

RDA

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1. Primer paso: cargar las librerías que necesitas.

```
library(ggplot2)
library(dplyr)
library(vegan)
```

2. Segundo paso: cargar los datos.

```
species=read.csv("data/RDA_species.csv", header=T, row.names=NULL, sep=",")
env=read.csv("data/RDA_envirometal.csv", header=T, row.names=NULL, sep=",")
```

3. Before we can use this explanatory matrix we need to check that its rows are in the same order as our response matrix `all.equal(rownames(species), rownames(env))`

```
all.equal(rownames(species), rownames(env))
```

```
## [1] TRUE
```

4. Remover la columna de sitios.

```
species_1 <- select(species, -site)
env_1 <- select(env, -site)
```

5. Transformar datos. Hellinger es una transformación recomendada por Legendre & Callagher (2001) en datos de abundancia y con una respuesta lineal

```
species_2 <- decostand(species_1, method = "hellinger")
```

- 6.

vegan requires that we write out each term if we are not going to

convert the factor to a dummy matrix

```
rda_tree_all = rda(species_2 ~ temperature + pH +
                    oxygen + conductivity + plants, data= env_1, scale=T)
rda_tree_all
```

```
## Call: rda(formula = species_2 ~ temperature + pH + oxygen +
## conductivity + plants, data = env_1, scale = T)
##
##              Inertia Proportion Rank
## Total          47.0000      1.0000
## Constrained     8.9073      0.1895    5
## Unconstrained 38.0927      0.8105   47
## Inertia is correlations
##
## Eigenvalues for constrained axes:
##  RDA1  RDA2  RDA3  RDA4  RDA5
## 4.067 2.255 1.376 0.792 0.417
##
## Eigenvalues for unconstrained axes:
##  PC1  PC2  PC3  PC4  PC5  PC6  PC7  PC8
## 5.045 4.820 3.785 2.839 2.079 1.798 1.619 1.404
## (Showing 8 of 47 unconstrained eigenvalues)
```

7. Summary http://dmcglinn.github.io/quant_methods/lessons/multivariate_models.html

Inertia is another name for variation or variance in this case. “Total” refers to total variance “Constrained” refers to the amount of variance explained by the explanatory variables, “Unconstrained” refers to the residual variance. Constrained + Unconstrained = Total.

An R2 statistic can be derived simply as Constrained / Total.

```
summary(rda_tree_all)
```

```
##
## Call:
## rda(formula = species_2 ~ temperature + pH + oxygen + conductivity +      plants, data = env_1, scale = T)
##
## Partitioning of correlations:
##              Inertia Proportion
## Total          47.000      1.0000
## Constrained     8.907      0.1895
## Unconstrained 38.093      0.8105
##
## Eigenvalues, and their contribution to the correlations
##
## Importance of components:
##              RDA1    RDA2    RDA3    RDA4    RDA5    PC1    PC2
## Eigenvalue      4.06679 2.25482 1.37627 0.79194 0.417482 5.0453 4.8203
## Proportion Explained 0.08653 0.04797 0.02928 0.01685 0.008883 0.1073 0.1026
## Cumulative Proportion 0.08653 0.13450 0.16378 0.18063 0.189517 0.2969 0.3994
##              PC3    PC4    PC5    PC6    PC7    PC8    PC9
## Eigenvalue      3.78471 2.83946 2.07941 1.79779 1.61889 1.40426 1.28896
## Proportion Explained 0.08053 0.06041 0.04424 0.03825 0.03444 0.02988 0.02742
```

```

## Cumulative Proportion 0.47995 0.54036 0.58461 0.62286 0.65730 0.68718 0.71460
## PC10 PC11 PC12 PC13 PC14 PC15 PC16
## Eigenvalue 1.19207 1.09439 1.08068 0.97083 0.91273 0.85041 0.78867
## Proportion Explained 0.02536 0.02328 0.02299 0.02066 0.01942 0.01809 0.01678
## Cumulative Proportion 0.73997 0.76325 0.78624 0.80690 0.82632 0.84441 0.86119
## PC17 PC18 PC19 PC20 PC21 PC22 PC23
## Eigenvalue 0.69918 0.61775 0.58582 0.57070 0.48347 0.46437 0.410574
## Proportion Explained 0.01488 0.01314 0.01246 0.01214 0.01029 0.00988 0.008736
## Cumulative Proportion 0.87607 0.88921 0.90168 0.91382 0.92411 0.93399 0.942723
## PC24 PC25 PC26 PC27 PC28 PC29
## Eigenvalue 0.384870 0.33090 0.309928 0.293196 0.235722 0.204967
## Proportion Explained 0.008189 0.00704 0.006594 0.006238 0.005015 0.004361
## Cumulative Proportion 0.950911 0.95795 0.964546 0.970784 0.975800 0.980161
## PC30 PC31 PC32 PC33 PC34 PC35
## Eigenvalue 0.191153 0.169063 0.125743 0.076653 0.072208 0.064563
## Proportion Explained 0.004067 0.003597 0.002675 0.001631 0.001536 0.001374
## Cumulative Proportion 0.984228 0.987825 0.990500 0.992131 0.993667 0.995041
## PC36 PC37 PC38 PC39 PC40
## Eigenvalue 0.049611 0.0419889 0.0381111 0.0342656 0.0228705
## Proportion Explained 0.001056 0.0008934 0.0008109 0.0007291 0.0004866
## Cumulative Proportion 0.996097 0.9969900 0.9978009 0.9985300 0.9990166
## PC41 PC42 PC43 PC44 PC45
## Eigenvalue 0.0163275 0.012502 0.0093315 0.0055293 1.296e-03
## Proportion Explained 0.0003474 0.000266 0.0001985 0.0001176 2.758e-05
## Cumulative Proportion 0.9993640 0.999630 0.9998285 0.9999462 1.000e+00
## PC46 PC47
## Eigenvalue 7.940e-04 4.408e-04
## Proportion Explained 1.689e-05 9.378e-06
## Cumulative Proportion 1.000e+00 1.000e+00
##
## Accumulated constrained eigenvalues
## Importance of components:
## RDA1 RDA2 RDA3 RDA4 RDA5
## Eigenvalue 4.0668 2.2548 1.3763 0.79194 0.41748
## Proportion Explained 0.4566 0.2531 0.1545 0.08891 0.04687
## Cumulative Proportion 0.4566 0.7097 0.8642 0.95313 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: 7.194377
##
##
## Species scores
##
## RDA1 RDA2 RDA3 RDA4 RDA5 PC1
## acan_speculum -0.56635 0.174225 0.012091 -0.059736 0.027177 0.0555015
## acan_trilobatum 0.22379 0.201319 -0.424041 0.085697 0.116983 -0.2831852
## ani_allopterum 0.34237 -0.225464 0.033024 0.034060 -0.054269 -0.4931210
## arg_anceps 0.53063 -0.068151 -0.074167 -0.076600 -0.191017 -0.0769561
## arg_ellongata 0.38020 -0.028739 -0.126081 -0.239406 -0.003290 -0.4432599
## arg_pulla 0.20645 0.199453 -0.416753 0.096749 0.093944 -0.2005521
## arg_translata 0.11795 -0.026002 -0.138746 -0.147740 0.038229 -0.1666081
## bra_furcata -0.19121 0.357038 0.273934 0.022463 0.037009 0.5482178

```

```

## can_vibex      0.16613  0.017311 -0.055460  0.040377  0.072448 -0.2712934
## dyt_nigra      0.06760  0.328213  0.117171  0.232796 -0.208999  0.4861273
## dyt_sterilis   0.42742  0.014951 -0.190910 -0.066271  0.081848 -0.3244196
## ena_civile     0.28133  0.051758 -0.076657 -0.222578 -0.034812  0.4988285
## ena_novaehispaniae 0.10535  0.175792 -0.011138 -0.282879 -0.132417  0.0889268
## erythe_attala  -0.58814  0.058109 -0.085068  0.050608  0.046613  0.1945645
## erythe_peruviana -0.40640  0.089686 -0.112724 -0.079167  0.065561 -0.0517349
## erythe_plebaja -0.36344 -0.069846 -0.132813  0.114418  0.061040  0.2363204
## erythe-vesiculosa 0.15599 -0.150890 -0.057331 -0.134456  0.178474  0.1744324
## erythr_fervida  -0.43529  0.123737  0.016983 -0.105057  0.074120  0.3420191
## erythr_funerea  0.14350  0.145748  0.254622 -0.268198  0.099007  0.2192590
## erythr_fusca    -0.57750  0.117559  0.098058 -0.308824 -0.052209 -0.0154398
## erythr_umbrata  0.09625  0.210565 -0.051355  0.214595 -0.160077  0.0542030
## het_cruentata   0.28978 -0.110885  0.013473 -0.128867 -0.149976 -0.3434451
## isc_capreola    -0.44929 -0.474919  0.090810  0.168794 -0.024459  0.2201268
## isc_ramburii    -0.12392 -0.566227  0.261880 -0.008813  0.085193  0.0888216
## les_tenuatus    0.17328 -0.007860  0.005584  0.051217  0.117939 -0.4603314
## lib_herculea    -0.31406 -0.081507 -0.354544 -0.077658 -0.161722  0.2355933
## mac_pseudimitans 0.08469  0.141945 -0.020065 -0.045587 -0.002069 -0.4095923
## mia_marcella    0.03101  0.369162  0.327434 -0.025711  0.079036  0.6348831
## mic_aequalis    -0.25930  0.132426 -0.062756  0.004040 -0.120485  0.0009114
## mic_atra        -0.18845 -0.005004 -0.034717  0.224143 -0.014931 -0.0803580
## mic_mengeri     0.06803  0.356810  0.133127  0.169256 -0.086707  0.5379574
## mic_ocellata    -0.55827  0.046166 -0.066868 -0.157877 -0.059001  0.0391176
## mic_schumanni   0.08663  0.095410  0.070262 -0.135939 -0.086617 -0.4900225
## neo_cultellatum -0.33112  0.258514  0.045463 -0.139860  0.078101  0.3507857
## oli_umbricola   0.00000  0.000000  0.000000  0.000000  0.000000  0.0000000
## ort_discolor    0.18884  0.271442 -0.320455  0.074843 -0.008280 -0.5106693
## ort_ferruginea  0.19892  0.335125  0.310869  0.076157  0.003996  0.6103688
## pal_lineatipes  0.16079 -0.079136 -0.023440  0.077224 -0.096927 -0.0946139
## pan_flavecens   0.18745  0.355312  0.278650  0.057720 -0.009532  0.6022441
## pan_hymenaea    0.14232  0.206311  0.190710  0.018467  0.184033  0.6116925
## per_mooma       -0.01314  0.559071 -0.103248  0.034689  0.066810  0.3170722
## rem_luteipennis 0.03717 -0.379952  0.187306  0.227218  0.120282 -0.4528407
## rhi_jalapensis  0.17012 -0.091011  0.098058  0.049158 -0.157195 -0.1159048
## tau_argo        0.00000  0.000000  0.000000  0.000000  0.000000  0.0000000
## tau_australis   0.01700  0.306013  0.029876  0.142745  0.039210  0.4338115
## tel_digiticolis -0.57986  0.034523 -0.128704  0.109802 -0.004543  0.2215035
## tel_filiola     -0.58657  0.044191 -0.201962  0.020802 -0.076858  0.2069809
## tel_salva       -0.26606  0.160484  0.062011 -0.020506 -0.076262 -0.0282824
## Gomphidae       0.18263  0.138073 -0.302768  0.054845  0.133397 -0.1991074
##
##
## Site scores (weighted sums of species scores)
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      PC1
## row1 -2.34062  0.367106 -0.86489  0.35331  1.398270  0.80689
## row2 -0.06932 -1.720847  0.96051  1.12267  0.647840  0.06049
## row3  1.20432  0.523913 -3.02251  0.22035  1.848212 -0.61954
## row4  0.76929 -0.265067 -0.63310 -0.19901  0.729802 -0.05932
## row5  0.13512 -1.136051  0.70430  0.18790  0.416868  0.08071
## row6  1.62816 -1.131078  0.22063 -0.90133 -5.543507 -0.78772
## row7 -3.06222  0.409328 -2.28831 -0.80906 -1.719443  1.05261
## row8 -0.06623 -1.669057  0.92494  1.02285  0.575982 -0.06461

```

```

## row9  0.75463  0.596024 -1.86921  0.97715  2.122455 -0.56325
## row10 0.47967 -1.177751  0.28321 -0.61564 -1.129926  1.79942
## row11 0.63178 -0.373815  0.04090 -0.81800 -0.709860  0.07991
## row12 0.67378 -1.354297 -0.09839 -1.34885 -2.442458 -0.38932
## row13 -3.04431  0.254577 -2.21428 -0.70320 -2.306937  1.20211
## row14 -0.30342 -1.584942  0.84487  0.98682 -0.002383 -0.75783
## row15  0.86311  0.835042 -2.97650  1.28609  2.804836 -0.36456
## row16  0.60442 -0.964110 -0.26359 -1.49993  3.174251  1.18549
## row17  0.46498  0.618156  0.58847  0.15026  0.162726 -0.10825
## row18  0.81394 -1.119690 -0.07207 -0.26968 -2.788060 -0.77797
## row19 -2.77075  1.005968 -0.47312  0.02145  1.091618  0.48056
## row20 -0.45553 -1.662763  0.66237  3.05968  0.096906 -0.54614
## row21  1.02234  1.867314 -2.71759  2.80580 -0.549668 -0.51699
## row22  0.34608  0.156511 -0.33556 -0.67849 -1.615253  0.35243
## row23  0.28405  0.783592  0.95821  0.39643 -0.804511  0.42092
## row24  1.33565 -1.061082 -0.64079 -0.12060 -5.316509 -0.64302
## row25 -0.55971 -0.006254  0.46939 -1.96208 -0.964995 -1.07580
## row26  0.01830 -1.513783  0.71931  0.77932  0.265327 -0.23655
## row27  0.40808  1.282277 -1.64128  0.03989  1.334484 -0.83463
## row28  0.37897  0.354380 -0.32374  0.21877  0.432733 -0.26413
## row29  0.92409  4.680181  4.16703  4.48033 -0.351811  2.94831
## row30  1.05812 -0.896667 -0.02988 -1.09425 -1.022010 -2.52276
## row31 -1.42812  0.689193 -0.12277 -0.24389  0.384007  0.01594
## row32 -0.14991 -1.693987  0.89385  0.95120  0.191491 -0.05879
## row33  0.80533  1.022034 -2.71260  1.11141  2.690842 -0.53659
## row34  0.19001  0.251339 -0.12070 -1.20899 -1.876603  0.46121
## row35  0.49174  2.861819  3.02607  3.59647 -4.164108  1.76896
## row36  1.23195 -0.689798 -0.22319  0.35051  0.128912 -2.14819
## row37 -2.71587  1.057302 -1.15422 -0.61626  0.231418  0.03008
## row38 -0.32729 -1.485983  0.86009  0.30837  0.307584 -0.44787
## row39  0.28076  0.476911 -0.20191 -1.08242 -0.802799 -0.07814
## row40  0.34499  1.715944  2.39958  0.65230 -0.340980  1.16210
## row41  0.97919 -0.925196 -0.20365  1.16152  0.081045 -1.26536
## row42 -2.17756  1.338554  0.09762 -1.24805  0.764429  0.05379
## row43 -0.27012 -1.712056  0.97535  0.77526  0.443011 -0.05352
## row44  1.09828  0.954697 -3.77708 -1.13249  2.684427 -0.77128
## row45  0.20924 -0.210026  1.34341 -3.22416  0.631511  0.04522
## row46  0.28275  1.441965  3.19228 -0.19459  2.430683  1.56899
## row47  0.92245 -0.901607 -0.55128 -0.77293  0.874007 -0.65333
## row48 -1.42792  0.908313 -0.48685  0.44698  0.384335  0.34872
## row49 -0.02002 -1.832898  0.92859  1.30624  0.352968 -0.05425
## row50  1.01503  0.898435 -3.23009 -0.82234  1.957650 -0.88713
## row51  0.33127  0.030597  0.31750 -1.72708  0.455291 -0.13242
## row52  0.40198  1.552848  3.46976 -1.21232  2.894735  2.36774
## row53  0.83082 -1.684325  0.53337  1.46966  0.794600 -0.37659
## row54 -3.40935  1.879938 -0.22944 -1.65410 -0.799397 -0.19222
## row55 -0.05115 -1.600289  0.89217  0.65607  0.238956 -0.37738
## row56 -0.44988  0.447030  0.01173 -3.19969 -1.110610  0.26519
## row57 -0.24346  0.780408  2.63104 -1.52506  2.015678  0.81961
## row58  1.12807 -1.668277  0.36204 -0.01055 -1.678064 -0.21195
##
##
## Site constraints (linear combinations of constraining variables)
##

```

| ## | RDA1 | RDA2 | RDA3 | RDA4 | RDA5 | PC1 |
|----------|----------|----------|----------|---------|----------|----------|
| ## row1 | -0.65000 | -0.75055 | 0.15653 | 0.6292 | 1.33209 | 0.80689 |
| ## row2 | -0.54753 | -2.76358 | 2.09802 | -1.0563 | -1.57350 | 0.06049 |
| ## row3 | 0.66503 | 0.14970 | -1.56316 | 0.4513 | 0.42498 | -0.61954 |
| ## row4 | 1.22005 | -0.76667 | 0.49217 | 0.3315 | -0.81750 | -0.05932 |
| ## row5 | 1.01834 | -0.77070 | 1.48895 | -0.9261 | -0.31878 | 0.08071 |
| ## row6 | 1.15621 | -0.61854 | 0.66643 | 0.3341 | -1.06834 | -0.78772 |
| ## row7 | -1.69726 | -0.20349 | -2.15655 | -0.2491 | -1.51435 | 1.05261 |
| ## row8 | -1.37717 | -0.87285 | -0.89998 | -0.3247 | 1.16402 | -0.06461 |
| ## row9 | 0.15802 | 1.03950 | -1.61860 | 0.1697 | 0.15007 | -0.56325 |
| ## row10 | 0.63955 | -1.79198 | -3.45850 | -1.2176 | -1.78612 | 1.79942 |
| ## row11 | 0.64080 | 0.39286 | 1.03709 | -0.1746 | -0.22942 | 0.07991 |
| ## row12 | 0.30816 | -0.49323 | -0.62302 | -2.1018 | -0.66262 | -0.38932 |
| ## row13 | -1.39786 | -0.52769 | -1.41072 | -0.4644 | -0.27426 | 1.20211 |
| ## row14 | -1.36713 | 0.47936 | 0.24234 | 2.1373 | -1.07550 | -0.75783 |
| ## row15 | 0.72744 | 0.21193 | -1.25614 | 0.7576 | 0.04036 | -0.36456 |
| ## row16 | 1.06015 | -1.02549 | -0.38964 | -0.9138 | 1.21296 | 1.18549 |
| ## row17 | 0.14044 | 1.78294 | 0.47397 | 0.6649 | -0.47310 | -0.10825 |
| ## row18 | 0.18867 | 0.68257 | -0.16099 | -0.5445 | -1.45764 | -0.77797 |
| ## row19 | -1.12879 | 0.39137 | 0.28438 | 1.1261 | 0.01184 | 0.48056 |
| ## row20 | -1.28076 | -0.03401 | -0.23595 | 1.5233 | -0.10148 | -0.54614 |
| ## row21 | 0.46829 | 1.01831 | -0.85022 | 0.9863 | -0.11149 | -0.51699 |
| ## row22 | 0.74606 | -0.06915 | -0.26568 | 0.1874 | -1.01673 | 0.35243 |
| ## row23 | 0.37931 | 1.21070 | -0.16373 | 0.5002 | 0.82385 | 0.42092 |
| ## row24 | 1.09275 | -0.53783 | -0.15931 | 0.5248 | -0.65874 | -0.64302 |
| ## row25 | -2.08785 | 0.61959 | 0.89390 | -2.1726 | -0.68515 | -1.07580 |
| ## row26 | -1.00180 | -1.40620 | 0.37423 | -0.5590 | 1.42044 | -0.23655 |
| ## row27 | 0.42139 | 0.93312 | -0.61545 | 0.4353 | 0.22463 | -0.83463 |
| ## row28 | 0.59675 | 0.73795 | 0.40260 | 0.3312 | -0.06071 | -0.26413 |
| ## row29 | 0.11551 | 2.07975 | 0.20305 | 0.9701 | 0.26648 | 2.94831 |
| ## row30 | 0.13014 | 0.58374 | 0.32038 | -1.6786 | 0.06746 | -2.52276 |
| ## row31 | -0.95014 | -0.33334 | 1.03067 | 0.5295 | -1.03234 | 0.01594 |
| ## row32 | -0.54577 | -1.48883 | 0.53941 | 1.4651 | -0.22507 | -0.05879 |
| ## row33 | 0.50123 | 0.86814 | -0.95071 | 0.4540 | 1.27682 | -0.53659 |
| ## row34 | 0.41459 | -0.10646 | -0.86407 | -0.4445 | -2.13238 | 0.46121 |
| ## row35 | 0.50477 | 1.11596 | 0.87242 | 1.2353 | -2.10859 | 1.76896 |
| ## row36 | 0.81845 | 0.28973 | 0.36544 | 0.7633 | -1.09268 | -2.14819 |
| ## row37 | -1.43302 | 0.56577 | 0.29116 | 0.2485 | 0.09561 | 0.03008 |
| ## row38 | -1.07949 | -0.78158 | -0.13619 | 0.4217 | 1.55971 | -0.44787 |
| ## row39 | 0.10510 | 1.17547 | -0.24151 | -0.8351 | 1.14091 | -0.07814 |
| ## row40 | 0.52242 | 0.48167 | 1.24928 | -0.6944 | 0.12505 | 1.16210 |
| ## row41 | 0.73457 | 0.25494 | 0.70733 | -0.2331 | 0.27141 | -1.26536 |
| ## row42 | -2.00027 | 0.83527 | -0.23406 | -1.5646 | 1.35328 | 0.05379 |
| ## row43 | -0.40769 | -1.87423 | 0.81736 | 1.0080 | 0.32826 | -0.05352 |
| ## row44 | 0.71952 | -0.39567 | -0.55517 | -0.7756 | 0.39529 | -0.77128 |
| ## row45 | 0.25292 | 0.65604 | 0.59784 | -1.2433 | 0.07913 | 0.04522 |
| ## row46 | 0.69085 | 0.05078 | 1.31213 | -1.0921 | 0.94963 | 1.56899 |
| ## row47 | 0.78271 | -0.07583 | -0.75293 | -0.2442 | 1.45722 | -0.65333 |
| ## row48 | -0.93692 | -0.09313 | 0.02035 | 0.8663 | 0.92379 | 0.34872 |
| ## row49 | -0.65649 | -1.42747 | -0.07534 | 1.0186 | 1.15738 | -0.05425 |
| ## row50 | 0.34891 | 0.30446 | -0.87894 | -0.6393 | -0.14767 | -0.88713 |
| ## row51 | 0.62508 | 0.15070 | 0.28948 | -0.6872 | 0.52651 | -0.13242 |
| ## row52 | 0.97592 | -0.10272 | 1.00056 | -0.1681 | 1.09398 | 2.36774 |
| ## row53 | 1.43720 | -0.71917 | -0.32373 | 1.0824 | 0.90989 | -0.37659 |

```
## row54 -1.80820  1.09070  0.42144 -0.1394 -0.51830 -0.19222
## row55 -0.97992 -0.83162  0.60896  1.0147 -0.54566 -0.37738
## row56  0.07891  0.88485  0.30888 -1.4075  0.22265  0.26519
## row57  0.22334  1.05859  1.19542 -0.6582 -0.35368  0.81961
## row58  1.72452 -1.23446  0.07813  1.0416  1.03610 -0.21195
##
##
## Biplot scores for constraining variables
##
##           RDA1    RDA2    RDA3    RDA4    RDA5 PC1
## temperature -0.43020  0.8404 -0.3197 -0.0630 -0.05065  0
## pH           0.09972  0.1058  0.3653  0.3928 -0.83137  0
## oxygen       0.22572  0.3153  0.3833 -0.7680 -0.33595  0
## conductivity 0.39715 -0.1615 -0.8061 -0.2094 -0.35005  0
## plants      -0.87704 -0.3946  0.1208  0.2338  0.07652  0
```

```
head (summary (rda_tree_all))
```

```
##
## Call:
## rda(formula = species_2 ~ temperature + pH + oxygen + conductivity +      plants, data = env_1, scal
##
## Partitioning of correlations:
##           Inertia Proportion
## Total           47.000    1.0000
## Constrained      8.907    0.1895
## Unconstrained   38.093    0.8105
##
## Eigenvalues, and their contribution to the correlations
##
## Importance of components:
##           RDA1    RDA2    RDA3    RDA4    RDA5    PC1    PC2
## Eigenvalue      4.06679 2.25482 1.37627 0.79194 0.417482 5.0453 4.8203
## Proportion Explained 0.08653 0.04797 0.02928 0.01685 0.008883 0.1073 0.1026
## Cumulative Proportion 0.08653 0.13450 0.16378 0.18063 0.189517 0.2969 0.3994
##           PC3    PC4    PC5    PC6    PC7    PC8    PC9
## Eigenvalue      3.78471 2.83946 2.07941 1.79779 1.61889 1.40426 1.28896
## Proportion Explained 0.08053 0.06041 0.04424 0.03825 0.03444 0.02988 0.02742
## Cumulative Proportion 0.47995 0.54036 0.58461 0.62286 0.65730 0.68718 0.71460
##           PC10   PC11   PC12   PC13   PC14   PC15   PC16
## Eigenvalue      1.19207 1.09439 1.08068 0.97083 0.91273 0.85041 0.78867
## Proportion Explained 0.02536 0.02328 0.02299 0.02066 0.01942 0.01809 0.01678
## Cumulative Proportion 0.73997 0.76325 0.78624 0.80690 0.82632 0.84441 0.86119
##           PC17   PC18   PC19   PC20   PC21   PC22   PC23
## Eigenvalue      0.69918 0.61775 0.58582 0.57070 0.48347 0.46437 0.410574
## Proportion Explained 0.01488 0.01314 0.01246 0.01214 0.01029 0.00988 0.008736
## Cumulative Proportion 0.87607 0.88921 0.90168 0.91382 0.92411 0.93399 0.942723
##           PC24   PC25   PC26   PC27   PC28   PC29
## Eigenvalue      0.384870 0.33090 0.309928 0.293196 0.235722 0.204967
## Proportion Explained 0.008189 0.00704 0.006594 0.006238 0.005015 0.004361
## Cumulative Proportion 0.950911 0.95795 0.964546 0.970784 0.975800 0.980161
##           PC30   PC31   PC32   PC33   PC34   PC35
## Eigenvalue      0.191153 0.169063 0.125743 0.076653 0.072208 0.064563
## Proportion Explained 0.004067 0.003597 0.002675 0.001631 0.001536 0.001374
```

```

## Cumulative Proportion 0.984228 0.987825 0.990500 0.992131 0.993667 0.995041
##          PC36      PC37      PC38      PC39      PC40
## Eigenvalue      0.049611 0.0419889 0.0381111 0.0342656 0.0228705
## Proportion Explained 0.001056 0.0008934 0.0008109 0.0007291 0.0004866
## Cumulative Proportion 0.996097 0.9969900 0.9978009 0.9985300 0.9990166
##          PC41      PC42      PC43      PC44      PC45
## Eigenvalue      0.0163275 0.012502 0.0093315 0.0055293 1.296e-03
## Proportion Explained 0.0003474 0.000266 0.0001985 0.0001176 2.758e-05
## Cumulative Proportion 0.9993640 0.999630 0.9998285 0.9999462 1.000e+00
##          PC46      PC47
## Eigenvalue      7.940e-04 4.408e-04
## Proportion Explained 1.689e-05 9.378e-06
## Cumulative Proportion 1.000e+00 1.000e+00
##
## Accumulated constrained eigenvalues
## Importance of components:
##          RDA1      RDA2      RDA3      RDA4      RDA5
## Eigenvalue      4.0668 2.2548 1.3763 0.79194 0.41748
## Proportion Explained 0.4566 0.2531 0.1545 0.08891 0.04687
## Cumulative Proportion 0.4566 0.7097 0.8642 0.95313 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: 7.194377
##
##
## Species scores
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      PC1
## acan_speculum -0.5664 0.17423 0.01209 -0.05974 0.02718 0.05550
## acan_trilobatum 0.2238 0.20132 -0.42404 0.08570 0.11698 -0.28319
## ani_allopterum 0.3424 -0.22546 0.03302 0.03406 -0.05427 -0.49312
## arg_anceps 0.5306 -0.06815 -0.07417 -0.07660 -0.19102 -0.07696
## arg_ellongata 0.3802 -0.02874 -0.12608 -0.23941 -0.00329 -0.44326
## arg_pulla 0.2065 0.19945 -0.41675 0.09675 0.09394 -0.20055
## ....
##
##
## Site scores (weighted sums of species scores)
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      PC1
## row1 -2.34062 0.3671 -0.8649 0.3533 1.3983 0.80689
## row2 -0.06932 -1.7208 0.9605 1.1227 0.6478 0.06049
## row3 1.20432 0.5239 -3.0225 0.2203 1.8482 -0.61954
## row4 0.76929 -0.2651 -0.6331 -0.1990 0.7298 -0.05932
## row5 0.13512 -1.1361 0.7043 0.1879 0.4169 0.08071
## row6 1.62816 -1.1311 0.2206 -0.9013 -5.5435 -0.78772
## ....
##
##
## Site constraints (linear combinations of constraining variables)
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      PC1

```



```
## row1 -0.6500 -0.7506  0.1565  0.6292  1.3321  0.80689
## row2 -0.5475 -2.7636  2.0980 -1.0563 -1.5735  0.06049
## row3  0.6650  0.1497 -1.5632  0.4513  0.4250 -0.61954
## row4  1.2200 -0.7667  0.4922  0.3315 -0.8175 -0.05932
## row5  1.0183 -0.7707  1.4889 -0.9261 -0.3188  0.08071
## row6  1.1562 -0.6185  0.6664  0.3341 -1.0683 -0.78772
## ....
##
##
## Biplot scores for constraining variables
##
##           RDA1      RDA2      RDA3      RDA4      RDA5 PC1
## temperature -0.43020  0.8404 -0.3197 -0.0630 -0.05065  0
## pH           0.09972  0.1058  0.3653  0.3928 -0.83137  0
## oxygen       0.22572  0.3153  0.3833 -0.7680 -0.33595  0
## conductivity 0.39715 -0.1615 -0.8061 -0.2094 -0.35005  0
## plants      -0.87704 -0.3946  0.1208  0.2338  0.07652  0
```

8. Test for colinearity

Then, we can calculate Variance Inflation Factors (VIF) for each of the constraints (variables) from the “env” matrix (environmental matrix). If we find an environmental variable with $VIF > 10$, we’ll know that this variable presents colinearity with another or other variables. In that case, we would have to delete the variable from our initial dataset and redo all the analysis. In our example, no variable is redundant with each other (all of them have $VIF < 10$).

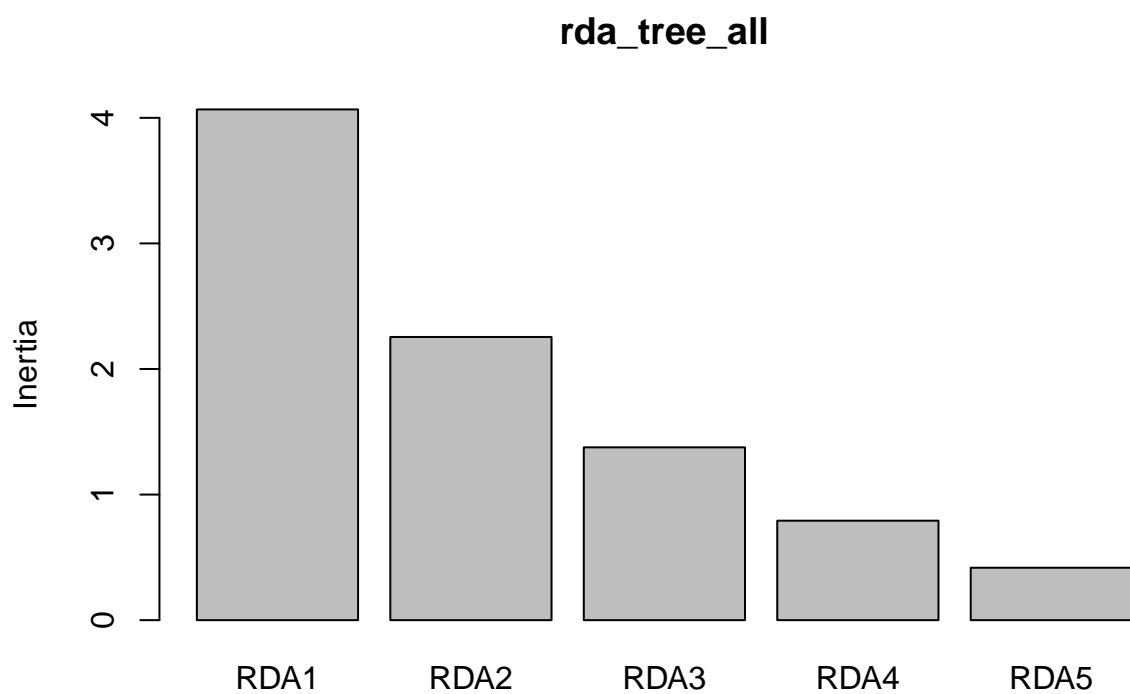
Linear dependencies can be explored by computing the variables’ variance inflation factors (VIF), which measure the proportion by which the variance of a regression coefficient is inflated in the presence of other explanatory variables. VIFs above 20 indicate strong collinearity. Ideally, VIFs above 10 should be at least examined, and avoided if possible. VIFs can be computed in *vegan* after RDA or CCA: (Bocard et al. page 175)

```
vif.cca(rda_tree_all)
```

```
## temperature      pH      oxygen conductivity      plants
##      1.020607      1.041448      1.459971      1.370939      1.781782
```

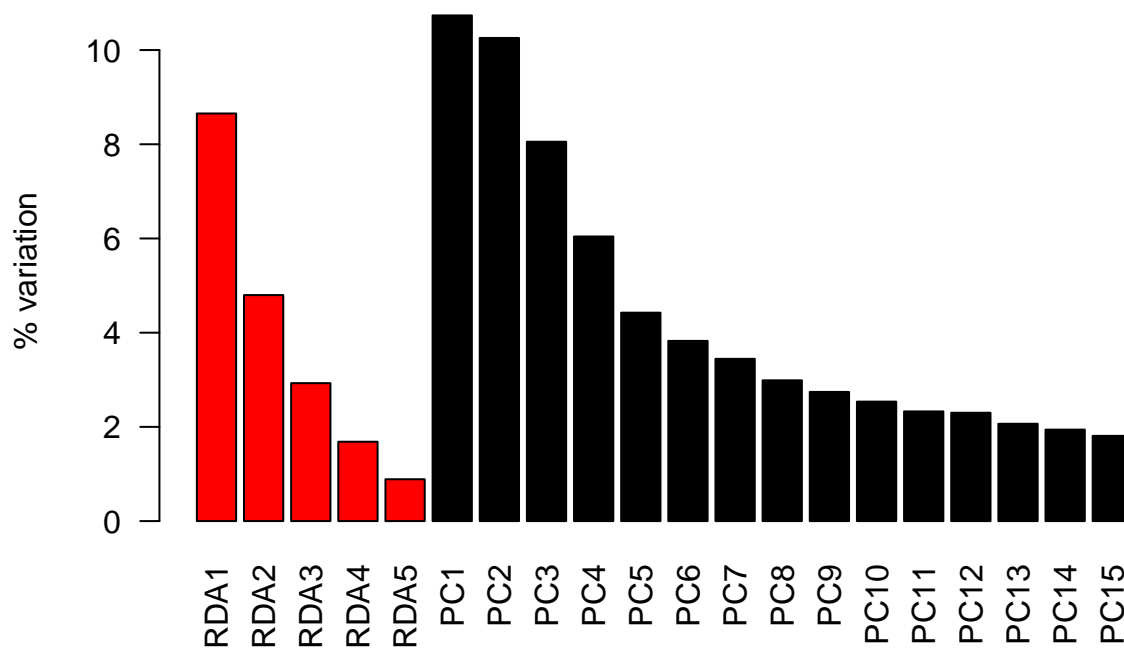
9. Plots

```
screeplot(rda_tree_all)
```



10. Percentage explained by constrained and unconstrained variables.

```
constrained_eig <- rda_tree_all$CCA$eig/rda_tree_all$tot.chi*100
unconstrained_eig <- rda_tree_all$CA$eig/rda_tree_all$tot.chi*100
expl_var <- c(constrained_eig, unconstrained_eig)
barplot (expl_var[1:20], col = c(rep ('red', length (constrained_eig)), rep ('black', length (unconstrained_eig))),
        las = 2, ylab = '% variation')
```



11. Ordination plots

Scaling 1 (distance biplot): Se prioriza que la distancia entre objetos en el gráfico respete tanto como sea posible las distancias euclídeas de la matriz original. Los ángulos entre vectores (variables) pueden ser distorsionados.

Scaling 2 (correlation biplot): Se prioriza que los ángulos entre vectores respeten la correlación original entre variables. La distancia entre objetos en el gráfico puede estar distorsionada.

En resumen, utilizaremos scaling 1 si nos interesa más ver cómo se diferencian los objetos, y scaling 2 si nos interesa más ver cómo se relacionan las distintas variables.

[https://bookdown.org/stephi_gascon/bookdown-demo-master__multivariant/__book/ordination.html](https://bookdown.org/stephi_gascon/bookdown-demo-master/__multivariant/__book/ordination.html)

#<https://fukamilab.github.io/BIO202/06-B-constrained-ordination.html>

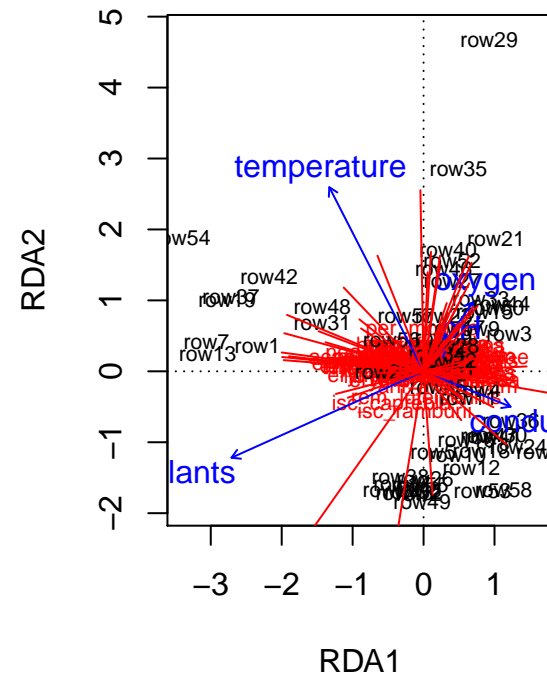
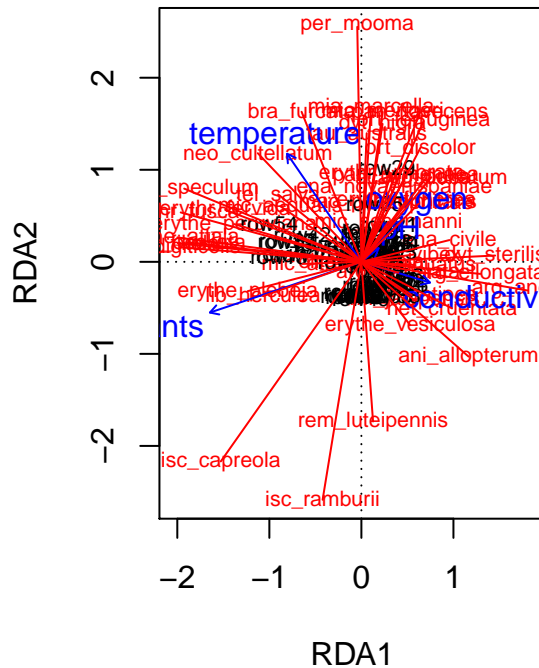
```
par(mfrow=c(1,2))

plot(rda_tree_all, scaling=1, main="Odonata in Urban ponds,, scaling=1")
spe.sc <- scores(rda_tree_all, choices=1:2, scaling=1, display="sp")
arrows(0,0,spe.sc[,1], spe.sc[,2], length=0, lty=1, col='red')

plot(rda_tree_all, scaling=2, main="Odonata in Urban ponds, scaling=2")
```

```
spe.sc <- scores(rda_tree_all, choices=1:2, scaling=1, display="sp")
arrows(0,0,spe.sc[,1], spe.sc[,2], length=0, lty=1, col='red')
```

Odonata in Urban ponds,, scaling Odonata in Urban ponds, scaling



12. Calcular las R

```
(R2 <- RsquareAdj(rda_tree_all)$r.squared)
```

```
## [1] 0.1895171
```

```
(R2adj <- RsquareAdj(rda_tree_all)$adj.r.squared)
```

```
## [1] 0.1115861
```

13a Testing the global significance of RDA

```
set.seed(1)
```

```
anova.cca(rda_tree_all, step=1000)
```

```
## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
```

```
##
## Model: rda(formula = species_2 ~ temperature + pH + oxygen + conductivity + plants, data = env_1, sc
##           Df Variance      F Pr(>F)
## Model      5      8.907 2.4319 0.001 ***
## Residual 52     38.093
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

13b Testing the significance of CCA axes (at least the first two or three should present a significant p value)
Hint Argument “step” gives the minimal number of permutations requested to assess if the F value of a test is obviously significant or not

```
set.seed(1)
```

```
anova.cca(rda_tree_all, by='axis', step=1000)
```

```
## Permutation test for rda under reduced model
## Forward tests for axes
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = species_2 ~ temperature + pH + oxygen + conductivity + plants, data = env_1, sc
##           Df Variance      F Pr(>F)
## RDA1      1      4.067 5.5515 0.001 ***
## RDA2      1      2.255 3.0780 0.005 **
## RDA3      1      1.376 1.8787 0.122
## RDA4      1      0.792 1.0811 0.699
## RDA5      1      0.417 0.5699 0.963
## Residual 52     38.093
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

13c Testing the significance of terms (environmental variables) Hint Argument “step” gives the minimal number of permutations requested to assess if the F value of a test is obviously significant or not

```
anova.cca(rda_tree_all, by='terms', step=1000)
```

```
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = species_2 ~ temperature + pH + oxygen + conductivity + plants, data = env_1, sc
##           Df Variance      F Pr(>F)
## temperature 1      2.490 3.3989 0.001 ***
## pH           1      0.654 0.8933 0.573
## oxygen       1      1.146 1.5642 0.073 .
## conductivity 1      1.631 2.2265 0.010 **
## plants       1      2.986 4.0763 0.001 ***
## Residual    52     38.093
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```