[LG_Y$I_R=="R",c(2,8:40)] # SUBSET OF REFERENCE SITES  
  
# CREATING RAREFIED RICHNESS METRICS FOR IMPACTED STATIONS  
RRI<-specpool(LG_Y_I, smallsample=T, pool=LG_Y_I$TSI)  
I_R <-c("I") # CREATING ONE VECTOR = IMPACTED  
RRI <-cbind(I_R, RRI) # MERGE THE RR METRICS AND THE VECTOR  
rownames_to_column(RRI, var = "TSI")  
RRI <- as_tibble(rownames_to_column(RRI, var = "TSI"))
```

Specpool computes several rarefied richness indices (Jackknife second order is preferred in the literature)



Console ~/RESERVOIRS AND WATER LEVELS REGULATION/DATA_HYDROQUEBEC/										
21	I	9	9.031250	0.1878252	9.500000	0.5000000	9.50000	9.250000	0.4330127	2
>	rownames_to_column(RRI, var = "TSI")									
1	-2	I	18	32.666667	15.1584227	25.333333	3.2231799	30.48485	21.048230	NaN 12
2	-1	I	17	24.555556	11.0330592	20.777778	2.3359773	23.49673	18.676221	NaN 18
3	0	I	23	30.578947	7.1175333	30.578947	3.3120279	34.35673	26.424486	NaN 19
4	1	I	14	16.476190	3.2636712	17.714286	2.3035022	18.76923	15.763971	NaN 14
5	2	I	17	21.178571	4.4926598	22.571429	3.2779411	24.54945	19.588185	NaN 14
6	3	I	16	18.461538	3.2466034	19.692308	2.2922561	20.75000	17.821018	NaN 13

(n = Nb. of sampling stations)

# Example 3: Qc reservoirs (visualizing $\beta D$ )

```
# CREATING RAREFIED RICHNESS FOR REFERENCE SITES
RRR<-specpool(LG_Y_R, smallsample=T, pool=LG_Y_R$TSI)
I_R <-c("R")
RRR <-cbind(I_R, RRR)
rownames_to_column(RRR, var = "TSI")
RRR <- as_tibble(rownames_to_column(RRR, var = "TSI"))

RR_IR<-bind_rows(list(RRI, RRR)) # combine both matrices
RR_IR$TSI<-as.integer(RR_IR$TSI)
```

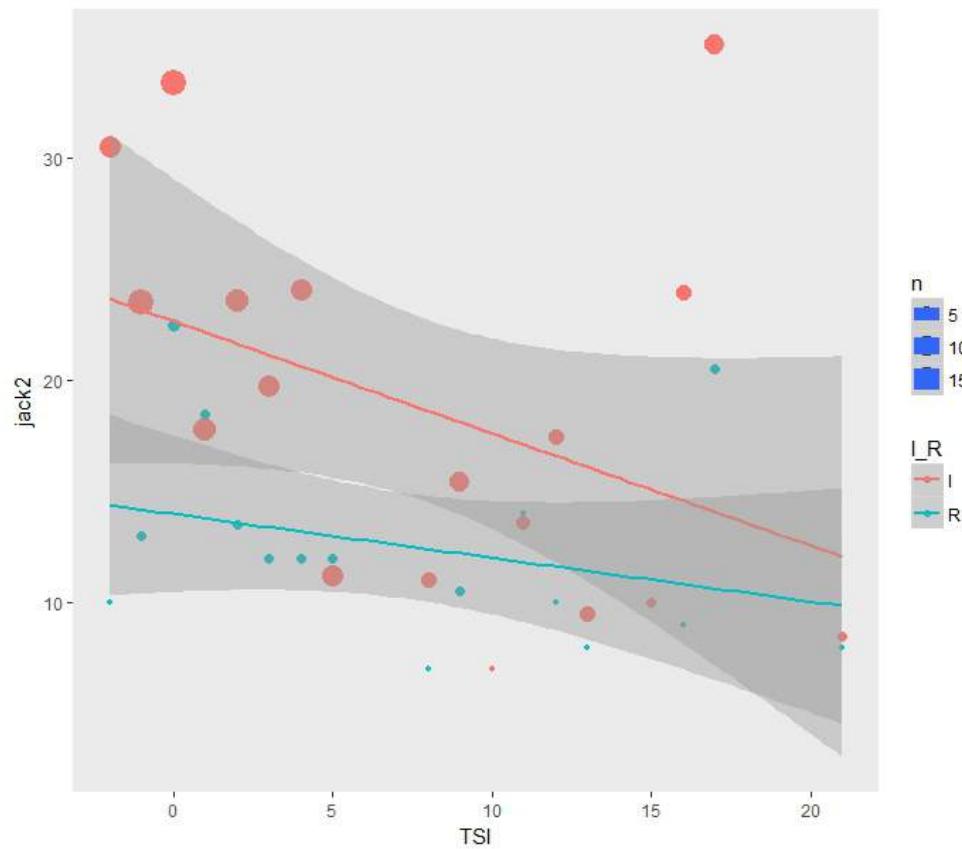
Is rarefied richness (gamma) at the complex level differs between impacted and references sites?

```
# LINEAR MODEL; RICHNESS IN RELATION TO TIME SINCE IMPOUNDMENT
RR_CBIR <- lm(jack2 ~ TSI*I_R, weight=RR_IR$n, data=RR_IR)
summary(RR_CBIR)
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	20.07848	0.90868	22.096	<2e-16 ***
TSI	-0.26520	0.11537	-2.299	0.0287 *
I_RR	-5.90095	2.62401	-2.249	0.0320 *
TSI:I_RR	0.09152	0.30021	0.305	0.7626

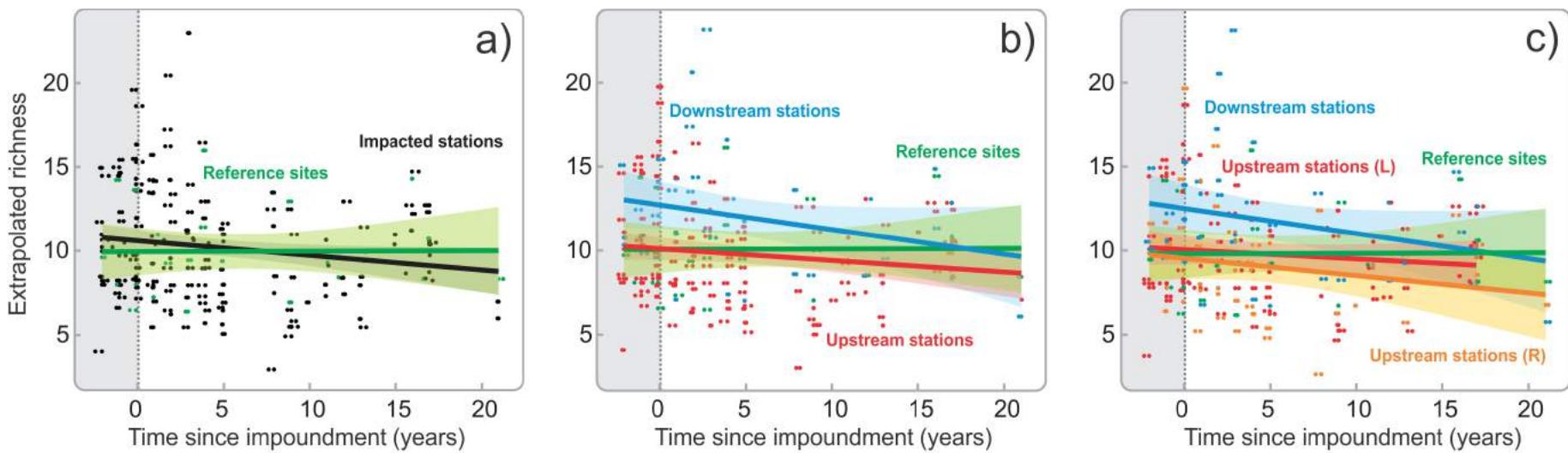
# Example 3: Qc reservoirs (visualizing $\beta D$ )

```
# GRAPH OF RICHNESS OVER TIME FOR IMPACTED AND REFERENCE SITES
ggplot(RR_IR, aes(TSI, jack2, color=I_R, size = n)) + geom_point() +
  geom_smooth(method = "lm", se= T) +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())
```



# Example 3: Qc reservoirs (visualizing $\beta D$ )

Overall, there is little change in gamma (previous slide) and **alpha** diversity metrics (richness, diversity and evenness) between impacted stations and reference sites in those boreal reservoirs



From Turgeon et al. (accepted)

What is going on with beta-diversity?

# Example 3: Qc reservoirs (visualizing $\beta D$ )

Let's explore  $\beta$ -diversity in space and time at the hydroelectric complex level with LCBD (local contributions to beta-diversity) and SCBD (species contribution to beta-diversity)

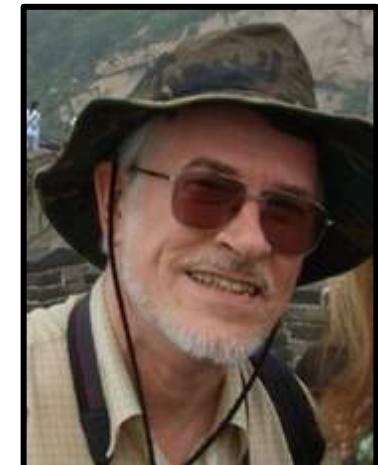


Idea and Perspective | Full Access

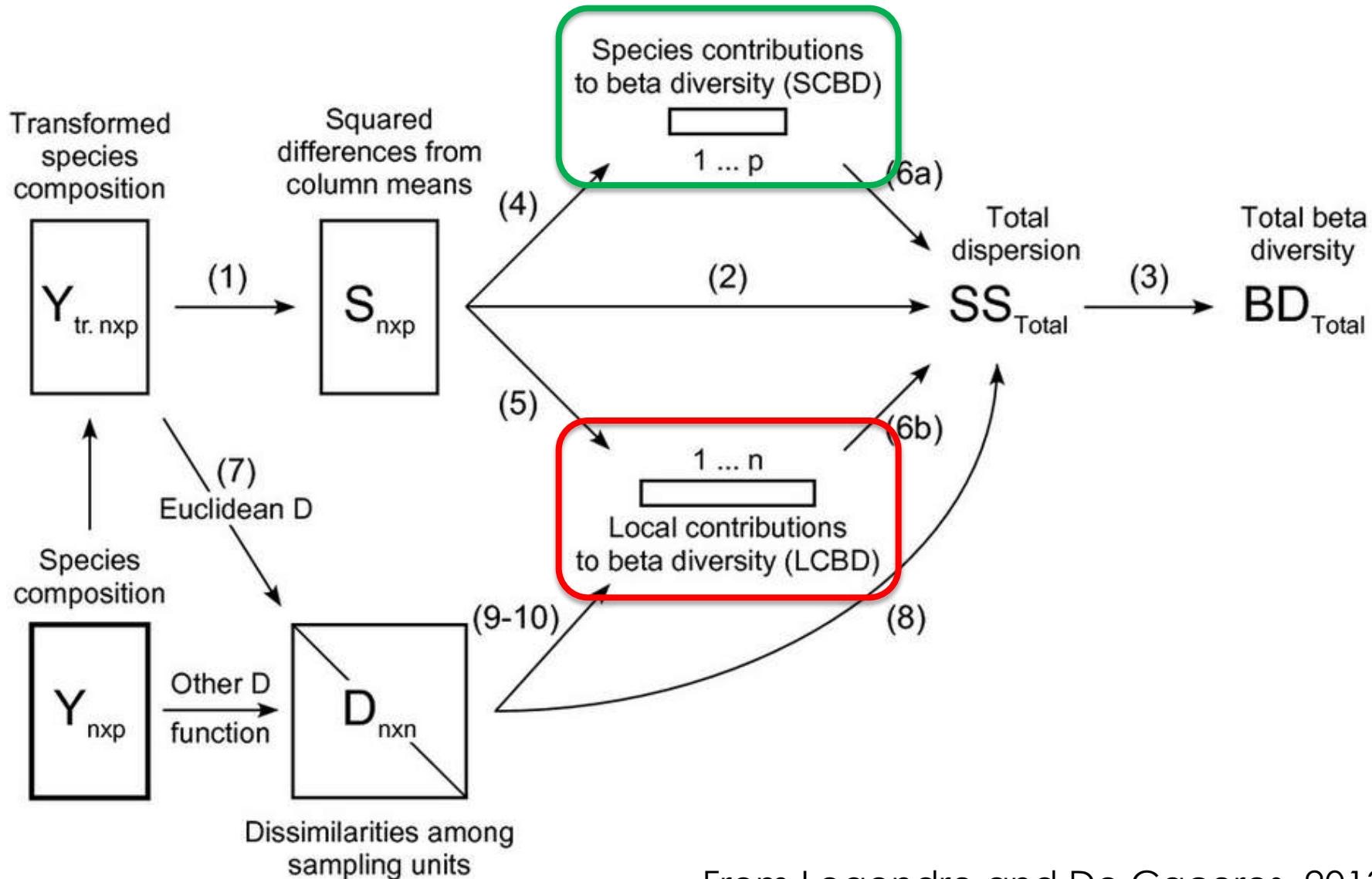
**Beta diversity as the variance of community data:  
dissimilarity coefficients and partitioning**

Pierre Legendre , Miquel De Cáceres

Volume 16, Issue 8  
August 2013  
Pages 951-963



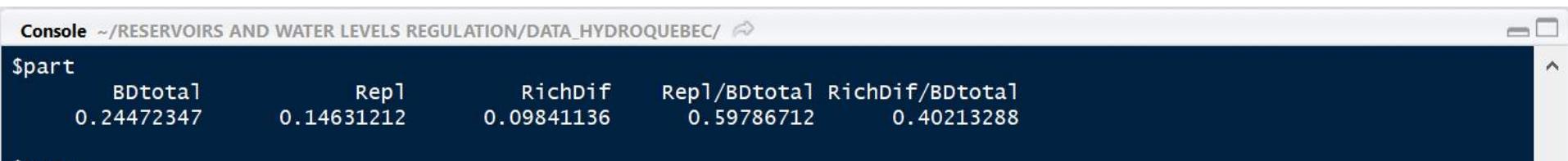
# Example 3: Qc reservoirs (visualizing $\beta D$ )



From Legendre and De Caceres, 2013

# Example 3: Qc reservoirs (visualizing $\beta D$ )

```
LG_com<-LG_Y[, -1:-7] #Keep only species columns  
  
BDLG_dec<-beta.div.comp(LG_com)  
BDLG_dec$part
```



The screenshot shows the RStudio console window with the title "Console ~/RESERVOIRS AND WATER LEVELS REGULATION/DATA\_HYDROQUEBEC/". The command `BDLG_dec$part` was run, resulting in the following output:

	BDtotal	Repl	RichDif	Repl/BDtotal	RichDif/BDtotal
\$part	0.24472347	0.14631212	0.09841136	0.59786712	0.40213288

At the complex level, 59% of the beta-diversity is due to replacement and 40% to richness difference

```
BDLG<-beta.div(LG_com, method="hellinger")  
?beta.div
```

Function that calculates LCBD and SCBD (after Hellinger transform in this case)

# Example 3: Qc reservoirs (visualizing $\beta D$ )

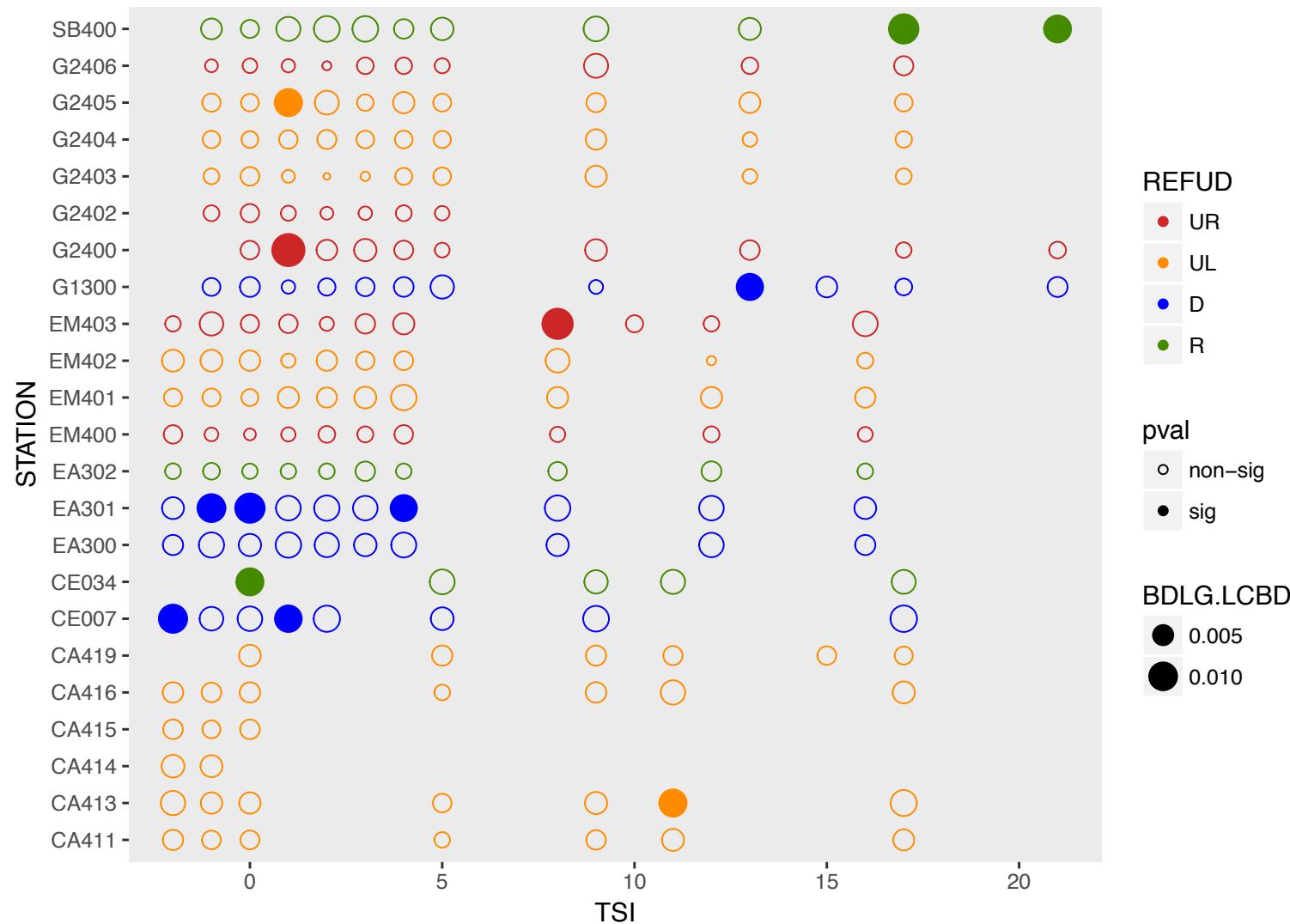
LCBD in space and time, graphically

```
LGLCBD = data.frame(BDLG$LCBD, BDLG$p.LCBD)
LGLCBD <- cbind(LGLCBD, LG_Y)
LGLCBD$pval <- ifelse(LG_LCBD$BDLG.p.LCBD >= 0.05, c("non-sig"),
c("sig"))

ggplot(LGLCBD, aes(TSI, STATION, color=REFUD, size =BDLG.LCBD,
shape=pval)) + geom_point() +
  scale_shape_manual(values=c(1, 19)) +
  scale_color_manual(values=c("firebrick3", "darkorange", "blue",
"chartreuse4")) +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())
```

## Example 3: Qc reservoirs (visualizing $\beta D$ )

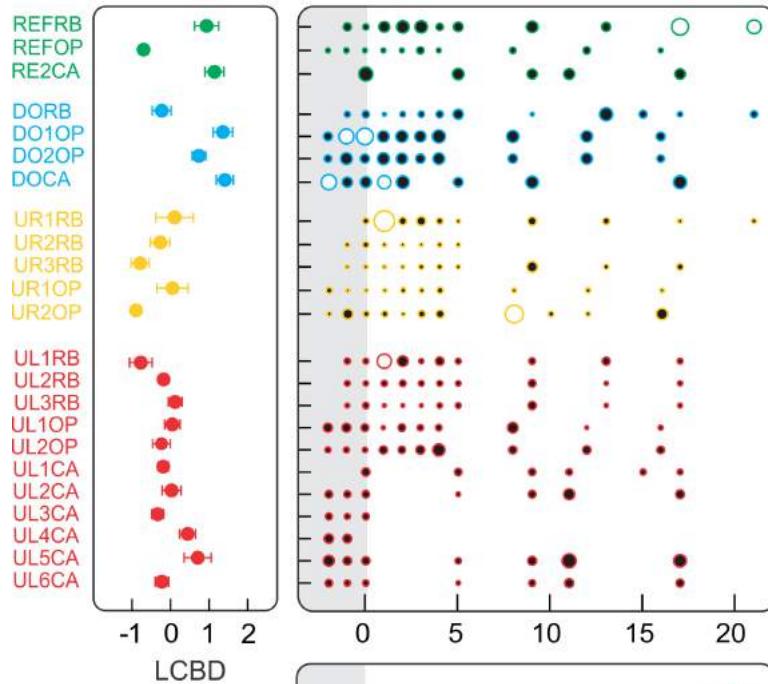
# LCBD in space and time, graphically



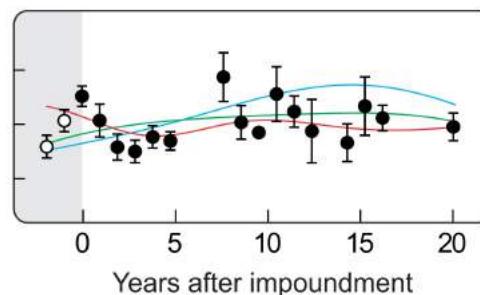
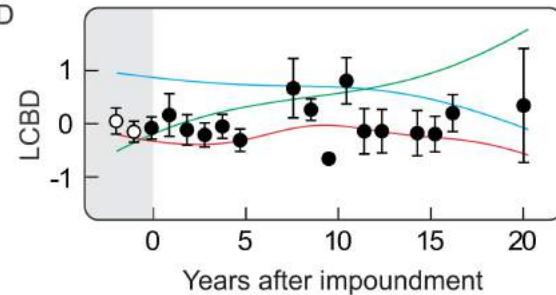
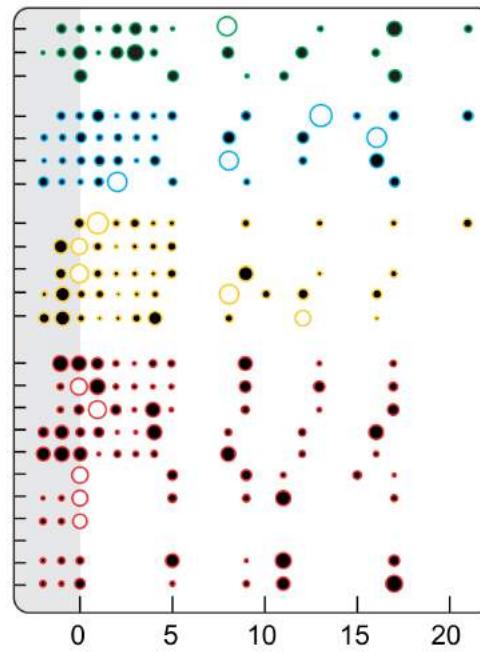
# Example 3: Qc reservoirs (visualizing $\beta D$ )

Scale matters! (high LCBD sites differ at various scales)

a) Complex scale



b) Sampling station scale



# Example 3: Qc reservoirs (visualizing $\beta D$ )

Species contribution to beta-diversity: SCBD

Let's explore which species contribute the most to b-diversity at the complex level

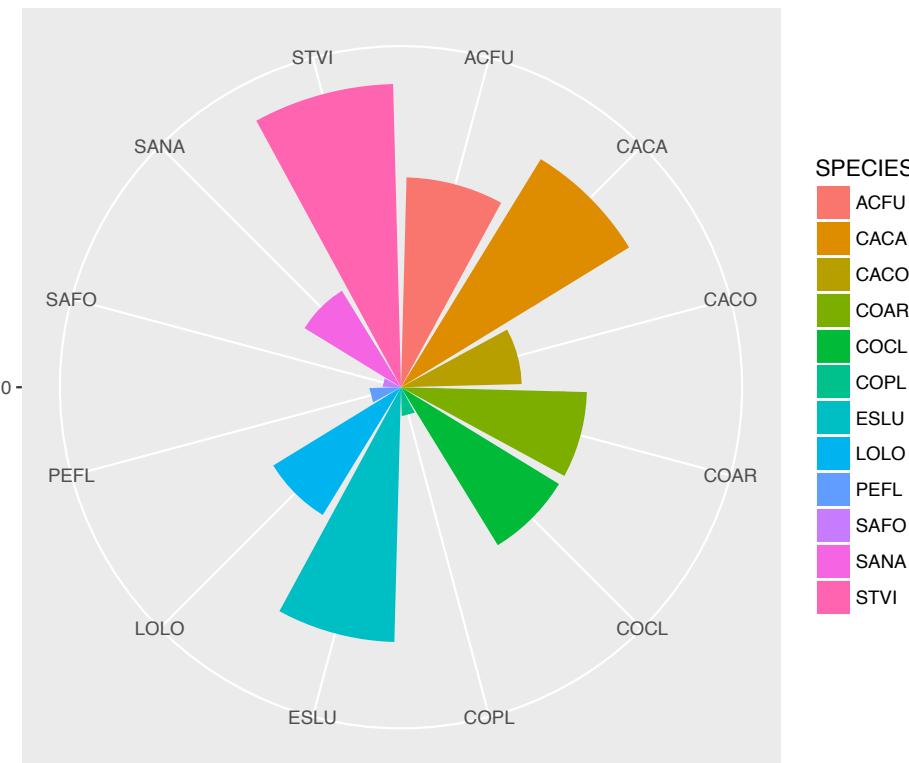
```
LGSCBD = data.frame(BDLG$SCBD)
LGSCBD <- as_tibble(rownames_to_column(LGSCBD, var = "SPECIES"))
LGSCBD_s <- LGSCBD[c(1:3,5,9,11,13,15,16,17,20,22),] # Select the most abundant species

# ROSE PLOT
ggplot(LGSCBD_s, aes(x=SPECIES, y=BDLG.SCBD)) +
  geom_bar(aes(fill=SPECIES), stat="identity") +
  scale_y_continuous(breaks = 0:10) +
  coord_polar() + labs(x = "", y = "")
```

This could be illustrated with radar chart (in the paper) or “rose plots”. Let's explore with rose plots.

# Example 3: Qc reservoirs (visualizing $\beta D$ )

Species contribution to beta-diversity: SCBD at the complex level



Walleye (STVI), Lake sturgeon (ACFU), Longnose sucker (CACA), Cisco (COAR), Whitefish (COCL) and Northern pike (ESLU) are contributing the most to beta-diversity

# Example 3: Qc reservoirs (visualizing $\beta D$ )

Species contribution to beta-diversity: SCBD

Do SCBDs differ across reservoirs?

Let's calculate SCBD per reservoir (3 reservoirs) and compare the rose plots. Starting with Robert-Bourassa:

```
# SUBSET for ROBERT-BOURASSA
RB_Y<-LG_Y[LG_Y$RES=="RB",-1:-7]

BDRB<-beta.div(RB_Y,method="hellinger")
RBSCBD = data.frame(BDRB$SCBD)
RBSCBD <- as_tibble(rownames_to_column(RBSCBD, var = "SPECIES"))
RBSCBD_s <- RBSCBD[c(1:3,5,9,11,13,15,16,17,20,22),]

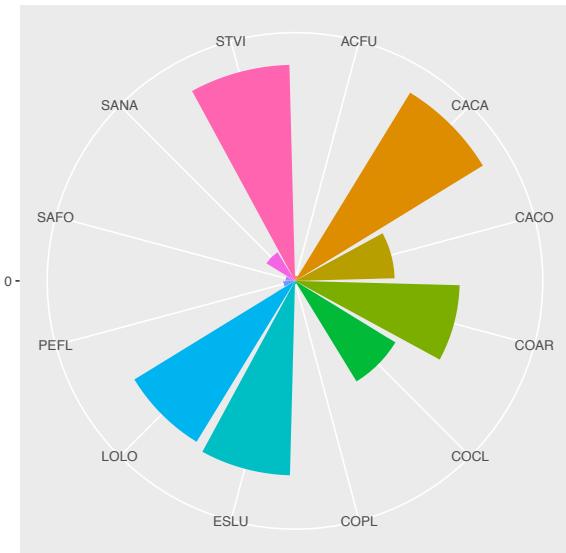
ggplot(RBSCBD_s, aes(x=SPECIES, y=BDRB.SCBD)) + geom_bar(aes(fill=SPECIES),
stat="identity") +
  scale_y_continuous(breaks = 0:10) +
  coord_polar() + labs(x = "", y = "")
```

Do the same for Opinaca and Caniapiscau!

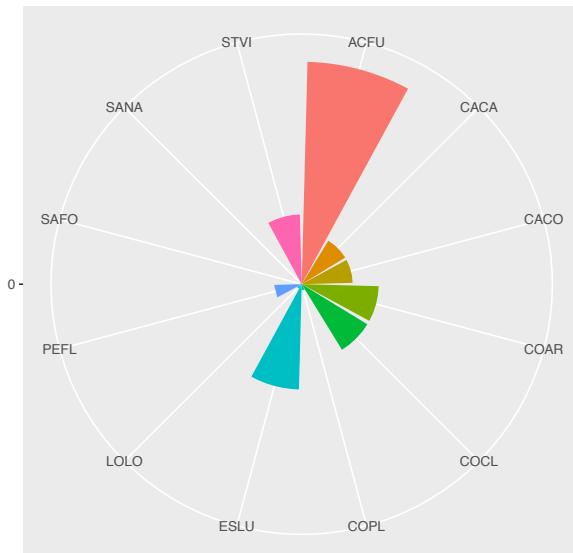
# Example 3: Qc reservoirs (visualizing $\beta D$ )

Species contribution to beta-diversity: SCBD  
Reservoirs strongly vary in their SCBD

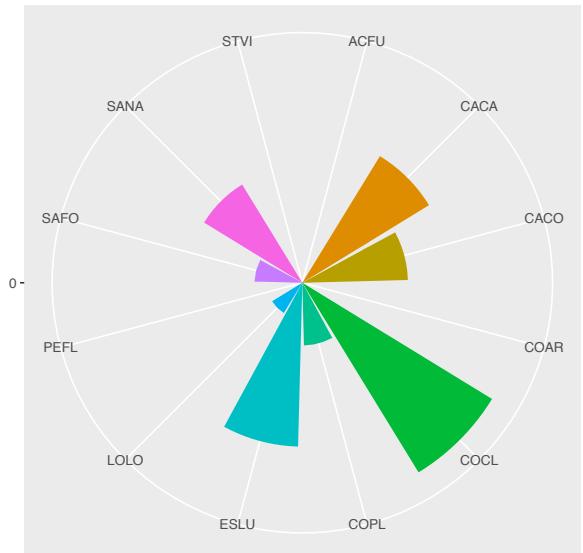
Robert-Bourassa



Opinaca



Caniapiscau

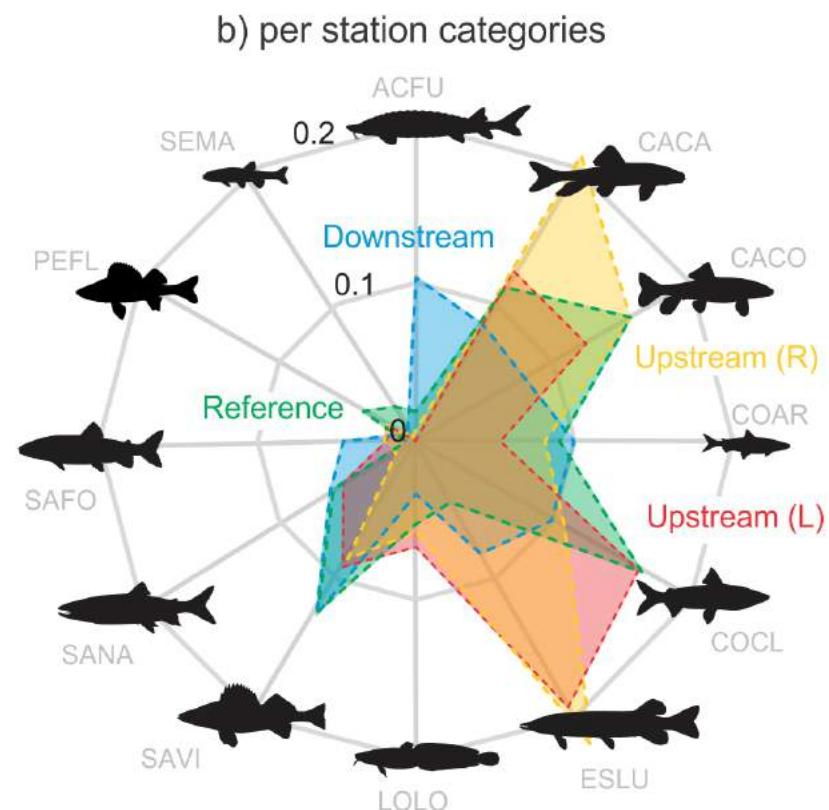
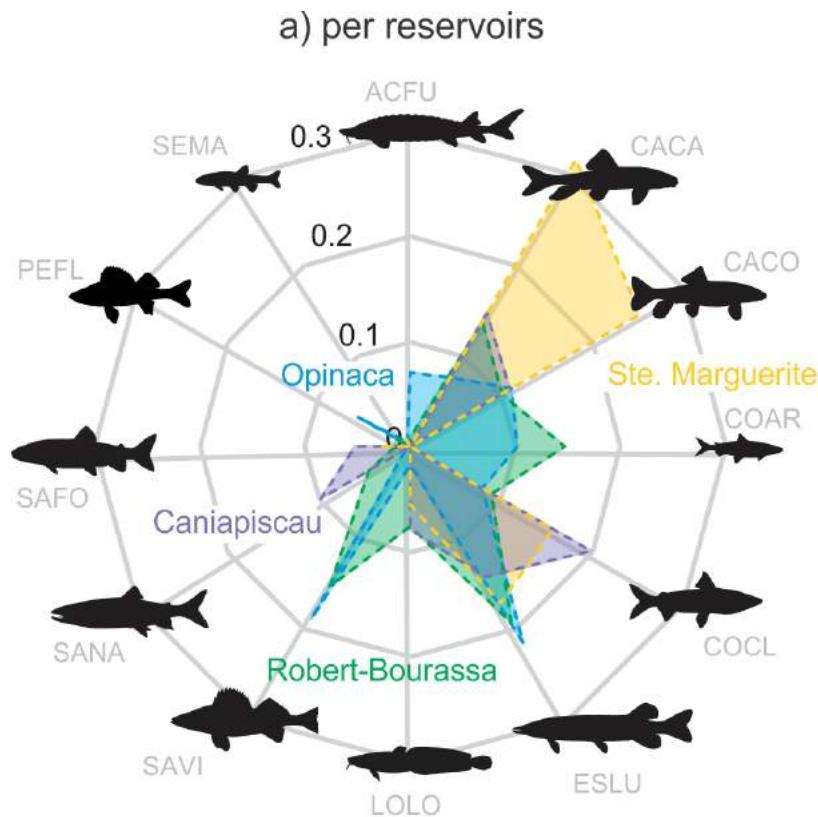


SPECIES
ACFU
CACA
CACO
COAR
COCL
COPL
ESLU
LOLO
PEFL
SAFO
SANA
STVI

# Example 3: Qc reservoirs (visualizing $\beta D$ )

Species contribution to beta-diversity: SCBD

Variation across reservoirs and sampling station categories



# Example 3: Qc reservoirs (visualizing $\beta D$ )

DOI: 10.1111/geb.12690

RESEARCH PAPER

WILEY

Global Ecology  
and Biogeography

A Journal of  
Macroecology

Concomitant impacts of climate change, fragmentation and non-native species have led to reorganization of fish communities since the 1980s

Lucie Kuczynski<sup>1</sup> | Pierre Legendre<sup>2</sup> | Gaël Grenouillet<sup>1,3</sup>

