

VEGAN: AN INTRODUCTION TO ORDINATION

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CONTENTS

Vegan is a package for community ecologists. This document explains how the commonly used ordination methods can be done in **vegan**. The document only is a very basic introduction. Another document (*vegan tutorial*) (<http://cc.oulu.fi/~jarioksa/opetus/method/vegantutor.pdf>) gives a longer and more detailed introduction to ordination. The current document only describes a small part of all **vegan** functions. For most functions, the canonical references are the **vegan** help pages, and some of the most important additional functions are listed at this document.

1. ORDINATION

The **vegan** package contains all common ordination methods: Principal component analysis (function `rda`, or `prcomp` in the base R), correspondence analysis (`cca`), detrended correspondence analysis (`decorana`) and a wrapper for non-metric multidimensional scaling (`metaMDS`). Functions `rda` and `cca` mainly are designed for constrained ordination, and will be discussed later. In this chapter I describe functions `decorana` and `metaMDS`.

1.1. Detrended correspondence analysis. Detrended correspondence analysis (DCA) is done like this:

```
> library(vegan)
> data(dune)
> ord <- decorana(dune)
```

This saves ordination results in `ord`:

```
> ord
```

Call:

```
decorana(veg = dune)
```

Detrended correspondence analysis with 26 segments.
Rescaling of axes with 4 iterations.

	DCA1	DCA2	DCA3	DCA4
Eigenvalues	0.5117	0.3036	0.12125	0.14266
Decorana values	0.5360	0.2869	0.08136	0.04814
Axis lengths	3.7004	3.1166	1.30057	1.47883

Date: Id: intro-vegan.Rnw 114 2007-11-09 14:22:36Z jarioksa processed with vegan 1.8-8 in R version 2.6.0 (2007-10-03) on November 19, 2007.

The display of results is very brief: only eigenvalues and used options are listed. Actual ordination results are not shown, but you can see them with command `summary(ord)`, or extract the scores with command `scores`. The `plot` function also automatically knows how to access the scores.

1.2. Non-metric multidimensional scaling. Function `metaMDS` is a bit special case. The actual ordination is performed by function `isoMDS` of the `MASS` package. Function `metaMDS` is a wrapper to perform non-metric multidimensional scaling (NMDS) like recommended in community ordination: it uses adequate dissimilarity measures (function `vegdist`), then it runs NMDS several times with random starting configurations, compares results (function `procrustes`), and stops after finding twice a similar minimum stress solution. Finally it scales and rotates the solution, and adds species scores to the configuration as weighted averages (function `wascores`):

```
> ord <- metaMDS(dune)
Run 0 stress 12.05894
Run 1 stress 11.97273
... New best solution
... procrustes: rmse 0.01949902  max resid 0.06034508
Run 2 stress 12.04546
Run 3 stress 11.97273
... New best solution
... procrustes: rmse 1.104428e-05  max resid 2.746860e-05
*** Solution reached

> ord
Call:
metaMDS(comm = dune)
```

Nonmetric Multidimensional Scaling using `isoMDS` (`MASS` package)

```
Data:      dune
Distance: bray
```

```
Dimensions: 2
Stress:      11.97273
Two convergent solutions found after 3 tries
Scaling: centring, PC rotation, halfchange scaling
```

2. ORDINATION GRAPHICS

Ordination is nothing but a way of drawing graphs, and it is best to inspect ordinations only graphically (which also implies that they should not be taken too seriously).

All ordination results of `vegan` can be displayed with a `plot` command (Fig. ??):

```
> plot(ord)
```

Default `plot` command uses either black circles for sites and red pluses for species, or black and red text for sites and species, resp. The choices depend on the number of items in the plot and ordination method. You can override the default choice by setting `type = "p"` for points, or `type = "t"` for text. For a better control of ordination graphics you can first draw an empty plot (`type = "n"`) and then add species and sites separately using `points` or `text` functions. In this way you can

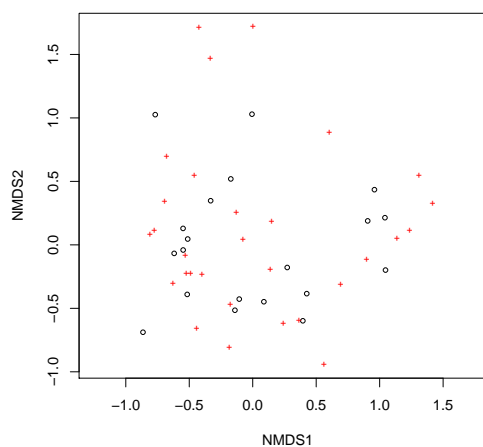


FIGURE 1. Default ordination plot.

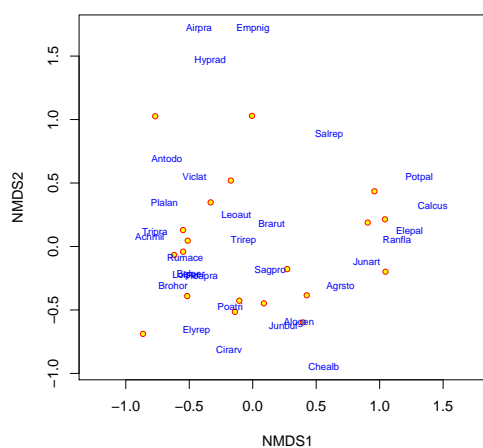


FIGURE 2. A more colourful ordination plot where sites are points, and species are text.

combine points and text, and you can select colours and character sizes freely (Fig. ??):

```
> plot(ord, type = "n")
> points(ord, display = "sites", cex = 0.8, pch = 21, col = "red",
+       bg = "yellow")
> text(ord, display = "spec", cex = 0.7, col = "blue")
```

All `vegan` ordination methods have a specific `plot` function. In addition, `vegan` has an alternative plotting function `ordiplot` that also knows many non-`vegan` ordination methods, such as `prcomp`, `cmdscale` and `isoMDS`. All `vegan` plot functions return invisibly an `ordiplot` object, so that you can use `ordiplot` support functions with the results (`points`, `text`, `identify`).

Function `ordirgl` (requires `rgl` package) provides dynamic three-dimensional graphics that can be spun around or zoomed into with your mouse. Function `ordiplot3d` (requires package `scatterplot3d`) displays simple three-dimensional scatterplots.

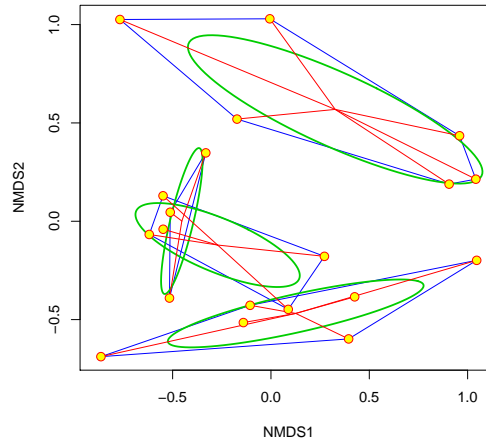


FIGURE 3. Convex hull, standard error ellipse and a spider web diagram for Management levels in ordination.

2.1. Cluttered plots. Ordination plots are often congested: there is a large number of sites and species, and it may be impossible to display all clearly. In particular, two or more species may have identical scores and are plotted over each other. **Vegan** does not have (yet?) automatic tools for clean plotting in these cases, but here some methods you can try:

- Zoom into graph setting axis limits `xlim` and `ylim`. You must typically set both, because **vegan** will maintain equal aspect ratio of axes.
- Use points and label only some of these with `identify` command.
- Use `select` argument in ordination `text` and `points` functions to only show the specified items.
- Use automatic `orditorp` function that uses text only if this can be done without overwriting previous labels, but points in other cases.

2.2. Adding items to ordination plots. **Vegan** has a group of functions for adding information about classification or grouping of points onto ordination diagrams. Function `ordihull` adds convex hulls, `ordiellipse` (which needs package `ellipse`) adds ellipses of standard deviation, standard error or confidence areas, and `ordispider` combines items to their centroid (Fig. ??):

```
> data(dune.env)
> attach(dune.env)

> plot(ord, disp = "sites", type = "n")
> ordihull(ord, Management, col = "blue")
> ordiellipse(ord, Management, col = 3, lwd = 2)
> ordispider(ord, Management, col = "red")
> points(ord, disp = "sites", pch = 21, col = "red", bg = "yellow",
+       cex = 1.3)
```

In addition, you can overlay a cluster dendrogram from `hclust` using `ordicluster` or a minimum spanning tree from `spantree` with its `lines` function. Segmented arrows can be added with `ordiarrows`, lines with `ordisegments` and regular grids with `ordigrid`.

3. FITTING ENVIRONMENTAL VARIABLES

Vegan provides two functions for fitting environmental variables onto ordination:

- `envfit` fits vectors of continuous variables and centroids of levels of class variables (defined as `factor` in R). The direction of the vector shows the direction of the gradient, and the length of the arrow is proportional to the correlation between the variable and the ordination.
- `ordisurf` (which requires package `mgcv`) fits smooth surfaces for continuous variables onto ordination using thinplate splines with cross-validators selection of smoothness.

Function `envfit` can be called with a `formula` interface, and it optionally can assess the “significance” of the variables using permutation tests:

```
> ord.fit <- envfit(ord ~ A1 + Management, data = dune.env,
+   perm = 1000)
```

```
> ord.fit
```

```
***VECTORS
```

```
      NMDS1  NMDS2    r2 Pr(>r)
A1 0.97950 0.20144 0.3689 0.017 *
```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
P values based on 1000 permutations.
```

```
***FACTORS:
```

```
Centroids:
```

```
      NMDS1  NMDS2
ManagementBF -0.4532 0.0011
ManagementHF -0.2712 -0.1209
ManagementNM 0.3267 0.5688
ManagementSF 0.1260 -0.4686
```

```
Goodness of fit:
```

```
      r2 Pr(>r)
Management 0.4206 0.006 **
```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
P values based on 1000 permutations.
```

The result can be drawn directly or added to an ordination diagram (Fig. ??):

```
> plot(ord, dis = "site")
```

```
> plot(ord.fit)
```

Function `ordisurf` directly adds a fitted surface onto ordination, but it returns the result of the fitted thinplate spline `gam` (Fig. ??):

```
> ordisurf(ord, A1, add = TRUE)
```

```
This is mgcv 1.3-27
```

```
Family: gaussian
```

```
Link function: identity
```

```
Formula:
```

```
y ~ s(x1, x2, k = knots)
```

```
Estimated degrees of freedom:
```

```
2 total = 3
```

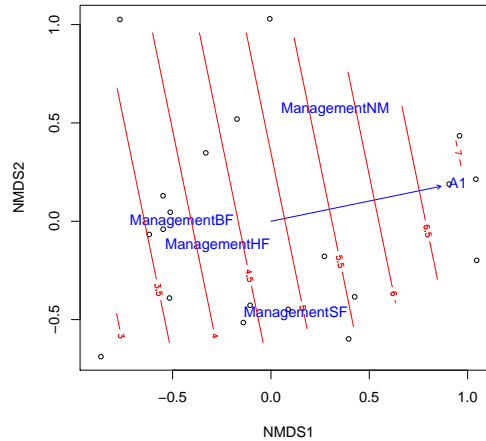


FIGURE 4. Fitted vector and smooth surface for the thickness of A1 horizon (A1, in cm), and centroids of Management levels.

GCV score: 3.941014

4. CONSTRAINED ORDINATION

`Vegan` has three methods of constrained ordination: constrained or “canonical” correspondence analysis (function `cca`), redundancy analysis (function `rda`) and constrained analysis of proximities (function `capscale`). All these functions also can have a conditioning term that is “partialled out”. I only demonstrate `cca`, but all functions accept similar commands and can be used in the same way.

The preferred way is to use `formula` interface, where the left hand side gives the community data frame and the right hand side lists the constraining variables:

```
> ord <- cca(dune ~ A1 + Management, data = dune.env)
> ord
```

Call:

```
cca(formula = dune ~ A1 + Management, data = dune.env)
```

```

              Inertia Rank
Total          2.1153
Constrained    0.7798   4
Unconstrained  1.3355  15
Inertia is mean squared contingency coefficient
```

Eigenvalues for constrained axes:

```

CCA1  CCA2  CCA3  CCA4
0.31875 0.23718 0.13217 0.09168
```

Eigenvalues for unconstrained axes:

```

CA1    CA2    CA3    CA4    CA5    CA6    CA7    CA8
0.362024 0.202884 0.152661 0.134549 0.110957 0.079982 0.076698 0.055267
CA9    CA10   CA11   CA12   CA13   CA14   CA15
0.044361 0.041528 0.031699 0.017786 0.011642 0.008736 0.004711
```

The results can be plotted with (Fig. ??):

```
> plot(ord)
```

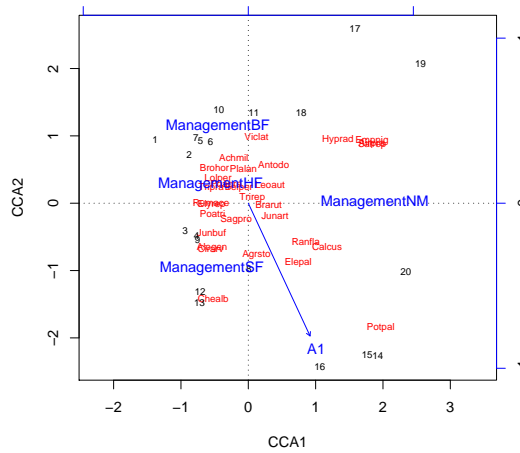


FIGURE 5. Default plot from constrained correspondence analysis.

There are three groups of items: sites, species and centroids (and biplot arrows) of environmental variables. All these can be added individually to an empty plot, and all previously explained tricks of controlling graphics still apply.

It is not recommended to perform constrained ordination with all environmental variables you happen to have: adding the number of constraints means slacker constraint, and you finally end up with solution similar to unconstrained ordination. In that case it is better to use unconstrained ordination with environmental fitting. However, if you really want to do so, it is possible with the following shortcut in formula:

```
> cca(dune ~ ., data = dune.env)
```

Call:

```
cca(formula = dune ~ A1 + Moisture + Management + Use + Manure, data = dune.env)
```

```

                Inertia Rank
Total                2.1153
Constrained          1.5032  12
Unconstrained        0.6121   7
Inertia is mean squared contingency coefficient
Some constraints were aliased because they were collinear (redundant)

```

Eigenvalues for constrained axes:

```

  CCA1  CCA2  CCA3  CCA4  CCA5  CCA6  CCA7  CCA8  CCA9
0.46713 0.34102 0.17606 0.15317 0.09528 0.07027 0.05887 0.04993 0.03183
  CCA10 CCA11 CCA12
0.02596 0.02282 0.01082

```

Eigenvalues for unconstrained axes:

```

  CA1  CA2  CA3  CA4  CA5  CA6  CA7
0.27237 0.10876 0.08975 0.06305 0.03489 0.02529 0.01798

```

4.1. **Significance tests.** *Vegan* provides permutation tests for the significance of constraints. The test mimics standard analysis of variance function (`anova`), and the default test analyses all constraints simultaneously:

```
> anova(ord)
```

Permutation test for cca under direct model

```
Model: cca(formula = dune ~ A1 + Management, data = dune.env)
      Df Chisq      F N.Perm Pr(>F)
Model   4 0.7798 2.1896   200 < 0.005 ***
Residual 15 1.3355
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The function actually used was `anova.cca`, but you do not need to give its name in full, because R automatically chooses the correct `anova` variant for the result of constrained ordination.

The `anova.cca` function tries to be clever and lazy: it automatically stops if the observed permutation significance probably differs from the targeted critical value (0.05 as default), but it will continue long in uncertain cases. You must set `step` and `perm.max` to same values to override this behaviour.

It is also possible to analyse terms separately:

```
> anova(ord, by = "term", permu = 200)
```

Permutation test for cca under direct model
Terms added sequentially (first to last)

```
Model: cca(formula = dune ~ A1 + Management, data = dune.env)
      Df Chisq      F N.Perm Pr(>F)
A1      1 0.2248 2.5245   200 0.025 *
Management 3 0.5550 2.0780   200 <0.005 ***
Residual 15 1.3355
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In this case, the function is unable to automatically select the number of iterations.

Moreover, it is possible to analyse significance of each axis:

```
> anova(ord, by = "axis", perm = 500)
```

Permutation test for cca under direct model

```
Model: cca(formula = dune ~ A1 + Management, data = dune.env)
      Df Chisq      F N.Perm Pr(>F)
CCA1   1 0.3187 3.5801   200 0.010 **
CCA2   1 0.2372 2.6640   500 0.046 *
CCA3   1 0.1322 1.4845   100 0.300
CCA4   1 0.0917 1.0297   100 0.450
Residual 15 1.3355
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Now the automatic selection works, but typically some of your axes will be very close to the critical value, and it may be useful to set a lower `perm.max` than the default 10000 (typically you use higher limits than in these examples: we used lower limits to save time when this document is automatically generated with this package).

4.2. Conditioned or partial ordination. All constrained ordination methods can have terms that are partialled out from the analysis before constraints:


```

> ord <- cca(dune ~ A1 + Management + Condition(Moisture),
+ data = dune.env)
> ord
Call:
cca(formula = dune ~ A1 + Management + Condition(Moisture), data = dune.env)

              Inertia Rank
Total              2.1153
Conditional        0.6283   3
Constrained        0.5109   4
Unconstrained     0.9761  12
Inertia is mean squared contingency coefficient

Eigenvalues for constrained axes:
  CCA1   CCA2   CCA3   CCA4
0.24932 0.12090 0.08160 0.05904

Eigenvalues for unconstrained axes:
  CA1   CA2   CA3   CA4   CA5   CA6   CA7   CA8
0.306366 0.131911 0.115157 0.109469 0.077242 0.075754 0.048714 0.037582
  CA9   CA10  CA11  CA12
0.031058 0.021024 0.012542 0.009277

This partials out the effect of Moisture before analysing the effects of A1 and
Management. This also influences the significances of the terms:
> anova(ord, by = "term", perm = 500)
Permutation test for cca under direct model
Terms added sequentially (first to last)

Model: cca(formula = dune ~ A1 + Management + Condition(Moisture), data = dune.env)
              Df  Chisq      F N.Perm Pr(>F)
A1              1 0.1154 1.4190   100  0.15
Management     3 0.3954 1.6205   100  0.01 **
Residual      12 0.9761
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
If we had a designed experiment, we may wish to restrict the permutations so that
the observations only are permuted within levels of strata:
> anova(ord, by = "term", perm = 500, strata = Moisture)
Permutation test for cca under direct model
Terms added sequentially (first to last)
Permutations stratified within `Moisture'

Model: cca(formula = dune ~ A1 + Management + Condition(Moisture), data = dune.env)
              Df  Chisq      F N.Perm Pr(>F)
A1              1 0.1154 1.4190   100  0.3
Management     3 0.3954 1.6205   100 <0.01 ***
Residual      12 0.9761
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```