

Bootstrapping

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Load Data and Codes

- Read dataset with id, site, period, species, abund

```
data <- read.csv("data.csv", h = T)
head(data)
```

```
##   ID Site Period      species Nr
## 1  1  42      1    Noctua pronuba 8
## 2  2  42      1 Atlantarctia tigrina 1
## 3  3  42      1    Anarta myrtilli 1
## 4  4  42      1 Lycophotia molothina 7
## 5  5  42      1    Harpyia milhauseri 1
## 6  6  42      1 Pseudoterpna coronillaria 1
```

```
library(xtable)
library(boot)
source('chao.R')
source('distanc.R')
```

Distances

The distances between pairs were calculated using QGIS for IPCC and IGeoE:

- Hayford Gauss IPCC:

```
dist <- read.csv("dist_mat_ipcc.csv", h = T)
dist <- dist[-1]
DIST1 <- distanc(dist)
head(DIST1)
```

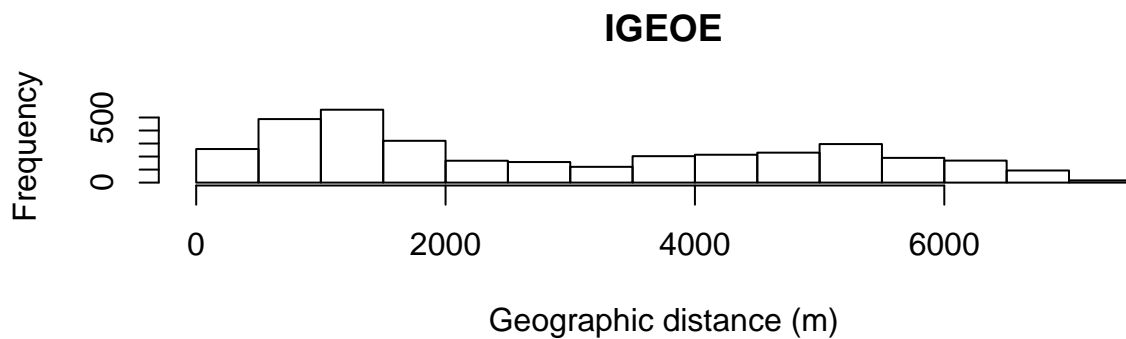
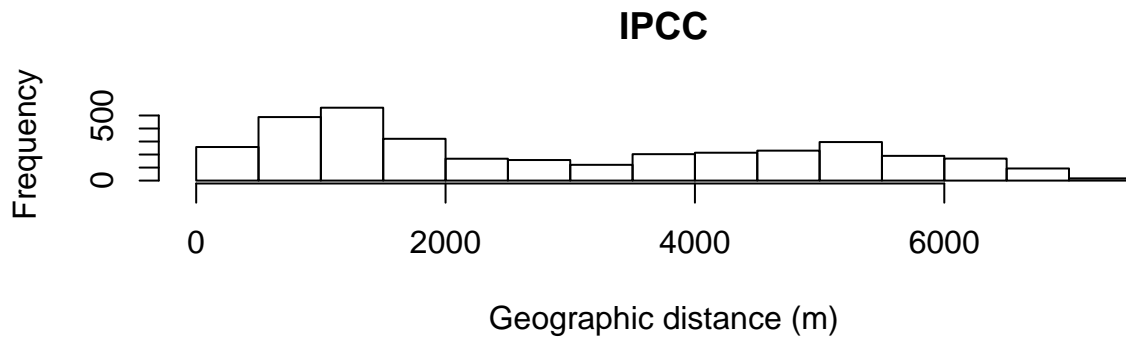
```
##      [,1] [,2] [,3]
## [1,]    1    2 60.00
## [2,]    1    3 60.00
## [3,]    1    4 84.85
## [4,]    1    5 247.39
## [5,]    1    6 247.40
## [6,]    1    7 339.41
```

- Hayford Gauss IGeoE

```
dist <- read.csv("dist_mat_igeoe.csv", h = T)
dist <- dist[-1]
DIST2 <- distanc(dist)
head(DIST2)
```

```
##      [,1] [,2]  [,3]
## [1,]    1    2 60.00
## [2,]    1    3 60.00
## [3,]    1    4 84.85
## [4,]    1    5 247.39
## [5,]    1    6 247.40
## [6,]    1    7 339.41
```

```
par(mfrow=c(2, 1))
hist(DIST1[, 3], main = "IPCC", xlab = "Geographic distance (m)", ylab = "Frequency")
hist(DIST2[, 3], main = "IGE0E", xlab = "Geographic distance (m)", ylab = "Frequency")
```



The histograms have the same behavior, then I chose the first vector of distances (IPCC) for analysing the data.

Data

Sorensen and Jaccard Estimators were estimated using unseen species (Chao et al 2005). The data-set was subsetted by sample. Variables created from the chao-function have the following columns:

```
sample1 <- chao(1, 1, "sample1")
sample2 <- chao(2, 2, "sample2")
sample3 <- chao(3, 3, "sample3")
sample4 <- chao(4, 4, "sample4")
sample5 <- chao(5, 5, "sample5")
sample6 <- chao(6, 6, "sample6")
```

- p: sampling period.

- s1: the code of sample 1.
- s2: the code of sample 2.
- n: the number of observed species in the sample 1.
- nsp1: the number of species in the sample 1.
- m: the number of observed species in the sample 2.
- nsp2: the number of species in the sample 2.
- nsh: the number of observed shared species in the two samples.
- fm1: the observed number of shared species that occur once in sample 2.
- fm2: the observed number of shared species that occur twice in sample 2.
- flm: the observed number of shared species that occur once in sample 1.
- f2m: the observed number of shared species that occur twice in sample 1.
- u_pt1: abundance sum of shared species divided by species number for the sample 1.
- v_pt1: abundance sum of shared species divided by species number for the sample 2.
- Junad: Jaccard unadjusted estimator.
- Lunad: Sorensen unadjusted estimator.
- U: u_pt1 plus unseen species for the sample 2.
- V: v_pt1 plus unseen species for the sample 1.
- Jabd: Jaccard adjusted estimator.
- Labd: Sorensen adjusted estimator.

```
head(sample1)
```

```
##      p s1 s2  n nsp1  m nsp2 nsh fm1 fm2 flm f2m  u_pt1  v_pt1  Junad
## [1,] 1  1  2 44   17  72   26  13  4  2  5  4 0.88636 0.6667 0.6142
## [2,] 1  1  3 44   17  73   33  13  5  1  5  5 0.86364 0.6301 0.5731
## [3,] 1  1  4 44   17  4    4  1  1  1  0  1 0.04545 0.2500 0.0400
## [4,] 1  1  5 44   17 114   33  12  2  1  4  4 0.86364 0.6754 0.6103
## [5,] 1  1  6 44   17  67   25  10  4  2  4  2 0.77273 0.4328 0.3840
## [6,] 1  1  7 44   17  97   29  12  3  1  5  4 0.81818 0.7216 0.6219
##      Lunad      U      V      Jabd      Labd
## [1,] 0.76098 1.0000 0.7854 0.78543 0.8798
## [2,] 0.72864 1.0000 0.7172 0.71715 0.8353
## [3,] 0.07692 0.0625 0.2500 0.05263 0.1000
## [4,] 0.75803 0.9312 0.7440 0.70526 0.8272
## [5,] 0.55487 1.0000 0.5495 0.54953 0.7093
## [6,] 0.76689 1.0000 0.9231 0.92315 0.9600
```

Exploratory Analysis

These functions were used to synthesize the samples for each year. Moth samplings were conducted for two years (2011 and 2012), each year had three sampling period.

```
trisamples <- function(base1, base2, base3, vr){
  base <- matrix(0, nrow = dim(base1)[1])
  for(i in 1:dim(base1)[1]){
    base[i] <- (base1[i, vr] + base2[i, vr] + base3[i, vr])/3
  }
  base
}

bisamples <- function(base1, base2){
```

```

base <- matrix(0, nrow = length(base1))
for(i in 1:length(base1)){
  base[i] <- (base1[i] + base2[i])/2
}
base
}

```

- Calculated the dissimilarity average per site for first year

```

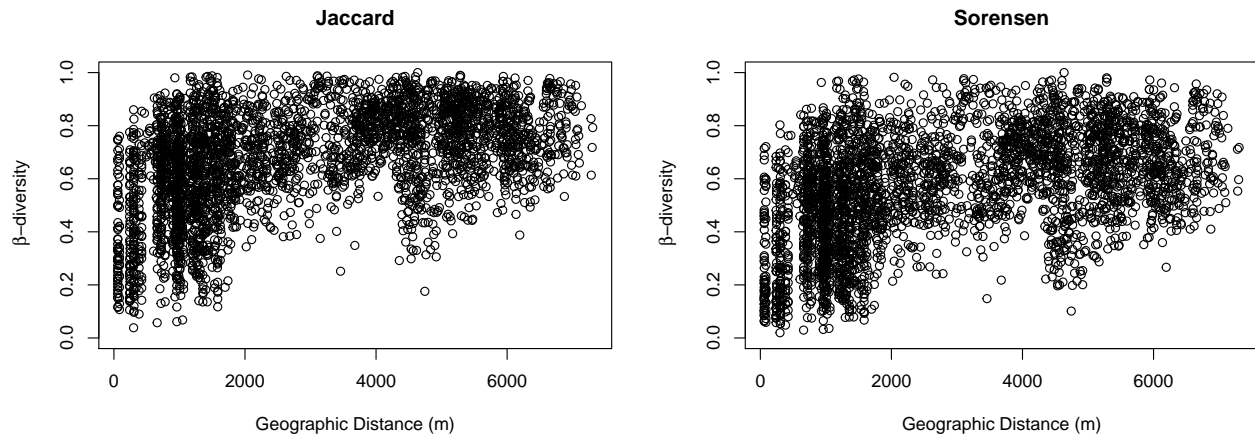
Jperiod1 <- trisamples(sample1, sample2, sample3, 19)
Lperiod1 <- trisamples(sample1, sample2, sample3, 20)

```

```

par(mfrow=c(1, 2))
plot(DIST1[, 3], (1 - Jperiod1), ylim = c(0, 1), xlab = "Geographic Distance (m)", ylab =
  expression(~beta*"-diversity"), main = "Jaccard")
plot(DIST1[, 3], (1 - Lperiod1), ylim = c(0, 1), xlab = "Geographic Distance (m)", ylab =
  expression(~beta*"-diversity"), main = "Sorensen")

```



- Calculated the dissimilarity average per site for second year

```

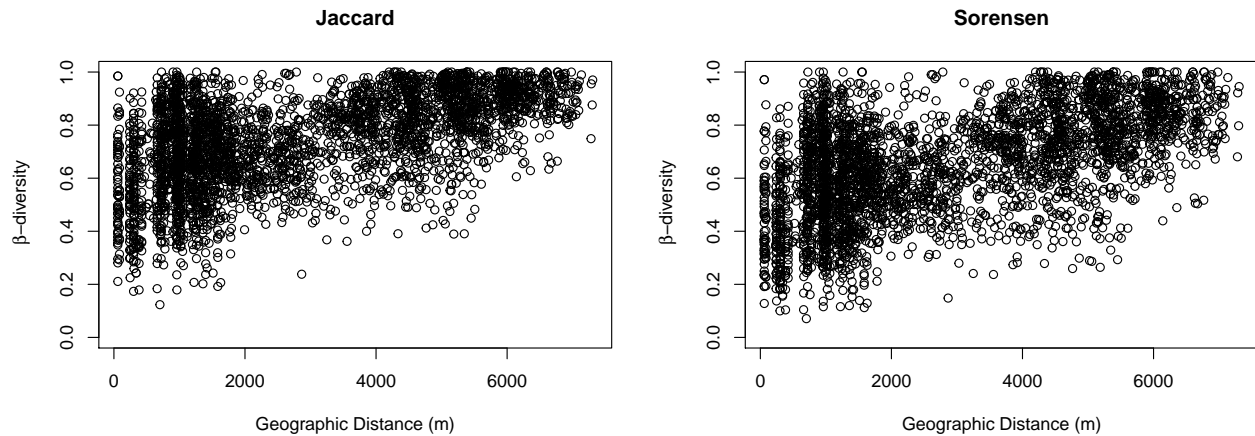
Jperiod2 <- trisamples(sample4, sample5, sample6, 19)
Lperiod2 <- trisamples(sample4, sample5, sample6, 20)

```

```

par(mfrow=c(1, 2))
plot(DIST1[, 3], (1 - Jperiod2), ylim = c(0, 1), xlab = "Geographic Distance (m)", ylab =
  expression(~beta*"-diversity"), main = "Jaccard")
plot(DIST1[, 3], (1 - Lperiod2), ylim = c(0, 1), xlab = "Geographic Distance (m)", ylab =
  expression(~beta*"-diversity"), main = "Sorensen")

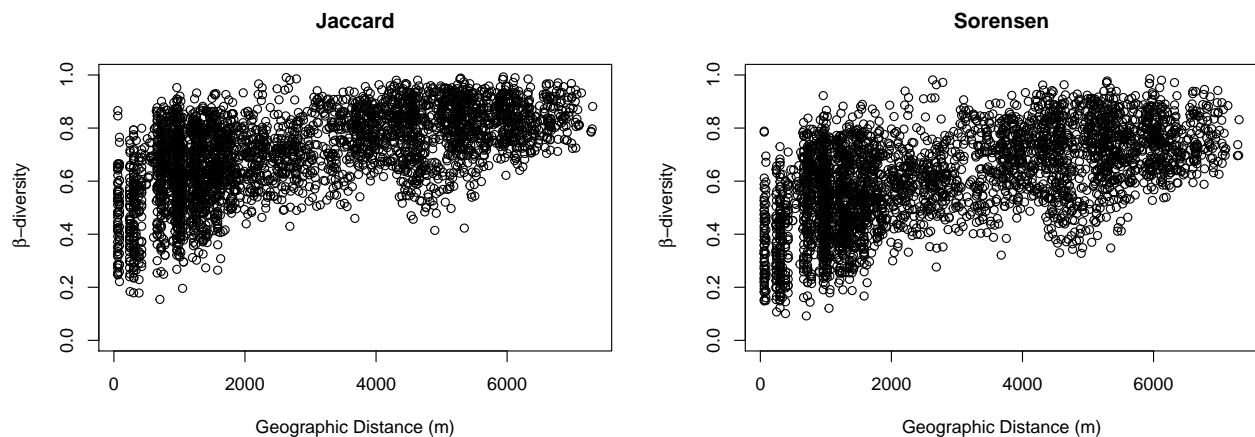
```



- Calculated the dissimilarity average per site for both years

```
Jperiod <- bisamples(Jperiod1, Jperiod2)
Lperiod <- bisamples(Lperiod1, Lperiod2)
```

```
par(mfrow=c(1, 2))
plot(DIST1[, 3], (1 - Jperiod), ylim = c(0, 1), xlab = "Geographic Distance (m)", ylab =
  expression(~beta*"-diversity"), main = "Jaccard")
plot(DIST1[, 3], (1 - Lperiod), ylim = c(0, 1), xlab = "Geographic Distance (m)", ylab =
  expression(~beta*"-diversity"), main = "Sorensen")
```



DATASET: I created a new database with six columns:

- p: no functionality, I created just to standardize with other functions previously created.
- s1: site 1
- s2: site 2
- Jabd: Jaccard adjusted estimator
- Labd: Sorensen adjusted estimator
- ipcc: distance between site 1 and site 2 (Hayford Gauss IPCC)

```
b.div.mean <- cbind(sample1[, 1], sample1[, 2], sample1[, 3], Jperiod, Lperiod, DIST1[, 3])
colnames(b.div.mean) <- c("p", "s1", "s2", "Jabd", "Labd", "ipcc")
head(b.div.mean)
```

```
##      p s1 s2  Jabd  Labd  ipcc
## [1,] 1  1  2 0.6520 0.7724 60.00
## [2,] 1  1  3 0.7169 0.8153 60.00
## [3,] 1  1  4 0.2347 0.3054 84.85
## [4,] 1  1  5 0.5494 0.6839 247.39
## [5,] 1  1  6 0.6330 0.7575 247.40
## [6,] 1  1  7 0.6073 0.7244 339.41
```

Samples were taken in three landscapes that represent the farmland abandonment gradient: meadow-dominated, shrub-dominated and forest-dominated. In each landscape had 28 fixed sampling sites divided into four biotopes (meadow, short shrub, tall shrub and woodland), totaling 84 sampling sites.

- forest-dominated:

```
mf <- c(56) #m - meadow
sf <- c(36, 39, 42, 45, 46) #s - short shrub
tf <- c(34, 49) #t - tall shrub
wf <- c(29, 30, 31, 32, 33, 35, 37, 38, 40, 41, 43, 44, 47, 48, 50, 51, 52, 53, 54, 55)
#w - woodland
```

- shrub-dominated (m - mixed)

```
mm <- c(68, 75, 77, 84)
sm <- c(60, 64, 65, 66, 67, 70, 78, 79, 82)
tm <- c(57, 58, 59, 61, 62, 63, 69, 71, 72, 74, 76)
wm <- c(73, 80, 81, 83)
```

- meadow-dominated (a - agriculture)

```
ma <- c(1, 9, 14, 15, 16, 17, 18, 19, 21, 23, 24, 25, 27)
sa <- c(2, 8, 10, 11, 12, 13, 20)
ta <- c(3, 4, 5, 6, 7, 28)
wa <- c(22, 26)
```

SECOND APPROACH

```
# function to obtain regression weights
bs.jac <- function(formula, data, ind){
  d <- data[ind,] # allows boot to select sample
  fit <- lm(formula, data = d)
  return(c(coef(fit), summary(fit)$r.square, mean(d[, 4])))
}

bs.sor <- function(formula, data, ind){
  d <- data[ind,] # allows boot to select sample
  fit <- lm(formula, data = d)
  return(c(coef(fit), summary(fit)$r.square, mean(d[, 5])))
}
```

within landscapes

```
agr.mea <- landsc_within(b.div.mean, ma, ma)
shr.shr <- landsc_within(b.div.mean, sm, sm)
tal.shr <- landsc_within(b.div.mean, tm, tm)
for.woo <- landsc_within(b.div.mean, wf, wf)
mix.shr <- landsc_within(b.div.mean, c(sm, tm), c(sm, tm))
```

This function creates a database for each landscape. Also, I analyzed separately short and tall shrub within the shrub-dominated landscape.

In this analysis only the biotopes that correspond the type of the landscape were considered.

Regression models

- Jaccard Estimator

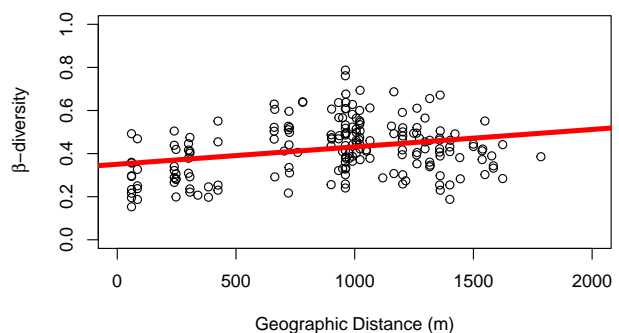
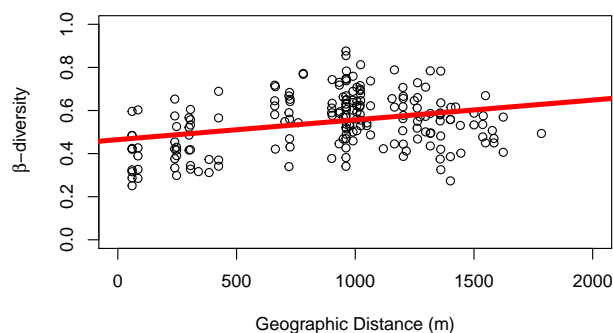
```
jmodelfor.woo <- lm((1 - for.woo[, 4]) ~ for.woo[, 6])
jmodelmix.shr <- lm((1 - mix.shr[, 4]) ~ mix.shr[, 6])
jmodelagr.mea <- lm((1 - agr.mea[, 4]) ~ agr.mea[, 6])
jmodelshr.shr <- lm((1 - shr.shr[, 4]) ~ shr.shr[, 6])
jmodeltal.shr <- lm((1 - tal.shr[, 4]) ~ tal.shr[, 6])
```

- Sorensen Estimator

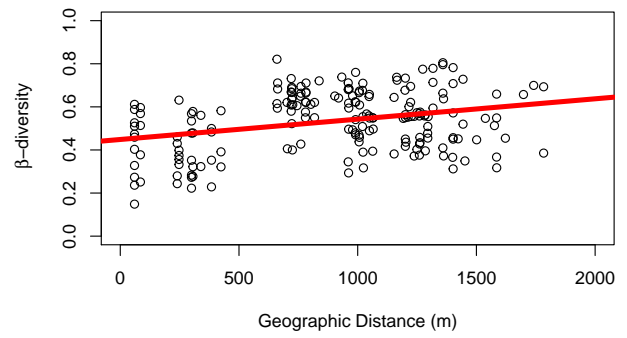
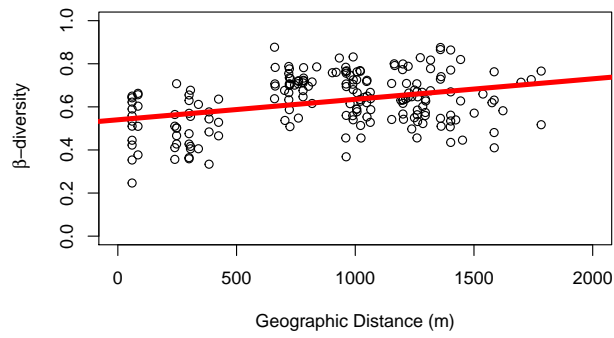
```
smodelfor.woo <- lm((1 - for.woo[, 5]) ~ for.woo[, 6])
smodelmix.shr <- lm((1 - mix.shr[, 5]) ~ mix.shr[, 6])
smodelagr.mea <- lm((1 - agr.mea[, 5]) ~ agr.mea[, 6])
smodelshr.shr <- lm((1 - shr.shr[, 5]) ~ shr.shr[, 6])
smodeltal.shr <- lm((1 - tal.shr[, 5]) ~ tal.shr[, 6])
```

- Short and tall shrubs are together in Shrub (right side: Jaccard and left side: Sorensen)

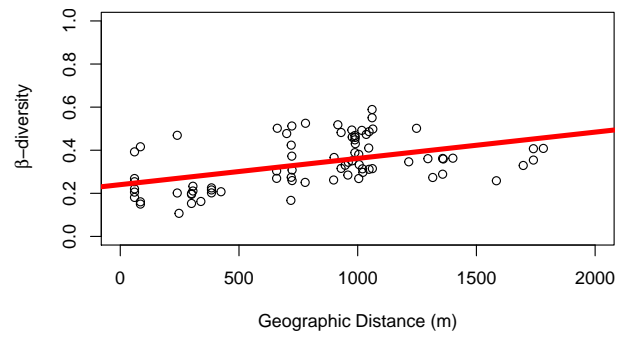
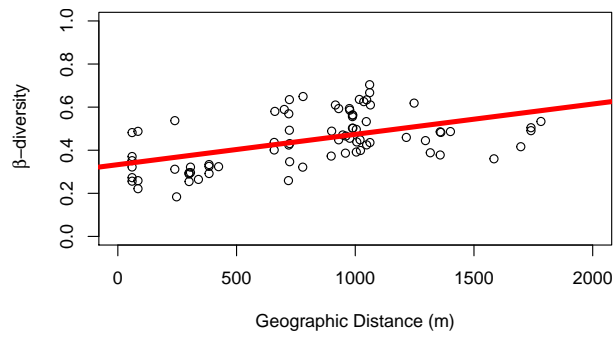
1. Forest



2. Shrub

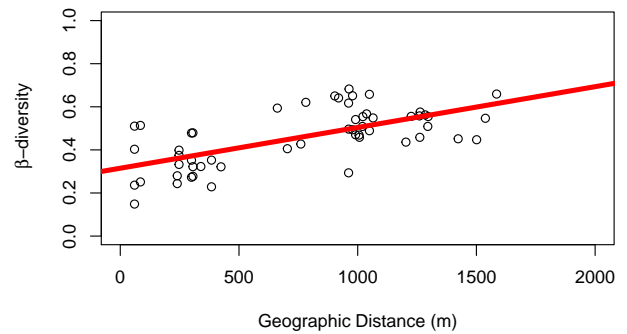
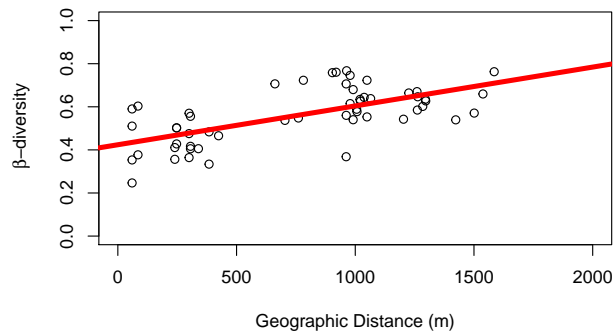


3. Meadow

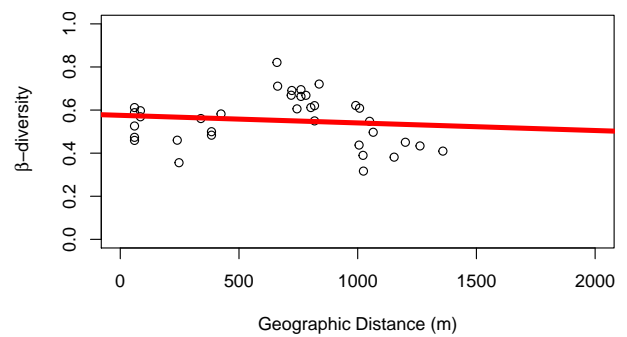
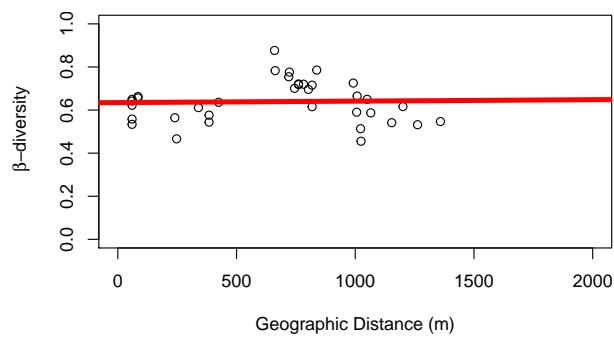


- Short and tall shrubs are separated (right side: Jaccard and left side: Sorensen)

4. Tall Shrub



5. Short Shrub



- Mean Dissimilarity for each landscape (with standard deviations)

```
par(mfrow=c(1, 2))
m.data <- c(mean(for.woo[, 4]), mean(mix.shr[, 4]), mean(agr.mea[, 4]))
m.li <- c(mean(for.woo[, 4]) - sd(for.woo[, 4]), mean(mix.shr[, 4]) - sd(mix.shr[, 4]),
          mean(agr.mea[, 4]) - sd(agr.mea[, 4]))
m.lu <- c(mean(for.woo[, 4]) + sd(for.woo[, 4]), mean(mix.shr[, 4]) + sd(mix.shr[, 4]),
          mean(agr.mea[, 4]) + sd(agr.mea[, 4]))
plot(1:3, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
     ylab = expression(~beta*"~diversity"), main = "Jaccard adjusted")
axis(1, at = 1:3, labels = c("Forest", "Shrub", "Meadow"))
segments(x0 = 1:3, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)

m.data <- c(mean(for.woo[, 5]), mean(mix.shr[, 5]), mean(agr.mea[, 5]))
m.li <- c(mean(for.woo[, 5]) - sd(for.woo[, 5]), mean(mix.shr[, 5]) - sd(mix.shr[, 5]),
          mean(agr.mea[, 5]) - sd(agr.mea[, 5]))
m.lu <- c(mean(for.woo[, 5]) + sd(for.woo[, 5]), mean(mix.shr[, 5]) + sd(mix.shr[, 5]),
          mean(agr.mea[, 5]) + sd(agr.mea[, 5]))
plot(1:3, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
     ylab = expression(~beta*"~diversity"), main = "Sorensen adjusted")
axis(1, at = 1:3, labels = c("Forest", "Shrub", "Meadow"))
segments(x0 = 1:3, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)
```



- Mean Dissimilarity for each landscape (with tall and short shrub separately)

```
par(mfrow=c(1, 2))
m.data <- c(mean(for.woo[, 4]), mean(tal.shr[, 4]), mean(shr.shr[, 4]), mean(agr.mea[, 4]))
m.li <- c(mean(for.woo[, 4]) - sd(for.woo[, 4]), mean(tal.shr[, 4]) - sd(tal.shr[, 4]),
          mean(shr.shr[, 4]) - sd(shr.shr[, 4]), mean(agr.mea[, 4]) - sd(agr.mea[, 4]))
m.lu <- c(mean(for.woo[, 4]) + sd(for.woo[, 4]), mean(tal.shr[, 4]) + sd(tal.shr[, 4]),
          mean(shr.shr[, 4]) + sd(shr.shr[, 4]), mean(agr.mea[, 4]) + sd(agr.mea[, 4]))
plot(1:4, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "", ylab =
     expression(~beta*"~diversity"), main = "Jaccard adjusted")
axis(1, at = 1:4, labels = c("Forest", "Tall", "Short", "Meadow"))
segments(x0 = 1:4, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)

m.data <- c(mean(for.woo[, 5]), mean(tal.shr[, 5]), mean(shr.shr[, 5]), mean(agr.mea[, 5]))
m.li <- c(mean(for.woo[, 5]) - sd(for.woo[, 5]), mean(tal.shr[, 5]) - sd(tal.shr[, 5]),
          mean(shr.shr[, 5]) - sd(shr.shr[, 5]), mean(agr.mea[, 5]) - sd(agr.mea[, 5]))
m.lu <- c(mean(for.woo[, 5]) + sd(for.woo[, 5]), mean(tal.shr[, 5]) + sd(tal.shr[, 5]),
          mean(shr.shr[, 5]) + sd(shr.shr[, 5]), mean(agr.mea[, 5]) + sd(agr.mea[, 5]))
plot(1:4, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
```

```
ylab = expression(~beta*"-diversity"), main = "Sorensen adjusted")
axis(1, at = 1:4, labels = c("Forest", "Tall", "Short", "Meadow"))
segments(x0 = 1:4, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)
```



between landscapes

```
landsc_between <- function(base, s1, s2){
  result <- NULL
  for(i in s1){
    for(j in s2){
      result <- rbind(result, base[(base[, 2] == i & base[, 3] == j) |
                                   (base[, 2] == j & base[, 3] == i), ])
    }
  }
  result
}
```

This function creates a database of pairs of biotypes of the same type, but are in different landscapes. Also, I analyzed separately short and tall shrub among landscapes.

```
mea <- landsc_between(b.div.mean, ma, c(mm, mf))
shr <- landsc_between(b.div.mean, sm, c(sa, sf))
tal <- landsc_between(b.div.mean, tm, c(ta, tf))
woo <- landsc_between(b.div.mean, wf, c(wa, wm))
mix <- rbind(shr, tal)
```

Regression models

- Jaccard Estimator

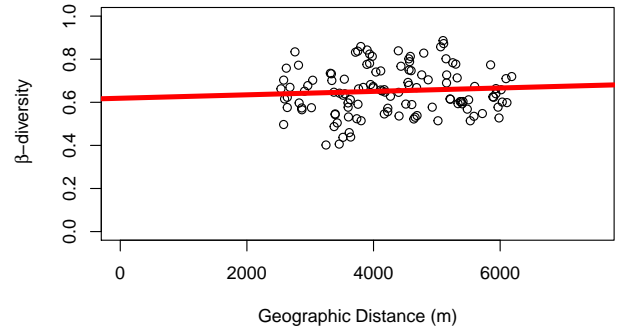
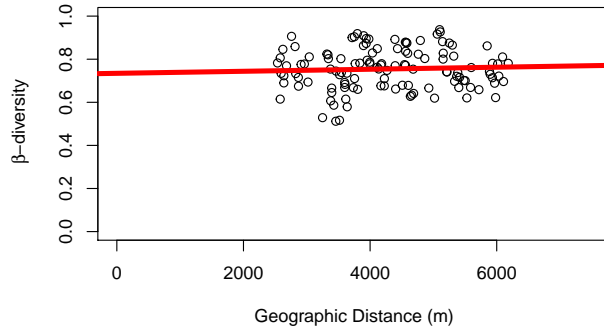
```
jmodelwoo <- lm((1 - woo[, 4]) ~ woo[, 6])
jmodelmix <- lm((1 - mix[, 4]) ~ mix[, 6])
jmodelmea <- lm((1 - mea[, 4]) ~ mea[, 6])
jmodelshr <- lm((1 - shr[, 4]) ~ shr[, 6])
jmodeltal <- lm((1 - tal[, 4]) ~ tal[, 6])
```

- Sorensen Estimator

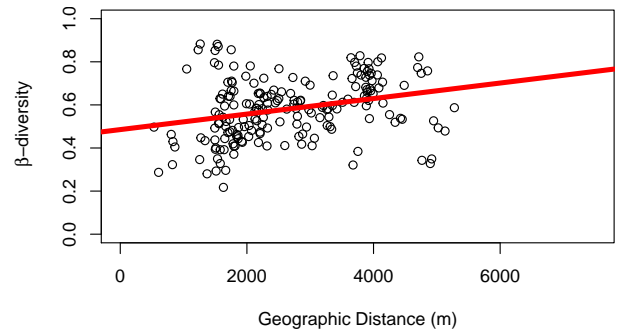
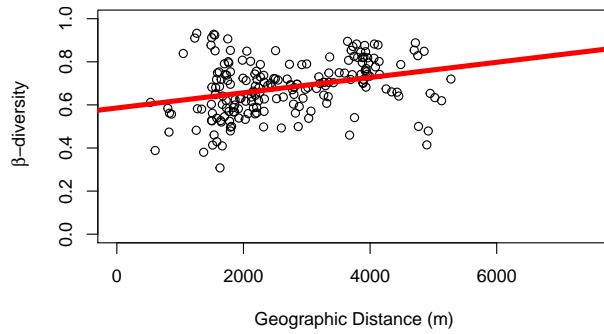
```
smodelwoo <- lm((1 - woo[, 5]) ~ woo[, 6])
smodelmix <- lm((1 - mix[, 5]) ~ mix[, 6])
smodelmea <- lm((1 - mea[, 5]) ~ mea[, 6])
smodelshr <- lm((1 - shr[, 5]) ~ shr[, 6])
smodeltal <- lm((1 - tal[, 5]) ~ tal[, 6])
```

- Short and tall shrubs are together in Shrub (right side: Jaccard and left side: Sorensen)

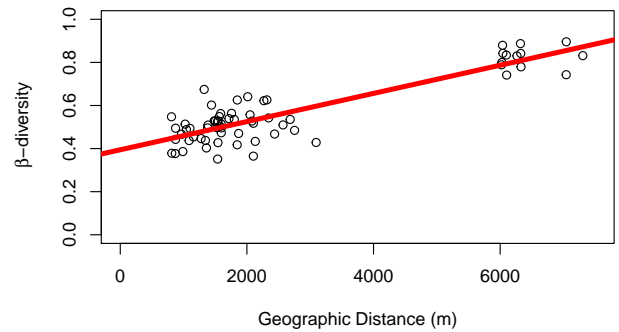
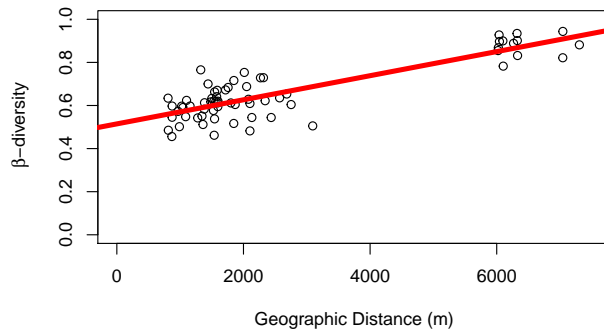
1. Forest



2. Shrub

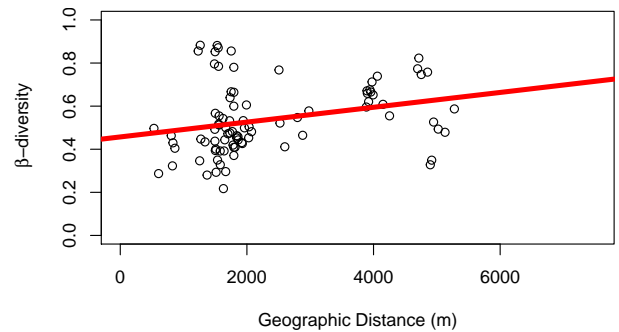
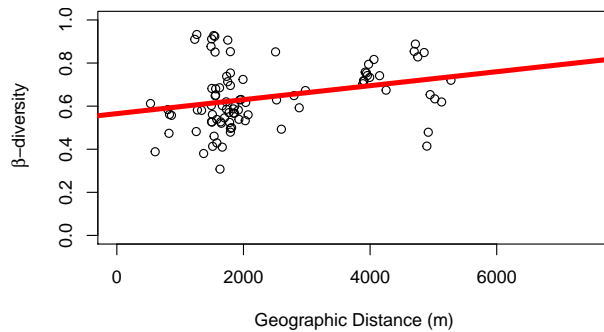


3. Meadow

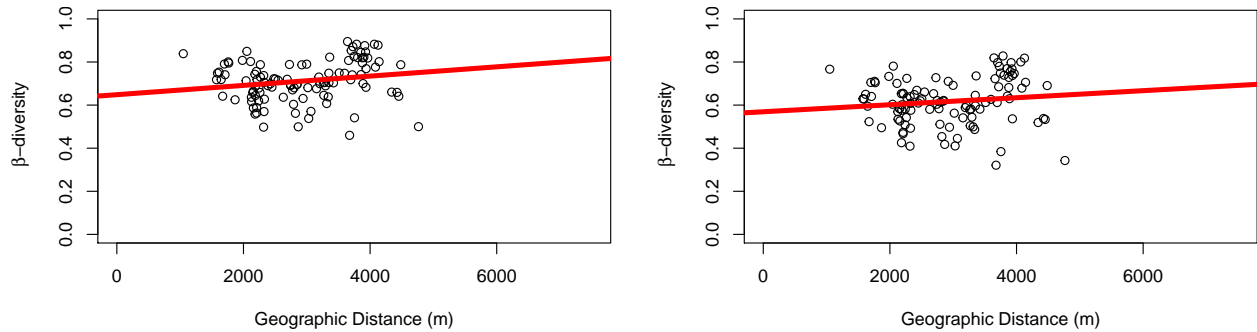


- Short and tall shrubs are separated (right side: Jaccard and left side: Sorensen)

4. Tall Shrub



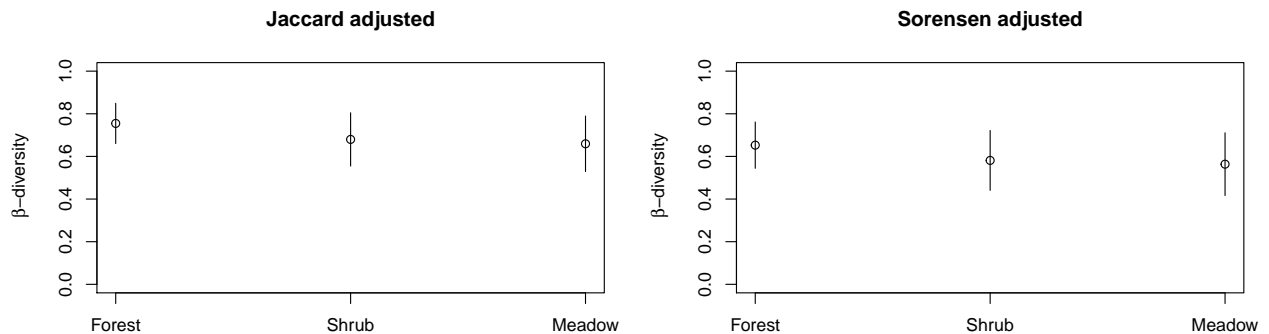
5. Short Shrub



- Mean Dissimilarity for each landscape (with standard deviations)

```
par(mfrow=c(1, 2))
m.data <- c(mean(woo[, 4]), mean(mix[, 4]), mean(mea[, 4]))
m.li <- c(mean(woo[, 4]) - sd(woo[, 4]), mean(mix[, 4]) - sd(mix[, 4]),
          mean(mea[, 4]) - sd(mea[, 4]))
m.lu <- c(mean(woo[, 4]) + sd(woo[, 4]), mean(mix[, 4]) + sd(mix[, 4]),
          mean(mea[, 4]) + sd(mea[, 4]))
plot(1:3, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
     ylab = expression(~beta*"~diversity"), main = "Jaccard adjusted")
axis(1, at = 1:3, labels = c("Forest", "Shrub", "Meadow"))
segments(x0 = 1:3, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)

m.data <- c(mean(woo[, 5]), mean(mix[, 5]), mean(mea[, 5]))
m.li <- c(mean(woo[, 5]) - sd(woo[, 5]), mean(mix[, 5]) - sd(mix[, 5]),
          mean(mea[, 5]) - sd(mea[, 5]))
m.lu <- c(mean(woo[, 5]) + sd(woo[, 5]), mean(mix[, 5]) + sd(mix[, 5]),
          mean(mea[, 5]) + sd(mea[, 5]))
plot(1:3, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
     ylab = expression(~beta*"~diversity"), main = "Sorensen adjusted")
axis(1, at = 1:3, labels = c("Forest", "Shrub", "Meadow"))
segments(x0 = 1:3, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)
```



- Mean Dissimilarity for each landscape (with tall and short shrub separately)

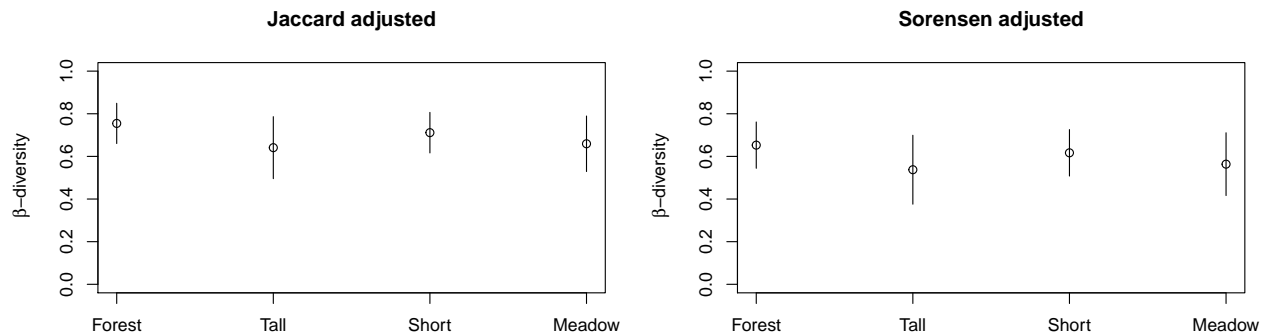
```
par(mfrow=c(1, 2))
m.data <- c(mean(woo[, 4]), mean(tal[, 4]), mean(shr[, 4]), mean(mea[, 4]))
m.li <- c(mean(woo[, 4]) - sd(woo[, 4]), mean(tal[, 4]) - sd(tal[, 4]),
```

```

      mean(shr[, 4]) - sd(shr[, 4]), mean(mea[, 4]) - sd(mea[, 4]))
m.lu <- c(mean(woo[, 4]) + sd(woo[, 4]), mean(tal[, 4]) + sd(tal[, 4]),
      mean(shr[, 4]) + sd(shr[, 4]), mean(mea[, 4]) + sd(mea[, 4]))
plot(1:4, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
      ylab = expression(~beta*"diversity"), main = "Jaccard adjusted")
axis(1, at = 1:4, labels = c("Forest", "Tall", "Short", "Meadow"))
segments(x0 = 1:4, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)

m.data <- c(mean(woo[, 5]), mean(tal[, 5]), mean(shr[, 5]), mean(mea[, 5]))
m.li <- c(mean(woo[, 5]) - sd(woo[, 5]), mean(tal[, 5]) - sd(tal[, 5]),
      mean(shr[, 5]) - sd(shr[, 5]), mean(mea[, 5]) - sd(mea[, 5]))
m.lu <- c(mean(woo[, 5]) + sd(woo[, 5]), mean(tal[, 5]) + sd(tal[, 5]),
      mean(shr[, 5]) + sd(shr[, 5]), mean(mea[, 5]) + sd(mea[, 5]))
plot(1:4, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
      ylab = expression(~beta*"diversity"), main = "Sorensen adjusted")
axis(1, at = 1:4, labels = c("Forest", "Tall", "Short", "Meadow"))
segments(x0 = 1:4, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)

```



Biotores

```

mfma <- c(mf, mm, ma)
sfma <- c(sf, sm, sa)
tfma <- c(tf, tm, ta)
wfma <- c(wf, wm, wa)
mixf <- c(sf, sm, sa, tf, tm, ta)

```

This function creates database for each biotope independent landscape.

```

mea.bio <- landsc_within(b.div.mean, mfma, mfma)
sho.bio <- landsc_within(b.div.mean, sfma, sfma)
tal.bio <- landsc_within(b.div.mean, tfma, tfma)
woo.bio <- landsc_within(b.div.mean, wfma, wfma)
mix.bio <- landsc_within(b.div.mean, mixf, mixf)

```

Regression models

- Jaccard Estimator

```

jmodelwoo.bio <- lm((1 - woo.bio[, 4]) ~ woo.bio[, 6])
jmodelmix.bio <- lm((1 - mix.bio[, 4]) ~ mix.bio[, 6])
jmodelmea.bio <- lm((1 - mea.bio[, 4]) ~ mea.bio[, 6])
jmodelsho.bio <- lm((1 - sho.bio[, 4]) ~ sho.bio[, 6])
jmodeltal.bio <- lm((1 - tal.bio[, 4]) ~ tal.bio[, 6])

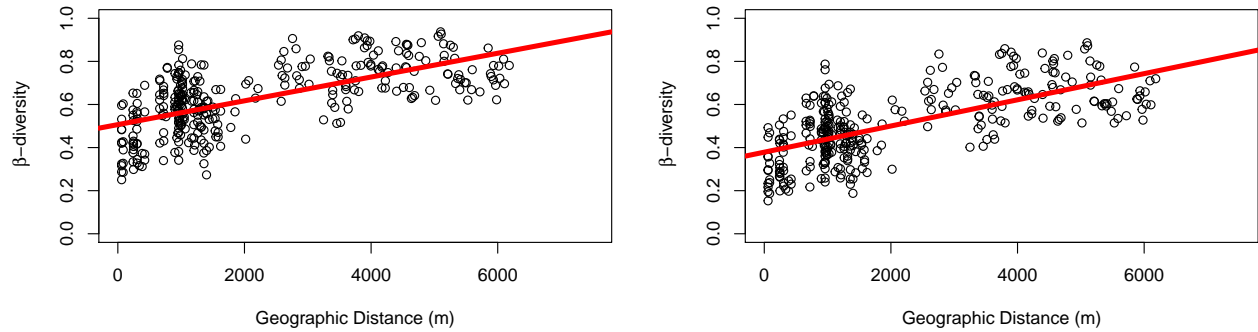
```

- Sorensen Estimator

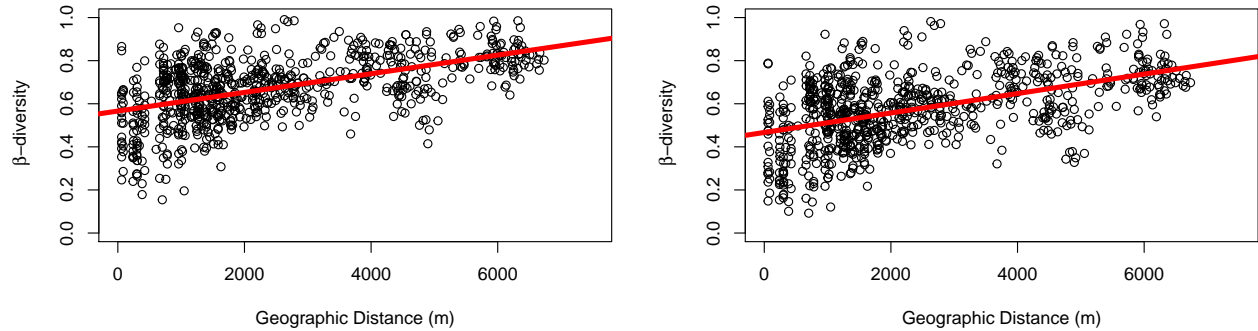
```
smodelwoo.bio <- lm((1 - woo.bio[, 5]) ~ woo.bio[, 6])
smodelmix.bio <- lm((1 - mix.bio[, 5]) ~ mix.bio[, 6])
smodelmea.bio <- lm((1 - mea.bio[, 5]) ~ mea.bio[, 6])
smodelsho.bio <- lm((1 - sho.bio[, 5]) ~ sho.bio[, 6])
smodeltal.bio <- lm((1 - tal.bio[, 5]) ~ tal.bio[, 6])
```

- Short and tall shrubs are together (right side: Jaccard and left side: Sorensen)

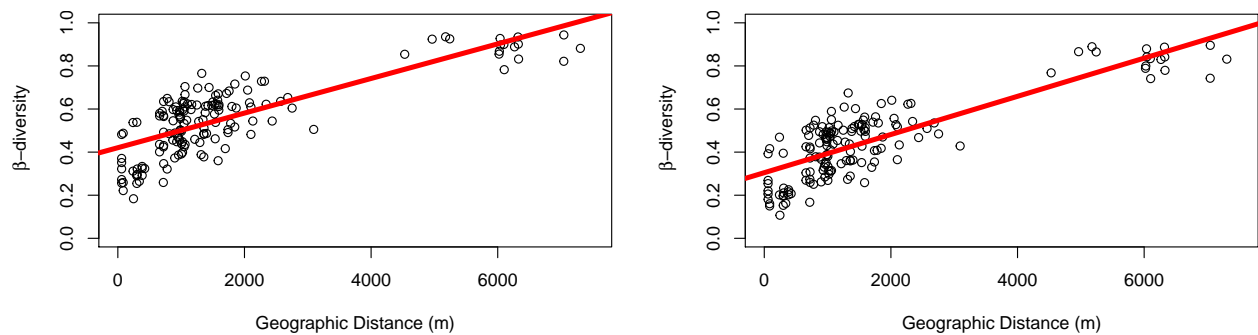
1. Forest



2. Shrub

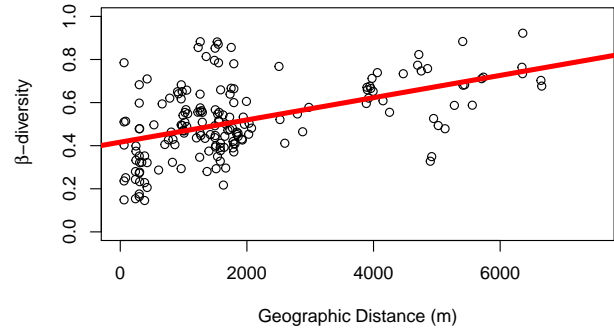
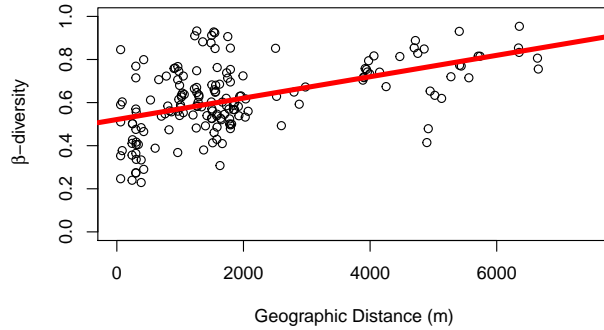


3. Meadow

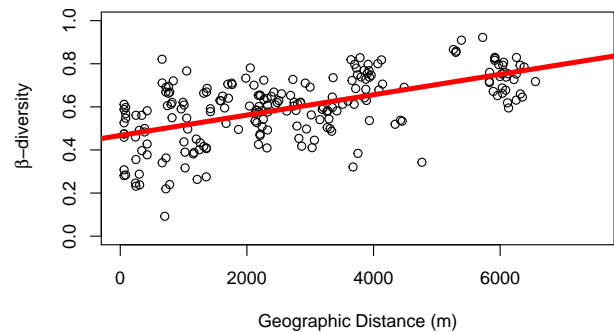
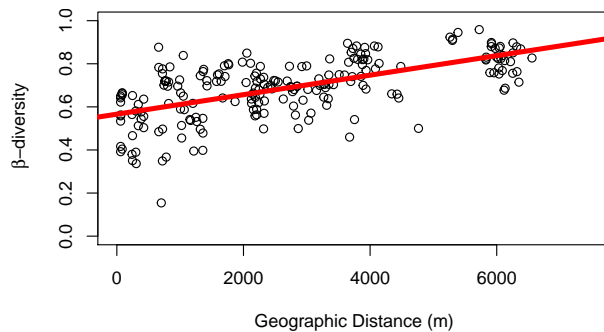


- Short and tall shrubs are separated (right side: Jaccard and left side: Sorensen)

4. Tall Shrub



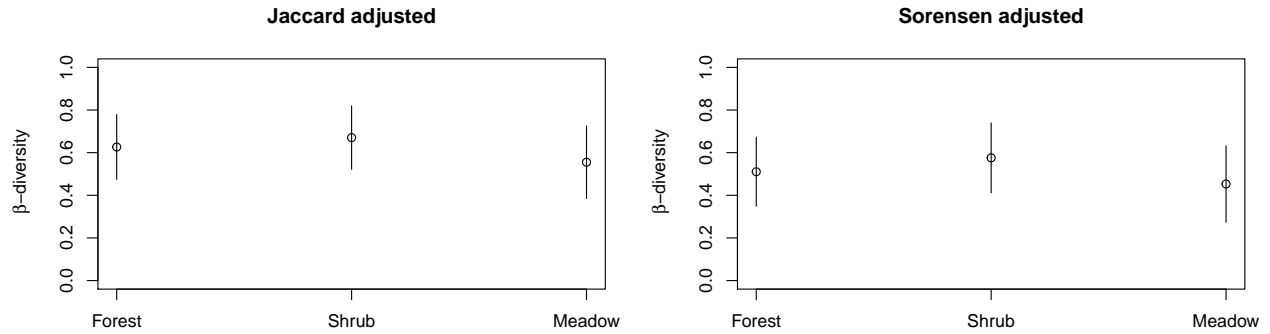
5. Short Shrub



- Mean Dissimilarity for each landscape (with standard deviations)

```
par(mfrow=c(1, 2))
m.data <- c(mean(woo.bio[, 4]), mean(mix.bio[, 4]), mean(mea.bio[, 4]))
m.li <- c(mean(woo.bio[, 4]) - sd(woo.bio[, 4]), mean(mix.bio[, 4]) - sd(mix.bio[, 4]),
          mean(mea.bio[, 4]) - sd(mea.bio[, 4]))
m.lu <- c(mean(woo.bio[, 4]) + sd(woo.bio[, 4]), mean(mix.bio[, 4]) + sd(mix.bio[, 4]),
          mean(mea.bio[, 4]) + sd(mea.bio[, 4]))
plot(1:3, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
     ylab = expression(~beta*"-diversity"), main = "Jaccard adjusted")
axis(1, at = 1:3, labels = c("Forest", "Shrub", "Meadow"))
segments(x0 = 1:3, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)

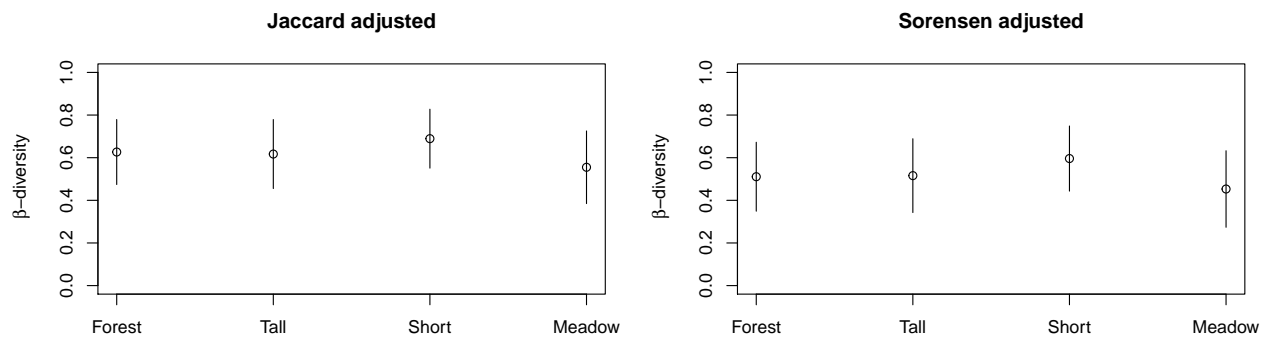
m.data <- c(mean(woo.bio[, 5]), mean(mix.bio[, 5]), mean(mea.bio[, 5]))
m.li <- c(mean(woo.bio[, 5]) - sd(woo.bio[, 5]), mean(mix.bio[, 5]) - sd(mix.bio[, 5]),
          mean(mea.bio[, 5]) - sd(mea.bio[, 5]))
m.lu <- c(mean(woo.bio[, 5]) + sd(woo.bio[, 5]), mean(mix.bio[, 5]) + sd(mix.bio[, 5]),
          mean(mea.bio[, 5]) + sd(mea.bio[, 5]))
plot(1:3, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
     ylab = expression(~beta*"-diversity"), main = "Sorensen adjusted")
axis(1, at = 1:3, labels = c("Forest", "Shrub", "Meadow"))
segments(x0 = 1:3, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)
```



- Mean Dissimilarity for each landscape (with tall and short shrubs separately)

```
par(mfrow=c(1, 2))
m.data <- c(mean(woo.bio[, 4]), mean(tal.bio[, 4]), mean(sho.bio[, 4]), mean(mea.bio[, 4]))
m.li <- c(mean(woo.bio[, 4]) - sd(woo.bio[, 4]), mean(tal.bio[, 4]) - sd(tal.bio[, 4]),
          mean(sho.bio[, 4]) - sd(sho.bio[, 4]), mean(mea.bio[, 4]) - sd(mea.bio[, 4]))
m.lu <- c(mean(woo.bio[, 4]) + sd(woo.bio[, 4]), mean(tal.bio[, 4]) + sd(tal.bio[, 4]),
          mean(sho.bio[, 4]) + sd(sho.bio[, 4]), mean(mea.bio[, 4]) + sd(mea.bio[, 4]))
plot(1:4, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
     ylab = expression(~beta*"~diversity"), main = "Jaccard adjusted")
axis(1, at = 1:4, labels = c("Forest", "Tall", "Short", "Meadow"))
segments(x0 = 1:4, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)

m.data <- c(mean(woo.bio[, 5]), mean(tal.bio[, 5]), mean(sho.bio[, 5]), mean(mea.bio[, 5]))
m.li <- c(mean(woo.bio[, 5]) - sd(woo.bio[, 5]), mean(tal.bio[, 5]) - sd(tal.bio[, 5]),
          mean(sho.bio[, 5]) - sd(sho.bio[, 5]), mean(mea.bio[, 5]) - sd(mea.bio[, 5]))
m.lu <- c(mean(woo.bio[, 5]) + sd(woo.bio[, 5]), mean(tal.bio[, 5]) + sd(tal.bio[, 5]),
          mean(sho.bio[, 5]) + sd(sho.bio[, 5]), mean(mea.bio[, 5]) + sd(mea.bio[, 5]))
plot(1:4, 1 - m.data, xaxt = "n", ylim=c(0, 1), xlab = "",
     ylab = expression(~beta*"~diversity"), main = "Sorensen adjusted")
axis(1, at = 1:4, labels = c("Forest", "Tall", "Short", "Meadow"))
segments(x0 = 1:4, y0 = 1 - m.li, y1 = 1 - m.lu, col = 1)
```



- Mean Dissimilarity for each scale

```
plot.scale <- function(base, estimator = 0){
  #if estimator == 0: Jaccard, otherwise: Sorensen (default is Jaccard)
  area <- base[, 6]
  if(estimator) div <- base[, 5]
  else div <- base[, 4]
```



```

plot(area, 1 - div, ylim = c(0, 1), xlim = c(0, 7500), xlab = "Geographic Distance (m)",
      ylab = expression(~beta*"~diversity"))
abline(v = c(115, 455, 1810), col = "gray", lwd = 1.5, lty = 2)
lines(1:115, rep(1 - mean(div[area <= 115]), 115), col = 2, lwd = 4.5)
lines(116:445, rep(1 - mean(div[(area <= 445) & (area > 115)]), 330), col = 2, lwd = 4.5)
lines(446:1810, rep(1 - mean(div[(area <= 1810) & (area > 445)]), 1365), col = 2, lwd = 4.5)
lines(1811:7500, rep(1 - mean(div[area > 1811]), 5690), col = 2, lwd = 4.5)
}

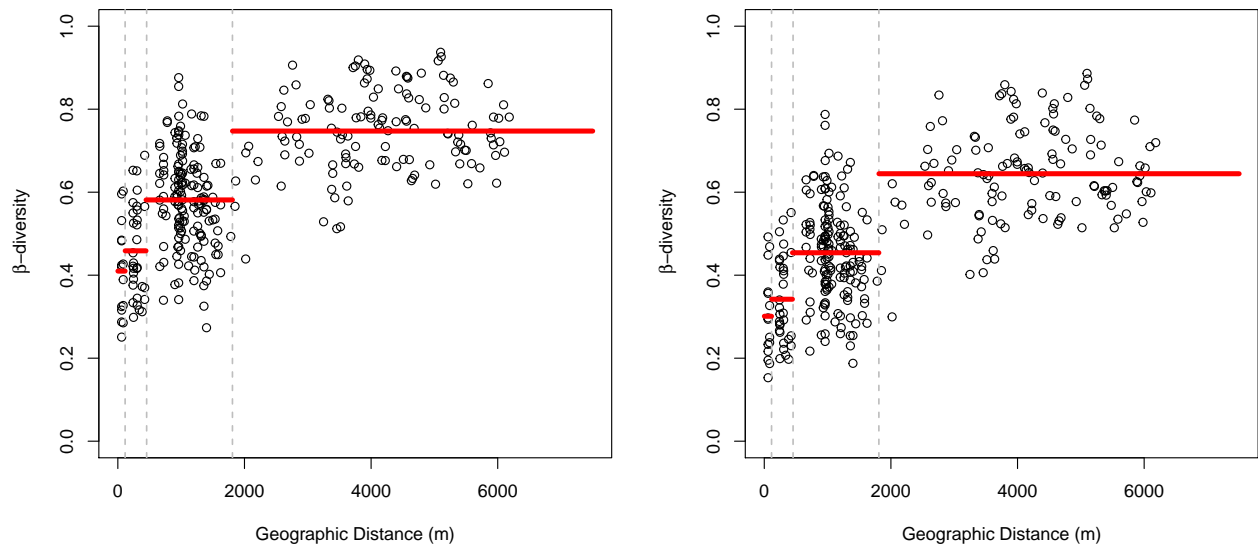
```

1. Forest

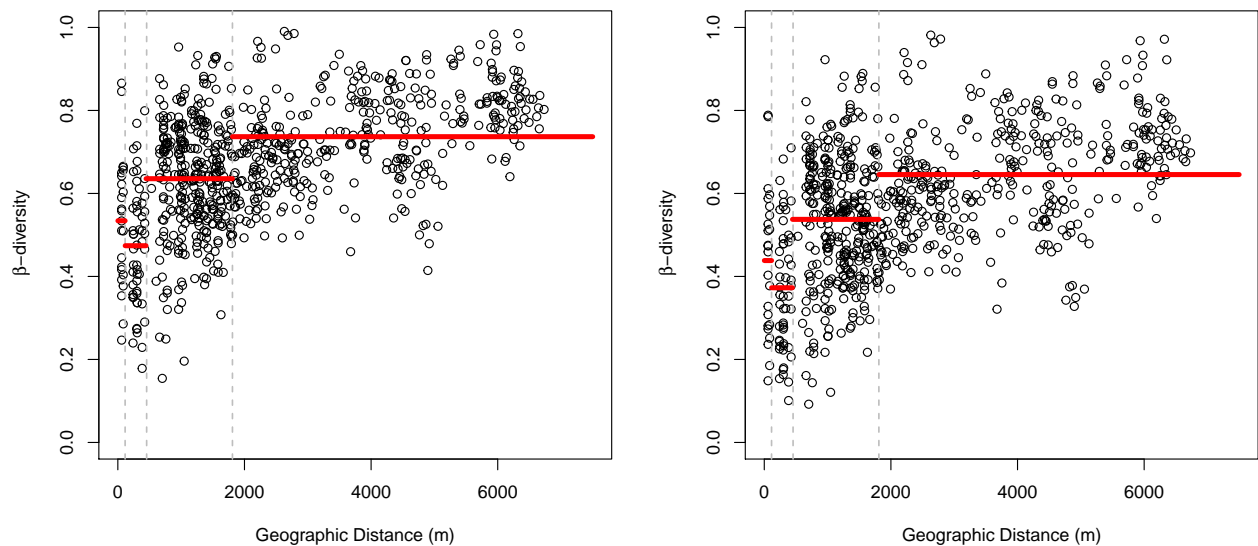
```

par(mfrow=c(1, 2))
plot.scale(woo.bio)
plot.scale(woo.bio, 1)

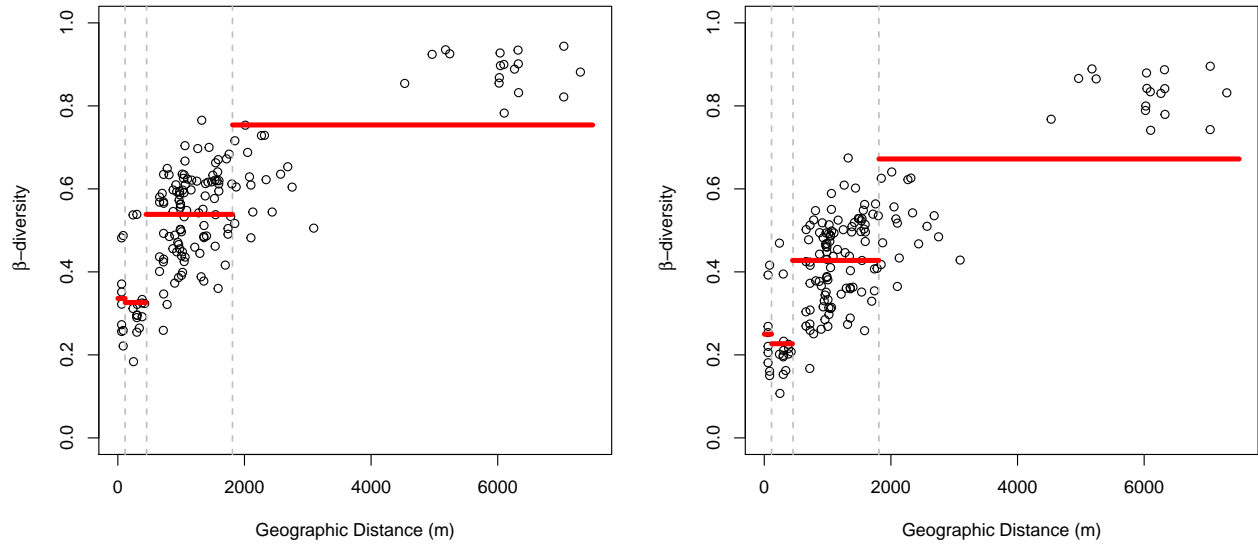
```



2. Shrub

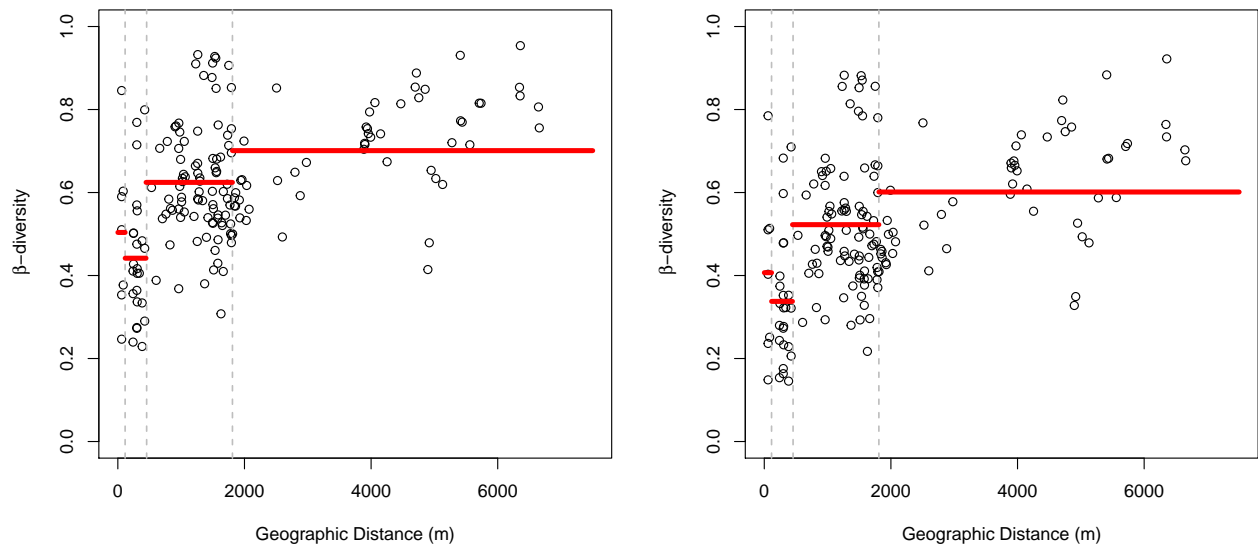


3. Meadow

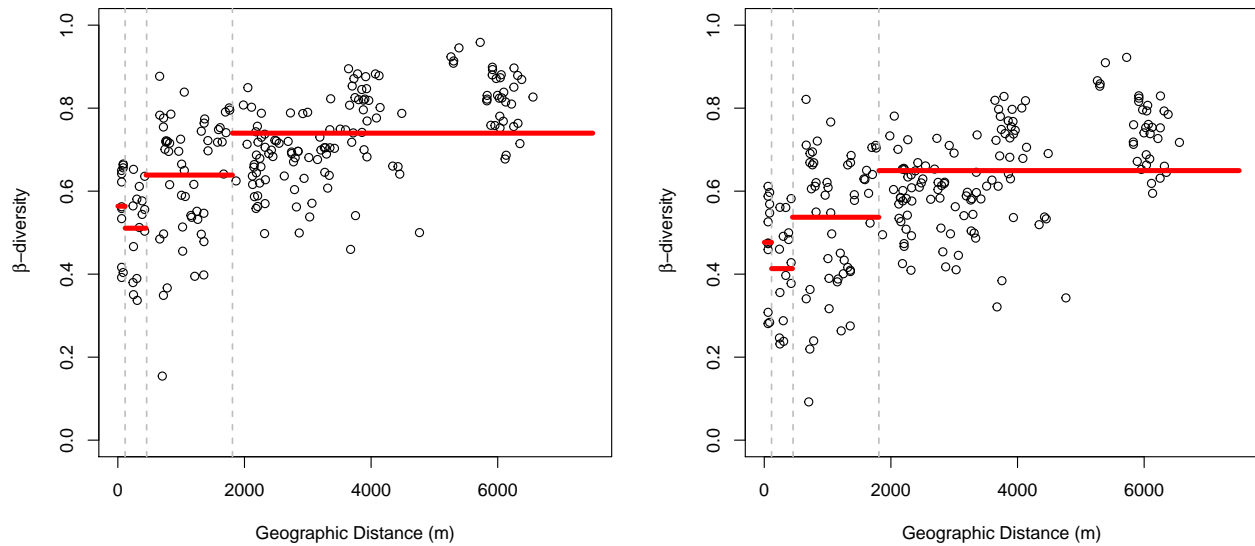


- Mean Dissimilarity for each scale (with tall and short shrubs separately)

4. Tall Shrub



5. Short Shrub



Bootstrapping 1

Mean Dissimilarity for each scale

```
mean.fun <- function(data, ind){
  mean(data[ind], na.rm = TRUE)
}

plot.boot <- function(base, ci.result, estimator = 0){
  #if estimator == 0: Jaccard, otherwise: Sorensen (default is Jaccard)
  area <- base[, 6]
  if(estimator) div <- base[, 5]
  else div <- base[, 4]
  plot(area, 1 - div, ylim = c(0, 1), xlim = c(0, 7500), xlab = "Geographic Distance (m)",
        ylab = expression(~beta*"diversity"))
  abline(v = c(115, 455, 1810), col = "gray", lwd = 1.5, lty = 2)
  lines(1:115, rep(ci.result[1, 1], 115), col = 2, lwd = 4.5)
  lines(116:445, rep(ci.result[2, 1], 330), col = 2, lwd = 4.5)
  lines(446:1810, rep(ci.result[3, 1], 1365), col = 2, lwd = 4.5)
  lines(1811:7500, rep(ci.result[4, 1], 5690), col = 2, lwd = 4.5)
  lines(1:115, rep(ci.result[1, 2], 115), col = 3, lwd = 4.5)
  lines(116:445, rep(ci.result[2, 2], 330), col = 3, lwd = 4.5)
  lines(446:1810, rep(ci.result[3, 2], 1365), col = 3, lwd = 4.5)
  lines(1811:7500, rep(ci.result[4, 2], 5690), col = 3, lwd = 4.5)
  lines(1:115, rep(ci.result[1, 3], 115), col = 3, lwd = 4.5)
  lines(116:445, rep(ci.result[2, 3], 330), col = 3, lwd = 4.5)
  lines(446:1810, rep(ci.result[3, 3], 1365), col = 3, lwd = 4.5)
  lines(1811:7500, rep(ci.result[4, 3], 5690), col = 3, lwd = 4.5)
}
```

1. Forest

```

jsf <- boot(data = 1 - woo.bio[woo.bio[, 6] <= 115, 4], statistic = mean.fun, R = 2000)
jmf <- boot(data = 1 - woo.bio[(woo.bio[, 6] <= 445) & (woo.bio[, 6] > 115), 4],
            statistic = mean.fun, R = 2000)
jlf <- boot(data = 1 - woo.bio[(woo.bio[, 6] <= 1810) & (woo.bio[, 6] > 445), 4],
            statistic = mean.fun, R = 2000)
jxf <- boot(data = 1 - woo.bio[woo.bio[, 6] > 1811, 4], statistic = mean.fun, R = 2000)

ci.jsf <- boot.ci(jsf, type = "bca")
ci.jmf <- boot.ci(jmf, type = "bca")
ci.jlf <- boot.ci(jlf, type = "bca")
ci.jxf <- boot.ci(jxf, type = "bca")

jci.for <- rbind(cbind(ci.jsf$t0, ci.jsf$bca[4], ci.jsf$bca[5]), cbind(ci.jmf$t0,
ci.jmf$bca[4], ci.jmf$bca[5]), cbind(ci.jlf$t0, ci.jlf$bca[4],
ci.jlf$bca[5]), cbind(ci.jxf$t0, ci.jxf$bca[4], ci.jxf$bca[5]))
colnames(jci.for) <- c("mean", "lower.ci", "upper.ci")
rownames(jci.for) <- c("small", "medium", "large", "extra-large")

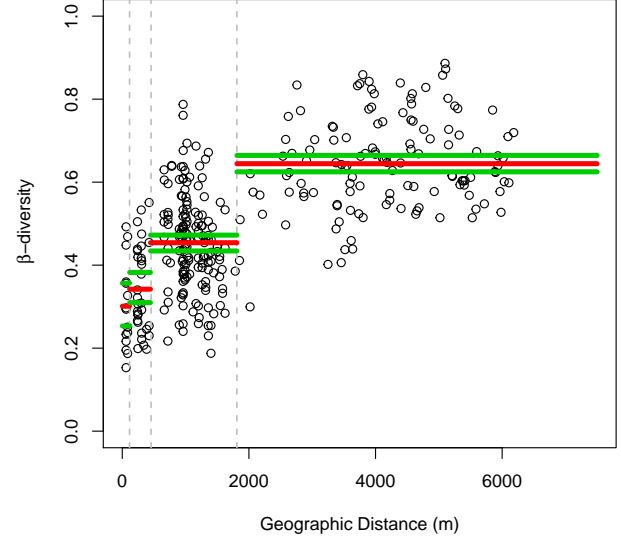
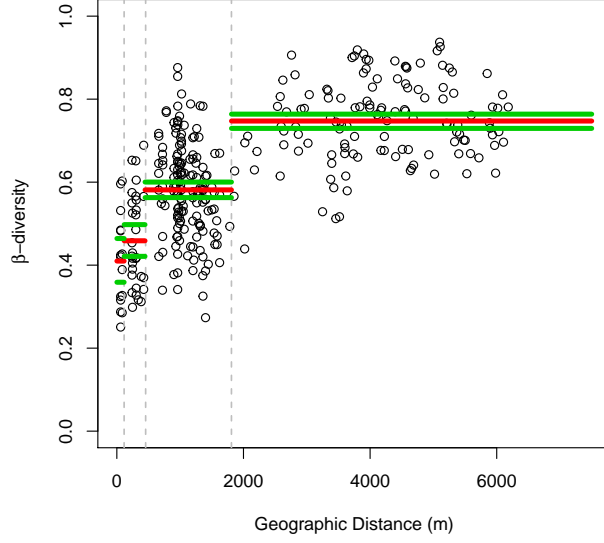
ssf <- boot(data = 1 - woo.bio[woo.bio[, 6] <= 115, 5], statistic = mean.fun, R = 2000)
smf <- boot(data = 1 - woo.bio[(woo.bio[, 6] <= 445) & (woo.bio[, 6] > 115), 5],
            statistic = mean.fun, R = 2000)
slf <- boot(data = 1 - woo.bio[(woo.bio[, 6] <= 1810) & (woo.bio[, 6] > 445), 5],
            statistic = mean.fun, R = 2000)
sxf <- boot(data = 1 - woo.bio[woo.bio[, 6] > 1811, 5], statistic = mean.fun, R = 2000)

ci.ssf <- boot.ci(ssf, type = "bca")
ci.smf <- boot.ci(smf, type = "bca")
ci.slf <- boot.ci(slf, type = "bca")
ci.sxf <- boot.ci(sxf, type = "bca")

sci.for <- rbind(cbind(ci.ssf$t0, ci.ssf$bca[4], ci.ssf$bca[5]), cbind(ci.smf$t0,
ci.smf$bca[4], ci.smf$bca[5]), cbind(ci.slf$t0, ci.slf$bca[4],
ci.slf$bca[5]), cbind(ci.sxf$t0, ci.sxf$bca[4], ci.sxf$bca[5]))
colnames(sci.for) <- c("mean", "lower.ci", "upper.ci")
rownames(sci.for) <- c("small", "medium", "large", "extra-large")

par(mfrow=c(1, 2))
plot.boot(woo.bio, jci.for)
plot.boot(woo.bio, sci.for, 1)

```



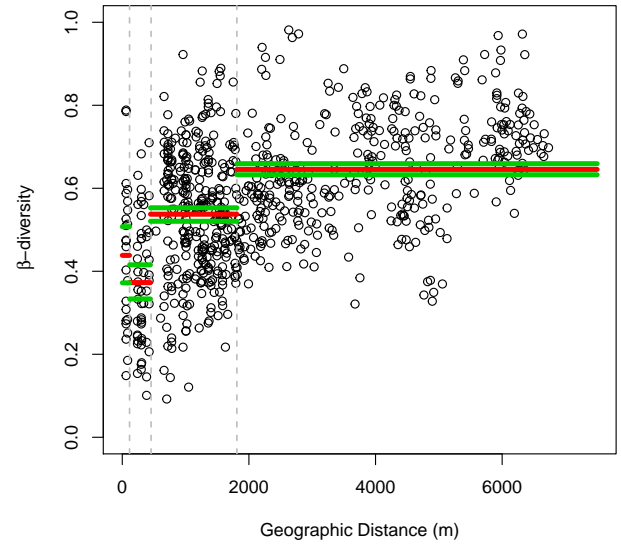
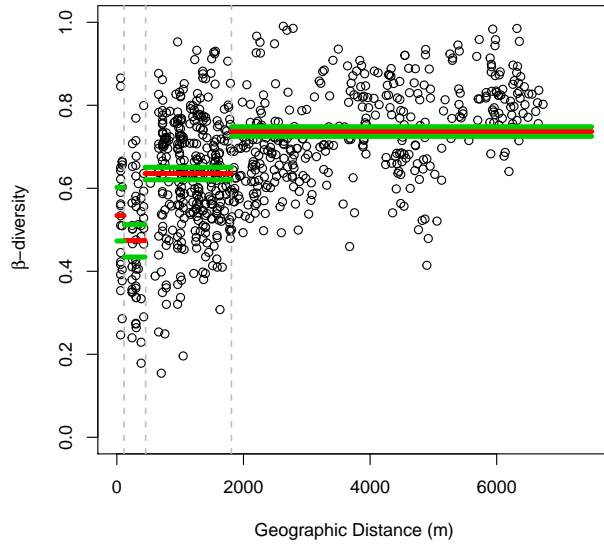
	mean	lower.ci	upper.ci
small	0.4099	0.3588	0.4642
medium	0.4588	0.4212	0.4976
large	0.5813	0.5628	0.6002
extra-large	0.7473	0.7295	0.7639

Table 1: Jaccard

	mean	lower.ci	upper.ci
small	0.3011	0.2534	0.3566
medium	0.3421	0.3097	0.3823
large	0.4541	0.4341	0.4723
extra-large	0.6445	0.6249	0.6644

Table 2: Sorensen

2. Shrub



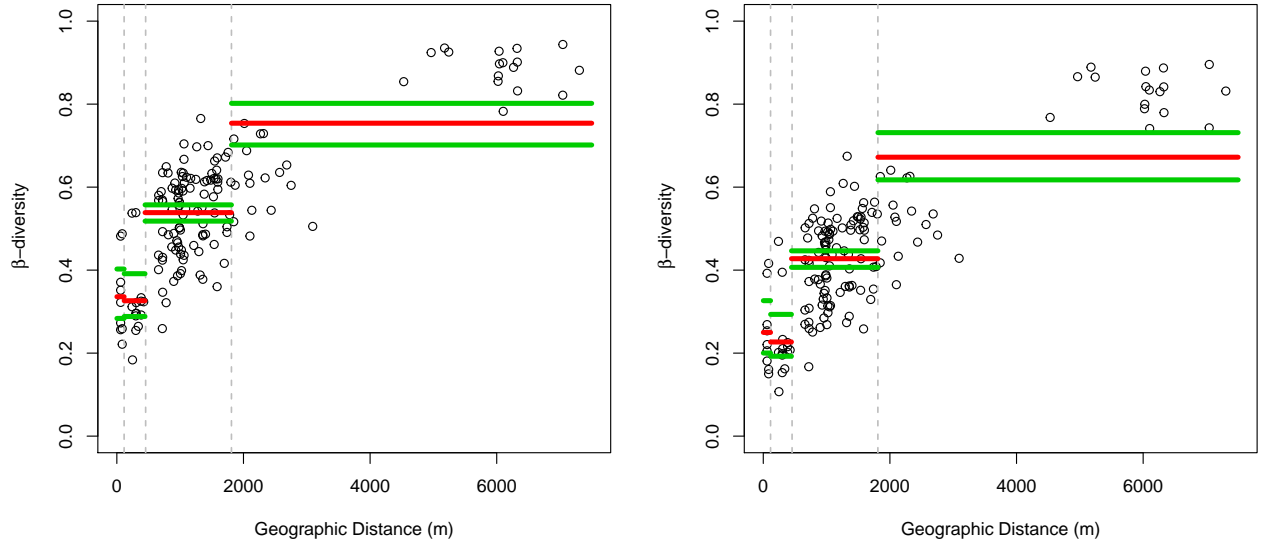
	mean	lower.ci	upper.ci
small	0.5342	0.4729	0.6020
medium	0.4740	0.4343	0.5123
large	0.6355	0.6204	0.6505
extra-large	0.7368	0.7251	0.7483

Table 3: Jaccard

	mean	lower.ci	upper.ci
small	0.4383	0.3721	0.5075
medium	0.3728	0.3333	0.4155
large	0.5375	0.5205	0.5530
extra-large	0.6455	0.6326	0.6592

Table 4: Sorensen

3. Meadow



	mean	lower.ci	upper.ci
small	0.3359	0.2836	0.4026
medium	0.3262	0.2883	0.3914
large	0.5386	0.5181	0.5573
extra-large	0.7540	0.7015	0.8019

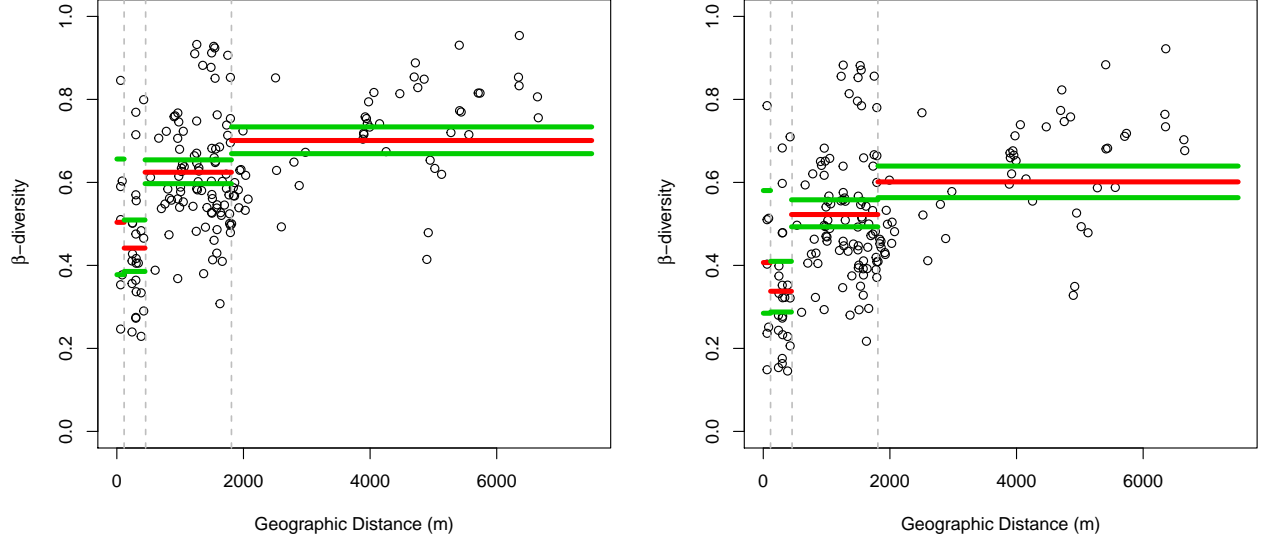
Table 5: Jaccard

- Mean Dissimilarity for each scale (with tall and short shrubs separately)

4. Tall Shrub

	mean	lower.ci	upper.ci
small	0.2499	0.2003	0.3264
medium	0.2269	0.1925	0.2933
large	0.4275	0.4067	0.4465
extra-large	0.6721	0.6175	0.7313

Table 6: Sorensen



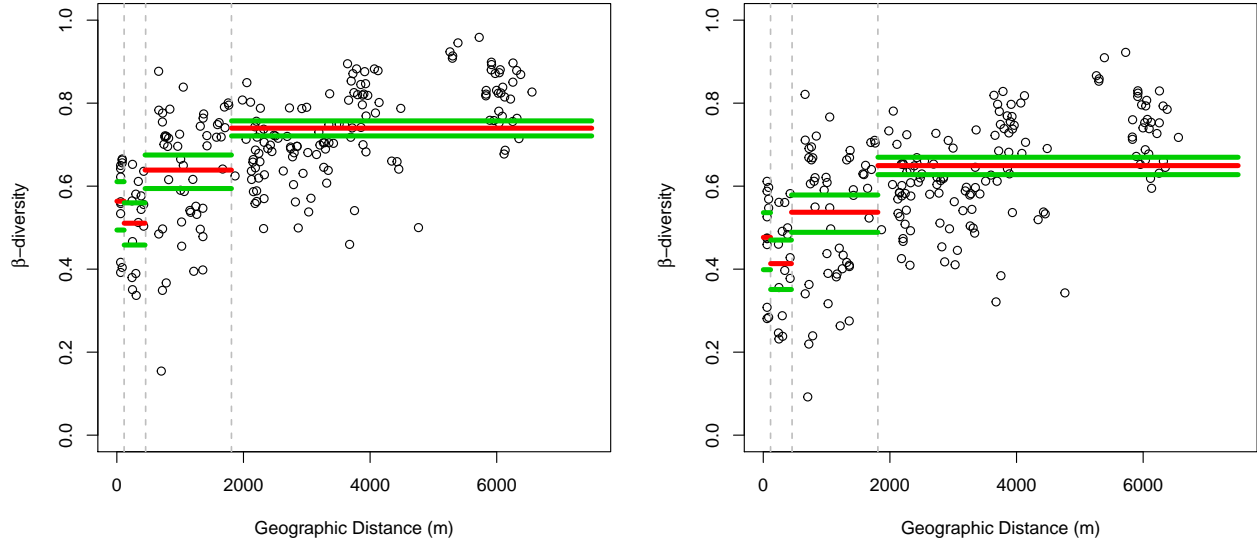
	mean	lower.ci	upper.ci
small	0.5038	0.3776	0.6563
medium	0.4417	0.3854	0.5094
large	0.6244	0.5969	0.6543
extra-large	0.7009	0.6693	0.7337

Table 7: Jaccard

	mean	lower.ci	upper.ci
small	0.4068	0.2847	0.5804
medium	0.3377	0.2876	0.4097
large	0.5226	0.4930	0.5581
extra-large	0.6012	0.5632	0.6394

Table 8: Sorensen

5. Short Shrub



	mean	lower.ci	upper.ci
small	0.5637	0.4942	0.6108
medium	0.5107	0.4582	0.5598
large	0.6387	0.5943	0.6750
extra-large	0.7397	0.7210	0.7573

Table 9: Jaccard

	mean	lower.ci	upper.ci
small	0.4766	0.3987	0.5361
medium	0.4133	0.3509	0.4701
large	0.5371	0.4887	0.5787
extra-large	0.6495	0.6277	0.6696

Table 10: Sorensen

Bootstrapping 2

Within Landscape

```
# bootstrapping with 2000 replications
wl.jforres <- boot(data = as.data.frame(for.woo), statistic = bs.jac, R = 2000,
  formula = (1 - Jabd) ~ ipcc)
wl.sforres <- boot(data = as.data.frame(for.woo), statistic = bs.sor, R = 2000,
  formula = (1 - Labd) ~ ipcc)

wl.jmixres <- boot(data = as.data.frame(mix.shr), statistic = bs.jac, R = 2000,
  formula = (1 - Jabd) ~ ipcc)
wl.smixres <- boot(data = as.data.frame(mix.shr), statistic = bs.sor, R = 2000,
  formula = (1 - Labd) ~ ipcc)

wl.jtalres <- boot(data = as.data.frame(tal.shr), statistic = bs.jac, R = 2000,
  formula = (1 - Jabd) ~ ipcc)
wl.stalres <- boot(data = as.data.frame(tal.shr), statistic = bs.sor, R = 2000,
```



```

        formula = (1 - Labd) ~ ipcc)

wl.jshrres <- boot(data = as.data.frame(shr.shr), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
wl.sshrres <- boot(data = as.data.frame(shr.shr), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

wl.jmeares <- boot(data = as.data.frame(agr.mea), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
wl.smeares <- boot(data = as.data.frame(agr.mea), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

```

Between Landscapes

```

# bootstrapping with 2000 replications
bl.jwoores <- boot(data = as.data.frame(woo), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
bl.swoores <- boot(data = as.data.frame(woo), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

bl.jmixres <- boot(data = as.data.frame(mix), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
bl.smixres <- boot(data = as.data.frame(mix), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

bl.jtalres <- boot(data = as.data.frame(tal), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
bl.stalres <- boot(data = as.data.frame(tal), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

bl.jshrres <- boot(data = as.data.frame(shr), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
bl.sshrres <- boot(data = as.data.frame(shr), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

bl.jmeares <- boot(data = as.data.frame(mea), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
bl.smeares <- boot(data = as.data.frame(mea), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

```

All Biotopes

```

# bootstrapping with 2000 replications
al.jforres <- boot(data = as.data.frame(woo.bio), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
al.sforres <- boot(data = as.data.frame(woo.bio), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

al.jmixres <- boot(data = as.data.frame(mix.bio), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)

```

```

al.smixres <- boot(data = as.data.frame(mix.bio), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

al.jtalres <- boot(data = as.data.frame(tal.bio), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
al.stalres <- boot(data = as.data.frame(tal.bio), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

al.jshrres <- boot(data = as.data.frame(sho.bio), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
al.sshrres <- boot(data = as.data.frame(sho.bio), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

al.jmeares <- boot(data = as.data.frame(mea.bio), statistic = bs.jac, R = 2000,
                  formula = (1 - Jabd) ~ ipcc)
al.smeares <- boot(data = as.data.frame(mea.bio), statistic = bs.sor, R = 2000,
                  formula = (1 - Labd) ~ ipcc)

```

Confidence Interval

Within Landscape - get 95% confidence intervals

Jaccard Estimator

```

wl.jforres.ci <- ci.boot(wl.jforres)
wl.jmixres.ci <- ci.boot(wl.jmixres)
wl.jtalres.ci <- ci.boot(wl.jtalres)
wl.jshrres.ci <- ci.boot(wl.jshrres)

```

Warning: extreme order statistics used as endpoints

```

wl.jmeares.ci <- ci.boot(wl.jmeares)

```

Sorensen Estimator

```

wl.sforres.ci <- ci.boot(wl.sforres)
wl.smixres.ci <- ci.boot(wl.smixres)
wl.stalres.ci <- ci.boot(wl.stalres)
wl.sshrres.ci <- ci.boot(wl.sshrres)
wl.smeares.ci <- ci.boot(wl.smeares)

```

Between Landscapes - get 95% confidence intervals

Jaccard Estimator

```

bl.jforres.ci <- ci.boot(bl.jwoores)
bl.jmixres.ci <- ci.boot(bl.jmixres)
bl.jtalres.ci <- ci.boot(bl.jtalres)
bl.jshrres.ci <- ci.boot(bl.jshrres)
bl.jmeares.ci <- ci.boot(bl.jmeares)

```

Sorensen Estimator

```
bl.sforres.ci <- ci.boot(bl.swoores)
bl.smixres.ci <- ci.boot(bl.smixres)
bl.stalres.ci <- ci.boot(bl.stalres)
bl.sshrres.ci <- ci.boot(bl.sshrres)
bl.smeares.ci <- ci.boot(bl.smeares)
```

All Biotopes - get 95% confidence intervals

Jaccard Estimator

```
al.jforres.ci <- ci.boot(al.jforres)
al.jmixres.ci <- ci.boot(al.jmixres)
al.jtalres.ci <- ci.boot(al.jtalres)
al.jshrres.ci <- ci.boot(al.jshrres)
al.jmeares.ci <- ci.boot(al.jmeares)
```

Sorensen Estimator

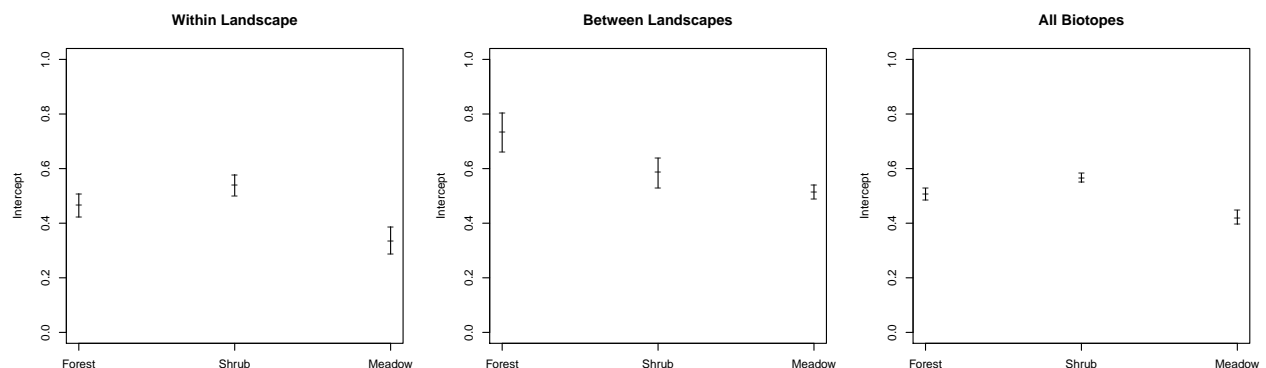
```
al.sforres.ci <- ci.boot(al.sforres)
al.smixres.ci <- ci.boot(al.smixres)
al.stalres.ci <- ci.boot(al.stalres)
al.sshrres.ci <- ci.boot(al.sshrres)
al.smeares.ci <- ci.boot(al.smeares)
```

Results 1

Jaccard

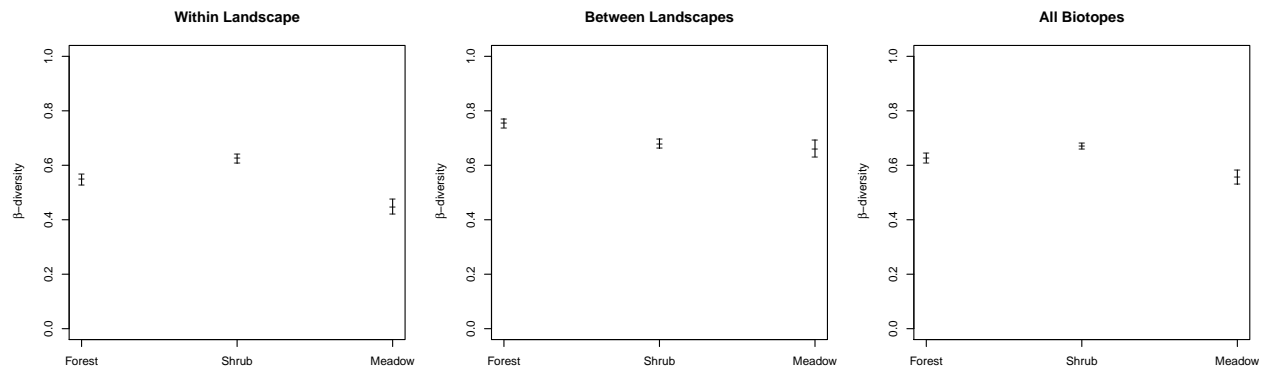
- Intercept

```
par(mfrow = c(1, 3))
interc.plot3(wl.jforres.ci, wl.jmixres.ci, wl.jmeares.ci)
title("Within Landscape", cex = 1.5)
interc.plot3(bl.jforres.ci, bl.jmixres.ci, bl.jmeares.ci)
title("Between Landscapes", cex = 1.5)
interc.plot3(al.jforres.ci, al.jmixres.ci, al.jmeares.ci)
title("All Biotopes", cex = 1.5)
```



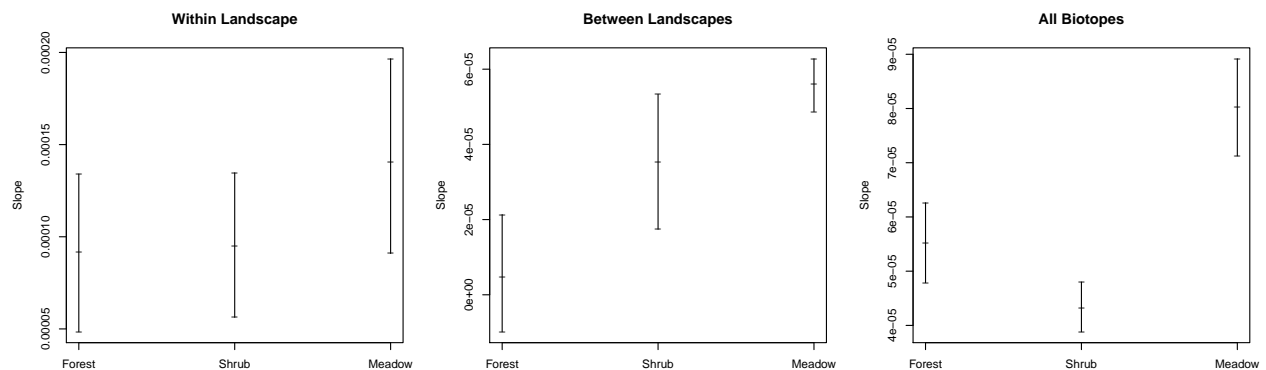
- Dissimilarity

```
par(mfrow = c(1, 3))
dissim.plot3(wl.jforres.ci, wl.jmixres.ci, wl.jmeares.ci)
title("Within Landscape", cex = 1.5)
dissim.plot3(bl.jforres.ci, bl.jmixres.ci, bl.jmeares.ci)
title("Between Landscapes", cex = 1.5)
dissim.plot3(al.jforres.ci, al.jmixres.ci, al.jmeares.ci)
title("All Biotopes", cex = 1.5)
```



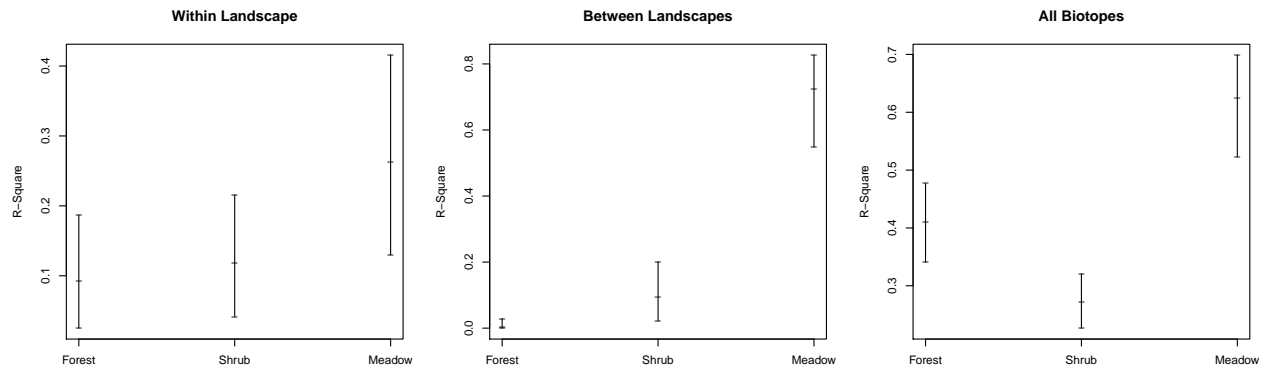
- Slope

```
par(mfrow = c(1, 3))
slope.plot3(wl.jforres.ci, wl.jmixres.ci, wl.jmeares.ci)
title("Within Landscape", cex = 1.5)
slope.plot3(bl.jforres.ci, bl.jmixres.ci, bl.jmeares.ci)
title("Between Landscapes", cex = 1.5)
slope.plot3(al.jforres.ci, al.jmixres.ci, al.jmeares.ci)
title("All Biotopes", cex = 1.5)
```



- R-Square

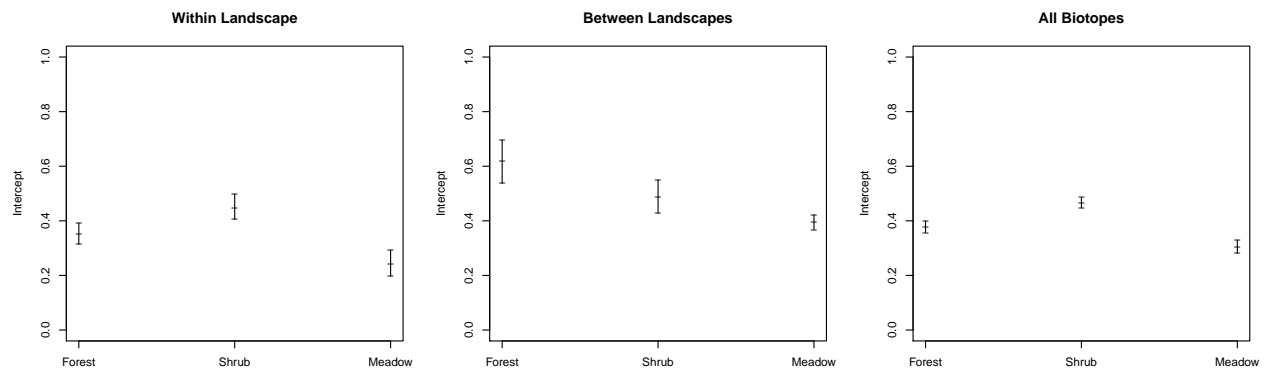
```
par(mfrow = c(1, 3))
rsquar.plot3(wl.jforres.ci, wl.jmixres.ci, wl.jmeares.ci)
title("Within Landscape", cex = 1.5)
rsquar.plot3(bl.jforres.ci, bl.jmixres.ci, bl.jmeares.ci)
title("Between Landscapes", cex = 1.5)
rsquar.plot3(al.jforres.ci, al.jmixres.ci, al.jmeares.ci)
title("All Biotopes", cex = 1.5)
```



Sorensen

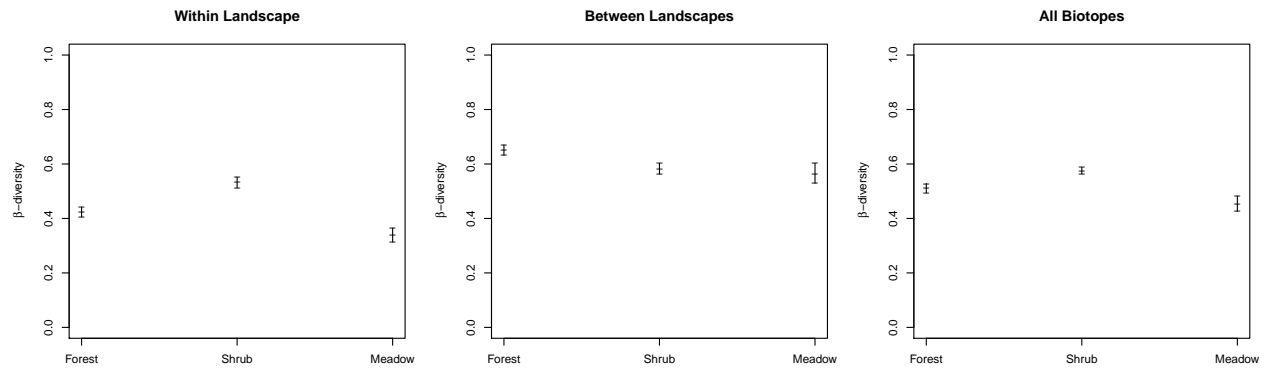
- Intercept

```
par(mfrow = c(1, 3))
interc.plot3(wl.sforres.ci, wl.smixres.ci, wl.smeares.ci)
title("Within Landscape", cex = 1.5)
interc.plot3(bl.sforres.ci, bl.smixres.ci, bl.smeares.ci)
title("Between Landscapes", cex = 1.5)
interc.plot3(al.sforres.ci, al.smixres.ci, al.smeares.ci)
title("All Biotopes", cex = 1.5)
```



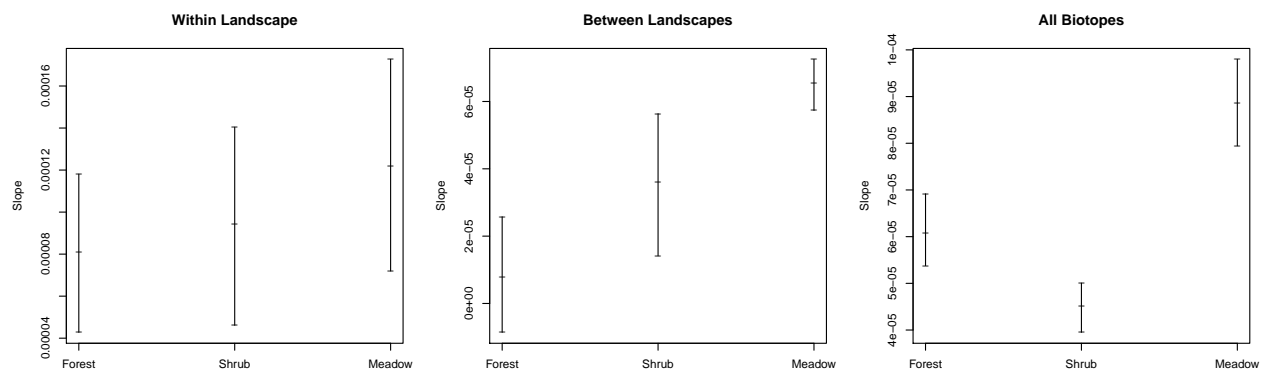
- Dissimilarity

```
par(mfrow = c(1, 3))
dissim.plot3(wl.sforres.ci, wl.smixres.ci, wl.smeares.ci)
title("Within Landscape", cex = 1.5)
dissim.plot3(bl.sforres.ci, bl.smixres.ci, bl.smeares.ci)
title("Between Landscapes", cex = 1.5)
dissim.plot3(al.sforres.ci, al.smixres.ci, al.smeares.ci)
title("All Biotopes", cex = 1.5)
```



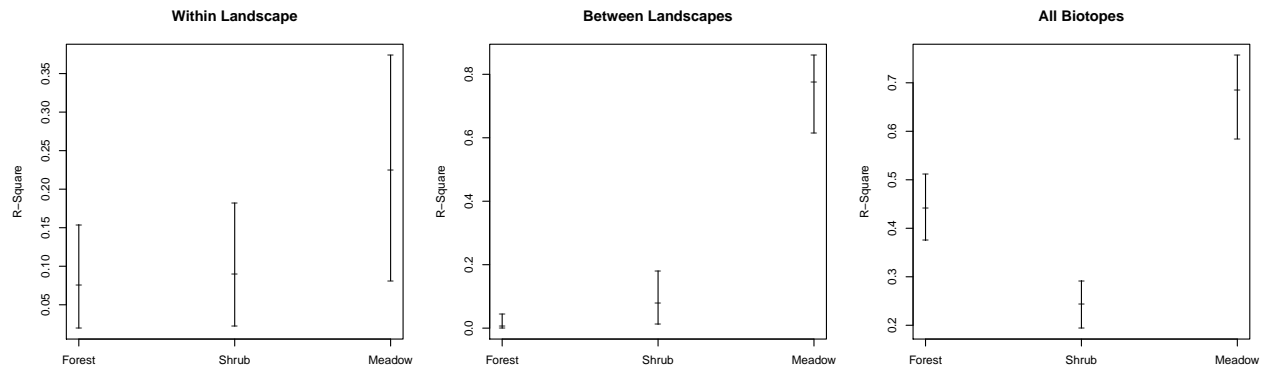
- Slope

```
par(mfrow = c(1, 3))
slope.plot3(wl.sforres.ci, wl.smixres.ci, wl.smeares.ci)
title("Within Landscape", cex = 1.5)
slope.plot3(bl.sforres.ci, bl.smixres.ci, bl.smeares.ci)
title("Between Landscapes", cex = 1.5)
slope.plot3(al.sforres.ci, al.smixres.ci, al.smeares.ci)
title("All Biotopes", cex = 1.5)
```



- R-Square

```
par(mfrow = c(1, 3))
rsquar.plot3(wl.sforres.ci, wl.smixres.ci, wl.smeares.ci)
title("Within Landscape", cex = 1.5)
rsquar.plot3(bl.sforres.ci, bl.smixres.ci, bl.smeares.ci)
title("Between Landscapes", cex = 1.5)
rsquar.plot3(al.sforres.ci, al.smixres.ci, al.smeares.ci)
title("All Biotopes", cex = 1.5)
```

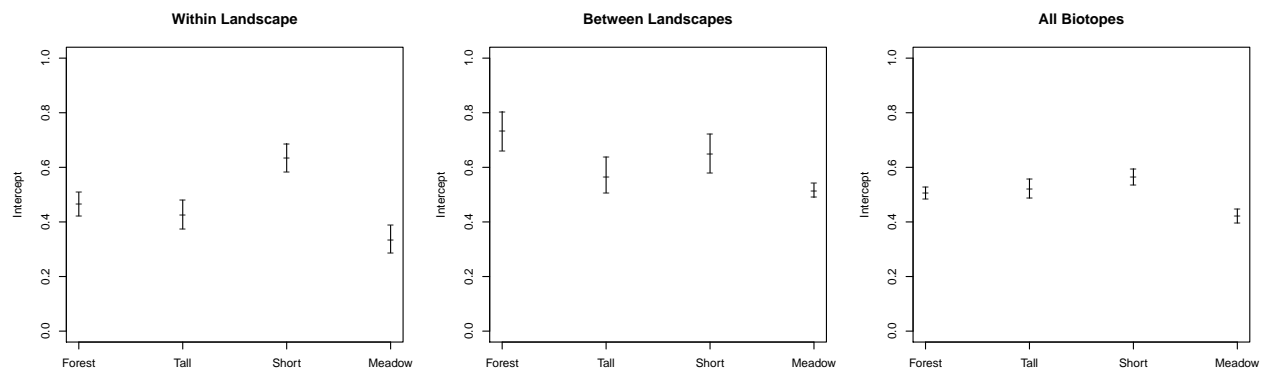


Results 2

Jaccard

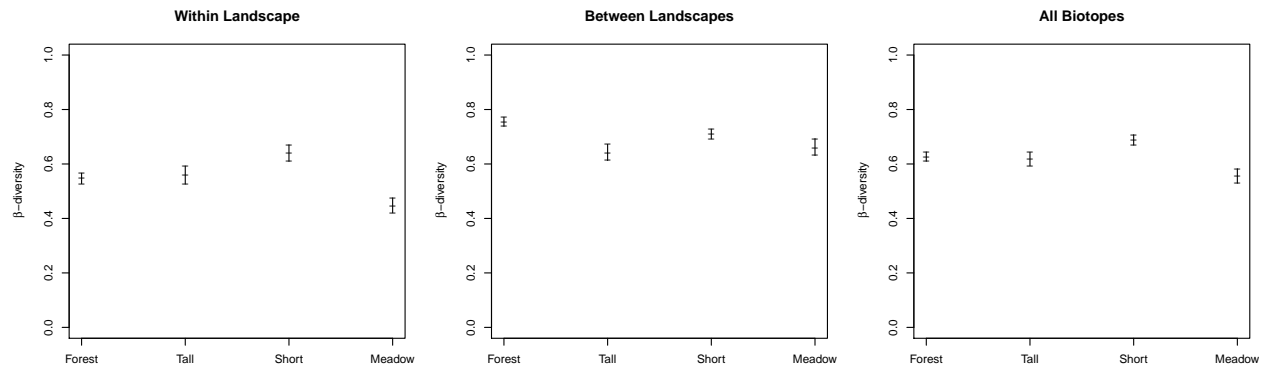
- Intercept

```
par(mfrow = c(1, 3))
interc.plot4(wl.jforres.ci, wl.jtalres.ci, wl.jshrres.ci, wl.jmeares.ci)
title("Within Landscape", cex = 1.5)
interc.plot4(bl.jforres.ci, bl.jtalres.ci, bl.jshrres.ci, bl.jmeares.ci)
title("Between Landscapes", cex = 1.5)
interc.plot4(al.jforres.ci, al.jtalres.ci, al.jshrres.ci, al.jmeares.ci)
title("All Biotopes", cex = 1.5)
```



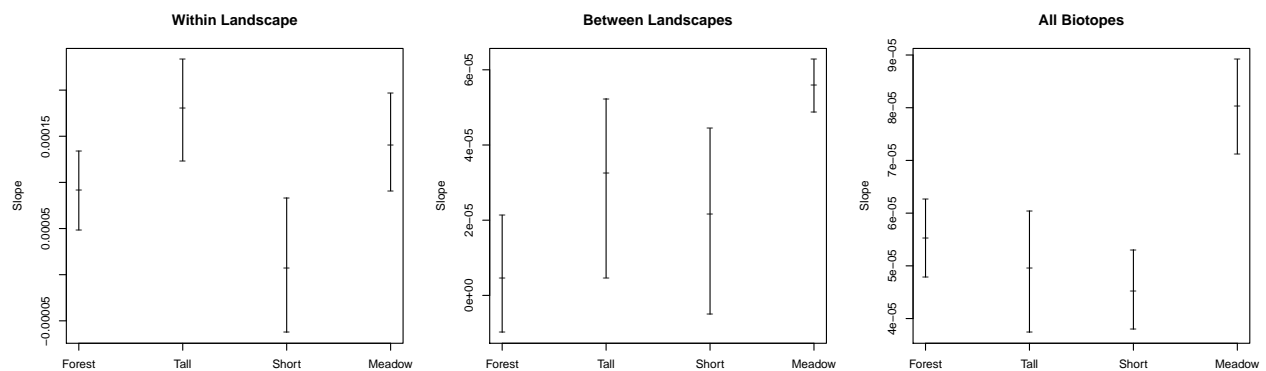
- Dissimilarity

```
par(mfrow = c(1, 3))
dissim.plot4(wl.jforres.ci, wl.jtalres.ci, wl.jshrres.ci, wl.jmeares.ci)
title("Within Landscape", cex = 1.5)
dissim.plot4(bl.jforres.ci, bl.jtalres.ci, bl.jshrres.ci, bl.jmeares.ci)
title("Between Landscapes", cex = 1.5)
dissim.plot4(al.jforres.ci, al.jtalres.ci, al.jshrres.ci, al.jmeares.ci)
title("All Biotopes", cex = 1.5)
```



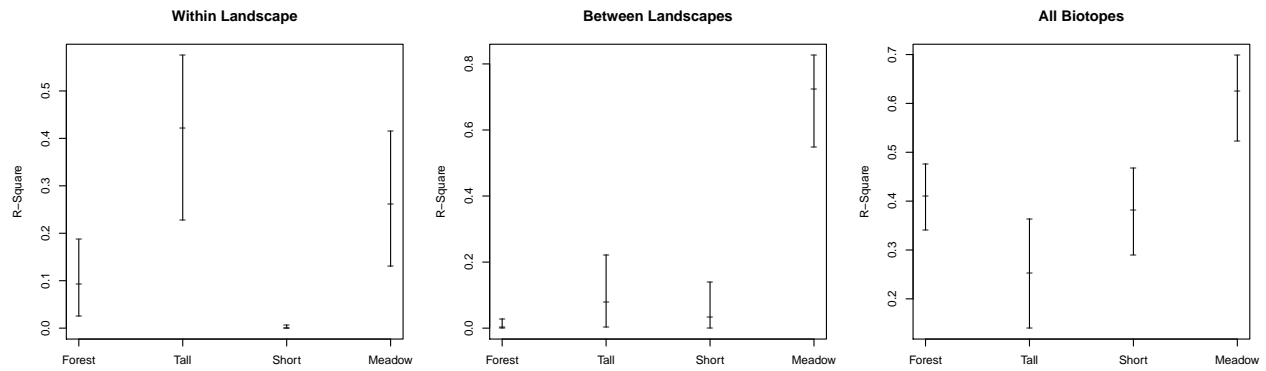
- Slope

```
par(mfrow = c(1, 3))
slope.plot4(wl.jforres.ci, wl.jtalres.ci, wl.jshrres.ci, wl.jmeares.ci)
title("Within Landscape", cex = 1.5)
slope.plot4(bl.jforres.ci, bl.jtalres.ci, bl.jshrres.ci, bl.jmeares.ci)
title("Between Landscapes", cex = 1.5)
slope.plot4(al.jforres.ci, al.jtalres.ci, al.jshrres.ci, al.jmeares.ci)
title("All Biotopes", cex = 1.5)
```



- R-Square

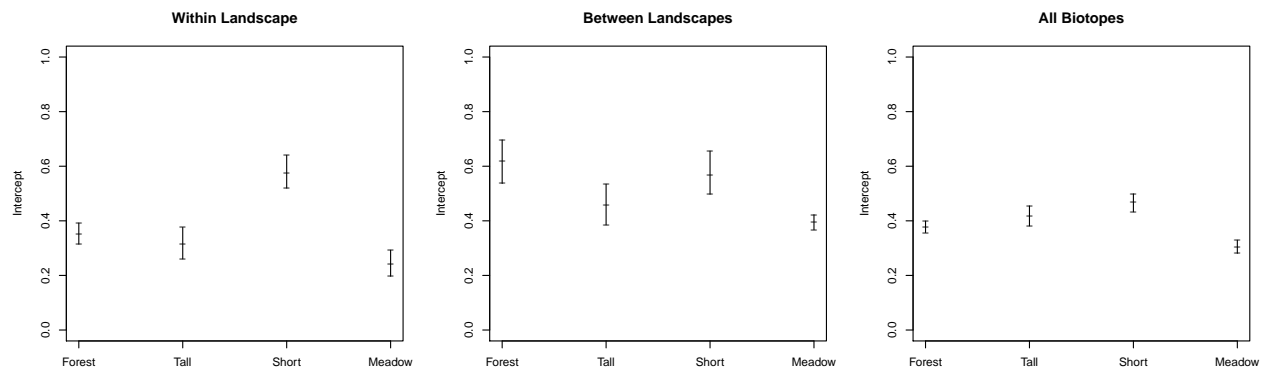
```
par(mfrow = c(1, 3))
rsquar.plot4(wl.jforres.ci, wl.jtalres.ci, wl.jshrres.ci, wl.jmeares.ci)
title("Within Landscape", cex = 1.5)
rsquar.plot4(bl.jforres.ci, bl.jtalres.ci, bl.jshrres.ci, bl.jmeares.ci)
title("Between Landscapes", cex = 1.5)
rsquar.plot4(al.jforres.ci, al.jtalres.ci, al.jshrres.ci, al.jmeares.ci)
title("All Biotopes", cex = 1.5)
```

Sorensen

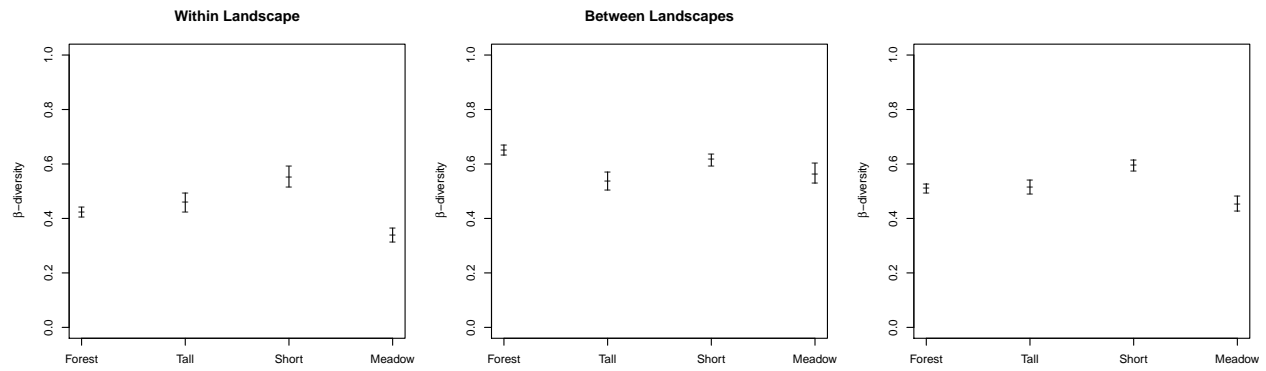
- Intercept

```
par(mfrow = c(1, 3))
interc.plot4(wl.sforres.ci, wl.stalres.ci, wl.sshrres.ci, wl.smeares.ci)
title("Within Landscape", cex = 1.5)
interc.plot4(bl.sforres.ci, bl.stalres.ci, bl.sshrres.ci, bl.smeares.ci)
title("Between Landscapes", cex = 1.5)
interc.plot4(al.sforres.ci, al.stalres.ci, al.sshrres.ci, al.smeares.ci)
title("All Biotopes", cex = 1.5)
```



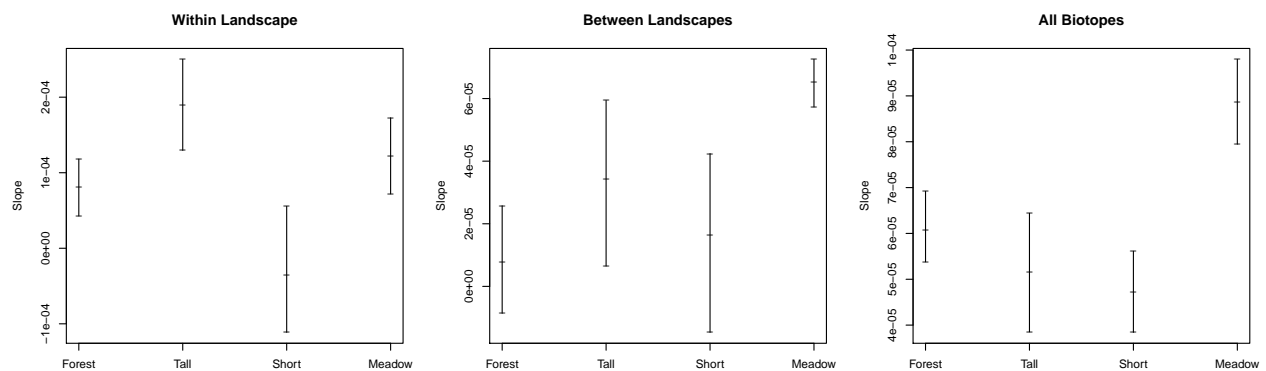
- Dissimilarity

```
par(mfrow = c(1, 3))
dissim.plot4(wl.sforres.ci, wl.stalres.ci, wl.sshrres.ci, wl.smeares.ci)
title("Within Landscape", cex = 1.5)
dissim.plot4(bl.sforres.ci, bl.stalres.ci, bl.sshrres.ci, bl.smeares.ci)
title("Between Landscapes", cex = 1.5)
dissim.plot4(al.sforres.ci, al.stalres.ci, al.sshrres.ci, al.smeares.ci)
```



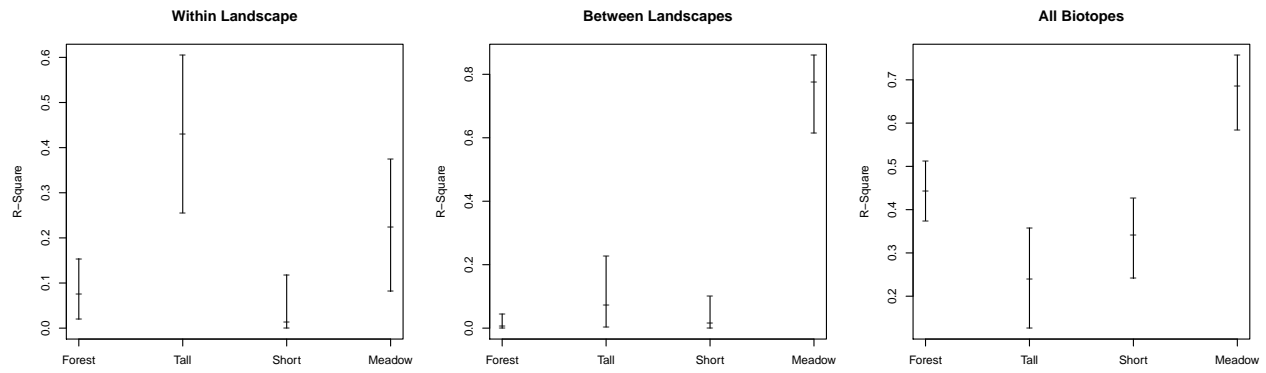
- Slope

```
par(mfrow = c(1, 3))
slope.plot4(wl.sforres.ci, wl.stalres.ci, wl.sshrres.ci, wl.smeares.ci)
title("Within Landscape", cex = 1.5)
slope.plot4(bl.sforres.ci, bl.stalres.ci, bl.sshrres.ci, bl.smeares.ci)
title("Between Landscapes", cex = 1.5)
slope.plot4(al.sforres.ci, al.stalres.ci, al.sshrres.ci, al.smeares.ci)
title("All Biotopes", cex = 1.5)
```



- R-Square

```
par(mfrow = c(1, 3))
rsquar.plot4(wl.sforres.ci, wl.stalres.ci, wl.sshrres.ci, wl.smeares.ci)
title("Within Landscape", cex = 1.5)
rsquar.plot4(bl.sforres.ci, bl.stalres.ci, bl.sshrres.ci, bl.smeares.ci)
title("Between Landscapes", cex = 1.5)
rsquar.plot4(al.sforres.ci, al.stalres.ci, al.sshrres.ci, al.smeares.ci)
title("All Biotopes", cex = 1.5)
```



Tables

Jaccard

1. Within landscape

	mean.ci	lower.ci	upper.ci
Forest	0.4648	0.4223	0.5081
Shrub	0.5400	0.5013	0.5782
Tall	0.4238	0.3746	0.4797
Short	0.6347	0.5842	0.6871
Meadow	0.3331	0.2872	0.3870

	mean.ci	lower.ci	upper.ci
Forest	0.5480	0.5660	0.5279
Shrub	0.6249	0.6405	0.6067
Tall	0.5611	0.5924	0.5262
Short	0.6391	0.6703	0.6095
Meadow	0.4466	0.4754	0.4209

	mean.ci	lower.ci	upper.ci
Forest	0.000092	0.000048	0.000134
Shrub	0.000095	0.000056	0.000135
Tall	0.000180	0.000123	0.000233
Short	0.000007	-0.000062	0.000083
Meadow	0.000141	0.000091	0.000197

	mean.ci	lower.ci	upper.ci
Forest	0.0921	0.0251	0.1870
Shrub	0.1178	0.0416	0.2156
Tall	0.4210	0.2278	0.5755
Short	0.0008	0.0000	0.0069
Meadow	0.2622	0.1300	0.4155

2. Between landscapes

	mean.ci	lower.ci	upper.ci
Forest	0.7345	0.6613	0.8044
Shrub	0.5857	0.5296	0.6384
Tall	0.5652	0.5070	0.6380
Short	0.6483	0.5805	0.7219
Meadow	0.5146	0.4896	0.5408

	mean.ci	lower.ci	upper.ci
Forest	0.7548	0.7716	0.7382
Shrub	0.6798	0.6978	0.6615
Tall	0.6410	0.6718	0.6126
Short	0.7114	0.7279	0.6925
Meadow	0.6592	0.6933	0.6310

	mean.ci	lower.ci	upper.ci
Forest	0.000005	-0.000010	0.000021
Shrub	0.000035	0.000017	0.000053
Tall	0.000032	0.000005	0.000052
Short	0.000022	-0.000005	0.000044
Meadow	0.000056	0.000049	0.000063

	mean.ci	lower.ci	upper.ci
Forest	0.0025	0.0000	0.0288
Shrub	0.0946	0.0220	0.2013
Tall	0.0806	0.0032	0.2224
Short	0.0350	0.0001	0.1401
Meadow	0.7247	0.5488	0.8265

3. All biotopes

	mean.ci	lower.ci	upper.ci
Forest	0.5066	0.4849	0.5278
Shrub	0.5661	0.5495	0.5824
Tall	0.5214	0.4874	0.5576
Short	0.5661	0.5358	0.5949
Meadow	0.4205	0.3961	0.4472

	mean.ci	lower.ci	upper.ci
Forest	0.6266	0.6441	0.6099
Shrub	0.6706	0.6807	0.6602
Tall	0.6171	0.6429	0.5937
Short	0.6892	0.7073	0.6694
Meadow	0.5551	0.5825	0.5293

	mean.ci	lower.ci	upper.ci
Forest	0.000055	0.000048	0.000063
Shrub	0.000043	0.000039	0.000048
Tall	0.000050	0.000037	0.000060
Short	0.000045	0.000038	0.000053
Meadow	0.000080	0.000071	0.000089

	mean.ci	lower.ci	upper.ci
Forest	0.4104	0.3408	0.4768
Shrub	0.2720	0.2267	0.3210
Tall	0.2536	0.1400	0.3640
Short	0.3827	0.2902	0.4679
Meadow	0.6253	0.5231	0.6988

Sorensen

1. Within landscape

	mean.ci	lower.ci	upper.ci
Forest	0.3505	0.3146	0.3918
Shrub	0.4486	0.4048	0.4980
Tall	0.3149	0.2606	0.3756
Short	0.5756	0.5198	0.6400
Meadow	0.2402	0.1970	0.2922

	mean.ci	lower.ci	upper.ci
Forest	0.4237	0.4413	0.4055
Shrub	0.5329	0.5517	0.5126
Tall	0.4591	0.4937	0.4250
Short	0.5524	0.5909	0.5156
Meadow	0.3386	0.3645	0.3134

	mean.ci	lower.ci	upper.ci
Forest	0.000081	0.000043	0.000118
Shrub	0.000094	0.000046	0.000140
Tall	0.000189	0.000130	0.000250
Short	-0.000035	-0.000111	0.000055
Meadow	0.000122	0.000072	0.000173

	mean.ci	lower.ci	upper.ci
Forest	0.0755	0.0197	0.1541
Shrub	0.0904	0.0222	0.1821
Tall	0.4295	0.2555	0.6049
Short	0.0146	0.0000	0.1183
Meadow	0.2246	0.0812	0.3739

2. Between landscapes

	mean.ci	lower.ci	upper.ci
Forest	0.6189	0.5369	0.6962
Shrub	0.4854	0.4280	0.5501
Tall	0.4571	0.3854	0.5340
Short	0.5691	0.4975	0.6554
Meadow	0.3945	0.3677	0.4224

	mean.ci	lower.ci	upper.ci
Forest	0.6529	0.6702	0.6317
Shrub	0.5812	0.6022	0.5632
Tall	0.5375	0.5708	0.5042
Short	0.6168	0.6355	0.5937
Meadow	0.5636	0.6025	0.5291

	mean.ci	lower.ci	upper.ci
Forest	0.000008	-0.000009	0.000026
Shrub	0.000036	0.000014	0.000056
Tall	0.000034	0.000007	0.000059
Short	0.000016	-0.000015	0.000042
Meadow	0.000065	0.000057	0.000073

	mean.ci	lower.ci	upper.ci
Forest	0.0054	0.0000	0.0446
Shrub	0.0778	0.0118	0.1806
Tall	0.0734	0.0038	0.2263
Short	0.0153	0.0000	0.0998
Meadow	0.7752	0.6151	0.8604

3. All biotopes

	mean.ci	lower.ci	upper.ci
Forest	0.3787	0.3572	0.3992
Shrub	0.4667	0.4480	0.4854
Tall	0.4163	0.3814	0.4545
Short	0.4673	0.4331	0.4988
Meadow	0.3046	0.2810	0.3289

	mean.ci	lower.ci	upper.ci
Forest	0.5107	0.5281	0.4937
Shrub	0.5757	0.5874	0.5639
Tall	0.5158	0.5412	0.4903
Short	0.5960	0.6160	0.5748
Meadow	0.4531	0.4823	0.4258

	mean.ci	lower.ci	upper.ci
Forest	0.000061	0.000054	0.000069
Shrub	0.000045	0.000040	0.000050
Tall	0.000052	0.000039	0.000064
Short	0.000047	0.000038	0.000056
Meadow	0.000089	0.000079	0.000098

	mean.ci	lower.ci	upper.ci
Forest	0.4419	0.3748	0.5116
Shrub	0.2442	0.1941	0.2921
Tall	0.2396	0.1262	0.3577
Short	0.3421	0.2410	0.4258
Meadow	0.6856	0.5846	0.7570