

# BCB743 Quantitative Ecology practical

*Tauriq Jamalie (3437177)*

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## Question 1 (2 marks)

Specify the dimensions of the three data sets.

```
# Dimensions -----
```

```
dim(env)
```

```
## [1] 28 3
```

```
dim(spa)
```

```
## [1] 28 2
```

```
dim(spe)
```

```
## [1] 28 17
```

```
dim(spe_mass)
```

```
## [1] 28 17
```

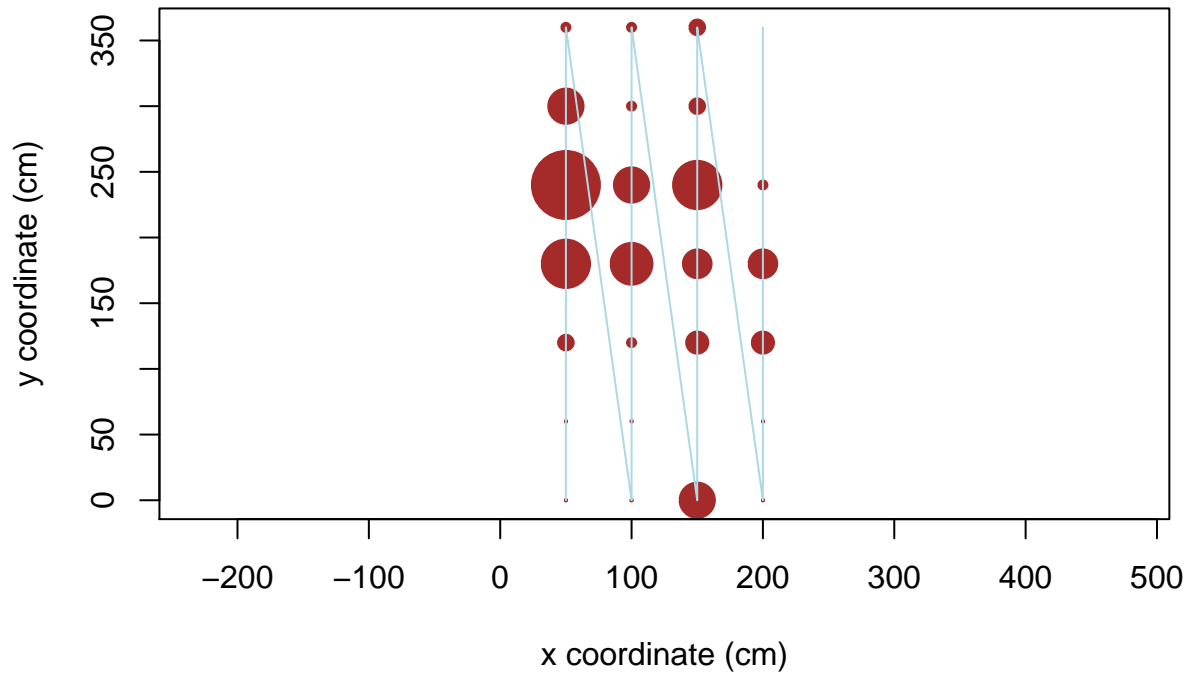
## Question 2 (6 marks)

i. Provide a plot on Cartesian (spatial) coordinates of a) the species richness, the b) Shannon-Weaver, and c) the Simpson's Index.

```
# Map of Species Richness
```

```
plot(spa, asp=1, main="Map of Species Richness", pch=21, col="white",  
     bg="brown", cex=5*sit.pres/max(sit.pres), xlab="x coordinate (cm)",  
     ylab="y coordinate (cm)")  
lines(spa, col="light blue")
```

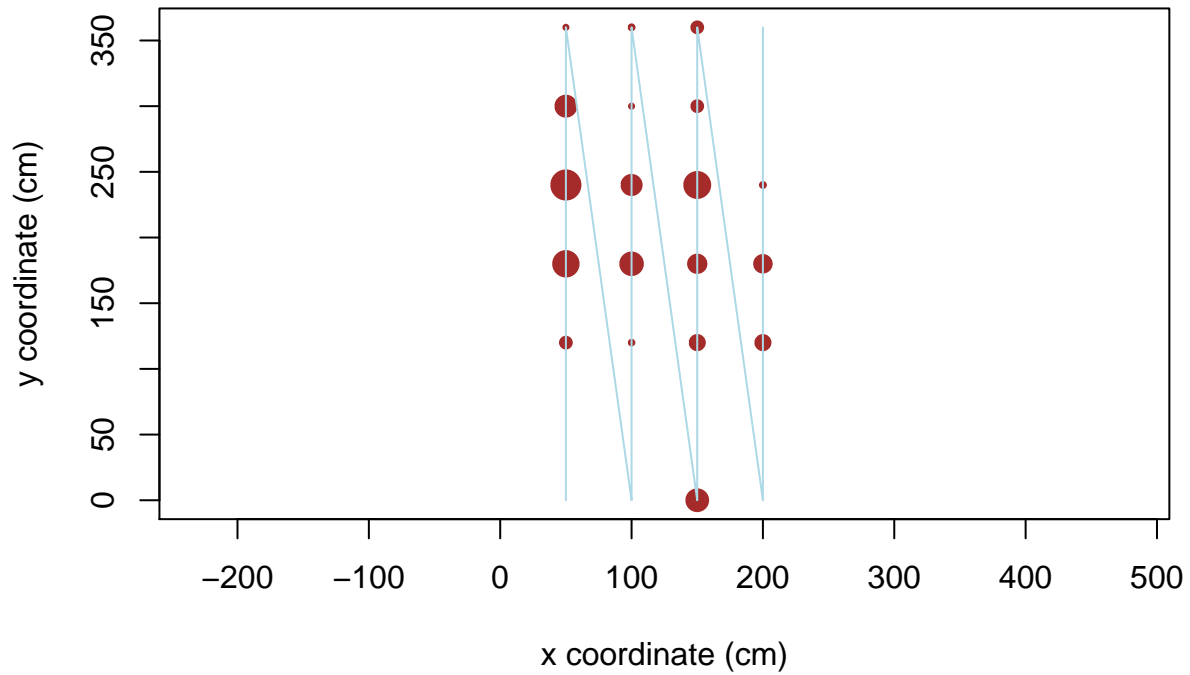
## Map of Species Richness



```
# b) Shannon-Weaver
```

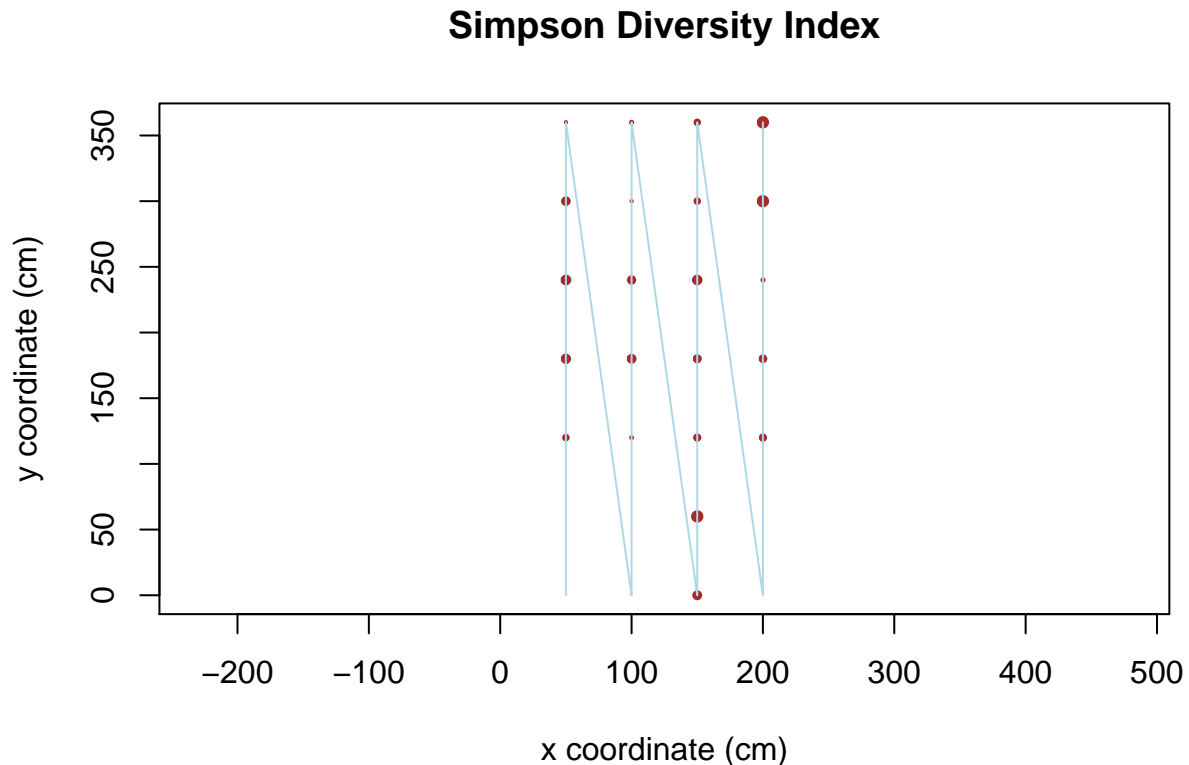
```
H <- as.tibble(diversity(spe, index = "shannon"))
plot(spa, asp=1, main="Shannon-Weaver Diversity Index", pch=21, col="white",
     bg="brown", cex=H$value, xlab="x coordinate (cm)",
     ylab="y coordinate (cm)")
lines(spa, col="light blue")
```

## Shannon–Weaver Diversity Index



*# c) Simpsons Index*

```
N2 <- as.tibble(diversity(spe, index = "simpson"))
plot(spa, asp=1, main="Simpson Diversity Index", pch=21, col="white",
     bg="brown", cex=N2$value, xlab="x coordinate (cm)",
     ylab="y coordinate (cm)")
lines(spa, col="light blue")
```



**ii. Explain each figure using your knowledge of how the ‘landscape was created’.**

- From the figure depicting species richness it becomes apparent that the highest species richness is occurs near the center of the landscape. This is as a result of the ‘species’ being thrown towards the centre of the landscape upon the simulated invasion.
- From the figure depicting the Shannon-Weaver index we observe the species richness incorporated with the relative abundances. It becomes apparent that the highest indices are found near the centre. Furthermore, the highest Shannon-Weaver indices are located between 100 and 300 cm along the y-axis of the landscape.
- From the figure depicting the Simpson’s index it becomes apparent that the species evenness increases as it tends toward the centre of the landscape, also increasing vertically along the x-axis at 50, 100, 150, 200 cm respectively. This is also as a result of the ‘species’ being thrown towards the centre of the landscape upon the simulated invasion.

**Question 3 (8 marks)**

**i. Calculate an association matrix for the species data. (1)**

```
# transpose the species data
trans_spe <- t(spe)
```

```
# bray-curtis (default)
bray_spe <- vegdist(trans_spe)
bray_spe
```

```
##          s_triangle b_triangle s_c_triangle b_c_triangle  s_square
## b_triangle      0.4666667
## s_c_triangle    0.8666667  0.5714286
## b_c_triangle    0.7777778  0.4117647    0.4117647
## s_square        0.6666667  0.4545455    0.6363636    0.5714286
## b_square        0.5384615  0.6666667    1.0000000    0.8666667  0.7777778
## b_c_square      0.7777778  0.5294118    0.5294118    0.4000000  0.5714286
## s_rect          0.6666667  0.7391304    0.7391304    0.7692308  0.9000000
## b_rect          0.4285714  0.5384615    0.6923077    0.6250000  0.8000000
## b_c_rect        0.8181818  0.8000000    0.8000000    0.8461538  0.4285714
## s_half          0.5714286  1.0000000    1.0000000    1.0000000  1.0000000
## b_half          0.7500000  0.4666667    0.8666667    0.6666667  0.6666667
## s_c_half        1.0000000  0.7777778    0.7777778    0.8333333  0.6666667
## b_c_half        0.7142857  0.5384615    0.5384615    0.5000000  0.6000000
## pink_el         0.8947368  0.8888889    0.6666667    0.7142857  0.8666667
## beans           0.8000000  0.5789474    0.7894737    0.7272727  0.8750000
## gums            1.0000000  1.0000000    1.0000000    1.0000000  1.0000000
##          b_square b_c_square  s_rect  b_rect b_c_rect  s_half
## b_triangle
## s_c_triangle
## b_c_triangle
## s_square
## b_square
## b_c_square      0.8666667
## s_rect          0.8095238  0.7692308
## b_rect          0.6363636  0.7500000  0.8181818
## b_c_rect        1.0000000  0.8461538  1.0000000  0.7777778
## s_half          0.8181818  1.0000000  0.8181818  0.6666667  1.0000000
## b_half          0.6923077  0.7777778  0.6666667  1.0000000  1.0000000  0.8571429
## s_c_half        1.0000000  0.6666667  0.8888889  1.0000000  1.0000000  1.0000000
## b_c_half        0.6363636  0.3750000  0.8181818  0.6666667  1.0000000  0.8333333
## pink_el         0.7500000  0.7142857  0.7037037  0.8823529  1.0000000  0.6470588
## beans           0.8823529  0.8181818  0.6428571  0.6666667  1.0000000  0.8888889
## gums            1.0000000  1.0000000  0.8823529  1.0000000  1.0000000  0.7142857
##          b_half s_c_half b_c_half  pink_el  beans
## b_triangle
## s_c_triangle
## b_c_triangle
## s_square
## b_square
## b_c_square
## s_rect
## b_rect
## b_c_rect
## s_half
## b_half
## s_c_half        0.8000000
## b_c_half        0.7142857  0.7500000
## pink_el         0.4736842  0.6923077  0.6470588
## beans           0.8000000  0.8571429  0.7777778  0.9130435
```

```
## gums      0.7777778 1.0000000 1.0000000 0.8333333 1.0000000
```

ii. Produce a plot that is suitable for showing the kinds of information contained in the association matrix. (3)

```
cor(spe)
```

```
##          s_triangle b_triangle s_c_triangle b_c_triangle  s_square
## s_triangle  1.0000000 0.42008403 -0.11915865 -0.078007645 0.14852213
## b_triangle  0.42008403 1.00000000 0.20261022 0.557086015 0.47140452
## s_c_triangle -0.11915865 0.20261022 1.00000000 0.474059555 0.20057389
## b_c_triangle -0.07800765 0.55708601 0.47405955 1.000000000 0.24072846
## s_square     0.14852213 0.47140452 0.20057389 0.240728460 1.00000000
## b_square     0.24878220 0.16151457 -0.22907152 -0.109972510 0.07613870
## b_c_square   0.01130828 0.37686733 0.41232874 0.589852555 0.47586687
## s_rect       0.34607182 0.10629880 0.00000000 -0.187522322 -0.16912036
## b_rect       0.40684075 0.42107596 0.21499202 0.531704532 0.02977457
## b_c_rect     0.02119044 0.05044333 0.04292540 -0.009367091 0.64203874
## s_half       0.46580257 -0.22176638 -0.18871497 -0.205904916 -0.15681251
## b_half       0.08251230 0.31426968 -0.13371593 0.014589604 0.16666667
## s_c_half     -0.09335201 0.33333333 0.28365431 0.185695338 0.47140452
## b_c_half     0.03537746 0.25264558 0.35832004 0.531704532 0.23819653
## pink_el     -0.08978568 0.02671658 0.20461341 0.074417177 0.18891478
## beans       -0.03567386 0.22645541 0.00000000 0.199745638 -0.10008010
## gums        -0.09335201 -0.11111111 -0.09455144 -0.103164077 -0.07856742
##          b_square  b_c_square      s_rect      b_rect      b_c_rect
## s_triangle  0.24878220 0.011308282 0.34607182 0.40684075 0.021190436
## b_triangle  0.16151457 0.376867331 0.10629880 0.42107596 0.050443327
## s_c_triangle -0.22907152 0.412328743 0.00000000 0.21499202 0.042925402
## b_c_triangle -0.10997251 0.589852555 -0.18752232 0.53170453 -0.009367091
## s_square     0.07613870 0.475866867 -0.16912036 0.02977457 0.642038738
## b_square     1.00000000 0.026086957 0.01716881 0.17682575 -0.122209985
## b_c_square   0.02608696 1.000000000 0.01716881 0.08161188 -0.008147332
## s_rect       0.01716881 0.017168805 1.00000000 -0.13427961 -0.193034347
## b_rect       0.17682575 0.081611884 -0.13427961 1.00000000 0.063721417
## b_c_rect     -0.12220999 -0.008147332 -0.19303435 0.06372142 1.000000000
## s_half       0.15521351 -0.179092509 -0.03536025 0.35484587 -0.100679707
## b_half       0.10151827 0.101518265 0.30065841 -0.23819653 -0.142675275
## s_c_half     -0.08973032 0.412759458 0.10629880 -0.08421519 -0.050443327
## b_c_half     0.17682575 0.843322797 -0.04028388 0.25531915 -0.114698551
## pink_el      0.12513841 0.306373352 0.10223787 -0.03374913 -0.133419667
## beans       -0.14630339 -0.018287924 0.26178233 0.24315507 -0.154212717
## gums        -0.08973032 -0.089730317 0.10629880 -0.08421519 -0.050443327
##          s_half      b_half      s_c_half      b_c_half      pink_el
## s_triangle  0.46580257 0.08251230 -0.09335201 0.03537746 -0.08978568
## b_triangle -0.22176638 0.31426968 0.33333333 0.25264558 0.02671658
## s_c_triangle -0.18871497 -0.13371593 0.28365431 0.35832004 0.20461341
## b_c_triangle -0.20590492 0.01458960 0.18569534 0.53170453 0.07441718
## s_square    -0.15681251 0.16666667 0.47140452 0.23819653 0.18891478
## b_square     0.15521351 0.10151827 -0.08973032 0.17682575 0.12513841
## b_c_square   -0.17909251 0.10151827 0.41275946 0.84332280 0.30637335
## s_rect      -0.03536025 0.30065841 0.10629880 -0.04028388 0.10223787
## b_rect       0.35484587 -0.23819653 -0.08421519 0.25531915 -0.03374913
```

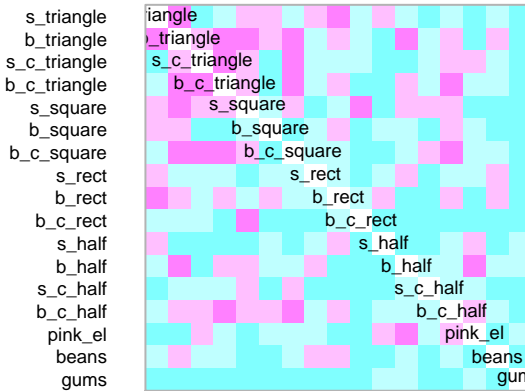
```

## b_c_rect      -0.10067971 -0.14267528 -0.05044333 -0.11469855 -0.13341967
## s_half        1.00000000  0.03484722 -0.07392213  0.09338049  0.30216685
## b_half        0.03484722  1.00000000  0.26189140  0.03969942  0.51636706
## s_c_half      -0.07392213  0.26189140  1.00000000  0.30878904  0.65010355
## b_c_half      0.09338049  0.03969942  0.30878904  1.00000000  0.43873874
## pink_el       0.30216685  0.51636706  0.65010355  0.43873874  1.00000000
## beans        -0.13810554 -0.13344013  0.15097027  0.04290972 -0.10890207
## gums          0.27104780  0.62853936 -0.03703704 -0.08421519  0.40074876
##              beans      gums
## s_triangle    -0.03567386 -0.09335201
## b_triangle     0.22645541 -0.11111111
## s_c_triangle  0.00000000 -0.09455144
## b_c_triangle  0.19974564 -0.10316408
## s_square      -0.10008010 -0.07856742
## b_square      -0.14630339 -0.08973032
## b_c_square    -0.01828792 -0.08973032
## s_rect         0.26178233  0.10629880
## b_rect         0.24315507 -0.08421519
## b_c_rect      -0.15421272 -0.05044333
## s_half        -0.13810554  0.27104780
## b_half        -0.13344013  0.62853936
## s_c_half      0.15097027 -0.03703704
## b_c_half      0.04290972 -0.08421519
## pink_el       -0.10890207  0.40074876
## beans          1.00000000 -0.11322770
## gums          -0.11322770  1.00000000

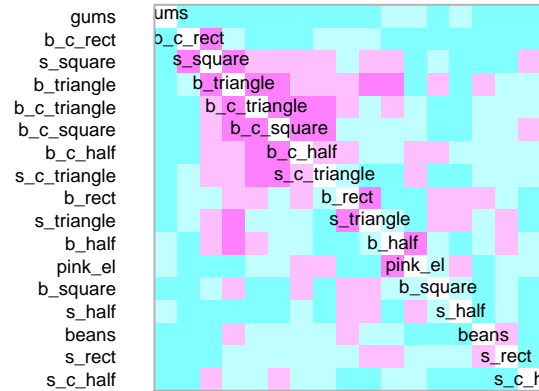
```

```
coldiss(bray_spe, byrank = FALSE, diag = TRUE)
```

## Dissimilarity Matrix



## Ordered Dissimilarity Matrix



iii. Briefly describe a few of the more ‘obvious’ positive and negative species associations. If possible, add an ‘ecological’ explanation for why this is so. (4)

In the dissimilarity matrix Magenta squares denote a dissimilarity that is close to 0 (Maximum similarity) and Cyan squares denote a dissimilarity that is close to 1 (minimum similarity).

## Question 4 (20)

i. Undertake a PCA on the species data. Comprehensively explain the various (all) components of the summary() of the PCA object. (20)

```
spe.pca <- rda(spe, scale = TRUE)
spe.pca

## Call: rda(X = spe, scale = TRUE)
##
##              Inertia Rank
## Total              17
## Unconstrained      17   17
## Inertia is correlations
##
## Eigenvalues for unconstrained axes:
```



```
##   PC1   PC2   PC3   PC4   PC5   PC6   PC7   PC8
## 3.791 2.475 2.124 1.733 1.573 1.217 1.057 0.898
## (Showed only 8 of all 17 unconstrained eigenvalues)
```

```
summary(spe.pca)
```

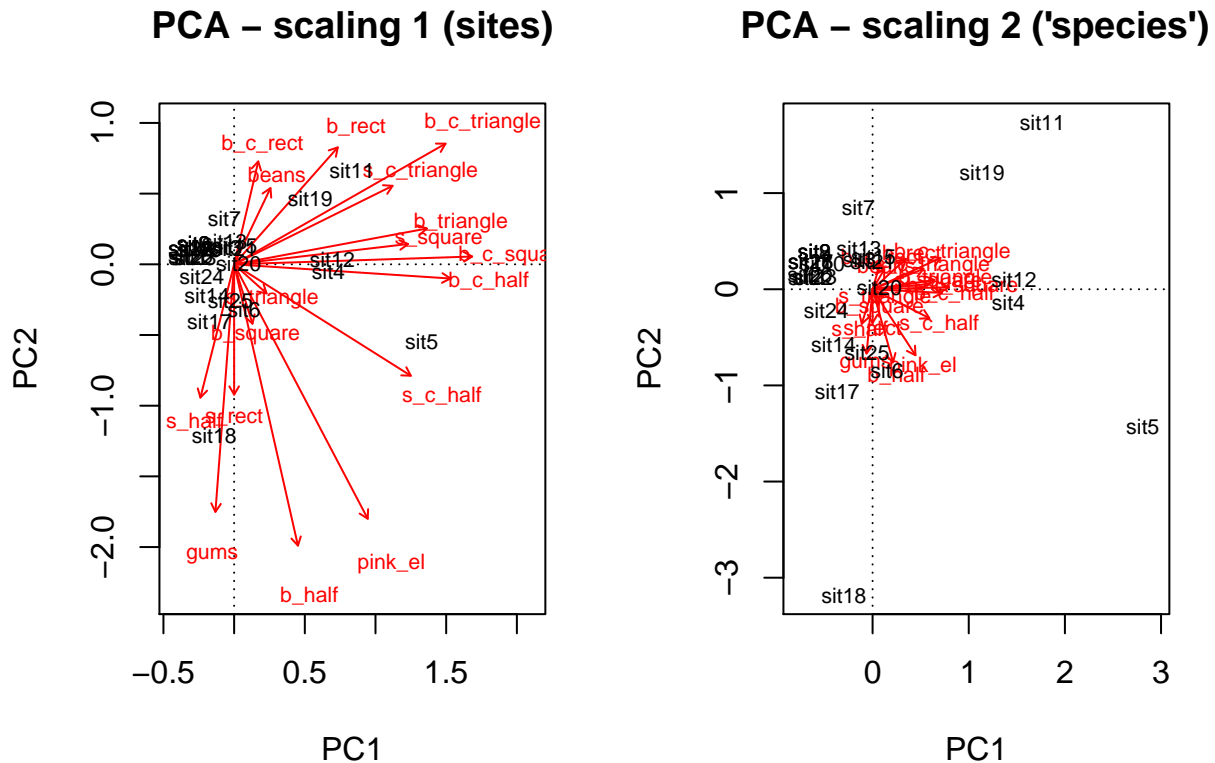
```
##
## Call:
## rda(X = spe, scale = TRUE)
##
## Partitioning of correlations:
##           Inertia Proportion
## Total           17           1
## Unconstrained    17           1
##
## Eigenvalues, and their contribution to the correlations
##
## Importance of components:
##           PC1   PC2   PC3   PC4   PC5   PC6   PC7
## Eigenvalue      3.791 2.4752 2.1244 1.7331 1.57261 1.21742 1.05653
## Proportion Explained 0.223 0.1456 0.1250 0.1019 0.09251 0.07161 0.06215
## Cumulative Proportion 0.223 0.3686 0.4936 0.5955 0.68802 0.75963 0.82178
##           PC8   PC9   PC10   PC11   PC12   PC13
## Eigenvalue      0.89815 0.68977 0.59409 0.29194 0.19075 0.153230
## Proportion Explained 0.05283 0.04057 0.03495 0.01717 0.01122 0.009014
## Cumulative Proportion 0.87461 0.91519 0.95013 0.96730 0.97853 0.987539
##           PC14   PC15   PC16   PC17
## Eigenvalue      0.084635 0.063794 0.034223 0.029192
## Proportion Explained 0.004979 0.003753 0.002013 0.001717
## Cumulative Proportion 0.992517 0.996270 0.998283 1.000000
##
## Scaling 2 for species and site scores
## * Species are scaled proportional to eigenvalues
## * Sites are unscaled: weighted dispersion equal on all dimensions
## * General scaling constant of scores: 4.628638
##
##
## Species scores
##
##           PC1   PC2   PC3   PC4   PC5   PC6
## s_triangle    0.1275428 -0.09235 0.91977 -0.26277 0.25511 -0.07041
## b_triangle    0.7575715 0.11366 0.36872 -0.11299 0.54400 0.08238
## s_c_triangle  0.6225770 0.24924 -0.26594 0.22170 -0.16960 0.21966
## b_c_triangle  0.8307310 0.38317 0.03427 0.25955 -0.09997 0.30889
## s_square      0.6835497 0.06453 -0.16697 -0.78616 0.20837 -0.01641
## b_square      0.0721410 -0.18860 0.53051 -0.21405 -0.13135 -0.64755
## b_c_square    0.9355258 0.02477 -0.16500 0.06740 -0.14607 -0.28537
## s_rect        0.0001674 -0.41384 0.22722 0.34946 0.66907 -0.15598
## b_rect        0.4073799 0.37131 0.76869 0.08860 -0.23081 0.41669
## b_c_rect      0.0949000 0.32664 -0.16948 -0.87722 0.09045 0.29810
## s_half        -0.1325307 -0.42314 0.67283 -0.08982 -0.55886 0.20951
## b_half        0.2508064 -0.89316 -0.04493 -0.10766 0.32961 0.16523
## s_c_half      0.6943703 -0.35376 -0.33096 0.02314 0.17929 -0.11137
## b_c_half      0.8502568 -0.04515 0.06680 0.22343 -0.43235 -0.29370
## pink_el       0.5250148 -0.80775 -0.14898 0.04851 -0.30313 0.01274
```

```
## beans      0.1428321  0.24205  0.14376  0.58712  0.49952  0.22143
## gums      -0.0735326 -0.78599 -0.06417 -0.02798 -0.09773  0.60988
##
##
## Site scores (weighted sums of species scores)
##
##          PC1      PC2      PC3      PC4      PC5      PC6
## sit1 -0.64351  0.12002 -0.37095  0.15479  0.12851 -0.29855
## sit2 -0.60326  0.39252 -0.40597  0.31467  0.04104  0.02467
## sit3 -0.13619  0.31125 -0.43109  0.36949 -0.04032 -0.24026
## sit4  1.41423 -0.13907  0.61923 -1.25972  0.27381 -1.59932
## sit5  2.81137 -1.43229 -1.33998  0.09368  0.72591 -0.45091
## sit6  0.14953 -0.84326  1.97133 -0.30132 -2.30698 -0.66593
## sit7 -0.14661  0.84907 -0.95751 -2.98739  0.21557  0.73362
## sit8 -0.60326  0.39252 -0.40597  0.31467  0.04104  0.02467
## sit9 -0.60326  0.39252 -0.40597  0.31467  0.04104  0.02467
## sit10 -0.52256  0.26593 -0.04638  1.44437  1.57508  0.15645
## sit11  1.76690  1.73565  0.96617  1.68843 -0.38392  1.97445
## sit12  1.47095  0.09827 -0.75153  1.08302 -1.46396 -1.19804
## sit13 -0.14055  0.42841 -0.75433  0.54655 -0.20177  0.25402
## sit14 -0.40553 -0.57722 -0.58055 -0.11166 -0.18220  0.04215
## sit15  0.01061  0.34158  1.67030  0.02934  0.90189 -0.59625
## sit16 -0.64356  0.28792 -0.47836 -0.04770 -0.29874 -0.16989
## sit17 -0.36672 -1.06804  0.14231  0.04205  0.50237 -1.29733
## sit18 -0.29772 -3.18234 -0.25982 -0.11330 -0.39570  2.46928
## sit19  1.13957  1.21491  0.40354 -1.84852  0.37550  1.19133
## sit20  0.07055  0.01593 -0.17857 -0.08208  0.56054  0.45010
## sit21  0.00403  0.29369 -0.72199  0.35158 -0.73282  0.41370
## sit22 -0.64351  0.12002 -0.37095  0.15479  0.12851 -0.29855
## sit23 -0.60484  0.13290  0.02969 -0.29897 -0.46867 -1.25203
## sit24 -0.48117 -0.21754  2.23500 -0.30977 -0.66854  0.57378
## sit25 -0.05629 -0.66294  1.34266  0.31147  2.68560 -0.19110
## sit26 -0.65209  0.15375  0.03639  0.24228 -0.45531  0.26503
## sit27 -0.64356  0.28792 -0.47836 -0.04770 -0.29874 -0.16989
## sit28 -0.64356  0.28792 -0.47836 -0.04770 -0.29874 -0.16989
```

Inertia describes the “variation” in the data. In Principle Component Analysis, the inertia is either the sum of the variances of the variables or, it is the sum of all correlations of the variables with themselves, which corresponds to the number of variables. Eigenvalues are the measures of the importance (variance) of the axes. They can be expressed as Proportions Explained, or proportions of variation accounted for, by dividing them by the total inertia. The species score depict the coordinates of the arrow heads of the variables. Site scores however denote the coordinates of the sites in an ordination diagram.

ii. Provide plots of the PCA. How many axes must be retained, and why? What patterns become visible from the biplot? Explain your findings in detail. (10)

```
par(mfrow = c(1, 2))
biplot(spe.pca, scaling = 1, main = "PCA - scaling 1 (sites)")
biplot(spe.pca, main = "PCA - scaling 2 ('species')")
```



Six axis must be retained as the cumulative proportion adds up to 0.76. In the figure on the left sites scaling (scaling 1) was used. These sites are scaled by eigenvalues. In this figure the distances in the multidimensional space are more accurately reflected on the graph plane, this shows the relationships between sites better. Sites that share similar environmental characteristics plots closer together and the ones that are further apart on the graph are also more dissimilar in their actual multidimensional space. Sites 1,2,3, 6, 7, 8,9,10,13, 14, 15,16, 17, 20, 21,22,23, 24, 26,27 and 28 are clustered in close proximity. Furthermore, sites 4, 5, 11, 12, 18, and 19 are a greater distance from the aforementioned cluster. The sites within the cluster have a low species composition. Site 5 has the highest values of s\_c\_half and site 18 has the highest value of s\_half\_rect and gums. The species scaling plots on the left show how the influential variables are tightly correlated with each other.

## Question 5 (10)

i.Undertake an NMDS on the species data, and provide plots of the NMDS. (2)

```
# remove the rows with NAs
sp.1 <- spe[-16,]
rm_sp <- sp.1[-26:-27,]

# run bray-curtis on new dataset with removed sites
spe.bray <- vegdist(rm_sp, method = "bray", binary = TRUE)

# run nmbs on bray data
spe.nmbs1 <- metaMDS(spe.bray)
```

```

## Run 0 stress 0.1325569
## Run 1 stress 0.1514949
## Run 2 stress 0.1398718
## Run 3 stress 0.1445479
## Run 4 stress 0.1268731
## ... New best solution
## ... Procrustes: rmse 0.1138616  max resid 0.234256
## Run 5 stress 0.1312789
## Run 6 stress 0.1325572
## Run 7 stress 0.1319957
## Run 8 stress 0.1530011
## Run 9 stress 0.135098
## Run 10 stress 0.1466686
## Run 11 stress 0.1268678
## ... New best solution
## ... Procrustes: rmse 0.002402212  max resid 0.008413946
## ... Similar to previous best
## Run 12 stress 0.1351016
## Run 13 stress 0.1319983
## Run 14 stress 0.1325572
## Run 15 stress 0.1396465
## Run 16 stress 0.161119
## Run 17 stress 0.170076
## Run 18 stress 0.136104
## Run 19 stress 0.1332218
## Run 20 stress 0.1364872
## *** Solution reached

dev.new(title="NMDS on fish species - Percentage difference")
plot(spe.nmds1, type = "t", main = paste("NMDS/Percentage difference", round(spe.nmds1$stress, 3)))

## species scores not available

par(mfrow = c(1, 2))
stressplot(spe.nmds1, spe.bray)
ordiplot(spe.nmds1, type = "t", display = c("sites"),
          main = "NMDS with site scores")
abline(v = 0, h = 0, lty = 3)

# dev.new(title="NMDS - Shepard plot", width=12, height=6)
par(mfrow=c(1,2))
stressplot(spe.nmds1, main = "Shepard plot")
gof <- goodness(spe.nmds1)
plot(spe.nmds1, type = "t", main = "Goodness of fit")

## species scores not available

points(spe.nmds1, display = "sites", cex = gof*300)

```

**ii. What patterns become visible from the ordination plot? Explain your findings in detail. (10)**

The relationship is non-linear, as can be seen in the Shepard diagram. The NMDS plot has a high stress, which means that the pairwise dissimilarities are not well represented in the ordination space (there is high scatter around the red line in the Shepard diagram). The graph has a poor linear relationship, with constant

stasis periods as it increases. The points on the graph are clustered between 0.2 and 0.8. The Goodness of fit indicates that sites 7, 8, 10, 22, and 25 are outliers. This means that they are dissimilar to the other sites. Overlapping sites have a high similarity.

## Question 6 (40)

i. Do a constrained analysis on the data, and comprehensively explain all the findings as per the output of the summary() of the NMDS object. (20)

```
spe.hel <- as.tibble(decostand(spe, "hellinger"))
spe.hel

## # A tibble: 28 x 17
##   s_triangle b_triangle s_c_triangle b_c_triangle s_square b_square
##   <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl>
## 1         0         0         0         0         0         0
## 2         0         0         0         0         0         0
## 3         0         0         0         0.577     0         0
## 4      0.333     0.333     0         0.333     0.333     0.333
## 5         0      0.258     0.258     0.258     0.258     0
## 6     0.354         0         0         0         0     0.354
## 7         0         0         0         0     0.577     0
## 8         0         0         0         0         0         0
## 9         0         0         0         0         0         0
## 10        0         0         0         0         0         0
## # ... with 18 more rows, and 11 more variables: b_c_square <dbl>,
## #   s_rect <dbl>, b_rect <dbl>, b_c_rect <dbl>, s_half <dbl>,
## #   b_half <dbl>, s_c_half <dbl>, b_c_half <dbl>, pink_el <dbl>,
## #   beans <dbl>, gums <dbl>

spe.rda <- rda(spe.hel ~ ., env)
spe.rda

## Call: rda(formula = spe.hel ~ Carpet + Cardboard + Wood, data =
## env)
##
##               Inertia Proportion Rank
## Total          0.70648    1.00000
## Constrained    0.05134    0.07267    2
## Unconstrained  0.65514    0.92733   16
## Inertia is variance
## Some constraints were aliased because they were collinear (redundant)
##
## Eigenvalues for constrained axes:
##   RDA1    RDA2
## 0.04097 0.01037
##
## Eigenvalues for unconstrained axes:
##   PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8    PC9
## 0.14899 0.11246 0.07950 0.06205 0.05427 0.05094 0.04292 0.03082 0.02809
##   PC10   PC11   PC12   PC13   PC14   PC15   PC16
## 0.01302 0.01273 0.00820 0.00469 0.00429 0.00143 0.00074
```

```
summary(spe.rda)
```

```
##
## Call:
## rda(formula = spe.hel ~ Carpet + Cardboard + Wood, data = env)
##
## Partitioning of variance:
##           Inertia Proportion
## Total          0.70648    1.00000
## Constrained    0.05134    0.07267
## Unconstrained  0.65514    0.92733
##
## Eigenvalues, and their contribution to the variance
##
## Importance of components:
##           RDA1    RDA2    PC1    PC2    PC3    PC4    PC5
## Eigenvalue      0.04097 0.01037 0.1490 0.1125 0.0795 0.06205 0.05427
## Proportion Explained 0.05800 0.01468 0.2109 0.1592 0.1125 0.08782 0.07682
## Cumulative Proportion 0.05800 0.07267 0.2836 0.4427 0.5553 0.64309 0.71991
##           PC6    PC7    PC8    PC9    PC10    PC11
## Eigenvalue      0.05094 0.04292 0.03082 0.02809 0.01302 0.01273
## Proportion Explained 0.07211 0.06075 0.04362 0.03976 0.01843 0.01802
## Cumulative Proportion 0.79201 0.85277 0.89639 0.93615 0.95458 0.97261
##           PC12    PC13    PC14    PC15    PC16
## Eigenvalue      0.008202 0.004688 0.004293 0.001432 0.0007387
## Proportion Explained 0.011609 0.006635 0.006076 0.002027 0.0010456
## Cumulative Proportion 0.984215 0.990851 0.996927 0.998954 1.0000000
##
## Accumulated constrained eigenvalues
## Importance of components:
##           RDA1    RDA2
## Eigenvalue      0.04097 0.01037
## Proportion Explained 0.79805 0.20195
## Cumulative Proportion 0.79805 1.00000
##
## Scaling 2 for species and site scores
## * Species are scaled proportional to eigenvalues
## * Sites are unscaled: weighted dispersion equal on all dimensions
## * General scaling constant of scores: 2.089857
##
##
## Species scores
##
##           RDA1    RDA2    PC1    PC2    PC3
## s_triangle -0.063242 -0.0037627 6.272e-02 -3.263e-02 -2.103e-01
## b_triangle -0.064737 -0.0038516 1.092e-01 9.832e-02 5.809e-02
## s_c_triangle -0.066106 -0.0039331 1.942e-01 1.259e-02 2.345e-01
## b_c_triangle -0.088445 -0.0052622 2.849e-01 1.705e-01 3.005e-01
## s_square -0.038116 -0.0022678 1.057e-01 1.021e-01 -1.302e-02
## b_square 0.084113 0.1565875 5.080e-02 7.876e-02 -3.088e-01
## b_c_square -0.066253 -0.0039418 2.255e-01 7.014e-02 2.269e-01
## s_rect 0.178347 0.0968708 5.476e-02 -7.495e-01 1.235e-01
## b_rect -0.048820 -0.0029046 4.437e-02 4.131e-02 -1.161e-01
## b_c_rect -0.029293 -0.0017429 6.307e-02 7.129e-02 -5.915e-02
```

```

## s_half      0.085935 -0.1229982 -7.456e-02  2.263e-02 -2.287e-01
## b_half      0.265460 -0.0137994  1.313e-01  1.136e-01  3.214e-02
## s_c_half    -0.009142 -0.0005439  2.268e-02  1.703e-02  4.617e-02
## b_c_half    -0.043012 -0.0025591  1.226e-01  9.513e-02  5.814e-02
## pink_el     0.257061 -0.0142991  1.897e-01  1.534e-01  4.186e-02
## beans      -0.148416 -0.0088303 -7.991e-01  1.376e-01  2.423e-01
## gums        0.130611 -0.1203402  7.426e-18  5.623e-17 -4.891e-18
##
##              PC4
## s_triangle  -3.015e-01
## b_triangle  -2.892e-01
## s_c_triangle 7.062e-02
## b_c_triangle -1.496e-01
## s_square    -4.824e-02
## b_square    -8.306e-02
## b_c_square  -1.866e-01
## s_rect      -9.653e-02
## b_rect      -2.314e-01
## b_c_rect     2.363e-02
## s_half      -6.315e-02
## b_half       6.513e-03
## s_c_half     -1.649e-03
## b_c_half     -8.999e-02
## pink_el     2.067e-01
## beans      -1.391e-01
## gums        -1.037e-17
##
##
## Site scores (weighted sums of species scores)
##
##              RDA1      RDA2      PC1      PC2      PC3      PC4
## row1  0.52147  1.21871  8.324e-02 -1.011e+00  1.816e-02  1.619e-01
## row2 -0.76853 -0.43034 -8.438e-01  2.645e-01  2.600e-01  5.098e-02
## row3 -0.12871  0.49706  3.780e-01 -3.560e-01  5.315e-01 -2.377e-01
## row4 -0.23745  0.32892  4.530e-01  4.141e-01 -7.196e-02 -6.457e-01
## row5  0.15743 -0.19084  2.713e-01  2.037e-01  5.522e-01 -1.973e-02
## row6  0.39539 -0.55076  1.939e-01  2.860e-01 -8.384e-01 -5.002e-02
## row7 -0.36391 -0.33521  1.460e-01  2.350e-01 -3.467e-01  3.912e-01
## row8 -0.76853 -0.43034 -8.438e-01  2.645e-01  2.600e-01  5.098e-02
## row9 -0.76853 -0.43034 -8.438e-01  2.645e-01  2.600e-01  5.098e-02
## row10 -0.19116  0.55653 -6.106e-01 -4.619e-01  3.078e-01 -2.645e-02
## row11 -0.98278 -0.48072  4.916e-02  4.241e-01  5.500e-01 -5.911e-01
## row12 -0.04407  0.03468  4.897e-01 -8.725e-03  5.642e-01  4.928e-02
## row13  0.01081  0.52986  2.303e-01 -5.411e-01  3.015e-01  4.186e-01
## row14  1.27603 -0.60255  2.702e-01  3.381e-01 -1.267e-01  8.066e-01
## row15 -0.28375  1.19849 -1.877e-01 -1.837e-01 -4.086e-01 -8.006e-01
## row16 -0.18261 -0.29258  2.379e-02  6.654e-02 -2.332e-01  4.136e-01
## row17  1.33372  1.55972 -1.704e-16  7.388e-16  8.664e-17 -1.383e-16
## row18  1.50925 -1.39057  1.456e-16 -1.400e-16  7.035e-17 -1.227e-16
## row19 -0.83166 -0.44519  4.420e-01  3.379e-01  6.999e-02 -6.117e-01
## row20  0.07330 -0.49897  3.531e-01  3.841e-01  2.259e-01 -2.371e-01
## row21  0.05104 -0.50420  4.430e-01  3.460e-01  4.445e-01  6.059e-01
## row22  0.52147  1.21871  8.324e-02 -1.011e+00  1.816e-02  1.619e-01
## row23  0.14945  2.15036  7.895e-02  1.798e-01 -8.615e-01  1.970e-01
## row24  0.07787 -0.83587  6.031e-02 -3.576e-01 -7.427e-01 -4.843e-01

```

```

## row25  0.19673  0.45748 -1.202e-01 -4.393e-01 -5.391e-02 -5.224e-01
## row26 -0.35703 -1.74687 -6.469e-01  2.295e-01 -2.136e-01  4.076e-02
## row27 -0.18261 -0.29258  2.379e-02  6.654e-02 -2.332e-01  4.136e-01
## row28 -0.18261 -0.29258  2.379e-02  6.654e-02 -2.332e-01  4.136e-01
##
##
## Site constraints (linear combinations of constraining variables)
##
##          RDA1      RDA2      PC1      PC2      PC3      PC4
## row1  -0.1093 -0.006506  8.324e-02 -1.011e+00  1.816e-02  1.619e-01
## row2  -0.1093 -0.006506 -8.438e-01  2.645e-01  2.600e-01  5.098e-02
## row3  -0.1093 -0.006506  3.780e-01 -3.560e-01  5.315e-01 -2.377e-01
## row4  -0.1093 -0.006506  4.530e-01  4.141e-01 -7.196e-02 -6.457e-01
## row5  -0.1093 -0.006506  2.713e-01  2.037e-01  5.522e-01 -1.973e-02
## row6  -0.1093 -0.006506  1.939e-01  2.860e-01 -8.384e-01 -5.002e-02
## row7  -0.1093 -0.006506  1.460e-01  2.350e-01 -3.467e-01  3.912e-01
## row8  -0.1093 -0.006506 -8.438e-01  2.645e-01  2.600e-01  5.098e-02
## row9  -0.1093 -0.006506 -8.438e-01  2.645e-01  2.600e-01  5.098e-02
## row10 -0.1093 -0.006506 -6.106e-01 -4.619e-01  3.078e-01 -2.645e-02
## row11 -0.1093 -0.006506  4.916e-02  4.241e-01  5.500e-01 -5.911e-01
## row12 -0.1093 -0.006506  4.897e-01 -8.725e-03  5.642e-01  4.928e-02
## row13 -0.1093 -0.006506  2.303e-01 -5.411e-01  3.015e-01  4.186e-01
## row14 -0.1093 -0.006506  2.702e-01  3.381e-01 -1.267e-01  8.066e-01
## row15 -0.1093 -0.006506 -1.877e-01 -1.837e-01 -4.086e-01 -8.006e-01
## row16 -0.1093 -0.006506  2.379e-02  6.654e-02 -2.332e-01  4.136e-01
## row17  1.3337  1.559717 -1.704e-16  7.388e-16  8.664e-17 -1.383e-16
## row18  1.5093 -1.390570  1.456e-16 -1.400e-16  7.035e-17 -1.227e-16
## row19 -0.1093 -0.006506  4.420e-01  3.379e-01  6.999e-02 -6.117e-01
## row20 -0.1093 -0.006506  3.531e-01  3.841e-01  2.259e-01 -2.371e-01
## row21 -0.1093 -0.006506  4.430e-01  3.460e-01  4.445e-01  6.059e-01
## row22 -0.1093 -0.006506  8.324e-02 -1.011e+00  1.816e-02  1.619e-01
## row23 -0.1093 -0.006506  7.895e-02  1.798e-01 -8.615e-01  1.970e-01
## row24 -0.1093 -0.006506  6.031e-02 -3.576e-01 -7.427e-01 -4.843e-01
## row25 -0.1093 -0.006506 -1.202e-01 -4.393e-01 -5.391e-02 -5.224e-01
## row26 -0.1093 -0.006506 -6.469e-01  2.295e-01 -2.136e-01  4.076e-02
## row27 -0.1093 -0.006506  2.379e-02  6.654e-02 -2.332e-01  4.136e-01
## row28 -0.1093 -0.006506  2.379e-02  6.654e-02 -2.332e-01  4.136e-01
##
##
## Biplot scores for constraining variables
##
##          RDA1      RDA2 PC1 PC2 PC3 PC4
## Carpet    -0.9982 -0.05939  0  0  0  0
## Cardboard  0.7354 -0.67760  0  0  0  0

```

The partitioning of variance depicts the overall variance which is then divided into constrained and unconstrained values. Constrained depicts 7.267% of the overall variance and unconstrained depicts 92.733% of the overall variance respectively. Furthermore, two canonical axes with eigenvalues labelled RDA1 and RDA2 and 16 additional respectively is produced. It also produces unconstrained axis for residuals- specifically PC1 to PC16. The summary() function produces eigenvalues depicting cumulative proportion of variance explained or represented. The last cumulative value is one. The cumulative contribution to the variance obtained is the proportion of the total variance of the response data explained by the RDA. It's the same value as the proportion constrained which is 0.07267. It becomes apparent that values are decreasing from RDA1 to RDA2. Furthermore, it becomes apparent that the first residual eigenvalue is larger than the last canonical eigenvalue.



The canonical (RDAx) eigenvalues indicate the amount of variance explained by the RDA model, unlike the residual eigenvalues which measure amounts of variance represented by the residual axes, this is not explained by the RDA model. The accumulated constrained eigenvectors depict the cumulative amounts of variance. This is expressed as proportions of the total explained variance. Species have been scaled proportional to eigenvalues with weighted dispersal equal in all direction. There is a general scaling constant of 2.089857. In RDA1, *b\_half* had the highest score (0.265460), and *beans* had the lowest score (-0.148416). In RDA2, *b\_square* had the highest score (0.1565875), and *s\_half* had the lowest score (-0.1229982). In PC1, PC2, PC3, and PC4 the highest scores were *b\_c\_triangle* (0.2849), *b\_c\_triangle* (0.1705), *b\_c\_triangle* (0.3005) and *pink\_el* (0.2067) respectively and the lowest scores were *beans* (-0.7991), *s\_rect* (-0.7495), *b\_square* (-0.3088) and *s\_triangle* (-0.3015) respectively. The biplot scores for RDA increased from -0.9987 to -0.05939 for carpet. Furthermore, the scores of PC1 to PC4 all equal 0. For cardboard the score RDA scores decreased from 0.7354 to -0.67760. The scores for PC1 to PC4 also equalled 0 for cardboard.

## ii. Run the necessary permutation tests. Explain the outcomes. (6)

```
# permutations

# Global test of the RDA result
anova(spe.rda, permutations = how(nperm = 999))

## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = spe.hel ~ Carpet + Cardboard + Wood, data = env)
##           Df Variance      F Pr(>F)
## Model      2  0.05134 0.9796  0.594
## Residual  25  0.65514

# Tests of all canonical axes
anova(spe.rda, by = "axis", permutations = how(nperm = 999))

## Permutation test for rda under reduced model
## Forward tests for axes
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = spe.hel ~ Carpet + Cardboard + Wood, data = env)
##           Df Variance      F Pr(>F)
## RDA1        1  0.04097 1.5636  0.194
## RDA2        1  0.01037 0.3957  0.950
## Residual  25  0.65514

anova(spe.rda, by = "term", permutations = how(nperm = 999))

## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = spe.hel ~ Carpet + Cardboard + Wood, data = env)
##           Df Variance      F Pr(>F)
## Carpet      1  0.04087 1.5594  0.095 .
## Cardboard   1  0.01048 0.3998  0.965
```

```
## Residual 25 0.65514
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Variance inflation factors (VIF)
vif.cca(spe.rda)
```

```
## Carpet Cardboard Wood
## 1.928571 1.928571 NA
```

```
# Apply Kaiser-Guttman criterion to residual axes
spe.rda$CA$eig[spe.rda$CA$eig > mean(spe.rda$CA$eig)]
```

```
## PC1 PC2 PC3 PC4 PC5 PC6
## 0.14898504 0.11246212 0.07949840 0.06204632 0.05426915 0.05094135
## PC7
## 0.04292241
```

For the global permutation test the  $Pr = 0.636$ . This indicates that the model is not significant. By testing all canonical axis it becomes apparent that the  $Pr$  for RDA1 and RDA2 have values of 0.178 and 0.940 respectively. In this case both canonical axes are non-significant. Both the carpet and cardboard have  $Pr$  scores of 0.069 and 0.966 respectively. These values are lower than 0.05. This means that they are both non-significant. The variance inflation factors measures the proportion the variance of a regression coefficient is inflated around other explanatory variables. Thus the carpet has a VIF score of 1.928571 as opposed to the cupboard that has a VIF score of 1.928571. The Kaiser-Guttman criterion computes the mean of all eigenvalues and interprets the axes with eigenvalues that are larger than the mean (PC1 to PC7). Where PC1 = 0.14898504, PC2 = 0.11246212, PC3 = 0.07949840, PC4 = 0.06204632, PC5 = 0.05426915, PC6 = 0.05094135 and PC7 = 0.0429224 respectively.

### iii. Produce the necessary biplots. Explain the findings. (14)

```
# Canonical coefficients from the rda object
coef(spe.rda)
```

```
## RDA1 RDA2
## Carpet -0.008631348 -0.009368001
## Cardboard 0.001049904 -0.017646464
## Wood NA NA
```

```
# Unadjusted R2 retrieved from the rda object
R2 <- RsquareAdj(spe.rda)$r.squared
R2
```

```
## [1] 0.07267347
```

```
# Adjusted R2 retrieved from the rda object
R2adj <- RsquareAdj(spe.rda)$adj.r.squared
R2adj
```

```
## [1] -0.001512655
```

```
# Triplots of the rda results (wa scores)
dev.new(title = "RDA scaling 1 + wa")
par(mfrow = c(2, 2))
plot(spe.rda, scaling = 1,
     main="Triplot RDA spe.hel ~ env2 - scaling 1 - wa scores")
spe.sc1 <- scores(spe.rda, choices = 1:2, scaling = 1, display = "sp")
```

```

arrows(0, 0, spe.sc1[, 1]*0.92, spe.sc1[, 2]*0.92, length = 0, lty = 1, col = "red")

# Scaling 2 (default): correlation triplot
# dev.new(title = "RDA scaling 2 + wa")
plot(spe.rda, main = "Triplot RDA spe.hel ~ env2 - scaling 2 - wa scores")
spe.sc2 <- scores(spe.rda, choices = 1:2, display = "sp")
arrows(0, 0, spe.sc2[, 1]*0.92, spe.sc2[, 2]*0.92, length = 0, lty = 1, col = "red")

# Triplots of the rda results (lc scores)
# dev.new(title = "RDA scaling 1 + lc")
# par(mfrow = c(1, 2))
plot(spe.rda, scaling = 1, display = c("sp", "lc", "cn"),
     main="Triplot RDA spe.hel ~ env2 - scaling 1 - lc scores")
arrows(0, 0, spe.sc1[, 1]*0.92, spe.sc1[, 2]*0.92, length = 0, lty = 1, col = "red")

# Scaling 2
# dev.new(title = "RDA scaling 2 + lc")
plot(spe.rda, display = c("sp", "lc", "cn"),
     main="Triplot RDA spe.hel ~ env2 - scaling 2 - lc scores")
arrows(0, 0, spe.sc2[,1]*0.92, spe.sc2[,2]*0.92, length = 0, lty = 1, col = "red")

```

On the figure on the top left the angles between the sites and the species in the biplot reflect the correlation. All sites are clustered around the centroid. There are outliers that lie within the top right of the plot. rows 17 and 23 are seen alongside b\_square and s\_rect. In the bottom right section, row 14 and 18 can be seen alongside the gums, c\_half and pink\_half species respectively. This means that these species are more related than the rest of the others. Also in the bottom right lies cardboard- this is the dispersal vector. Sites and species and therefore more closely related to this variable. Bulk of species are found in the bottom left section, thus strongly relating to the carpet variable. The figure on the top right depicts scaling 2. Sites are more spread out and species are centred around the centroid. In the top right section, rows 22, 23, 25 and 27 are visible depicting that these sites are positively correlated. Species b\_square and s\_rect can be seen in the top\_right section indicating that they are positively correlated. Short arrows indicate that they are less important for this plot. In the bottom right section, rows 5, 6, 14 and 18 are all visible but are spread out. These variables are positively correlated with one another as well as the dispersal vector- cardboard. In the bottom left section, site 7, 11, 26, 27 and 28 are visible. 26 is an outliers. These sites are positively correlated with the carpet variable, these are spread further than the rows in the bottom right section where cardboard lies. In the top left section, rows 3, 4, 10 and 15 are positively correlated but with this lacks the species. Row 2 is very close to the centroid. Rows 20 and 24 is located on the negative y axis and site 13 is located on the positive y axis. Triplot RDA spe.hel ~ env2 - lc scores triplots indicate that the sites are clustered close to the centroid. Lc scores indicate that they are closely related. In the first lc triplot row 17 plays is correlated with the locations of b\_square and s\_rect on the plot. In row 18 gums and s\_half are found in the bottom right section of the plot where cardboard is the main influencing factor. In the bottom left section of the plot carpet is the main factor influencing the rest of the species. From scaling 2 of this triplot, rows 17 and rows 18 have a decreased arrow length thus have less influence on the species.

## Question 7 (10)

**Write down your understanding of the ‘ecology’ of the landscape that was sampled and analysed in the various steps, above.**

The study site spanned an area of 200cmx360cm. This area comprised of carpet, cardboard and wood. Species immigration occurred at different angles towards the center. Wind was the main dispersal vector. Thus species richness and relative abundance increases toward the centre of the landscape. Samples were taken with the

use of 50cmx50cm transects. 7 sections were sampled across the y-coordinate and 4 sections were sampled across the x-axis. Species lying in the transect was tallied and data was collated on excel. Comma delimited csv's were then generated for the data collected. The species richness, Shannon-Weaver and Simpson's indices, indicated that the centre of the study site had the highest species richness, and relative abundance and evenness in the landscape. The association matrix for the species data indicated that the 'gums' species was the most dissimilar to the other species. A PCA analysis revealed that PC1 to PC6 should be retained as it shows more than 75% of the total variation. The biplots from the PCA analysis indicate that species are located more to the right of the biplot with wind as a vector. Thus wind generated with cardboard is the main factor influencing species.