

# VEGAN: AN INTRODUCTION TO ORDINATION

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**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

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 12.04546
... New best solution
... procrustes: rmse 0.003129778  max resid 0.01072834
Run 2 stress 18.23000
Run 3 stress 12.04547
... procrustes: rmse 7.29894e-05  max resid 0.0001937243
*** Solution reached
> ord
Call:
metaMDS(comm = dune)
```

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

Data: dune  
 Distance: bray

Dimensions: 2  
 Stress: 12.04546  
 Two convergent solutions found after 3 tries  
 Scaling: centring, PC rotation, halfchange scaling  
 Species: expanded scores

## 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).

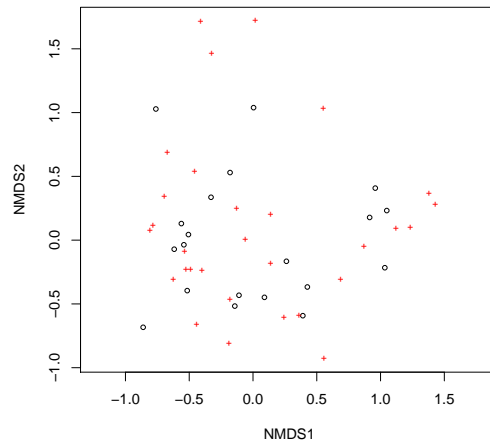


FIGURE 1. Default ordination plot.

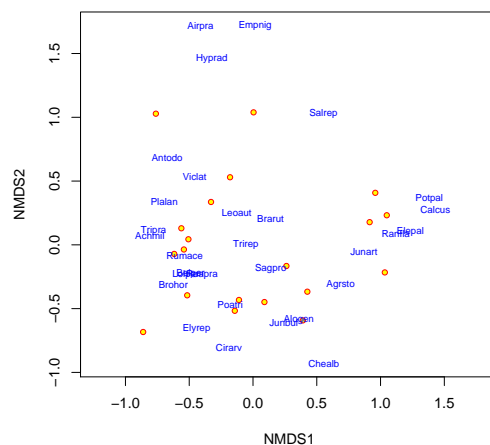


FIGURE 2. A more colourful ordination plot where sites are points, and species are text.

All ordination results of **vegan** can be displayed with a **plot** command (Fig. 1):

```
> 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 combine points and text, and you can select colours and character sizes freely (Fig. 2):

```
> 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.

**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.
- Use interactive `orditkplot` function that draws both points and labels for ordination scores, and allows you to drag labels to better positions. You can export the results of the edited graph to encapsulated postscript, pdf, png or jpeg files, or copy directly to encapsulated postscript, or return the edited positions to R for further processing.

**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. 3):

```
> 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.

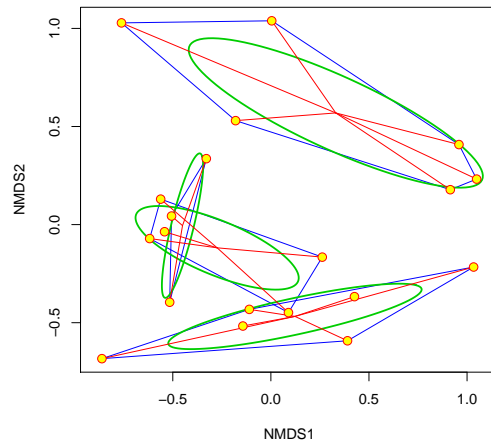


FIGURE 3. Convex hull, standard error ellipse and a spider web diagram for Management levels in ordination.

- `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	0.997182	0.075019	0.3863	0.021 *

---  
 Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
 P values based on 1000 permutations.

\*\*\*FACTORS:

Centroids:

	NMDS1	NMDS2
ManagementBF	-0.4504	-0.0052
ManagementHF	-0.2740	-0.1183
ManagementNM	0.3308	0.5692
ManagementSF	0.1227	-0.4679

Goodness of fit:

	r2	Pr(>r)
Management	0.422	0.003 **

---

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. 4):

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

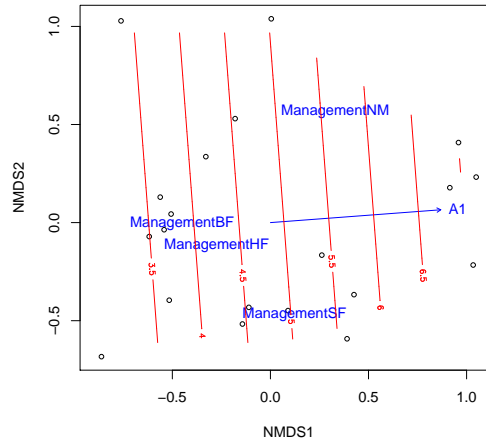


FIGURE 4. Fitted vector and smooth surface for the thickness of A1 horizon (A1, in cm), and centroids of Management levels.

Function `ordisurf` directly adds a fitted surface onto ordination, but it returns the result of the fitted thinplate spline `gam` (Fig. 4):

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

This is mgcv 1.3-29

Family: gaussian

Link function: identity

Formula:

$y \sim s(x1, x2, k = \text{knots})$

Estimated degrees of freedom:

2 total = 3

GCV score: 3.832127

#### 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

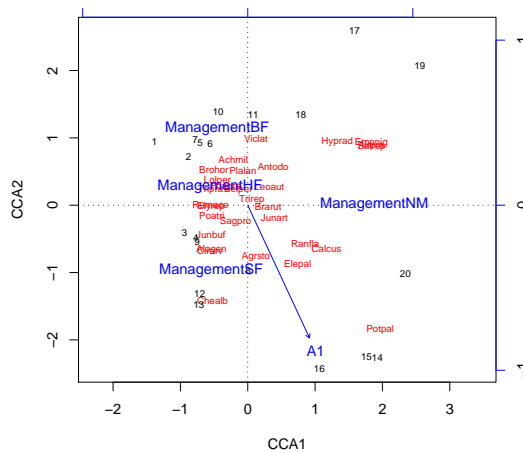


FIGURE 5. Default plot from constrained correspondence analysis.

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. 5):

```
> plot(ord)
```

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   199 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   199 0.015 *
Management 3 0.5550 2.0780   199 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. This test is sequential: the terms are analysed in the order they happen to be in the model. You can also analyse significances of marginal effects ("Type III effects"):

```
> anova(ord, by = "mar")
```

Permutation test for cca under direct model

Marginal effects of terms

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

```
      Df  Chisq      F N.Perm Pr(>F)
A1      1 0.1759 1.9761  1299 0.03385 *
Management 3 0.5550 2.0780   199 0.01000 **
Residual 15 1.3355
```



---

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

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	199	0.010 **
CCA2	1	0.2372	2.6640	499	0.048 *
CCA3	1	0.1322	1.4845	99	0.290
CCA4	1	0.0917	1.0297	99	0.460
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	99	0.16
Management	3	0.3954	1.6205	99	0.06 .
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	99	0.22
Management	3	0.3954	1.6205	99	0.01 **
Residual	12	0.9761			

```
---
```

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