This presentation contains material by Steve Juggins, Guillaume Blanchet and Richard Telford

Jack Williams did not contribute to this presentation

Canonical correspondence analysis and weighted

averaging

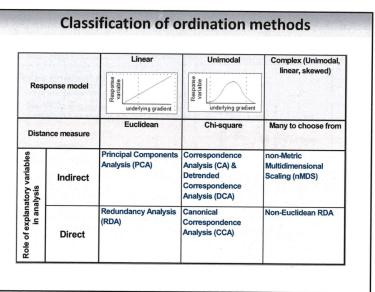
Types of ordinations:

We talked about two types of ordinations and about two types of response models:

What is the main difference between the two ordination types?

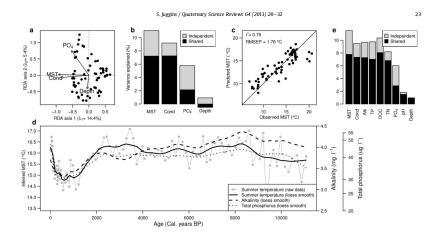
What is the main difference between the two response models?

Ordination types:



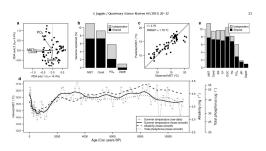
Juggins (2012)

Application of ordinations and reconstructions



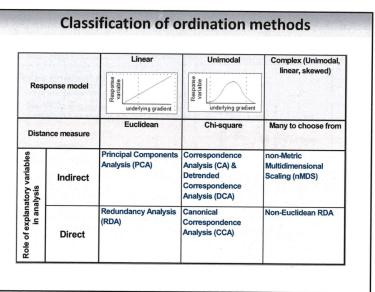
Juggins (2013)

Application of ordinations and reconstructions



- ► Constrained ordination
- Independent and shared variance
- Transfer function
- Reconstructions
- Variable selection

Ordination types:



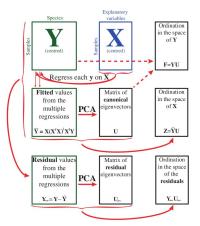
Juggins (2012)

Canonical correspondence analysis

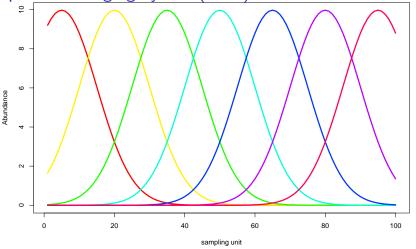
Same principle as redundancy analysis:

regression: weighted regression

ordination: correspondence analysis



Reciprocal averaging by Hill (1973):



The method of gradient analysis is to take some well-marked gradient and to assign scores to the species according to their [...] preferences. Sites are then ordinated by taking averages of the scores of the species which occur in them. Hill, 1973

Gradient analysis: Reciprocal averaging

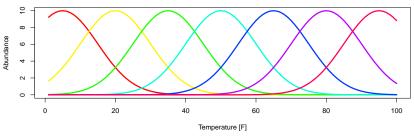
| | species 1 | species 2 | species i | Σ |
|-------------|--|--|-----------------------|--|
| site 1 | P ₁₁ P ₂₁ | P ₁₂ P ₂₂ | p_{1i} p_{2i} | p_{1+} p_{2+} |
| site M Σ | р _{М1} р ₊₁ | р _{м2} р ₊₂ | РМі Р+і | p _{M+} p ₊₊ |

Site scores: x

Species scores: y

Start with random site scores (assign a random env. variable)

Canonical correspondence analysis



| | species 1 | species 2 | species i | Σ | Env. var. |
|------------------|------------------------------------|--|--|--|-------------------|
| site 1 site 2 | P ₁₁ P ₂₁ | P ₁₂ P ₂₂ | , | $p_{1+} \\ p_{2+}$ | $env1_1$ $env1_2$ |
| site M Σ | ρ _{M1} ρ ₊₁ | р _{М2} р ₊₂ | р _{Мі} р _{+і} | p _{M+} p ₊₊ | env1 _M |

Environmental variable: env

Canonical correspondence analysis

| | species 1 | species 2 | species i | Σ | Env. var. |
|-------------|---|--|----------------|-------------------|-------------------|
| site 1 | <i>p</i> ₁₁ <i>p</i> ₂₁ | p ₁₂ p ₂₂ | • | p_{1+} p_{2+} | $env1_1$ $env1_2$ |
| site M Σ | р _{М1} р ₊₁ | р _{м2} р ₊₂ | РМі Р+і | p_{M+} p_{++} | env1 _M |

Environmental variable: env

Start with environmental variable to calculate species scores

Species score: environmental preference of a species

$$scores_{species} = \frac{p_{11}}{p_{+1}} env1_1 + \frac{p_{21}}{p_{+1}} env1_2 + ... + \frac{p_{M1}}{p_{+1}} env1_M$$

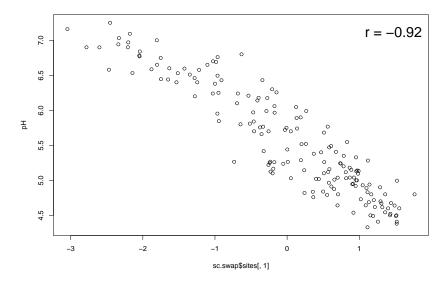
Canonical correspondence analysis: site scores

| | species 1 | species 2 | species i | Σ | Env. var. |
|-------------|--|--|------------------------------------|--------------------|-------------------|
| site 1 | p ₁₁ p ₂₁ | P ₁₂ P ₂₂ | p _{1i} p _{2i} | $p_{1+} \\ p_{2+}$ | $env1_1$ $env1_2$ |
| site M Σ | р _{М1} р ₊₁ | р _{м2} р ₊₂ | Р _{Мі} Р+і | p_{M+} p_{++} | env1 _M |

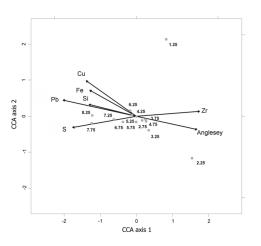
Site scores: environmental conditions at a site as determined by the environmental preferences of species found at that site

$$scores_{site} = \frac{p_{11}}{p_{1+}} scores_{spec,1} + \frac{p_{12}}{p_{1+}} scores_{spec,2} + ... + \frac{p_{1N}}{p_{1+}} scores_{spec,N}$$

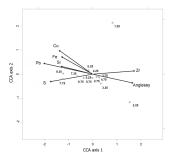
Compare site scores to environmental variable; Diatoms and $\ensuremath{\mathsf{pH}}$



CCA: bi or triplot



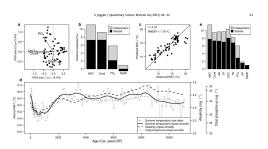
Variable selection:



Issues:

- many, highly correlated variables
- ▶ 7 variables for 14 samples
 - which variables are really important?
 - ▶ how do we select them?

Variable selection:

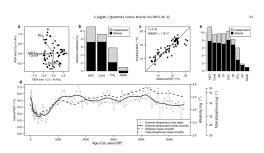


Different selection and inclusion criteria

- forward selection
- backward elimination
- ▶ Reviewed in Borcard et al. (2011, see github repository)
- ► Always use your ecological knowledge

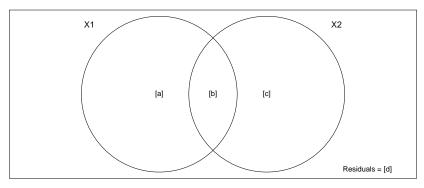
Correlated environmental variables:

Part of the variance explained is shared between the variables



Correlated environmental variables:

Part of the variance explained is shared between variables

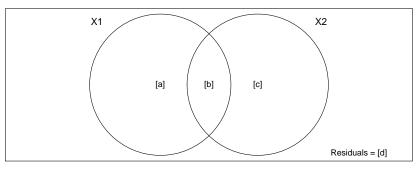


a: variance exclusively explained by X1

c: variance exclusively explained by X2

b: variance shared between X1 and X2

Variance partitioning:



Step1: Remove influence of one environmental variable (X1) on species assemblage

fit model with env variable you want to condition on ([a] + [b]) and then take residuals

Step2: Constrain residuals using second environmental variable (**X2**) (**[c]**)

Variance partitioning: RDA

varpart in vegan package

```
##
                 Df R.squared Adj.R.squared Testable
  [a+b] = X1
                  1 0.2289742
                                 0.2280408
                                              TRUE
  [b+c] = X2 1 0.1482025
                                 0.1471713
                                              TRUE
\#\# [a+b+c] = X1+X2  2  0.2895756
                                 0.2878534
                                              TRUE
##
                 Df R.squared Adj.R.squared Testable
  [a] = X1|X2
##
                          NΑ
                                 0.1406821
                                              TRUE
##
  [b]
                  0
                          NA
                                 0.0873587
                                             FALSE
  [c] = X2|X1
                          NA
                                 0.0598126
                                              TRUE
  [d] = Residuals NA
                          NA
                                 0.7121466
                                             FALSE
```

Variance partitioning: CCA

cca in vegan

```
 \begin{aligned} & cca.cond.tjul <- \ cca(sqrt(arctic.pollen) \sim taug \ + \ Condition(tjul), \\ & data = \ arctic.env) \\ & cca.cond.taug <- \ cca(sqrt(arctic.pollen) \sim tjul \ + \ Condition(taug), \\ & data = \ arctic.env) \end{aligned}
```

Conditional: [a] + [b] or [b]+[c]

Constrained: [c] or [a]

Unconstrained: residuals [d]

Conditional + Constrained = [a] + [b] + [c]

No adjusted R^2

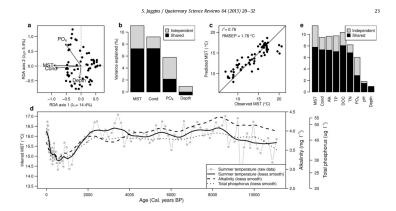
Variance partitioning:

Transform data following Legendre and Gallagher (2001) and then run rda

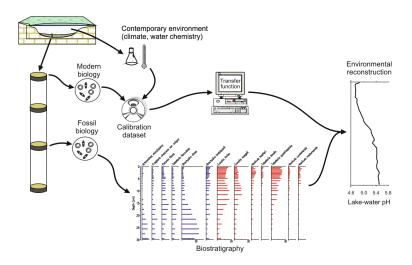
decostand() in vegan

varpart

Environmental reconstructions

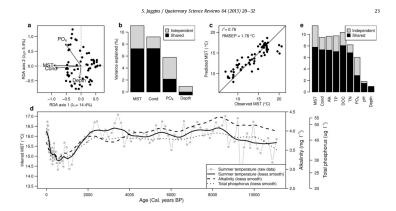


Environmental reconstructions



Juggins and Birks (2012)

Environmental reconstructions



Modern analogue technique vs weighted averaging

MAT: local solution (use k closest analogues and average environment of these analogues)

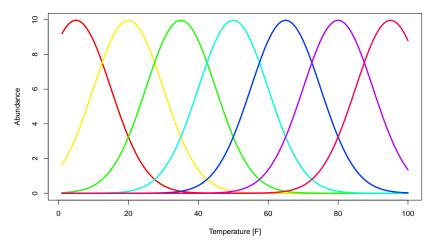
k: number of analogues (usually a few)

WA: global solution estimating optimal environmental conditions for species/taxa

From optimal conditions for species estimate past environment based on species composition

Have we encountered this procedure before?

WA: unimodal response



Estimate species optimum

Using species optima, estimate environmental conditions at a site

WA and CCA: Optima and species scores

| | species 1 | species 2 | species i | Σ | Env. var. |
|-------------|---|--|-------------------|--|--------------------------------------|
| site 1 | <i>p</i> ₁₁ <i>p</i> ₂₁ | p ₁₂ p ₂₂ | p_{1i} p_{2i} | p_{1+} p_{2+} | env ₁ env ₂ |
| site M Σ | р _{М1} р ₊₁ | р _{м2} р ₊₂ | Рмі Р+і | р _{М+} р ₊₊ | env _M |

Optimum: environmental preference of a species

Environmental variable: env

$$Optimum_{species1} = \frac{p_{11}}{p_{+1}}env_1 + \frac{p_{21}}{p_{+1}}env_2 + \ldots + \frac{p_{M1}}{p_{+1}}env_M$$

 $\label{eq:ccapacity} \textbf{Optimum} = \textbf{CCA} \text{ species scores}$

WA and CCA: Predicted value and site scores

| | species 1 | species 2 | species N | Σ | Env. var. |
|-------------|---------------------------------|--|----------------|-------------------|-------------------|
| site 1 | P ₁₁ P ₂₁ | P ₁₂ P ₂₂ | P1N P2N | p_{1+} p_{2+} | $env1_1$ $env1_2$ |
| site M Σ | $p_{M1} p_{+1}$ | р _{М2} р ₊₂ | РМN Р+N | p_{M+} p_{++} | env1 _M |

Predicted values: environmental conditions at a site as determined by the environmental preferences of species found at that site

$$Pred_{site} = rac{p_{11}}{p_{1+}} Opt_{spec1} + rac{p_{12}}{p_{1+}} Opt_{spec2} + ... + rac{p_{1N}}{p_{1+}} Opt_{specN}$$

Predicted values = CCA site scores

Deshrinking

```
max(Optima) <= max(env)
min(Optima) >= min(env)
max(predicted value) <= max(Optima)
min(predicted value) >= min(Optima)
```

Reconstructed values have less variance than environmental variables

Deshrinking: increase variance of reconstructed values

- inverse
- classical
- monotonic (predicted values no longer equal to CCA site scores but still monotonically related)

Cross-validation

CCA and apparent WA: method knows environmental conditions it is supposed to estimate

Should test model on (hopefully) independent data: **calibration** and **validation**

| | ◀ Total Number of Dataset → | |
|--------------|-----------------------------|------------|
| Experiment 1 | | |
| Experiment 2 | | Training |
| Experiment 3 | | |
| Experiment 4 | | Validation |
| Experiment 5 | | |

Cross-validation

- Divide data set in two parts
 - construct model (calibrate) on part one
 - test model (validate) on part two

Leave-one-out:

 Use all except one sample to calibrate model, predict omitted sample (validate)

k-fold:

- Divide data set into k-parts (e.g. k = 10)
- ▶ Use k-1 parts to calibrate and one part to validate
- repeat k times

Outlook

- Weighted averaging partial least squares (WA-PLS)
- Validate predictions/reconstructions
- Cautionary notes