

ECOL 592: RDA and CCA

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Canonical correspondence analysis (CCA)

Load Data

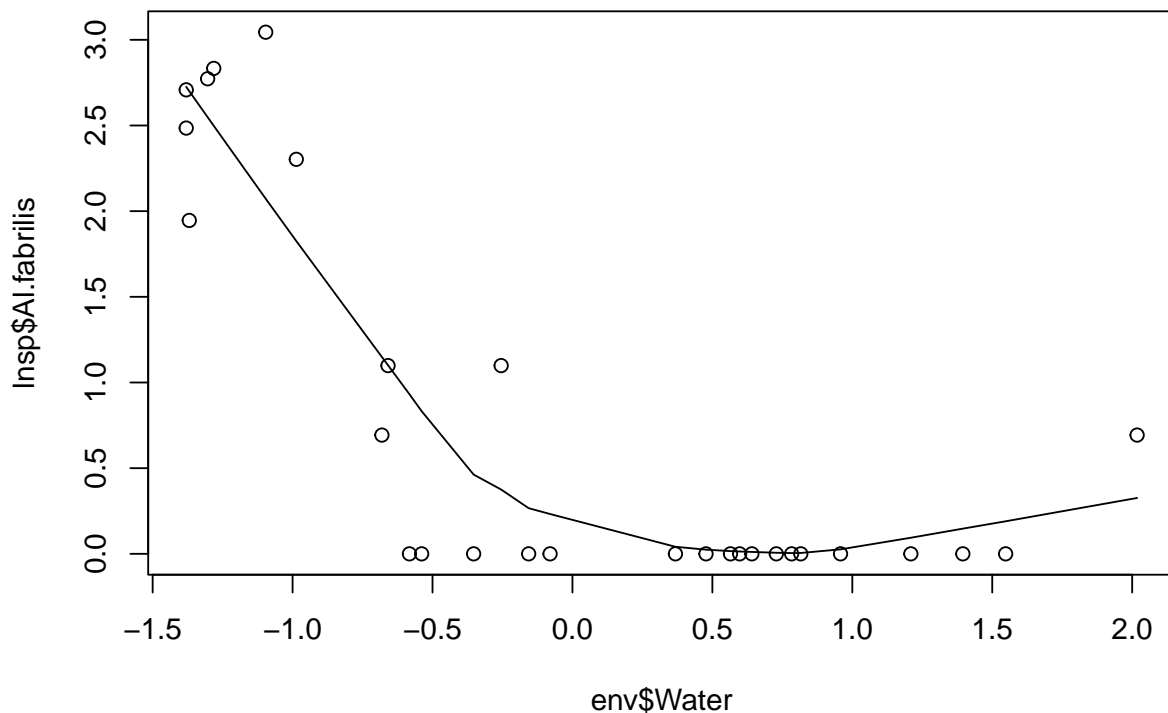
```
spider <- read.csv("Makarenkov2002.csv")
# species count data
spider[,2:13] %>% dplyr::glimpse()
```

```
## Rows: 28
## Columns: 12
## $ Al.accent      <int> 25, 0, 15, 2, 1, 0, 2, 0, 1, 3, 15, 16, 3, 0, 0, 0, 0, 0, ~
## $ A.cuneata      <int> 10, 2, 20, 6, 20, 6, 7, 11, 1, 0, 1, 13, 43, 2, 0, 3, 0, ~
## $ Al.fabrilllis   <int> 0, 0, 2, 0, 0, 0, 0, 0, 0, 0, 1, 2, 0, 1, 0, 0, 0, 0, ~
## $ Ar.lutetiana    <int> 0, 0, 2, 1, 2, 6, 12, 0, 0, 0, 0, 0, 2, 1, 0, 0, 0, 0, ~
## $ Ar.perita       <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
## $ Au.albimana     <int> 4, 30, 9, 24, 9, 6, 16, 7, 0, 0, 1, 0, 18, 4, 0, 0, 0, 0, ~
## $ Pa.lugubris     <int> 0, 1, 1, 1, 1, 0, 1, 55, 0, 0, 0, 0, 1, 3, 6, 6, 2, 5, 12~
## $ Pa.monticola    <int> 60, 1, 29, 7, 2, 11, 30, 2, 26, 22, 95, 96, 24, 14, 0, 0, ~
## $ Pa.nigriceps    <int> 12, 15, 18, 29, 135, 27, 89, 2, 1, 0, 0, 1, 53, 15, 0, 2, ~
## $ Pa.pullata      <int> 45, 37, 45, 94, 76, 24, 105, 1, 1, 0, 1, 8, 72, 72, 0, 0, ~
## $ Tr.terricola    <int> 57, 65, 66, 86, 91, 63, 118, 30, 2, 1, 4, 13, 97, 94, 25, ~
## $ Zo.spinimana    <int> 4, 9, 1, 25, 17, 34, 16, 3, 0, 0, 0, 0, 22, 32, 3, 4, 2, ~
```

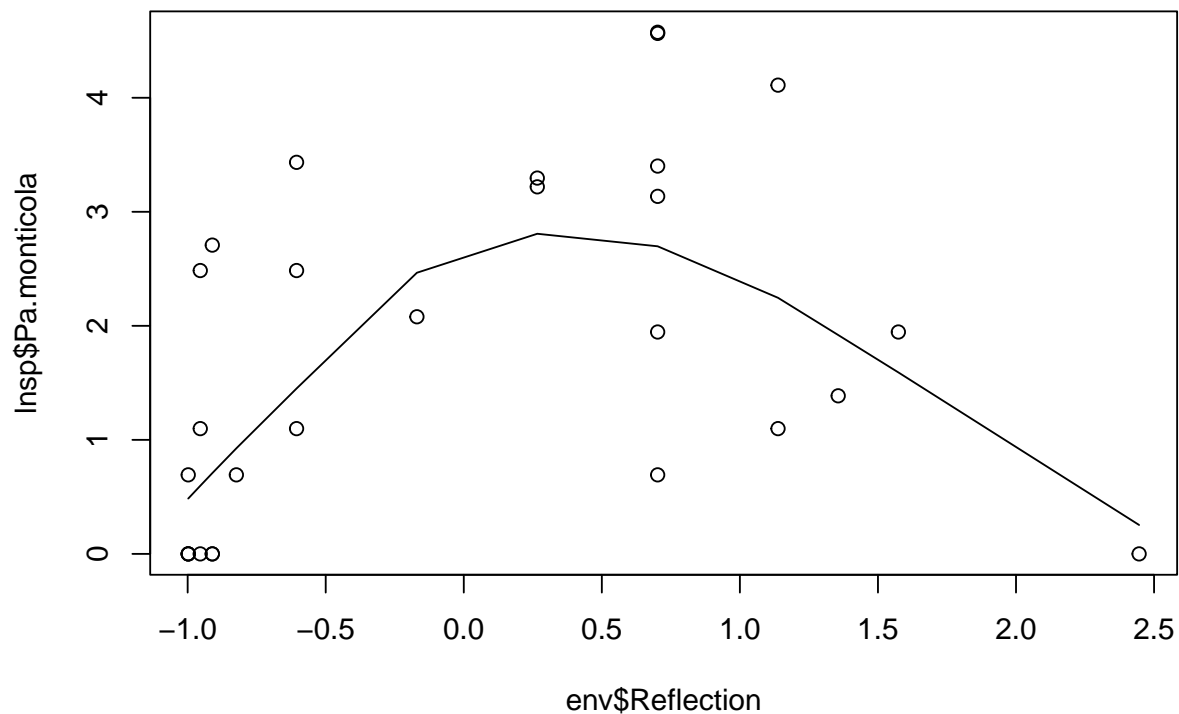
```
lnsp <- log(spider[,2:13]+1)
# environmental data
spider[,c(14:17)] %>% dplyr::glimpse()
```

```
## Rows: 28
## Columns: 4
## $ Water.content <dbl> 10.3, 21.1, 12.9, 14.5, 20.4, 29.4, 24.0, 13.8, 12.0, 9.~
## $ Reflection    <int> 50, 5, 40, 20, 10, 2, 10, 2, 30, 40, 40, 40, 30, 3, 2, 1~
## $ Calmagrostis  <int> 50, 80, 30, 100, 90, 10, 90, 10, 0, 0, 0, 2, 80, 20, 0, ~
## $ Corynephorus  <int> 0, 0, 0, 0, 0, 0, 0, 0, 20, 20, 30, 50, 0, 0, 0, 0, 0, 0~
```

```
env <- spider[,c(14:17)]
colnames(env)[1] <- "Water"
# scale environmental data
env <- as.data.frame(scale(env))
# create polynomials of environmental data
env$Water2 <- env$Water^2
env$Reflection2 <- env$Reflection^2
env$Waterref <- env$Water*env$Reflection
# explore some species
{plot(env$Water,lnsp$Al.fabrilis)
lines(lowess(env$Water,lnsp$Al.fabrilis))}
```



```
{plot(env$Reflection,lnsp$Pa.monticola)
lines(lowess(env$Reflection,lnsp$Pa.monticola))}
```



PCA

`princomp` performs a principal components analysis

```
# princomp performs a principal components analysis
# on the given numeric data matrix and returns the
# results as an object of class princomp.
pcares <- stats::princomp(lnsp, cor = TRUE)
pcares$loadings %>% str()
```

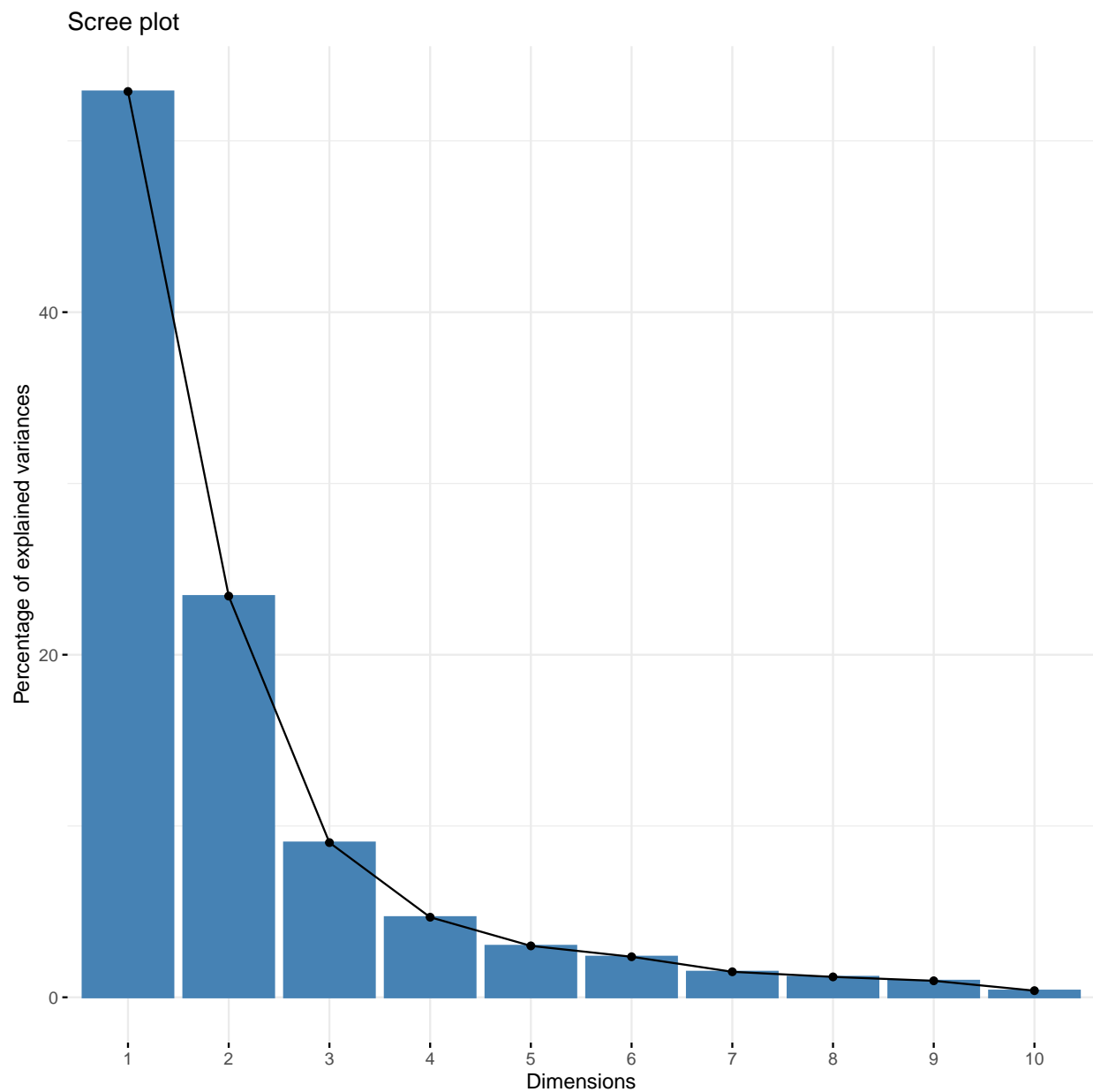
```
## 'loadings' num [1:12, 1:12] 0.135 -0.329 0.262 -0.293 0.259 ...
## - attr(*, "dimnames")=List of 2
## ..$ : chr [1:12] "Al.accent" "A.cuneata" "Al.fabrilis" "Ar.lutetiana" ...
## ..$ : chr [1:12] "Comp.1" "Comp.2" "Comp.3" "Comp.4" ...
```

```
pcares$scores %>% str()
```

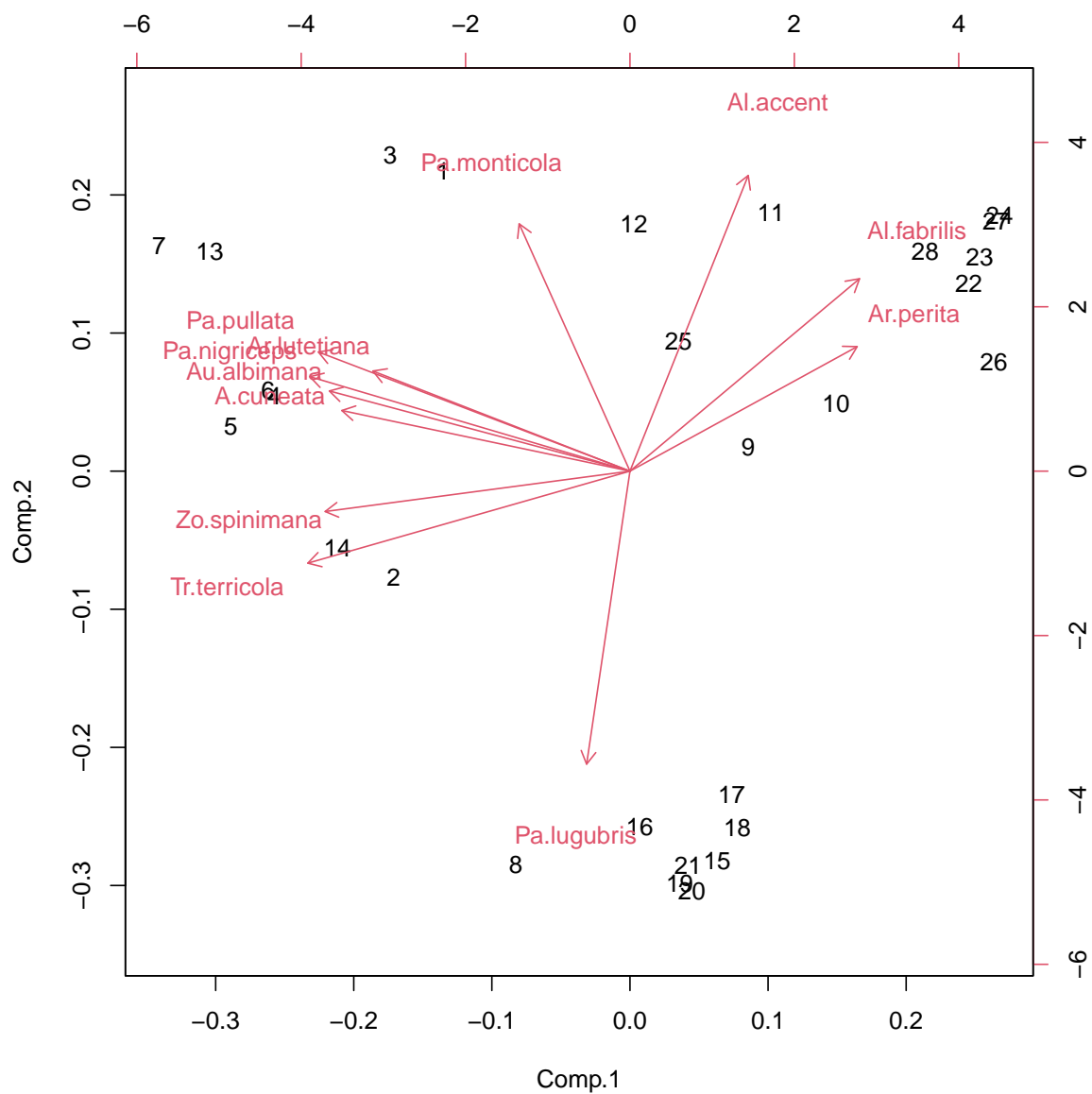
```
## num [1:28, 1:12] -1.8 -2.28 -2.31 -3.43 -3.85 ...
```

```
## - attr(*, "dimnames")=List of 2
## ..$ : NULL
## ..$ : chr [1:12] "Comp.1" "Comp.2" "Comp.3" "Comp.4" ...
```

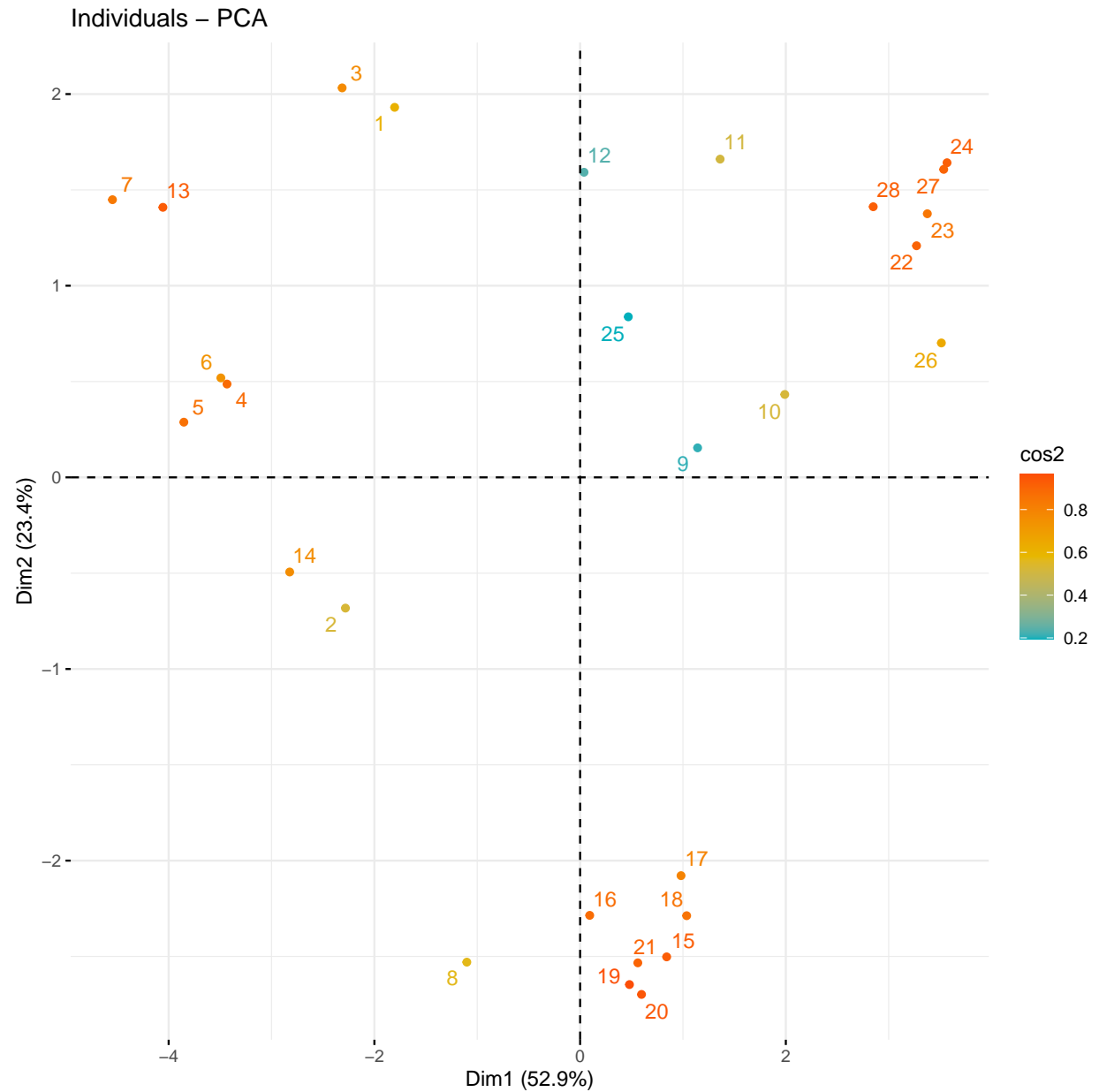
```
# Extract and visualize the eigenvalues/variances of dimensions
factoextra::fviz_eig(pcares)
```



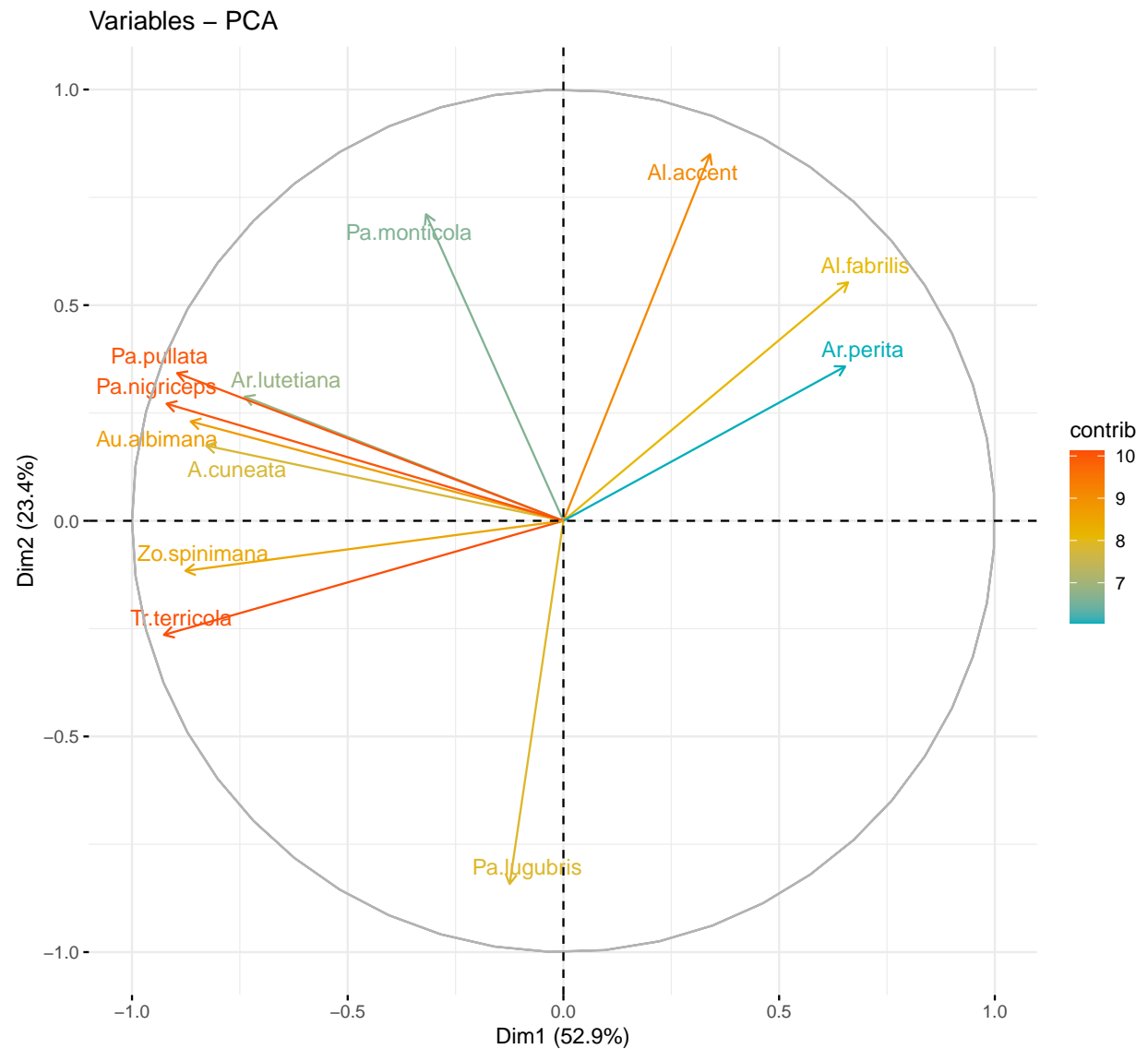
```
# Biplot of Multivariate Data
stats::biplot(pcares)
```



```
# Visualize Principal Component Analysis
# Color by the quality of representation
factoextra::fviz_pca_ind(pcares,
  col.ind = "cos2", # Color by the quality of representation
  gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
  repel = TRUE      # Avoid text overlapping
)
```



```
# Visualize Principal Component Analysis
# Color by contributions to the PC
factoextra::fviz_pca_var(pcares,
  col.var = "contrib", # Color by contributions to the PC
  gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
  repel = TRUE      # Avoid text overlapping
)
```



ASSIGNMENT

Linear Redundancy analysis

```
# rda performs redundancy analysis
rdamodel <- vegan::rda(lnsp~., env[,1:4])
# do forward, backward or stepwise model selection using permutation tests
finalrda<- vegan::ordistep(rdamodel, scope=formula(rdamodel))
```

```
##
## Start: lnsp ~ Water + Reflection + Calmagrostis + Corynephorus
```

```
# look at model output
summary(finalrda)
```

```
##
## Call:
## rda(formula = lnsf ~ Water + Reflection + Calmagrostis + Corynephorus,      data = env[, 1:4])
##
## Partitioning of variance:
##           Inertia Proportion
## Total           20.367      1.0000
## Constrained      13.735      0.6744
## Unconstrained     6.632      0.3256
##
## Eigenvalues, and their contribution to the variance
##
## Importance of components:
##           RDA1   RDA2   RDA3   RDA4   PC1   PC2   PC3
## Eigenvalue      9.776 3.3058 0.54311 0.110063 3.2978 0.99988 0.66883
## Proportion Explained 0.480 0.1623 0.02667 0.005404 0.1619 0.04909 0.03284
## Cumulative Proportion 0.480 0.6423 0.66895 0.674357 0.8363 0.88537 0.91821
##           PC4   PC5   PC6   PC7   PC8   PC9
## Eigenvalue      0.54883 0.30578 0.25436 0.178535 0.172157 0.095643
## Proportion Explained 0.02695 0.01501 0.01249 0.008766 0.008453 0.004696
## Cumulative Proportion 0.94515 0.96017 0.97265 0.981420 0.989873 0.994568
##           PC10  PC11  PC12
## Eigenvalue      0.060812 0.029855 0.0199568
## Proportion Explained 0.002986 0.001466 0.0009799
## Cumulative Proportion 0.997554 0.999020 1.0000000
##
## Accumulated constrained eigenvalues
## Importance of components:
##           RDA1   RDA2   RDA3   RDA4
## Eigenvalue      9.7757 3.3058 0.54311 0.110063
## Proportion Explained 0.7118 0.2407 0.03954 0.008014
## Cumulative Proportion 0.7118 0.9524 0.99199 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: 4.842538
##
##
## Species scores
##
##           RDA1   RDA2   RDA3   RDA4   PC1   PC2
## Al.accent      -0.5481 0.98279 0.1025369 0.120663 -0.3363 0.171126
## A.cuneata        0.8063 0.21269 -0.1297274 -0.076903 -0.6051 -0.424717
## Al.fabrilis     -0.7190 0.50595 0.3860684 0.031398 0.1577 0.514089
## Ar.lutetiana    0.4574 0.07049 -0.0286888 -0.118161 -0.2617 0.236615
## Ar.perita       -0.4676 0.37753 0.3145314 -0.201397 0.3065 0.157655
## Au.albimana     1.0960 0.29596 0.2301312 0.123337 -0.3843 0.023341
## Pa.lugubris      0.1586 -0.82105 0.0970379 0.150984 0.1778 -0.608752
## Pa.monticola    0.1069 0.88112 -0.4822572 0.065282 -1.1343 0.050759
```



```

## Pa.nigriceps 1.4774 0.33229 0.2035952 0.058396 -0.6925 0.233187
## Pa.pullata 1.6376 0.66096 -0.0005806 -0.059465 -0.8569 0.005137
## Tr.terricola 1.4122 -0.48184 -0.0285569 -0.038140 -0.5607 -0.309197
## Zo.spinimana 1.1241 -0.27216 0.1093981 0.008408 -0.3692 0.269707
##
##
## Site scores (weighted sums of species scores)
##
##          RDA1      RDA2      RDA3      RDA4      PC1      PC2
## row1  0.8209  1.55299 -1.86883  1.70909 -1.5150016 -1.238670
## row2  1.1264 -0.24069  1.46442  0.42873  1.2579824  0.212165
## row3  0.9123  1.45062 -0.58809  1.30777 -2.0535200 -0.840085
## row4  1.4999  0.51806  0.64706  0.65905  0.5888077 -0.342951
## row5  1.6544  0.29865  1.17868 -1.41500  0.4840189  0.051754
## row6  1.2623  0.18176 -0.43449 -2.70427 -1.7299853  1.974875
## row7  1.7178  0.94944 -0.38413 -0.51248 -0.1288916  0.869591
## row8  0.3102 -1.38975  0.21465  3.22503 -0.4512602 -2.242890
## row9 -0.5750  0.26374 -2.65231 -0.29155 -0.2098404 -0.072304
## row10 -0.9469  0.32945 -2.04977  1.00610  0.1426042  0.098391
## row11 -0.6938  1.16908 -2.60527  2.81558 -0.6008475  0.044961
## row12 -0.1156  1.28729 -3.76310  0.05468 -0.9047830 -1.334112
## row13  1.6154  1.03642 -0.09280  0.28146 -0.0007028  0.106498
## row14  1.2657 -0.07091 -0.49356 -0.46631 -1.6218085  0.666615
## row15 -0.3772 -1.69008  0.14044 -0.46242  0.9325534  0.086228
## row16 -0.0977 -1.54648  0.24459 -0.81549  0.2376842 -0.381822
## row17 -0.4279 -1.47660 -0.03771 -1.46692  1.0049003  0.526730
## row18 -0.4682 -1.51896 -0.26980 -1.15869  0.7997130 -0.596876
## row19 -0.2432 -1.70884  0.32398  0.21081  0.4189845 -0.613747
## row20 -0.3328 -1.74211 -0.02464 -0.28545  0.6715414 -0.850787
## row21 -0.2757 -1.50164 -0.43687  0.28125  0.2925909 -0.836447
## row22 -1.2036  0.48101  1.76551 -1.41077  0.3037491  0.764504
## row23 -1.2352  0.68812  1.61450  0.34481  0.5229776 -0.008712
## row24 -1.3286  0.78622  1.86395 -0.90528  0.8398280  1.000214
## row25 -0.2158  0.36384  0.84018  3.79837 -1.3438404  1.521139
## row26 -1.1790  0.06218  2.62279 -4.97822  0.8904746 -0.634298
## row27 -1.3365  0.76988  2.11156 -0.23879  0.7321187  1.228212
## row28 -1.1323  0.69728  0.66906  0.98889  0.4399524  0.841825
##
##
## Site constraints (linear combinations of constraining variables)
##
##          RDA1      RDA2      RDA3      RDA4      PC1      PC2
## row1  0.29361  0.9923  1.36137 -0.62198 -1.5150016 -1.238670
## row2  1.57197  0.3211  0.06477  0.91995  1.2579824  0.212165
## row3  0.02421  0.3691  1.02761 -0.69107 -2.0535200 -0.840085
## row4  1.68401  1.1035  0.77539  1.27060  0.5888077 -0.342951
## row5  1.72494  0.6272  0.18255  0.86770  0.4840189  0.051754
## row6  0.37717 -1.0679 -0.72097 -1.10734 -1.7299853  1.974875
## row7  1.83457  0.5943 -0.11204  0.34693 -0.1288916  0.869591
## row8 -0.09788 -0.9254  0.55560  1.14930 -0.4512602 -2.242890
## row9 -0.57840  0.1524 -0.71222  0.13334 -0.2098404 -0.072304
## row10 -0.74086  0.4251 -0.36767 -0.02682  0.1426042  0.098391
## row11 -0.74316  0.6991 -1.22478  0.20963 -0.6008475  0.044961
## row12 -0.69666  1.2797 -2.96136  0.66783 -0.9047830 -1.334112

```

Table 1: CCA model coefficients

	RDA1	RDA2	RDA3	RDA4
Water	0.058	-0.017	-0.155	-0.273
Reflection	-0.034	0.116	0.047	-0.281
Calmagrostis	0.148	0.125	0.008	0.101
Corynephorus	-0.002	0.075	-0.228	0.072

```
## row13  1.77792  0.8193 -0.71866 -2.38804 -0.0007028  0.106498
## row14  0.35151 -0.7978 -0.08636  0.06173 -1.6218085  0.666615
## row15  0.07293 -1.2166 -0.47827 -0.80246  0.9325534  0.086228
## row16 -0.09049 -1.1900 -0.02992  0.06703  0.2376842 -0.381822
## row17  0.11759 -1.2076 -0.60747 -1.10779  1.0049003  0.526730
## row18 -0.04381 -1.1592 -0.17377 -0.34111  0.7997130 -0.596876
## row19 -0.15444 -1.1709  0.14193  0.37081  0.4189845 -0.613747
## row20 -0.03872 -1.2056 -0.16903 -0.17888  0.6715414 -0.850787
## row21 -0.12399 -1.1800  0.06010  0.22615  0.2925909 -0.836447
## row22 -0.92238  0.2596  1.69700 -0.27430  0.3037491  0.764504
## row23 -1.01468  1.0032  0.29908 -0.36181  0.5229776 -0.008712
## row24 -0.92126  0.8632  0.09407 -0.33960  0.8398280  1.000214
## row25 -0.57506 -0.8192  1.24688  1.64420 -1.3438404  1.521139
## row26 -1.20873  1.1881  1.38484 -1.75735  0.8904746 -0.634298
## row27 -0.93576  0.4835  0.15605  0.89898  0.7321187  1.228212
## row28 -0.94415  0.7594 -0.68470  1.16436  0.4399524  0.841825
```

```
##
```

```
##
```

```
## Biplot scores for constraining variables
```

```
##
```

```
##           RDA1    RDA2    RDA3    RDA4 PC1 PC2
## Water       0.7088 -0.5343 -0.2942 -0.35447  0  0
## Reflection  -0.5062  0.8006  0.1851 -0.26179  0  0
## Calmagrostis 0.9016  0.3986  0.1474  0.08125  0  0
## Corynephorus -0.5552  0.5415 -0.6022  0.18961  0  0
```

```
# coefficients
```

```
coef(finalrda) %>%
```

```
  kableExtra::kbl(caption = "CCA model coefficients", digits = 3) %>%
```

```
  kableExtra::kable_paper()
```

```
# r-squared
```

```
vegan::RsquareAdj(finalrda)$r.squared
```

```
## [1] 0.6743569
```

```
vegan::RsquareAdj(finalrda)$adj.r.squared
```

```
## [1] 0.6177233
```

analyse linear dependencies among constraints and conditions

Table 2: CCA model VIF

	x
Water	2.762
Reflection	2.593
Calmagrostis	1.289
Corynephorus	1.690

Table 3: CCA model goodness of fit

	RDA1	RDA2	RDA3	RDA4
Al.accent	0.168	0.706	0.712	0.720
A.cuneata	0.435	0.466	0.477	0.481
Al.fabrilis	0.355	0.530	0.633	0.633
Ar.lutetiana	0.411	0.421	0.423	0.450
Ar.perita	0.289	0.477	0.608	0.661
Au.albimana	0.701	0.753	0.784	0.792
Pa.lugubris	0.019	0.516	0.523	0.540
Pa.monticola	0.004	0.299	0.387	0.389
Pa.nigriceps	0.718	0.755	0.768	0.770
Pa.pullata	0.655	0.762	0.762	0.763
Tr.terricola	0.715	0.798	0.798	0.799
Zo.spinimana	0.695	0.736	0.743	0.743

```
# analyse linear dependencies among constraints and conditions
vegan::vif.cca(finalrda) %>%
  kableExtra::kbl(caption = "CCA model VIF", digits = 3) %>%
  kableExtra::kable_paper()
```

Results above present the variance inflation factors (VIF) for each constraint or contrast in factor constraints. A common rule is that values over 10 indicate redundant constraints. The value below 4 in these results indicates no significant relationship between the variables.

assess the goodness of fit for individual sites or species

```
# assess the goodness of fit for individual sites or species.
# ?vegan::goodness
vegan::goodness(finalrda) %>%
  kableExtra::kbl(caption = "CCA model goodness of fit", digits = 3) %>%
  kableExtra::kable_paper()
```

The results above give cumulative proportion of inertia accounted by species up to chosen axes. The proportions can be assessed either by species or by sites. In these results, any species that have a coefficient above 0.6 indicates that the variation in species can be explained by the environmental variables.

1.1. Anova analysis (Permutation test)

```
# implement ANOVA-like permutation tests for the joint effect of constraints in cca, rda
vegan::anova.cca(finalrda)
```

```
## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = lnspl ~ Water + Reflection + Calmagrostis + Corynephorus, data = env[, 1:4])
##           Df Variance      F Pr(>F)
## Model      4  13.7347 11.907  0.001 ***
## Residual  23   6.6324
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
vegan::anova.cca(finalrda, by="terms")
```

```
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = lnspl ~ Water + Reflection + Calmagrostis + Corynephorus, data = env[, 1:4])
##           Df Variance      F Pr(>F)
## Water      1   5.9151 20.5125  0.001 ***
## Reflection  1   1.2905  4.4754  0.008 **
## Calmagrostis 1   5.7746 20.0254  0.001 ***
## Corynephorus 1   0.7544  2.6161  0.049 *
## Residual   23   6.6324
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
vegan::anova.cca(finalrda, by="axis")
```

```
## Permutation test for rda under reduced model
## Forward tests for axes
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = lnspl ~ Water + Reflection + Calmagrostis + Corynephorus, data = env[, 1:4])
##           Df Variance      F Pr(>F)
## RDA1      1   9.7757 33.9005  0.001 ***
## RDA2      1   3.3058 11.4639  0.001 ***
## RDA3      1   0.5431  1.8834  0.262
## RDA4      1   0.1101  0.3817  0.872
## Residual  23   6.6324
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The results above implement ANOVA-like permutation tests for the joint effect of constraints in CCA. The overall model tested shows significant differences in species abundances across the environmental variables tested. All of the environmental variables except 'Corynephorus' had impacts on species abundances which were significantly different from zero. Lastly, only the first two principal components (RDA1 and RDA2) had statistically significant explanatory power for describing differences in species abundances. Environmental variables and principal components that are not statistically significant can be removed from the model.

Table 4: CCA model coefficients

	RDA1	RDA2	RDA3	RDA4
Water	0.058	-0.017	-0.155	-0.273
Reflection	-0.034	0.116	0.047	-0.281
Calmagrostis	0.148	0.125	0.008	0.101
Corynephorus	-0.002	0.075	-0.228	0.072

Table 5: CCA model VIF

	x
Water	2.762
Reflection	2.593
Calmagrostis	1.289
Corynephorus	1.690

1.2. Diagnostics tests

```
# coefficients
coef(finalrda) %>%
  kableExtra::kbl(caption = "CCA model coefficients", digits = 3) %>%
  kableExtra::kable_paper()
# r-squared
vegan::RsquareAdj(finalrda)$r.squared
vegan::RsquareAdj(finalrda)$adj.r.squared
```

```
## [1] 0.6743569
## [1] 0.6177233
```

analyse linear dependencies among constraints and conditions

```
# analyse linear dependencies among constraints and conditions
vegan::vif.cca(finalrda) %>%
  kableExtra::kbl(caption = "CCA model VIF", digits = 3) %>%
  kableExtra::kable_paper()
```

Results above present the variance inflation factors (VIF) for each constraint or contrast in factor constraints. A common rule is that values over 10 indicate redundant constraints. The value below 4 in these results indicates no significant relationship between the variables.

assess the goodness of fit for individual sites or species

```
# assess the goodness of fit for individual sites or species.
# ?vegan::goodness
vegan::goodness(finalrda) %>%
  kableExtra::kbl(caption = "CCA model goodness of fit", digits = 3) %>%
  kableExtra::kable_paper()
```

The results above give cumulative proportion of inertia accounted by species up to chosen axes. The proportions can be assessed either by species or by sites. In these results, any species that have a coefficient above 0.6 indicates that the variation in species can be explained by the environmental variables.

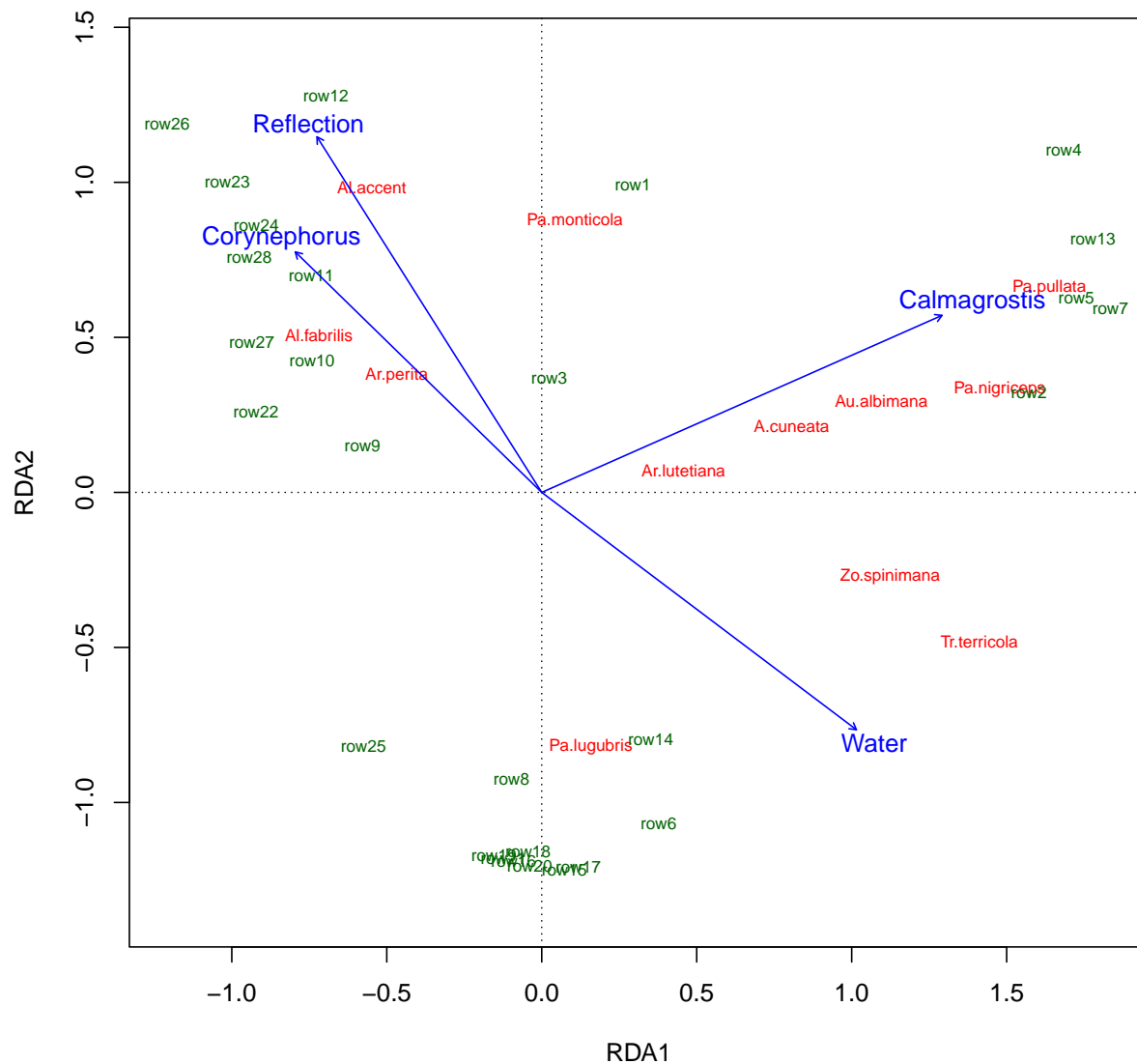
Table 6: CCA model goodness of fit

	RDA1	RDA2	RDA3	RDA4
Al.accent	0.168	0.706	0.712	0.720
A.cuneata	0.435	0.466	0.477	0.481
Al.fabrilis	0.355	0.530	0.633	0.633
Ar.lutetiana	0.411	0.421	0.423	0.450
Ar.perita	0.289	0.477	0.608	0.661
Au.albimana	0.701	0.753	0.784	0.792
Pa.lugubris	0.019	0.516	0.523	0.540
Pa.monticola	0.004	0.299	0.387	0.389
Pa.nigriceps	0.718	0.755	0.768	0.770
Pa.pullata	0.655	0.762	0.762	0.763
Tr.terricola	0.715	0.798	0.798	0.799
Zo.spinimana	0.695	0.736	0.743	0.743

1.3. Generating plot

```
plot(finalrda,
      scaling = 2,
      display = c("sp", "lc", "cn"),
      main = "Triplot RDA Species ~ Environment - scaling 1 - lc scores"
    )
```

Triplot RDA Species ~ Environment – scaling 1 – Ic scores



Interpretation of these plots should be based on the goodness test.

1.4. Quadratic model

```
rdamodel2 <- vegan::rda(lnsp~., env)
#model selection
finalrda2<- vegan::ordistep(rdamodel2, scope=formula(rdamodel2))
```

```
##
```

```
## Start: lnsp ~ Water + Reflection + Calmagrostis + Corynephorus + Water2 +      Reflection2 + Wateref
```

```
# look at model output
summary(finalrda2)
```

```
##
## Call:
## rda(formula = lnsf ~ Water + Reflection + Calmagrostis + Corynephorus +      Water2 + Reflection2 + V
##
## Partitioning of variance:
##           Inertia Proportion
## Total           20.37      1.0000
## Constrained      15.75      0.7731
## Unconstrained     4.62      0.2269
##
## Eigenvalues, and their contribution to the variance
##
## Importance of components:
##           RDA1    RDA2    RDA3    RDA4    RDA5    RDA6
## Eigenvalue    10.0961  3.8044  1.26657  0.33756  0.148998  0.079931
## Proportion Explained  0.4957  0.1868  0.06219  0.01657  0.007316  0.003925
## Cumulative Proportion  0.4957  0.6825  0.74468  0.76126  0.768574  0.772498
##           RDA7    PC1    PC2    PC3    PC4    PC5    PC6
## Eigenvalue    0.0130688  2.6367  0.57125  0.32371  0.28278  0.24591  0.179747
## Proportion Explained  0.0006417  0.1295  0.02805  0.01589  0.01388  0.01207  0.008825
## Cumulative Proportion  0.7731397  0.9026  0.93065  0.94654  0.96042  0.97250  0.981324
##           PC7    PC8    PC9    PC10    PC11    PC12
## Eigenvalue    0.166995  0.083969  0.060809  0.033756  0.024903  0.0099475
## Proportion Explained  0.008199  0.004123  0.002986  0.001657  0.001223  0.0004884
## Cumulative Proportion  0.989523  0.993646  0.996632  0.998289  0.999512  1.0000000
##
## Accumulated constrained eigenvalues
## Importance of components:
##           RDA1    RDA2    RDA3    RDA4    RDA5    RDA6
## Eigenvalue    10.0961  3.8044  1.26657  0.33756  0.148998  0.079931
## Proportion Explained  0.6412  0.2416  0.08043  0.02144  0.009462  0.005076
## Cumulative Proportion  0.6412  0.8828  0.96319  0.98463  0.994094  0.999170
##           RDA7
## Eigenvalue    0.0130688
## Proportion Explained  0.0008299
## Cumulative Proportion 1.0000000
##
## 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: 4.842538
##
##
## Species scores
##
##           RDA1    RDA2    RDA3    RDA4    RDA5    RDA6
## Al.accent    -0.5357  1.08697 -0.05362 -0.17069  0.002098  0.08053
## A.cuneata     0.8887  0.26114  0.27646 -0.16652  0.162578 -0.17394
## Al.fabrilis  -0.7919  0.53887 -0.54006 -0.25871 -0.076106 -0.04693
## Ar.lutetiana  0.4243  0.06835 -0.14312  0.14873 -0.129892 -0.08762
```



```

## Ar.perita      -0.5278  0.23432 -0.50908  0.13919  0.266041 -0.09558
## Au.albimana    1.0952  0.28187 -0.27310 -0.17002  0.045753  0.08300
## Pa.lugubris     0.2031 -0.85107  0.16173 -0.29863  0.142366  0.07919
## Pa.monticola    0.2248  1.07605  0.69750 -0.06358 -0.034024 -0.04982
## Pa.nigriceps    1.4702  0.32641 -0.30715 -0.10703 -0.013615  0.03439
## Pa.pullata      1.6542  0.62562 -0.10694  0.27488  0.069619  0.08913
## Tr.terricola    1.4502 -0.48237  0.11799 -0.03509 -0.007114 -0.02288
## Zo.spinimana    1.0815 -0.29723 -0.31741 -0.11399 -0.151899 -0.10480
##
##
## Site scores (weighted sums of species scores)
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## row1  0.83903  1.50229  1.08938 -0.02403  0.6234  1.0321
## row2  1.08742 -0.31361 -1.10676  0.78461  0.3788  3.8001
## row3  0.92053  1.38282  0.45395 -0.96721  1.5871  0.5341
## row4  1.46668  0.42951 -0.73643  0.24144 -0.1975  1.5213
## row5  1.61288  0.20223 -1.06896  0.20331  0.5999 -0.8251
## row6  1.22949  0.14663 -0.44065  1.24184 -2.9414 -4.1777
## row7  1.68917  0.86647 -0.29633  0.71897 -1.5392 -0.6716
## row8  0.32160 -1.26584  0.67999 -3.12792  3.7967  0.3600
## row9 -0.54268  0.30843  1.50691  1.70756 -0.8672 -0.1679
## row10 -0.91482  0.37899  1.18065  1.00219 -2.0007  0.6524
## row11 -0.64744  1.20792  1.68784 -0.30299 -1.3620  0.6438
## row12 -0.06158  1.31485  2.42315  0.64945  1.2960 -1.5915
## row13  1.59803  0.96573 -0.16679 -1.36802  0.5845 -3.2306
## row14  1.24133 -0.08778 -0.07078  1.06455 -1.2644  0.1825
## row15 -0.38140 -1.57515  0.11024  0.45204 -0.8073  0.9484
## row16 -0.10208 -1.43781  0.10192 -0.51973  0.2171 -1.5424
## row17 -0.43295 -1.38219  0.07241  1.19467 -1.2524  0.5668
## row18 -0.46008 -1.40981  0.52628  0.68011  0.9491  1.0843
## row19 -0.24522 -1.58895  0.15438 -0.50038  0.3133  0.4605
## row20 -0.32736 -1.61131  0.44808 -0.45578  1.0688 -0.1735
## row21 -0.26676 -1.38289  0.65799 -0.03716  0.9974  1.1035
## row22 -1.20503  0.40000 -1.17344  0.18284 -0.0418 -0.4013
## row23 -1.22403  0.61360 -0.81778 -0.94736  1.4675  0.3377
## row24 -1.32730  0.68337 -1.24874 -0.05509  0.1239 -0.3270
## row25 -0.21652  0.39919 -0.41794 -2.97508 -3.0155 -0.7579
## row26 -1.19451 -0.07963 -1.81085  1.73573  2.6315 -1.3471
## row27 -1.33653  0.66187 -1.34307 -0.03692  0.2381  1.3247
## row28 -1.11986  0.67108 -0.39464 -0.54164 -1.5836  0.6612
##
##
## Site constraints (linear combinations of constraining variables)
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## row1  0.50257  1.1129  0.08782  0.099021  1.056157  0.667805
## row2  1.44512 -0.1253 -0.78158  0.382327  0.137800  0.774258
## row3  0.31810  0.8504  0.91593 -0.044665  0.519075  0.679452
## row4  1.64955  0.9710 -0.70144 -0.113656  0.082024  1.491302
## row5  1.63245  0.3112 -0.65334  0.409477  0.057805  0.935940
## row6  0.06252 -1.0469 -0.64276  1.182117 -1.350132 -1.070344
## row7  1.66002  0.3147 -0.79335  0.826688 -0.317993  0.436958
## row8  0.08556 -0.9991  0.25130 -1.767459  0.804027  0.403866

```

```
## row9 -0.33332 0.5202 1.63740 -0.009389 -0.073176 0.301759
## row10 -0.57344 0.7404 1.10634 0.109484 -0.077159 0.284668
## row11 -0.56435 0.8356 1.46375 0.319528 0.032488 0.025169
## row12 -0.48377 1.0456 2.21990 0.760510 0.310548 -0.500159
## row13 1.85761 1.3632 0.01746 -1.304013 -0.262580 -3.687459
## row14 0.35245 -0.8861 0.15576 0.256351 -0.007608 0.216516
## row15 -0.05379 -1.1649 0.02979 0.835214 -0.730631 -0.540578
## row16 -0.01194 -1.2371 0.46192 -0.107047 0.224247 0.144196
## row17 -0.07563 -1.0808 -0.13403 0.995836 -1.092022 -0.871030
## row18 -0.01274 -1.0924 0.47061 0.319664 -0.166695 -0.025519
## row19 -0.01879 -1.2245 0.52382 -0.579403 0.479453 0.267302
## row20 -0.01652 -1.2431 0.35989 0.229327 -0.018133 -0.007771
## row21 -0.01380 -1.2312 0.50318 -0.346638 0.364020 0.217587
## row22 -1.12440 0.6579 -1.33326 -0.110185 -0.855653 0.675502
## row23 -1.18486 0.7085 -0.97983 0.690740 0.254410 -0.121079
## row24 -0.94069 0.7816 -0.14856 0.507996 0.283882 0.005276
## row25 -0.48977 -0.4507 -0.49983 -3.363492 -0.066731 0.172451
## row26 -1.22676 -0.1113 -1.82810 0.775695 3.421796 -1.222141
## row27 -1.21622 0.7920 -1.00542 -0.576025 -1.540229 0.297245
## row28 -1.22514 0.8879 -0.70338 -0.378003 -1.468991 0.048828
##
##
## Biplot scores for constraining variables
##
##           RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## Water          0.6970 -0.50100 0.1350 0.19183 -0.23255 -0.37882
## Reflection    -0.4971 0.74099 -0.1745 0.14187 0.36270 -0.10468
## Calmagrostis  0.8858 0.35091 -0.2694 0.03420 0.04365 0.10638
## Corynephorus -0.5375 0.53043 0.3790 0.17656 -0.05487 -0.05546
## Water2        -0.1127 0.16810 -0.4633 0.01754 -0.30324 -0.80536
## Reflection2   -0.4371 -0.10268 -0.4463 0.26693 0.69844 -0.19985
## Wateref       0.5355 0.08181 0.4991 -0.61040 -0.25890 0.13224
```

implement ANOVA-like permutation tests for the joint effect of constraints in cca, rda

```
# implement ANOVA-like permutation tests for the joint effect of constraints in cca, rda
vegan::anova.cca(finalrda2)
```

```
## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = lnsp ~ Water + Reflection + Calmagrostis + Corynephorus + Water2 + Reflection2
##           Df Variance      F Pr(>F)
## Model      7  15.7466 9.7371 0.001 ***
## Residual  20   4.6205
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
vegan::anova.cca(finalrda2, by="terms")
```

```
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
```

```
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = lnsp ~ Water + Reflection + Calmagrostis + Corynephorus + Water2 + Reflection2
##           Df Variance      F Pr(>F)
## Water      1   5.9151 25.6038 0.001 ***
## Reflection  1   1.2905  5.5862 0.006 **
## Calmagrostis 1   5.7746 24.9958 0.001 ***
## Corynephorus 1   0.7544  3.2654 0.023 *
## Water2      1   0.7100  3.0731 0.041 *
## Reflection2 1   0.8017  3.4702 0.033 *
## Wateref     1   0.5003  2.1654 0.095 .
## Residual    20   4.6205
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
vegan::anova.cca(finalrda2, by="axis")
```

```
## Permutation test for rda under reduced model
## Forward tests for axes
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = lnsp ~ Water + Reflection + Calmagrostis + Corynephorus + Water2 + Reflection2
##           Df Variance      F Pr(>F)
## RDA1      1  10.0961 43.7014 0.001 ***
## RDA2      1   3.8044 16.4675 0.001 ***
## RDA3      1   1.2666  5.4824 0.045 *
## RDA4      1   0.3376  1.4611 0.774
## RDA5      1   0.1490  0.6449 0.981
## RDA6      1   0.0799  0.3460 0.992
## RDA7      1   0.0131  0.0566 1.000
## Residual  20   4.6205
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The results above implement ANOVA-like permutation tests for the joint effect of constraints in CCA. The overall model tested shows significant differences in species abundances across the environmental variables tested. All of the environmental variables except 'Wateref' had impacts on species abundances which were significantly different from zero. Lastly, only the first two principal components (RDA1 and RDA2) had statistically significant explanatory power for describing differences in species abundances (alpha = 0.05 level). Environmental variables and principal components that are not statistically significant can be removed from the model.

model coefficients

```
# coefficients
coef(finalrda2) %>%
  kableExtra::kbl(caption = "CCA quadratic model coefficients", digits = 3) %>%
  kableExtra::kable_paper()
# r-squared
RsquareAdj(finalrda2)$r.squared
RsquareAdj(finalrda2)$adj.r.squared
```

Table 7: CCA quadratic model coefficients

	RDA1	RDA2	RDA3	RDA4	RDA5	RDA6	RDA7
Water	0.092	-0.005	0.230	0.194	0.081	-0.162	0.149
Reflection	0.007	0.187	0.173	0.117	0.075	-0.060	0.363
Calmagrostis	0.128	0.072	-0.129	0.026	0.016	0.054	-0.158
Corynephorus	-0.002	0.026	0.082	0.054	0.019	-0.067	-0.269
Water2	-0.027	0.011	-0.139	-0.123	-0.096	-0.140	-0.082
Reflection2	0.023	-0.082	-0.010	-0.132	0.260	-0.129	-0.180
Wateref	0.060	0.018	0.152	-0.350	0.219	-0.186	-0.057

Table 8: CCA quadratic model VIF

	x
Water	4.163
Reflection	5.936
Calmagrostis	1.814
Corynephorus	2.364
Water2	1.701
Reflection2	4.727
Wateref	3.991

```
## [1] 0.7731397
## [1] 0.6937386
```

analyse linear dependencies among constraints and conditions

```
# analyse linear dependencies among constraints and conditions
vegan::vif.cca(finalrda2) %>%
  kableExtra::kbl(caption = "CCA quadratic model VIF", digits = 3) %>%
  kableExtra::kable_paper()
```

Results above present the variance inflation factors (VIF) for each constraint or contrast in factor constraints. A common rule is that values over 10 indicate redundant constraints. The values below 4 in these results indicate no significant relationship between the variables. Values above 4 were found for ‘Water’, ‘Reflection’, and ‘Reflection2’.

assess the goodness of fit for individual sites or species

```
# assess the goodness of fit for individual sites or species.
# ?vegan::goodness
vegan::goodness(finalrda2, choices = 1:2) %>%
  kableExtra::kbl(caption = "CCA quadratic model goodness of fit", digits = 3) %>%
  kableExtra::kable_paper()
```

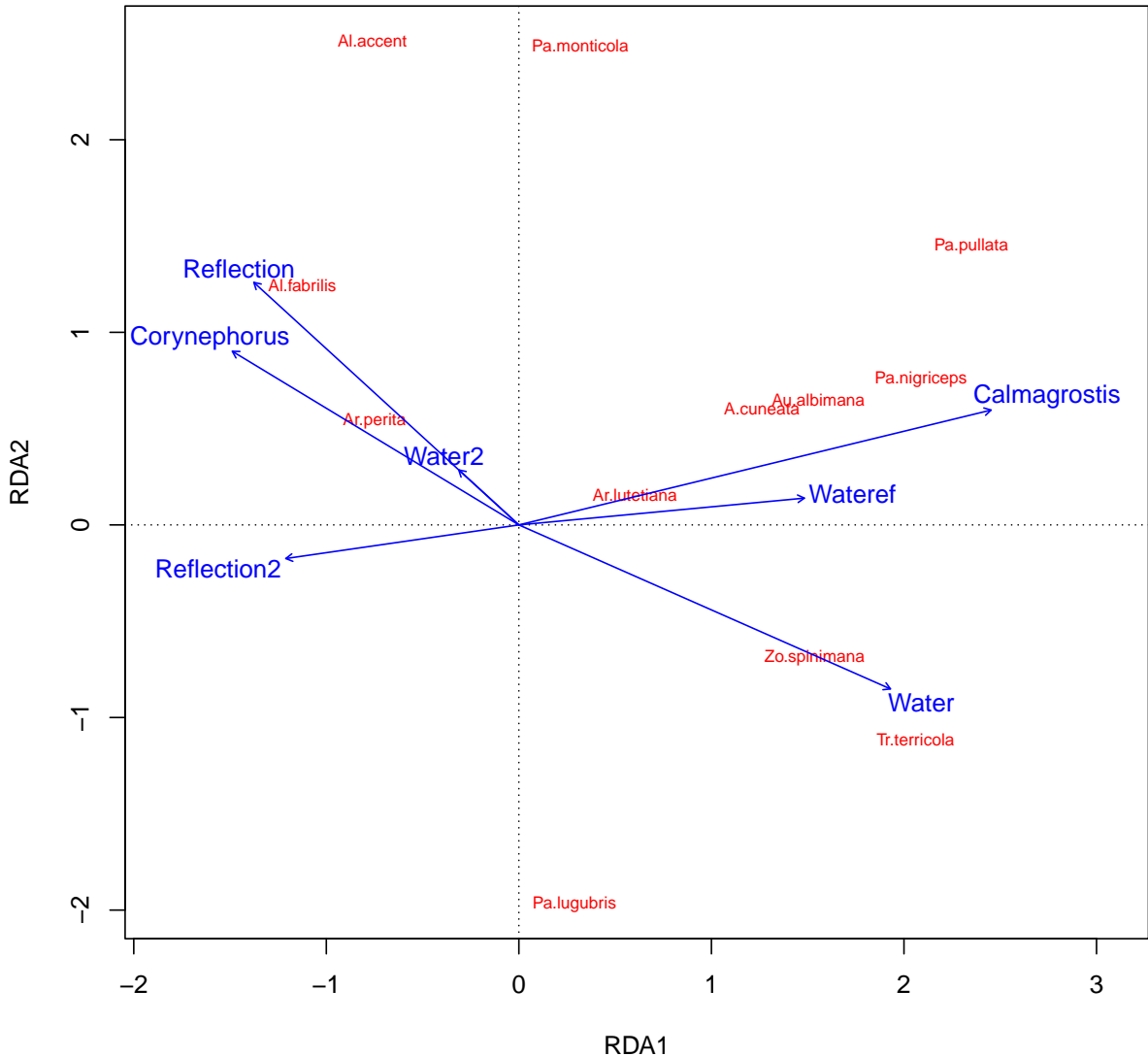
The results above give cumulative proportion of inertia accounted by species up to chosen axes. The proportions can be assessed either by species or by sites. In these results, any species that have a coefficient above 0.6 indicates that the variation in species can be explained by the environmental variables.

```
plot(finalrda2,
  scaling = 1,
  display = c("sp", "cn"),
  main = "Triplot RDA Species ~ Environment - scaling 1 - lc scores"
)
```

Table 9: CCA quadratic model goodness of fit

	RDA1	RDA2
Al.accent	0.160	0.819
A.cuneata	0.529	0.574
Al.fabrilis	0.430	0.630
Ar.lutetiana	0.354	0.363
Ar.perita	0.368	0.440
Au.albimana	0.700	0.747
Pa.lugubris	0.030	0.565
Pa.monticola	0.019	0.458
Pa.nigriceps	0.711	0.747
Pa.pullata	0.669	0.764
Tr.terricola	0.754	0.837
Zo.spinimana	0.644	0.692

Triplot RDA Species ~ Environment – scaling 1 – Ic scores



Interpretation of these plots should be based on the goodness test.

Reference

- Borcard, D., Gillet, F., & Legendre, P. (2011). Numerical ecology with R (Vol. 2, p. 688). New York: springer.
- Makarek, V., & Legendre, P. (2002). Nonlinear redundancy analysis and canonical correspondence analysis based on polynomial regression. *Ecology*, 83(4), 1146-1161.
- Leaw, Chui Pin; Lim, Po Teen; Lee, Li Keat (2020). R script and datasets - CCA. figshare. Dataset. <https://doi.org/10.6084/m9.figshare.12356519.v3>