COMMUNITY DATA ANALYSIS USING VEGAN

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CONSTRAINED ORDINATION

CCA is the constrained form of CA; fitted using `cca()`.

Two interfaces for specifying models

- basic; `cca1 <- cca(X = varespec, Y = varechem)`
- formula; `cca1 <- cca(varespec ~ ., data = varechem)`

Formula interface is the more powerful — *recommended*

```r
cca1 <- cca(varespec ~ ., data = varechem)
cca1
```

```
Call: cca(formula = varespec ~ N + P + K + Ca + Mg + S + Al + Fe +
Mn + Zn + Mo + Baresoil + Humdepth + pH, data = varechem)

              Inertia Proportion Rank
Total          2.0832     1.0000
Constrained    1.4415     0.6920   14
Unconstrained  0.6417     0.3080    9
Inertia is mean squared contingency coefficient

Eigenvalues for constrained axes:
  CCA1   CCA2   CCA3   CCA4   CCA5   CCA6   CCA7   CCA8   CCA9  CCA10
0.4389 0.2918 0.1628 0.1421 0.1180 0.0890 0.0703 0.0584 0.0311 0.0133
 CCA11  CCA12  CCA13  CCA14
0.0084 0.0065 0.0062 0.0047

Eigenvalues for unconstrained axes:
    CA1     CA2     CA3     CA4     CA5     CA6     CA7     CA8     CA9
0.19776 0.14193 0.10117 0.07079 0.05330 0.03330 0.01887 0.01510 0.00949
```

RDA is the constrained form of PCA; fitted using `rda()`.

```r
rda1 <- rda(varespec ~ ., data = varechem)
rda1
```

```
Call: rda(formula = varespec ~ N + P + K + Ca + Mg + S + Al + Fe +
Mn + Zn + Mo + Baresoil + Humdepth + pH, data = varechem)

                Inertia Proportion Rank
Total         1825.6594     1.0000
Constrained   1459.8891     0.7997   14
Unconstrained  365.7704     0.2003    9
Inertia is variance

Eigenvalues for constrained axes:
 RDA1  RDA2  RDA3  RDA4  RDA5  RDA6  RDA7  RDA8  RDA9 RDA10 RDA11 RDA12
820.1 399.3 102.6  47.6  26.8  24.0  19.1  10.2   4.4   2.3   1.5   0.9
RDA13 RDA14
  0.7   0.3

Eigenvalues for unconstrained axes:
   PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8    PC9
186.19  88.46  38.19  18.40  12.84  10.55   5.52   4.52   1.09
```

THE `cca.object`

- Objects of class `"cca"` are complex with many components
- Entire class described in `?cca.object`
- Depending on what analysis performed some components may be `NULL`
- Used for (C)CA, PCA, RDA, and CAP (`capscale()`)

THE `cca.object`

`cca1` has a large number of components

- **`$call`** how the function was called
- **`$grand.total`** in (C)CA sum of ‘rowsum}
- **`$rowsum`** the row sums
- **`$colsum`** the column sums
- **`$tot.chi`** total inertia, sum of Eigenvalues
- **`$pCCA`** Conditioned (partial-ed out) components
- **`$CCA`** Constrained components
- **`$CA`** Unconstrained components
- **`$method`** Ordination method used
- **`$inertia`** Description of what inertia is

THE `cca.object`

Depending on how one called `cca()` etc some of these components will be `NULL`

`$pCCA` is only filled in if a *partial* constrained ordination fitted

`rda()` returns objects with classes `"rda"` and `"cca"`, but in most cases those objects work like those of class `"cca"`

The Eigenvalues and axis scores are now spread about the `$CA` and `$CCA` components (also `$pCCA` if a *partial* CCA)

Thankfully we can use *extractor* functions to get at such things

EIGENVALUES

Use `eigenvals()` to extract Eigenvalues from a fitted ordination object

```
eigenvals(cca1)
```

```
     CCA1      CCA2      CCA3      CCA4      CCA5      CCA6      CCA7
0.4388704 0.2917753 0.1628465 0.1421302 0.1179519 0.0890291 0.0702945
     CCA8      CCA9     CCA10     CCA11     CCA12     CCA13     CCA14
0.0583592 0.0311408 0.0132944 0.0083644 0.0065385 0.0061563 0.0047332
      CA1       CA2       CA3       CA4       CA5       CA6       CA7
0.1977645 0.1419256 0.1011741 0.0707868 0.0533034 0.0332994 0.0188676
      CA8       CA9
0.0151044 0.0094876
```

`summary()` method for `eigenvals()` shows more information

```
summary(eigenvals(cca1, constrained = TRUE))
```

```
Importance of components:
                        CCA1   CCA2   CCA3   CCA4    CCA5    CCA6    CCA7
Eigenvalue            0.4389 0.2918 0.1628 0.1421 0.11795 0.08903 0.07029
Proportion Explained  0.3045 0.2024 0.1130 0.0986 0.08183 0.06176 0.04877
Cumulative Proportion 0.3045 0.5069 0.6198 0.7184 0.80027 0.86203 0.91080
                         CCA8    CCA9   CCA10    CCA11    CCA12    CCA13
Eigenvalue            0.05836 0.03114 0.01329 0.008364 0.006538 0.006156
Proportion Explained  0.04049 0.02160 0.00922 0.005800 0.004540 0.004270
Cumulative Proportion 0.95128 0.97288 0.98211 0.987910 0.992450 0.996720
                         CCA14
Eigenvalue            0.004733
Proportion Explained  0.003280
Cumulative Proportion 1.000000
```

To extract a range of scores from a fitted ordination use `scores()`

- takes an ordination object as the first argument
- `choices` — which axes? Defaults to `c(1,2)`
- `display` — which type(s) of scores to return
    - `"sites"` or `"wa"`: scores for samples in response matrix
    - `"species"`: scores for variables/columns in response
    - `"lc"`: linear combination site scores
    - `"bp"`: biplot scores (coords of arrow tip)
    - `"cn"`: centroid scores (coords of factor centroids)

EXTRACTING AXIS SCORES

```
str(scores(cca1, choices = 1:4, display = c("species","sites")), max = 1)
```

```
List of 2
 $ species: num [1:44, 1:4] 0.0753 -0.1813 -1.0535 -1.2774 -0.1526 ...
  ..- attr(*, "dimnames")=List of 2
 $ sites  : num [1:24, 1:4] 0.178 -0.97 -1.28 -1.501 -0.598 ...
  ..- attr(*, "dimnames")=List of 2
```

```
head(scores(cca1, choices = 1:2, display = "sites"))
```

```
         CCA1       CCA2
18  0.1784733 -1.0598842
15 -0.9702382 -0.1971387
24 -1.2798478  0.4764498
27 -1.5009195  0.6521559
23 -0.5980933 -0.1840362
19 -0.1102881  0.7143142
```

SCALINGS...

When we draw the results of many ordinations we display 2 or more sets of data

Can't display all of these and maintain relationships between the scores

Solution scale one set of scores relative to the other via the `scaling` argument

- `scaling = 1` — Focus on sites, scale site scores by λ_i
- `scaling = 2` — Focus on species, scale species scores by λ_i
- `scaling = 3` — Symmetric scaling, scale both scores by $\sqrt{\lambda_i}$
- `scaling = -1` — As above, but
- `scaling = -2` — For `cca()` multiply results by $\sqrt{(1/(1-\lambda_i))}$
- `scaling = -3` — this is Hill's scaling
- `scaling < 0` — For `rda()` divide species scores by species' σ
- `scaling = 0` — raw scores

```r
scores(cca1, choices = 1:2, display = "species", scaling = 3)
```

Partial constrained ordinations remove the effect of one or more variables *then* fit model of interest

Argument `Z` is used for a data frame of variables to partial out

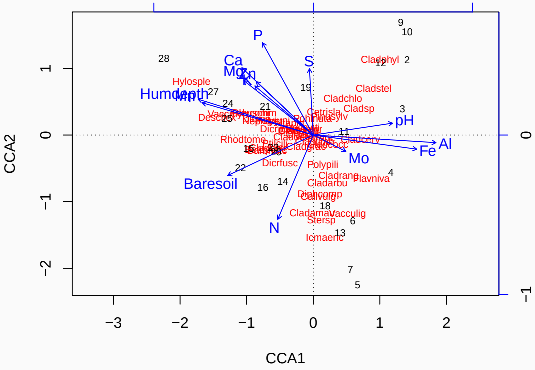
Or with the formula interface use the `Condition()` function

```
pcca <- cca(X = varespec,
            Y = varechem[, "Ca", drop = FALSE],
            Z = varechem[, "pH", drop = FALSE])
pcca <- cca(varespec ~ Ca + Condition(pH), data = varechem) ## easier!
```

TRIPLOTS

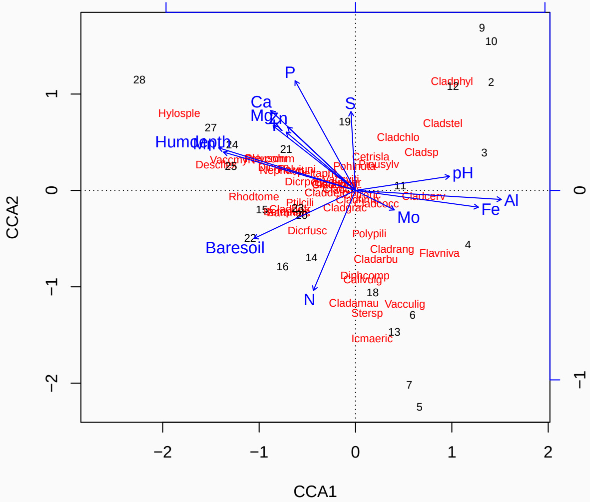
Triplots will generally produce a mess; we can really only display a couple of bits approximately anyway Trying to cram three things in is a recipe for a mess... but we can do it

```r
plot(cca1)
```



TRIPLOTS

```r
plot(cca1)
```



If we don't want to think it's easy to fit a poor model with many constraints

That's what we just did with `cca1` and `rda1`

Remember, CCA and RDA are *just regression methods* — everything you know about regression applies here

A better approach is to *think* about the important variables and include only those

The formula interface allows you to create interaction or quadratic terms easily (though be careful with latter)

It also handles factor or class constraints automatically unlike the basic interface

```r
vare.cca <- cca(varespec ~ Al + P*(K + Baresoil), data = varechem)
vare.cca
```

```

Call: cca(formula = varespec ~ Al + P * (K + Baresoil), data =
varechem)

              Inertia Proportion Rank
Total           2.083      1.000
Constrained     1.046      0.502    6
Unconstrained   1.038      0.498   17
Inertia is mean squared contingency coefficient

Eigenvalues for constrained axes:
  CCA1   CCA2   CCA3   CCA4   CCA5   CCA6
0.3756 0.2342 0.1407 0.1323 0.1068 0.0561

Eigenvalues for unconstrained axes:
    CA1     CA2     CA3     CA4     CA5     CA6     CA7     CA8
0.27577 0.15411 0.13536 0.11803 0.08887 0.05511 0.04919 0.03781
(Showed only 8 of all 17 unconstrained eigenvalues)
```

For CCA we have little choice but to do

1. Fit well-chosen set of candidate models & compare, or
2. Fit a *full* model of well-chosen variables & then do stepwise selection

But automatic approaches to model building should be used cautiously!

The standard `step()` function can be used as **vegan** provides two helper methods, `deviance()` and `extractAIC()`, used by `step()`

Vegan also provides methods for class `"cca"` for `add1()` and `drop1()`

`step()` uses AIC which is a fudge for RDA/CCA. Alternatively use function `ordistep()`

1. Define an upper and lower model scope, say the full model and the null model
2. To step from the lower scope or null model we use

```
upr <- cca(varespec ~ ., data = varechem)
lwr <- cca(varespec ~ 1, data = varechem)
set.seed(1)
mods <- ordistep(lwr, scope = formula(upr), trace = 0)
```

`trace = 0` is used her to turn off printing of progress

Permutation tests are used (more on these later); the theory for an AIC for ordination is somewhat loose

The object returned by `ordistep()` is a standard `"cca"` object with an extra component `$anova`

```
mods
```

```
Call: cca(formula = varespec ~ Al + P + K, data = varechem)

              Inertia Proportion Rank
Total          2.0832     1.0000
Constrained    0.6441     0.3092    3
Unconstrained  1.4391     0.6908   20
Inertia is mean squared contingency coefficient

Eigenvalues for constrained axes:
  CCA1   CCA2   CCA3
0.3616 0.1700 0.1126

Eigenvalues for unconstrained axes:
   CA1    CA2    CA3    CA4    CA5    CA6    CA7    CA8
0.3500 0.2201 0.1851 0.1551 0.1351 0.1003 0.0773 0.0537
(Showed only 8 of all 20 unconstrained eigenvalues)
```

STEPWISE SELECTION IN CCA

The `$anova` component contains a summary of the steps involved in automatic model building

```
mods$anova
```

```
     Df    AIC      F Pr(>F)
+ Al  1 128.61 3.6749  0.005 **
+ P   1 127.91 2.5001  0.005 **
+ K   1 127.44 2.1688  0.035 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Step-wise model selection is fairly fragile; if we start from the full model we won't end up with the same final model

```
mods2 <- ordistep(upr, scope = list(lower = formula(lwr), upper = formula(upr)), trace = 0)
```

```
mods2
```

```
Call: cca(formula = varespec ~ P + K + S + Mo + Baresoil +
Humdepth, data = varechem)

              Inertia Proportion Rank
Total          2.0832     1.0000
Constrained    0.9377     0.4501    6
Unconstrained  1.1455     0.5499   17
Inertia is mean squared contingency coefficient

Eigenvalues for constrained axes:
  CCA1   CCA2   CCA3   CCA4   CCA5   CCA6
0.3712 0.2356 0.1364 0.0974 0.0813 0.0159

Eigenvalues for unconstrained axes:
   CA1    CA2    CA3    CA4    CA5    CA6    CA7    CA8
0.3295 0.1893 0.1548 0.1269 0.0968 0.0616 0.0464 0.0337
(Showed only 8 of all 17 unconstrained eigenvalues)
```

ADJUSTED r^2 FOR *LINEAR* MODELS

As with ordinary R^2, that of an RDA is biased for the same reasons as for a linear regression

- adding a variable to constraints will increase R^2
- the larger the number of constraints in the model the larger R^2 is due to random correlations

Can attempt to account for this bias via an *adjusted* R^2 measure

$$R^2_{adj} = 1 - \frac{n-1}{n-m-1}(1-R^2)$$

- n is number of samples m is number of constraints (model degrees of freedom)
- Can be used up to $\sim M > n/2$ before becomes too conservative
- Can be negative
- Compute using `RsquareAdj()`

STEPWISE SELECTION VIA ADJUSTED r^2

The problems with stepwise selection in regression models are myriad. Affects RDA, CCA, etc as well

Blanchet, Legendre, and Borcard (2008) proposed a two-step solution for models where R^2_{adj} makes sense

- *Global test* of all constraints
    - Proceed **only** if this test is significant
    - Helps prevent inflation of overall type I error
- Proceed with forward selection, but with *two* stopping rules
    - Usual significance threshold α
    - The global R^2_{adj}
    - Stop if next candidate model is non-significant or if R^2_{adj} exceeds the global R^2_{adj}

Available in `ordiR2step()`

PERMUTATION TESTS

RDA has lots of theory behind it, CCA not as much. However, ecological/environmental data invariably violate what little theory we have

Instead we use permutation tests to assess the *importance* of fitted models — the data are shuffled in some way and the model refitted to derive a Null distribution under some hypothesis of *no effect*

What *is* shuffled and *how* is of **paramount** importance for the test to be valid

- No conditioning (partial) variables then rows of the species data are permuted
- With conditioning variables, two options are available, both of which *permute residuals* from model fits
    - The *full model* uses residuals from model $Y = X + Z + \varepsilon$
    - The *reduced model* uses residuals from model $Y = X + Z + \varepsilon$
- In **vegan** which is used can be set via argument `model` with `"direct"`, ~~`"full"`~~, and `"reduced"` respectively
- In current **vegan** option `method = "full"` is disabled

A test statistic is required, computed for observed model & each permuted model

vegan uses a pseudo-F statistic

$$F = \frac{\chi^2_{model} / df_{model}}{\chi^2_{resid} / df_{resid}}$$

Evaluate whether F is unusually large relative to the null (permutation) distribution of F

PERMUTATION TESTS IN VEGAN: `anova()`

- The main user function is the **`anova()`** method
- It is an interface to the lower-level function **`permutest.cca()`**
- At its most simplest, the **`anova()`** method tests whether the "model" as a whole is significant

$$F = \frac{1.4415/14}{0.6417/9} = 1.4441$$

```r
set.seed(42)
(perm <- anova(cca1, permutations = 499))
```

```
Permutation test for cca under reduced model
Permutation: free
Number of permutations: 499

Model: cca(formula = varespec ~ N + P + K + Ca + Mg + S + Al + Fe + Mn + Zn + Mo + Baresoil + Humdepth + pH, data = varechem)
         Df ChiSquare      F Pr(>F)
Model    14   1.44148 1.4441  0.048 *
Residual  9   0.64171
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

PERMUTATION TESTS IN VEGAN: `anova()`

`anova.cca()` has a number of arguments

```
function (object, ..., permutations = how(nperm = 999), by = NULL,
    model = c("reduced", "direct", "full"), parallel = getOption("mc.cores"),
    strata = NULL, cutoff = 1, scope = NULL)
NULL
```

- `permutations` controls the permutation test; one of
    1. a number of (unrestricted) permutations to do
    2. a matrix of pre-generated permutations
    3. an object returned by `how()`
- `by` determines what is tested; the default is to test the model
- More direct control can be achieved via `permutest.cca()`
- `parallel` allows for running the permutations on multiple CPU cores

A number of types of test can be envisaged

- Testing the overall significance of the model
- Testing constrained (canonical) axes
- Testing individual model terms *sequentially*
- The *marginal* effect of a single variable

The first is the default in `anova()`

The other three can be selected via the argument `by`

PERMUTATION TESTS | TESTING CANONICAL AXES

- The constrained (canonical) axes can be individually tests by specifying `by = "axis"`
- The first axis is tested in terms of variance explained compared to residual variance
- The second axis is tested after partialling out the first axis… and so on

```
set.seed(1)
anova(mods, by = "axis", permutations = 499)
```

```
Permutation test for cca under reduced model
Marginal tests for axes
Permutation: free
Number of permutations: 499

Model: cca(formula = varespec ~ Al + P + K, data = varechem)
         Df ChiSquare      F Pr(>F)
CCA1      1   0.36156 5.0249  0.002 **
CCA2      1   0.16996 2.3621  0.014 *
CCA3      1   0.11262 1.5651  0.114
Residual 20   1.43906
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- The individual terms in the model can be tested using `by = "terms"`
- The terms are assessed in the order they were specified in the model, sequentially from first to last
- Test is of the additional variance explained by adding the kth variable to the model
- **Ordering of the terms** will affect the results

```
set.seed(5)
anova(mods, by = "terms", permutations = 499)
```

```
Permutation test for cca under reduced model
Terms added sequentially (first to last)
Permutation: free
Number of permutations: 499

Model: cca(formula = varespec ~ Al + P + K, data = varechem)
         Df ChiSquare      F Pr(>F)
Al        1   0.29817 4.1440  0.002 **
P         1   0.18991 2.6393  0.012 *
K         1   0.15605 2.1688  0.030 *
Residual 20   1.43906
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- The marginal *effect* of a model term can be assessed using `by = "margin"`
- The marginal *effect* is the effect of a particular term when all other model terms are included in the model

```
set.seed(10)
anova(mods, by = "margin", permutations = 499)
```

```
Permutation test for cca under reduced model
Marginal effects of terms
Permutation: free
Number of permutations: 499

Model: cca(formula = varespec ~ Al + P + K, data = varechem)
         Df ChiSquare      F Pr(>F)
Al        1   0.31184 4.3340  0.002 **
P         1   0.16810 2.3362  0.014 *
K         1   0.15605 2.1688  0.032 *
Residual 20   1.43906
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Example & data taken from Leps & Smilauer, Case Study 2

Spring fen meadow vegetation in westernmost Carpathian mountains

```r
## load vegan
library("vegan")

## load the data
spp <- read.csv("data/meadow-spp.csv", header = TRUE, row.names = 1)
env <- read.csv("data/meadow-env.csv", header = TRUE, row.names = 1)
```

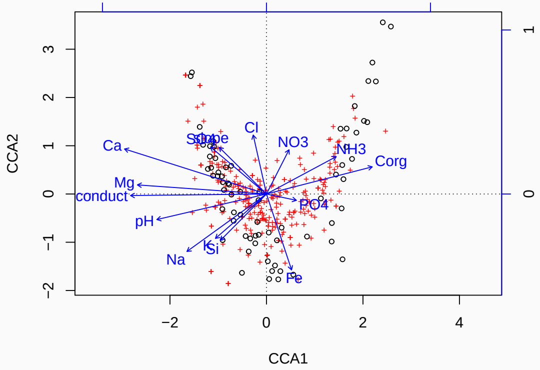
CCA a reasonable starting point as the gradient is long here (check with `decorana()` if you want)

```
m1 <- cca(spp ~ ., data = env)
set.seed(32)
anova(m1, permutations = 499)
```

```
Permutation test for cca under reduced model
Permutation: free
Number of permutations: 499

Model: cca(formula = spp ~ Ca + Mg + Fe + K + Na + Si + SO4 + PO4 + NO3 + NH3 + Cl + Corg + pH + conduct + slope,
         Df ChiSquare     F Pr(>F)
Model    15    1.5597 1.497  0.002 **
Residual 54    3.7509
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
plot(m1)
```


CCA2
CCA1
−2
0
2
4
3
2
1
0
−1
−2
1
0
Ca
Mg
conduct
pH
Na
K
Si
SO4
Slope
Cl
NO3
NH3
Corg
PO4
Fe

```r
set.seed(67)
lwr <- cca(spp ~ 1, data = env)
m2 <- ordistep(lwr, scope = formula(m1), trace = FALSE, permutations = 99)
```

```r
m2
```

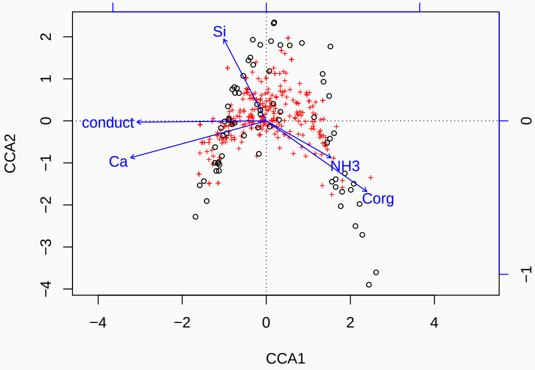
```
Call: cca(formula = spp ~ Ca + conduct + Corg + NH3 + Si, data =
env)

              Inertia Proportion Rank
Total          5.3107     1.0000
Constrained    0.8034     0.1513    5
Unconstrained  4.5073     0.8487   64
Inertia is mean squared contingency coefficient

Eigenvalues for constrained axes:
  CCA1   CCA2   CCA3   CCA4   CCA5
0.4221 0.1195 0.1036 0.0807 0.0775

Eigenvalues for unconstrained axes:
    CA1     CA2     CA3     CA4     CA5     CA6     CA7     CA8
0.29763 0.19604 0.17163 0.15357 0.14613 0.14229 0.13519 0.12476
(Showed only 8 of all 64 unconstrained eigenvalues)
```

```
plot(m2)
```



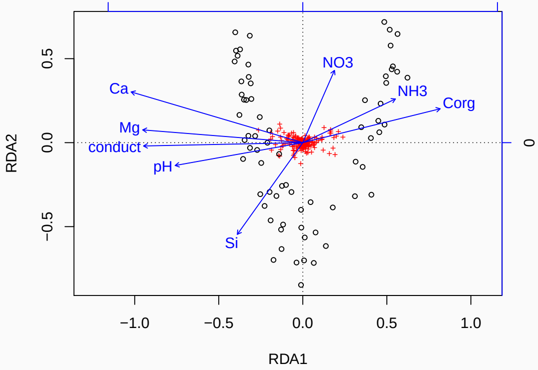
```r
m2$anova
```

```
          Df    AIC      F Pr(>F)   
+ Ca       1 453.14 4.7893   0.01 **
+ conduct  1 453.29 1.7915   0.01 **
+ Corg     1 453.61 1.6011   0.01 **
+ NH3      1 453.96 1.5533   0.01 **
+ Si       1 454.42 1.4231   0.01 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Alternative is RDA with a transformation

```
spph <- decostand(spp, method = "hellinger")
m3 <- rda(spph ~ ., data = env)
lwr <- rda(spph ~ 1, data = env)
m4 <- ordistep(lwr, scope = formula(m3), trace = FALSE, permutations = 99)
```

```r
plot(m4)
```



Stepwise using R^2_{adj}

```r
m5 <- ordiR2step(lwr, scope = formula(m3), trace = FALSE, permutations = 99)
m5$anova
```

```
                 R2.adj Df     AIC       F Pr(>F)   
+ Ca            0.12588  1 -41.779 10.9370   0.01 **
+ NH3           0.14628  1 -42.468  2.6242   0.01 **
+ conduct       0.16322  1 -42.925  2.3570   0.01 **
+ Si            0.17711  1 -43.164  2.1136   0.01 **
+ Corg          0.18518  1 -42.940  1.6442   0.01 **
+ NO3           0.19257  1 -42.680  1.5853   0.02 * 
+ pH            0.19966  1 -42.417  1.5583   0.01 **
<All variables> 0.20332                             
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

vegan provides a series of diagnostics to help assess the model fit

- `goodness()`
- `inertcomp()`
- `spenvcor()`
- `intersetcor()`
- `vif.caa()`

RESTRICTED PERMUTATION TESTS

RESTRICTED PERMUTATION TESTS

What *is* shuffled and *how* is of **paramount** importance for the test to be valid

Complete randomisation (default in **vegan**) assumes a null hypothesis where all observations are *independent*

Ecological / environmental data often aren't independent

- Temporal or spatial correlation
- Clustering, repeated measures
- Nested sampling designs (Split-plots designs)
- Blocks
- ...

Permutation *must* give null distribution of the test statistic whilst preserving the *dependence* between observations

Trick is to shuffle the data whilst preserving that dependence

Canoco has had restricted permutations for a *long* time. **vegan** has only recently caught up & we're not (quite) there yet

vegan used to only know how to completely randomise data or completely randomise within blocks (via `strata` in **vegan**)

The newish package **permute** grew out of initial code in the **vegan** repository to generate the sorts of restricted permutations available in Canoco

We have now fully integrated **permute** into **vegan**…

vegan depends on **permute** so it will already be installed & loaded when using **vegan**

permute follows Canoco closely — at the chiding of Cajo ter Braak when it didn't do what he wanted!

Samples can be thought of as belonging to three levels of a hierarchy

- the *sample* level; how are individual samples permuted
- the *plot* level; how are samples grouped at an intermediate level
- the *block* level; how are samples grouped at the outermost level

Blocks define groups of plots, each of which can contain groups of samples

Blocks are *never* permuted; if defined, only plots or samples *within* the blocks get shuffled & samples are **never** swapped between blocks

Plots or samples within plots, or both can be permuted following one of four simple permutation types

1. Free permutation (randomisation)
2. Time series or linear transect, equal spacing
3. Spatial grid designs, equal regular spacing
4. Permutation of plots (groups of samples)
5. Fixed (no permutation)

Multiple plots per block, multiple samples per plot; plots could be arranged in a spatial grid and samples within each of the plots form a time series

Blocks are a random factor that does not interact with factors that vary within blocks

Blocks form groups of samples that are never permuted between blocks, only within blocks

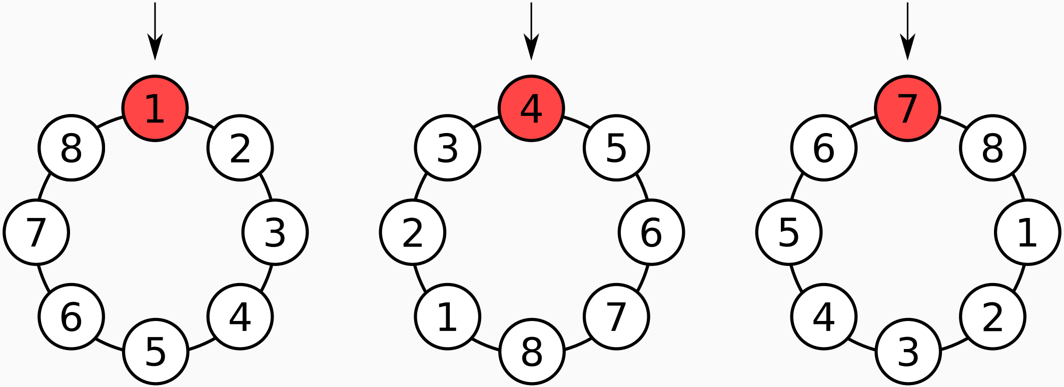
Using blocks you can achieve what the `strata` argument used to in **vegan**; needs to be a factor variable

The variation *between* blocks should be excluded from the test; **permute** doesn't do this for you!

Use `+ Condition(blocks)` in the model formula where `blocks` is a factor containing the block membership for each observation

Can *randomly* link starting point of one series to any time point of another series if series are stationary under null hypothesis that the series are unrelated

Achieve this via cyclic shift permutations — wrap series into a circle by joining start and end points



Works OK if there are no trends or cyclic pattern — autocorrelation structure only broken at the end points *if* series are stationary

Can detrend to make series stationary but not if you want to test significance of a trend

```
shuffle(10, control = how(within = Within(type = "series")))
```

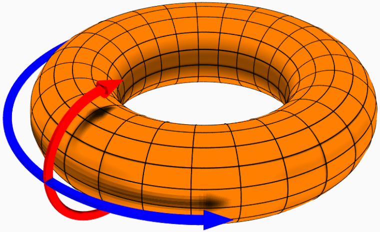
```
 [1] 10  1  2  3  4  5  6  7  8  9
```

The trick of cyclic shifts can be extended to two dimensions for a regular spatial grid arrangement of points

Now shifts are *toroidal* as we join the end point in the *x* direction together and in the *y* direction together

```
matrix(perm, ncol = 3)
```

```
     [,1] [,2] [,3]
[1,]    6    9    3
[2,]    4    7    1
[3,]    5    8    2
```



Source: Dave Burke, Wikimedia

Split-plot designs are hierarchical with two levels of units

1. **whole-plots** , which contain
2. **split-plots** (the samples)

Can permute one or both of these but whole-plots must be of equal size

Essentially allows more than one error stratum to be analyzed

Test effect of constraints that vary *between* whole plots by permuting the whole-plots whilst retaining order of split-splots (samples) within the whole-plots

Test effect of constraints that vary *within* whole-plots by permuting the split-plots within whole-plots without permuting the whole-plots

Whole-plots or split-plots can be time series, linear transects or rectangular grids in which case the appropriate restricted permutation is used

If the split-plots are parallel time series & `time` is an autocorrelated error component affecting all series then the same cyclic shift can be applied to each time series (within each whole-plot) (`constant = TRUE`)

(Without wanting to get *too* technical) Mirroring in restricted permutations allows for isotropy in dependencies by reflecting the ordering of samples in time or spatial dimensions

For a linear transect, technically the autocorrelation at lag *h* is equal to that at lag -*h* (also in a trend-free time series)

Hence the series `(1, 2, 3, 4)` and `(4, 3, 2, 1)` are equivalent fom this point of view & we can draw permutations from either version

Similar argument can be made for spatial grids

Using `mirror = TRUE` then can double (time series, linear transects) or quadruple (spatial grids) the size of the set of permutations

Using restricted permutations can severely reduce the size of the set of allowed permutations

As the minimum *p* value obtainable is $1/np$ where np is number of allowed permutations (including the observed) this can impact the ability to detect signal/pattern

If we don't want mirroring

- in a time series of 20 samples the minimum *p* is 1/20 (0.05)
- in a time series of 100 samples the minimum *p* is 1/100 (0.01)
- in a data set with 10 time series each of 20 observations (200 total), if we assume an autocorrelated error component over all series (`constant = TRUE`) then there are only 20 permutations of the data and minimum *p* is 0.05

When the set of permutations is small it is better to switch to an exact test & evaluate all permutations in the set rather than randomly sample from the set

In `permute`, we set up a permutation scheme with `how()`

We sample from the permutation scheme with

- `shuffle()`, which gives a single draw from scheme, or
- `shuffleSet()`, which returns a set of `n` draws from the scheme

`allPerms()` can generated the entire set of permutations — **note** this was designed for small sets of permutations & is slow if you request it for a scheme with many thousands of permutations!

`how()` has three main arguments

1. `within` — takes input from helper `Within()`
2. `plots` — takes input from helper `Plots()`
3. `blocks` — takes a factor variable as input

```
plt <- gl(3, 10)
h <- how(within = Within(type = "series"), plots = Plots(strata = plt))
```

Helper functions make it easy to change one or a few aspects of permutation scheme, rest left at defaults

```r
args(Within)
```

```
function (type = c("free", "series", "grid", "none"), constant = FALSE,
    mirror = FALSE, ncol = NULL, nrow = NULL)
NULL
```

```r
args(Plots)
```

```
function (strata = NULL, type = c("none", "free", "series", "grid"),
    mirror = FALSE, ncol = NULL, nrow = NULL)
NULL
```

`how()` has additional arguments, many of which control the heuristics that kick in to stop you shooting yourself in the foot and demanding 9999 permutations when there are only 10

- `complete` should we enumerate the entire set of permutations?
- `minperm` lower bound on the size of the set of permutations at & below which we turn on complete enumeration

```r
args(how)
```

```
function (within = Within(), plots = Plots(), blocks = NULL,
    nperm = 199, complete = FALSE, maxperm = 9999, minperm = 5040,
    all.perms = NULL, make = TRUE, observed = FALSE)
NULL
```

Time series within 3 plots, 10 observation each

```
plt <- gl(3, 10)
h <- how(within = Within(type = "series"),
         plots = Plots(strata = plt))
set.seed(4)
p <- shuffle(30, control = h)
do.call("rbind", split(p, plt)) ## look at perms in context
```

```
  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
1    7    8    9   10    1    2    3    4    5     6
2   12   13   14   15   16   17   18   19   20    11
3   24   25   26   27   28   29   30   21   22    23
```

Time series within 3 plots, 10 observation each, same permutation within each

```
plt <- gl(3, 10)
h <- how(within = Within(type = "series", constant = TRUE),
         plots = Plots(strata = plt))
set.seed(4)
p <- shuffle(30, control = h)
do.call("rbind", split(p, plt)) ## look at perms in context
```

```
  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
1    7    8    9   10    1    2    3    4    5     6
2   17   18   19   20   11   12   13   14   15    16
3   27   28   29   30   21   22   23   24   25    26
```

Now we've seen how to drive **permute**, we can use the same **how( )** commands to set up permutation designs within **vegan** functions

```
## Analyse the Ohraz data Case study 5 of Leps & Smilauer

## load vegan
library("vegan")

## load the data
spp <- read.csv("data/ohraz-spp.csv", header = TRUE, row.names = 1)
env <- read.csv("data/ohraz-env.csv", header = TRUE, row.names = 1)
molinia <- spp[, 1]
spp <- spp[, -1]

## Year as numeric
env <- transform(env, year = as.numeric(as.character(year)))
```

```r
c1 <- rda(spp ~ year + year:mowing + year:fertilizer + year:removal + Condition(plotid), data = env)
(h <- how(nperm = 499, within = Within(type = "none"),
          plots = with(env, Plots(strata = plotid, type = "free"))))
```

```
Permutation Design:

Blocks:
  Defined by: none

Plots:
  Plots: plotid
  Permutation type: free
  Mirrored?: No

Within Plots:
  Permutation type: none

Permutation details:
  Number of permutations: 499
  Max. number of permutations allowed: 9999
  Evaluate all permutations?: No.  Activation limit: 5040
```

```r
set.seed(23)
anova(c1, permutations = h, model = "reduced")
```

```
Permutation test for rda under reduced model
Plots: plotid, plot permutation: free
Permutation: none
Number of permutations: 499

Model: rda(formula = spp ~ year + year:mowing + year:fertilizer + year:removal + Condition(plotid), data =
         Df Variance      F Pr(>F)
Model     4   158.85 6.4247  0.002 **
Residual 90   556.30
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
set.seed(24)
anova(c1, permutations = h, model = "reduced", by = "axis")
```

```
Permutation test for rda under reduced model
Marginal tests for axes
Plots: plotid, plot permutation: free
Permutation: none
Number of permutations: 499

Model: rda(formula = spp ~ year + year:mowing + year:fertilizer + year:removal + Condition(plotid), data =
         Df Variance       F Pr(>F)
RDA1      1    89.12 14.4173  0.002 **
RDA2      1    34.28  5.5458  0.004 **
RDA3      1    26.52  4.2900  0.004 **
RDA4      1     8.94  1.4458  0.640
Residual 90   556.30
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Variation in communities may exist at various scales, sometimes hierarchically

A firt step in understanding this variation is to test for its exisistence

In this example from Leps & Smilauer (2014) uses crayfish data from Spring River, Arkansas/Missouri, USA, collected by Dr.~Camille Flinders.

567 records of 5 species (each sub-divided into *Large* & *Small* individuals

```r
## load data
crayfish <- head(read.csv("data/crayfish-spp.csv")[, -1], -1)
design <- read.csv("data/crayfish-design.csv", skip = 1)[, -1]

## fixup the names
names(crayfish) <- gsub("\\.", "", names(crayfish))
names(design) <- c("Watershed", "Stream", "Reach", "Run",
                   "Stream.Nested", "ReachNested", "Run.Nested")
```

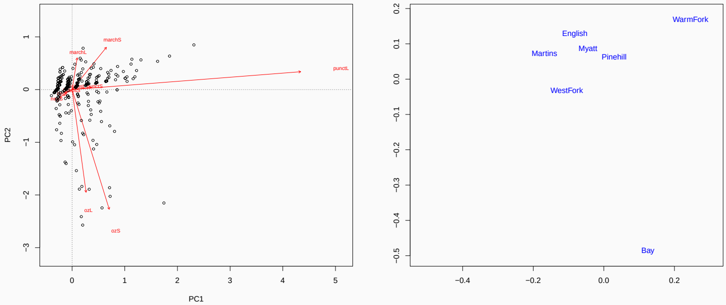
Number of samples have 0 crayfish, which excludes unimodal methods

```r
m.pca <- rda(crayfish)
summary(eigenvals(m.pca))
```

```
Importance of components:
                         PC1    PC2    PC3    PC4     PC5     PC6     PC7
Eigenvalue            3.5728 1.8007 1.1974 0.9012 0.79337 0.38886 0.28132
Proportion Explained  0.3818 0.1924 0.1280 0.0963 0.08478 0.04155 0.03006
Cumulative Proportion 0.3818 0.5742 0.7022 0.7985 0.88325 0.92480 0.95486
                          PC8     PC9     PC10
Eigenvalue            0.21225 0.20528 0.004881
Proportion Explained  0.02268 0.02194 0.000520
Cumulative Proportion 0.97754 0.99948 1.000000
```

HIERARCHICAL ANALYSIS OF CRAYFISH — UNCONSTRAINED

```r
layout(matrix(1:2, ncol = 2))
biplot(m.pca, type = c("text", "points"), scaling = "species")
set.seed(23)
ev.pca <- envfit(m.pca ~ Watershed, data = design, scaling = "species")
plot(ev.pca, labels = levels(design$Watershed), add = FALSE)
layout(1)
```



HIERARCHICAL ANALYSIS OF CRAYFISH — WATERSHED SCALE

```r
m.ws <- rda(crayfish ~ Watershed, data = design)
m.ws
```

```
Call: rda(formula = crayfish ~ Watershed, data = design)

              Inertia Proportion Rank
Total          9.3580     1.0000     
Constrained    1.7669     0.1888    6
Unconstrained  7.5911     0.8112   10
Inertia is variance 

Eigenvalues for constrained axes:
  RDA1   RDA2   RDA3   RDA4   RDA5   RDA6 
0.7011 0.5540 0.3660 0.1064 0.0381 0.0013 

Eigenvalues for unconstrained axes:
   PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8    PC9   PC10 
3.0957 1.2109 0.9717 0.7219 0.5333 0.3838 0.2772 0.2040 0.1879 0.0048 
```

HIERARCHICAL ANALYSIS OF CRAYFISH — WATERSHED SCALE

```r
summary(eigenvals(m.ws, constrained = TRUE))
```

```
Importance of components:
                        RDA1   RDA2   RDA3   RDA4    RDA5     RDA6
Eigenvalue            0.7011 0.5540 0.3660 0.1064 0.03814 0.001279
Proportion Explained  0.3968 0.3135 0.2072 0.0602 0.02159 0.000720
Cumulative Proportion 0.3968 0.7103 0.9175 0.9777 0.99928 1.000000
```

```r
set.seed(1)
ctrl <- how(nperm = 499,
            within = Within(type = "none"),
            plots = with(design, Plots(strata = Stream, type = "free")))
(sig.ws <- anova(m.ws, permutations = ctrl))
```

```
Permutation test for rda under reduced model
Plots: Stream, plot permutation: free
Permutation: none
Number of permutations: 499

Model: rda(formula = crayfish ~ Watershed, data = design)
          Df Variance      F Pr(>F)
Model      6   1.7669 21.724  0.002 **
Residual 560   7.5911
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
m.str <- rda(crayfish ~ Stream + Condition(Watershed), data = design)
m.str
```

```
Call: rda(formula = crayfish ~ Stream + Condition(Watershed), data
= design)

              Inertia Proportion Rank
Total          9.3580     1.0000     
Conditional    1.7669     0.1888    6
Constrained    1.1478     0.1227   10
Unconstrained  6.4433     0.6885   10
Inertia is variance 
Some constraints were aliased because they were collinear (redundant)

Eigenvalues for constrained axes:
  RDA1   RDA2   RDA3   RDA4   RDA5   RDA6   RDA7   RDA8   RDA9  RDA10 
0.4928 0.2990 0.2058 0.0782 0.0372 0.0224 0.0063 0.0030 0.0029 0.0002 

Eigenvalues for unconstrained axes:
   PC1    PC2    PC3    PC4    PC5    PC6    PC7    PC8    PC9   PC10 
2.7853 0.8528 0.7737 0.6317 0.5144 0.2808 0.2517 0.1923 0.1559 0.0046 
```

HIERARCHICAL ANALYSIS OF CRAYFISH — STREAM SCALE

```r
summary(eigenvals(m.str, constrained = TRUE))
```

```
Importance of components:
                        RDA1   RDA2   RDA3    RDA4    RDA5    RDA6
Eigenvalue            0.4928 0.2990 0.2058 0.07824 0.03719 0.02235
Proportion Explained  0.4293 0.2605 0.1793 0.06816 0.03240 0.01947
Cumulative Proportion 0.4293 0.6898 0.8691 0.93731 0.96971 0.98918
                          RDA7     RDA8     RDA9     RDA10
Eigenvalue            0.006326 0.003042 0.002894 0.0001546
Proportion Explained  0.005510 0.002650 0.002520 0.0001300
Cumulative Proportion 0.994690 0.997340 0.999870 1.0000000
```

```r
set.seed(1)
ctrl <- how(nperm = 499,
            within = Within(type = "none"),
            plots = with(design, Plots(strata = Reach, type = "free")),
            blocks = with(design, Watershed))
(sig.str <- anova(m.str, permutations = ctrl))
```

```
Permutation test for rda under reduced model
Blocks:  with(design, Watershed)
Plots: Reach, plot permutation: free
Permutation: none
Number of permutations: 499

Model: rda(formula = crayfish ~ Stream + Condition(Watershed), data = design)
          Df Variance      F Pr(>F)
Model     14   1.1478 6.9477  0.004 **
Residual 546   6.4433
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
m.re <- rda(crayfish ~ Reach + Condition(Stream), data = design)
m.re
```

```
Call: rda(formula = crayfish ~ Reach + Condition(Stream), data =
design)

              Inertia Proportion Rank
Total          9.3580     1.0000
Conditional    2.9148     0.3115   20
Constrained    1.4829     0.1585   10
Unconstrained  4.9603     0.5301   10
Inertia is variance
Some constraints were aliased because they were collinear (redundant)

Eigenvalues for constrained axes:
  RDA1   RDA2   RDA3   RDA4   RDA5   RDA6   RDA7   RDA8   RDA9  RDA10
```

```
m.run <- rda(crayfish ~ Run + Condition(Reach), data = design)
m.run
```

```
Call: rda(formula = crayfish ~ Run + Condition(Reach), data =
design)

              Inertia Proportion Rank
Total          9.3580     1.0000
Conditional    4.3977     0.4699   62
Constrained    1.8225     0.1948   10
Unconstrained  3.1378     0.3353   10
Inertia is variance
Some constraints were aliased because they were collinear (redundant)

Eigenvalues for constrained axes:
  RDA1   RDA2   RDA3   RDA4   RDA5   RDA6   RDA7   RDA8   RDA9  RDA10
```

RE-USE

Blanchet, F Guillaume, Pierre Legendre, and Daniel Borcard. 2008. “Forward Selection of Explanatory Variables.” *Ecology* 89 (9). Eco Soc America: 2623–32.