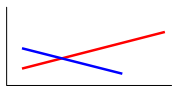


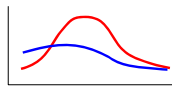
## Other Unconstrained Ordination Techniques

### Linear



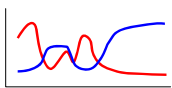
- Factor analysis (FA)
- Multidimensional scaling (MDS/PCO)
- **ML-Unconstrained linear ordination (ULO)**

### Quadratic



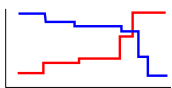
- Correspondence analysis (CA & DCA)
- **ML-Unconstrained quadratic ordination (UQO)**

### Smooth



- **ML-Unconstrained additive ordination (UAO)**

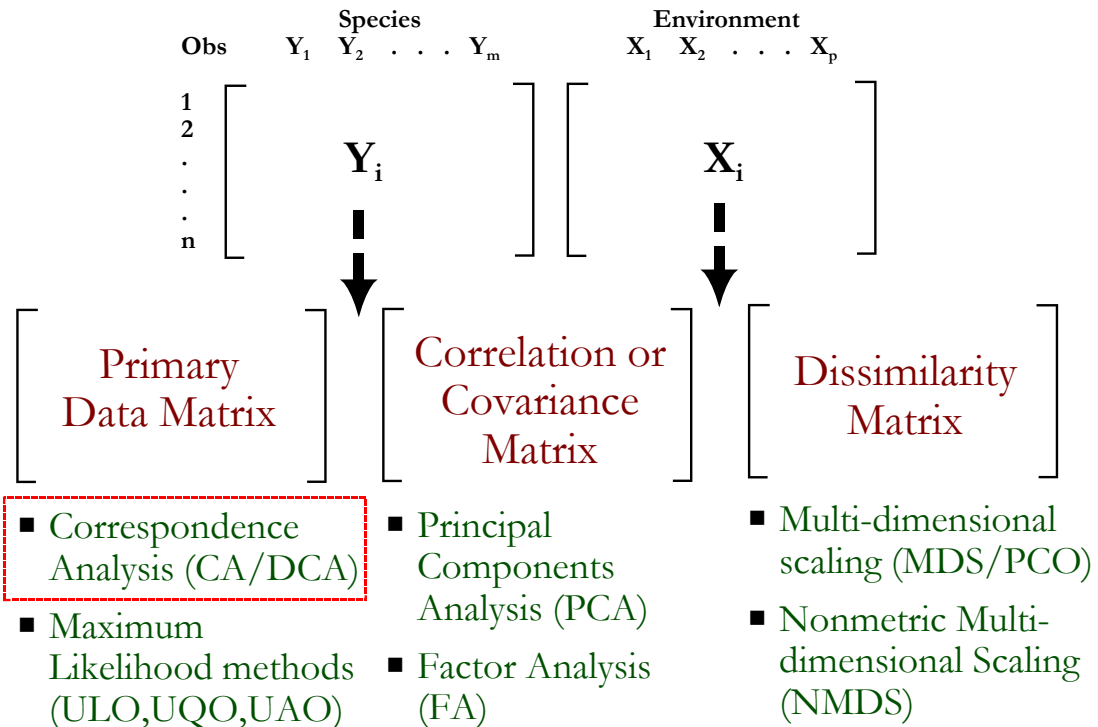
### Nonlinear



- **Nonmetric multidimensional scaling (NMDS)**

1

## Indirect (Unconstrained) Ordination Techniques



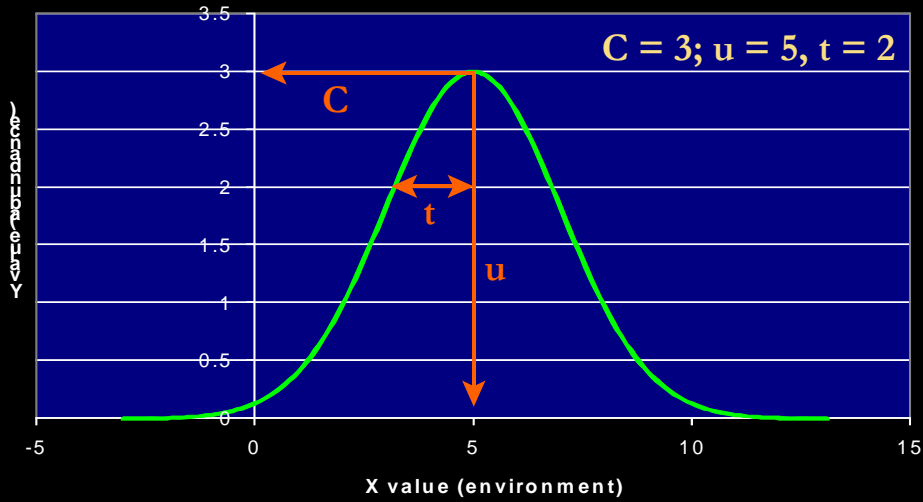
2

# Derivation of the CA Model

*From Gaussian Regression to Weighted-Averaging*

## Parametric Gaussian Function

$$E_{y_{ik}} = c_k \exp\left(- (x_i - u_k)^2 / 2t_k^2\right)$$

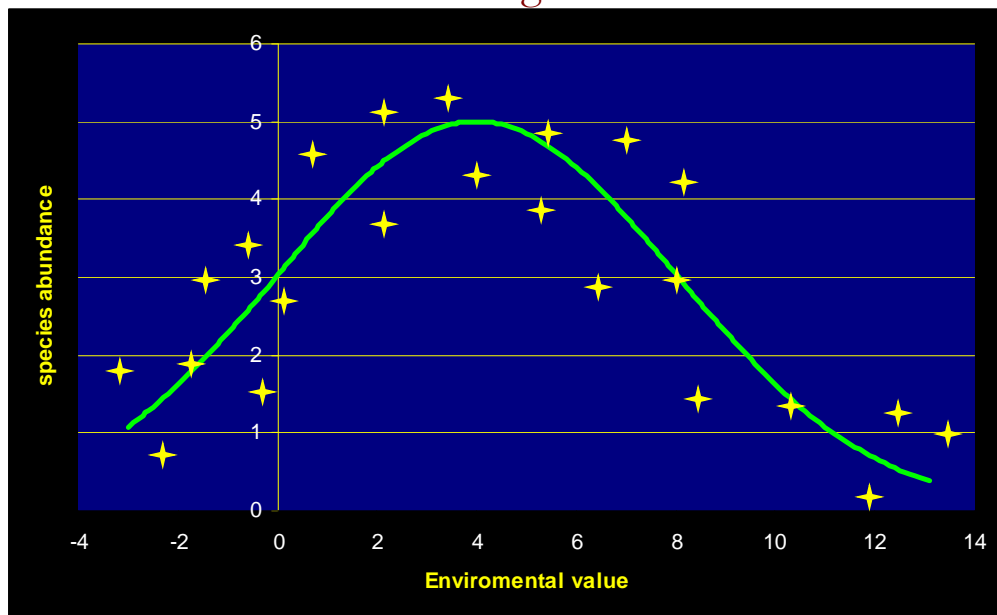


3

# Derivation of the CA Model

*From Gaussian Regression to Weighted-Averaging*

## Gaussian Regression



4

## Derivation of the CA Model

### *From Gaussian Regression to Weighted-Averaging*

- Gaussian regression has a counterpart in the family of heuristic methods based on weighted-averaging.
- Weighted averaging methods have the advantage of ease of computation and under certain conditions are maximally efficient estimators of the optima of Gaussian curves.
- The estimate for the optimum of a species is:

$$w_k = \frac{\sum_{i=1}^n y_{ik} x_i}{\sum_{i=1}^n y_{ik}}$$

$y_{ik}$  = abundance of species  $k$  at site  $i$ .  
 $x_i$  = value of the environmental variable at site  $i$ .

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## Derivation of the CA Model

### *From Gaussian Regression to Weighted-Averaging*

- Weighted-average and weighted-average standard deviation are 'simple-minded' estimates of the optimum and tolerance of the Gaussian curve.
- For presence/absence data the method reduces to the mean and standard deviation of the environmental values for 'presence'.
- Weighted-average is an unbiased estimator of the optimum if  $x$  has a uniform distribution and the response function is symmetric.

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## Derivation of the CA Model

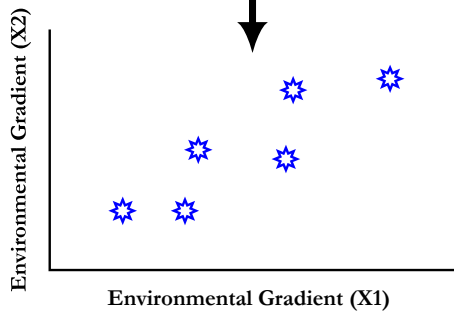
### *Weighted-Averaging (Whittaker 1956)*

Goal: Order species along environmental gradient(s)

Obs	Species	Environment
	$Y_1 \quad Y_2 \quad \dots \quad Y_m$	$X_1 \quad X_2 \quad \dots \quad X_p$
1	$\mathbf{Y}_i$	$\mathbf{X}_i$
2		
⋮		
⋮		
n		

Assume:  
Unimodal response function

Direct mapping of species into measured environmental space using *weighted averaging*



$$w_k = \frac{\sum_{i=1}^n y_{ik} x_i}{\sum_{i=1}^n y_{ik}}$$

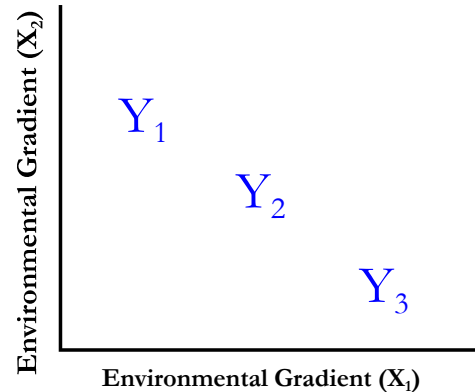
7

## Derivation of the CA Model

### *Weighted-Averaging (Whittaker 1956)*

Obs	Species	Environment
	$Y_1 \quad Y_2 \quad Y_3$	$X_1 \quad X_2$
1	$\begin{bmatrix} 5 & 1 & 0 \\ 10 & 5 & 10 \\ 0 & 2 & 5 \end{bmatrix}$	$\begin{bmatrix} 5 & 4 \\ 10 & 2 \\ 20 & 1 \end{bmatrix}$
2		
3		

$$w_k = \frac{\sum_{i=1}^n y_{ik} x_i}{\sum_{i=1}^n y_{ik}}$$



*Environmental Gradient (X<sub>1</sub>)*

Species Y1 = (5/15)(5) + (10/15)(10) + (0)(20) = 8.35  
 Species Y2 = (1/8)(5) + (5/8)(10) + (2/8)(20) = 11.88  
 Species Y3 = (0)(5) + (10/15)(10) + (5/15)(20) = 13.34

*Environmental Gradient (X<sub>2</sub>)*

Species Y1 = (5/15)(4) + (10/15)(2) + (0)(1) = 2.66  
 Species Y2 = (1/8)(4) + (5/8)(2) + (2/8)(1) = 2.00  
 Species Y3 = (0)(4) + (10/15)(2) + (5/15)(1) = 1.66

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# Derivation of the CA Model

## *Weighted-Averaging (Whittaker 1956)*

Obs	Species			Species Weights		
	Y <sub>1</sub>	Y <sub>2</sub>	Y <sub>3</sub>	Y <sub>1</sub>	Y <sub>2</sub>	Y <sub>3</sub>
1	5	1	0	Dry site indicator	Med site indicator	Wet site indicator
2	10	5	10	w <sub>1</sub> = 0	w <sub>2</sub> = 50	w <sub>3</sub> = 100
3	0	2	5			

$$v_i = \frac{\sum_{k=1}^p y_{ik} w_k}{\sum_{k=1}^p y_{ik}}$$

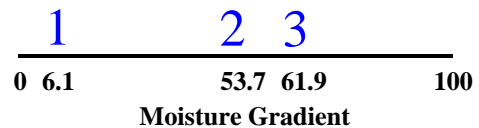
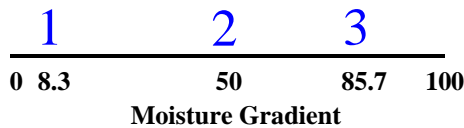
$$w_k = \frac{\sum_{i=1}^n y_{ik} v_i}{\sum_{i=1}^n y_{ik}}$$

*Sample Ordination:*

Obs 1 = (5)(0)+(1)(50)+(0)(100) / 6 = 8.3  
 Obs 2 = (10)(0)+(5)(50)+(10)(100) / 25 = 50  
 Obs 3 = (0)(0)+(2)(50)+(5)(100) / 7 = 85.7

*Species Ordination:*

Sp 1 = (5)(8.3)+(10)(50)+(0)(85.7) / 15 = 6.1  
 Sp 2 = (1)(8.3)+(5)(50)+(2)(85.7) / 8 = 53.7  
 Sp 3 = (0)(8.3)+(10)(50)+(5)(85.7) / 15 = 61.9

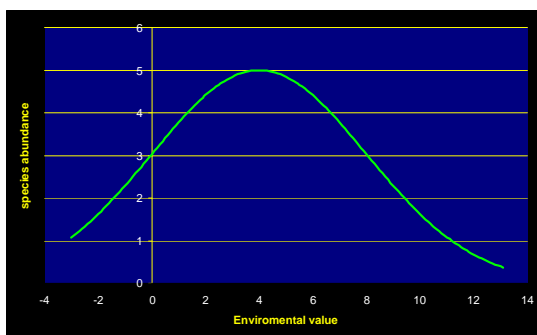


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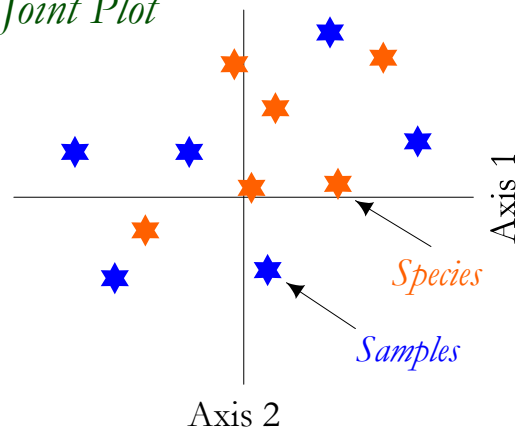
## Correspondence Analysis (CA)

Goal: Simultaneous ordination of samples and species into reduced ordination space such that correlation between sample and species ordination scores is maximized.

*Unimodal Response Model*



*Joint Plot*



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# Correspondence Analysis (CA)

## *Reciprocal Averaging Algorithm*

Hill (1973) ‘(re)discovered’ reciprocal averaging and proposed it as an alternative to ML-Gaussian ordination. Under assumptions of the species packing model the first CA axis is a good approximation of the latent variable in ML-Gaussian ordination.

- Assign arbitrary weights to samples.
- ➔ ■ Compute species scores as weighted averages.
- Compute sample scores as weighted averages.
- For subsequent axes, orthogonalize site scores.
- Rescale (standardize) sample scores.
- Stop on convergence.

# Correspondence Analysis (CA)

Sample	Species		
	A	B	C
1	5	1	0
2	10	5	10
3	0	2	5

② 1.6667, 2.125, 2.3333

⑤ -0.4417, 0.2024, 0.5005

⑧ -0.4415, 0.2025, 0.5006

*Species Scores*

Sample	Species		
	A	B	C
1	5	1	0
2	10	5	10
3	0	2	5

5.3333, 2.125, 2.3333

0.4547, -0.1913, -0.4879

-0.4416, 0.2025, 0.5006

	①	③	④	⑥	⑦
1	1.7431	-1.4427		-0.3343	-1.4428
2	2.025	0.0588		0.064	0.0591
3	2.2738	1.3839		0.4153	1.3837

2.014  
0.1878

0.0483  
0.2652

*Standardize*

*Arbitrary scores*

*Sample Scores*

8	4.7986	1.4306		0.347	1.4428
4	3.4917	-0.0333		-0.0516	-0.059
2	2.2738	-1.3973		-0.4032	-1.3838

3.5214  
0.8928

-0.0359  
0.2654

## Correspondence Analysis (CA)

### *Eigenanalysis Algorithm*

Given:

$$A = \begin{array}{c} \text{Obs} \\ 1 \\ 2 \\ 3 \end{array} \begin{array}{c} \text{Species} \\ Y_1 \quad Y_2 \quad Y_3 \\ \left[ \begin{array}{ccc} & & \\ & a_{ij} & \\ & & \end{array} \right] \\ (\text{nxp}) \end{array}$$

$$V = \begin{array}{c} \text{Sample weights} \\ \left[ \begin{array}{cc} \swarrow & 0 \\ v_i = \frac{1}{a_{i+}} & \\ 0 & \searrow \end{array} \right] \\ (\text{nxn}) \end{array}$$

$$W = \begin{array}{c} \text{Species weights} \\ \left[ \begin{array}{cc} \swarrow & 0 \\ w_j = \frac{1}{a_{+j}} & \\ 0 & \searrow \end{array} \right] \\ (\text{pxp}) \end{array}$$

Weighted data matrix:  $B = V^{1/2} A W^{1/2} = \begin{array}{c} \text{Obs} \\ 1 \\ 2 \\ 3 \end{array} \begin{array}{c} \text{Species} \\ Y_1 \quad Y_2 \quad Y_3 \\ \left[ \begin{array}{ccc} & & \\ & b_{ij} = \frac{a_{ij}}{\sqrt{a_{i+} \cdot a_{+j}}} & \\ & & \end{array} \right] \\ (\text{nxp}) \end{array}$  Simultaneous weighting by row and column totals

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## Correspondence Analysis (CA)

### *Eigenanalysis Algorithm*

Find Eigenvalues:  $|S - \lambda I| = 0$

$$A = \begin{array}{c} \text{Obs} \\ 1 \\ 2 \\ 3 \end{array} \begin{array}{c} \text{Species} \\ Y_1 \quad Y_2 \quad Y_3 \\ \left[ \begin{array}{ccc} & & \\ & a_{ij} & \\ & & \end{array} \right] \\ (\text{nxp}) \end{array}$$



$$B = \begin{array}{c} \text{Obs} \\ 1 \\ 2 \\ 3 \end{array} \begin{array}{c} \text{Species} \\ Y_1 \quad Y_2 \quad Y_3 \\ \left[ \begin{array}{ccc} & & \\ & b_{ij} = \frac{a_{ij}}{\sqrt{a_{i+} \cdot a_{+j}}} & \\ & & \end{array} \right] \\ (\text{nxp}) \end{array}$$



$$S_{(nxn)} = BB' = V^{1/2} AWA'V^{1/2}$$

Where: S = covariance matrix (as below)  
 $\lambda$  = vector of eigenvalue solutions  
 I = identity matrix

S is covariance matrix as in PCA except that cross-products are weighted by reciprocals of square roots of sample and species totals.

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## Correspondence Analysis (CA)

### *Eigenanalysis Algorithm*

**Find Eigenvectors:**

$$\left| V^{1/2} A W A' V^{1/2} - \lambda_i I \right| x_i = 0$$

$$\left| W^{1/2} A' V A W^{1/2} - \lambda_i I \right| y_i = 0$$

Where:  $\lambda_i$  = eigenvalue for  $k^{\text{th}}$  dimension  
 $x_i$  = sample eigenvector for the  $k^{\text{th}}$  dimension  
 $y_i$  = species eigenvector for  $k^{\text{th}}$  dimension

**Sample ordination:**

$$X_{(nxk)} = A_{(nxp)} \cdot Y_{(pxk)}$$

**Species ordination:**

$$Y_{(pxk)} = A'_{(pxn)} \cdot X_{(nxk)}$$

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## Correspondence Analysis (CA)

### *Eigenanalysis Algorithm*

**Sample scores:** For  $i^{\text{th}}$  sample on  $k^{\text{th}}$  dimension:

$$X = A \cdot Y \quad x_{ik} = a_{i1} y_{1k}^* + a_{i2} y_{2k}^* + \dots + a_{ip} y_{pk}^*$$

**Scaling factor:**

$$y_{jk}^* = y_{jk} \cdot \sqrt{a_{++} / a_{+j}}$$

**Species scores:** For  $j^{\text{th}}$  species on  $k^{\text{th}}$  dimension:

$$Y = A' \cdot X \quad y_{jk} = a_{j1} x_{1k}^* + a_{j2} x_{2k}^* + \dots + a_{jn} x_{nk}^*$$

**Scaling factor:**

$$x_{ik}^* = x_{ik} \cdot \sqrt{a_{++} / a_{i+}}$$

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## Correspondence Analysis (CA)

### *Eigenanalysis Algorithm*

#### *Likeness to PCA*

- $S$  is a covariance matrix as in PCA, except that the cross-products are weighted by the reciprocals of the square roots of the sample and species totals.
- Eigenvectors are derived as in PCA, except that two sets are produced, one for the sample ordination ( $X$ ) and one for the species ordination ( $Y$ ), such that they are maximally correlated.
- As in PCA, each axis can be represented as a linear combination of the original variables (eigenvectors contain the coefficients), although after doubly weighting by row and column totals.

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## Correspondence Analysis (CA)

### *Important differences with PCA*

- PCA preserves the *Euclidean distances* among samples, while CA preserves the *chi-square distances* among samples and species. Chi-square distances are similar to Euclidean distances except they have been doubly weighted by row and column totals. *Both are heavily criticized for use with community data.*
- CA and PCA scale scores differently.
- In PCA, eigenvalues represent '*variance*' explained; whereas in CA, eigenvalues represent '*inertia*', where total inertia equals the Chi-squared statistic of the data matrix standardized to unit total.

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## Correspondence Analysis (CA)

*Important differences with PCA*

### Correspondence Analysis Results:

```
Inertia Rank
Total      0.7405
Unconstrained 0.7405  20
Inertia is mean squared contingency coefficient

Eigenvalues for unconstrained axes:
CA1  CA2  CA3  CA4  CA5  CA6  CA7  CA8
0.24219 0.12414 0.07552 0.06561 0.04671 0.04307 0.03416 0.02672
(Shown only 8 of all 20 unconstrained eigenvalues)
```

#### Pearson's Chi-squared test

```
data: rip.veg/sum(rip.veg)
X-squared = 0.7405 df = 987, p-value = 1
```

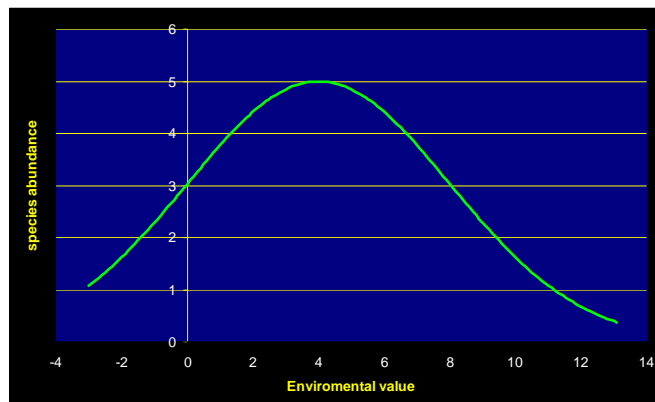
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## Correspondence Analysis (CA)

*Important differences with PCA*

- PCA assumes species respond *linearly* to underlying gradients, while CA assumes *unimodal* response; in effect, CA uses central tendencies of species on the gradient to position samples and vice-versa.

Unimodal  
Response Model



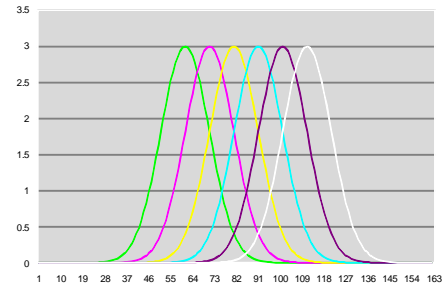
20

## Correspondence Analysis (CA)

### *Unimodal Assumption*

Chi-square distance in CA is an approximate solution to representing unimodal species responses if:

- Samples are equally spaced along the gradients and closely spaced in comparison with the species' tolerance.
- Species optima are either equal or independent of position on gradients.
- Species optima are equally spaced along the gradients and closely spaced in comparison with their tolerances.
- Species have equal tolerances or tolerances are independent of species position on gradients.

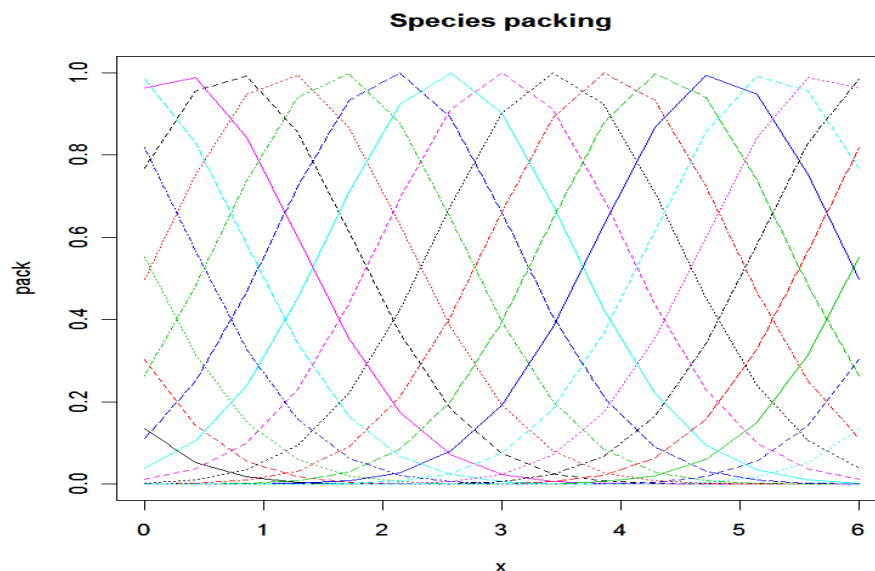


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## Correspondence Analysis (CA)

### *Unimodal Assumption*

This amounts to the assumption of a “species packing model”



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## Correspondence Analysis (CA)

### *“Arch” and “Compression” Effects*

- CA approximates the ML Gaussian ordinations under the *species packing model* - However, CA can never be exactly equivalent to ML ordination, because the assumptions needed for exact correspondence require both that the range of site scores is broad enough to include the range of all the species, and that there must be species with their optima situated beyond the edge of the range of site scores – *it is not possible to meet both of these assumptions.*

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## Correspondence Analysis (CA)

### *“Arch” and “Compression” Effects*

As a result:

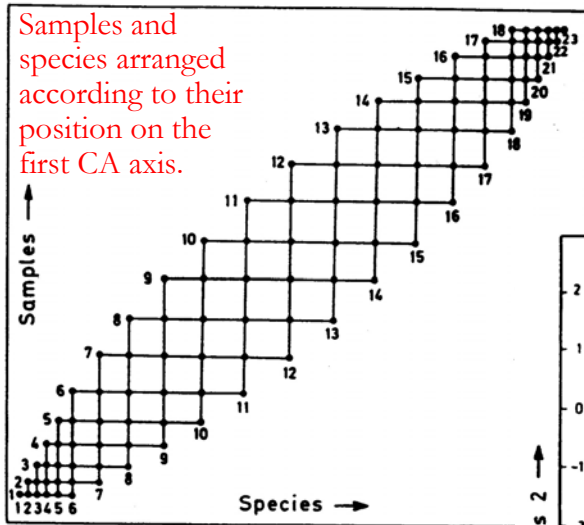
- CA shows a “*compression*” effect - the site scores near the ends of the axes become compressed relative to the middle.
- CA shows an “*arch*” effect – which arises because axes are extracted sequentially in order of decreasing variance – if RA has extracted a first axis that approximates the species packing model, then a possible second axis is obtained by folding the first axis in the middle. Even if there is a strong second gradient, RA will not associate it with the second axis if it separates the species less than a folded first axis.

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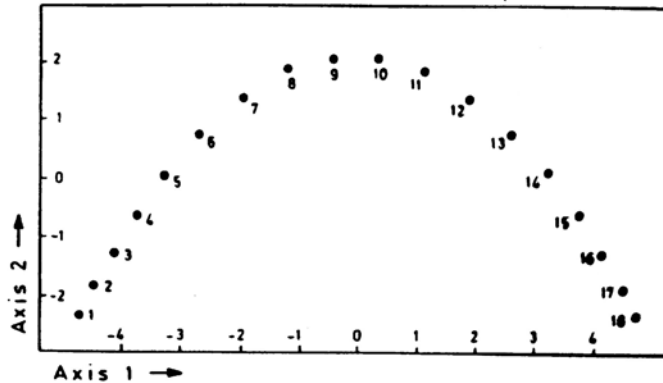
# Correspondence Analysis (CA)

*“Arch” and “Compression” Effects*

Samples and species arranged according to their position on the first CA axis.



- The arch is a mathematical artifact having no basis in the structure of the data.

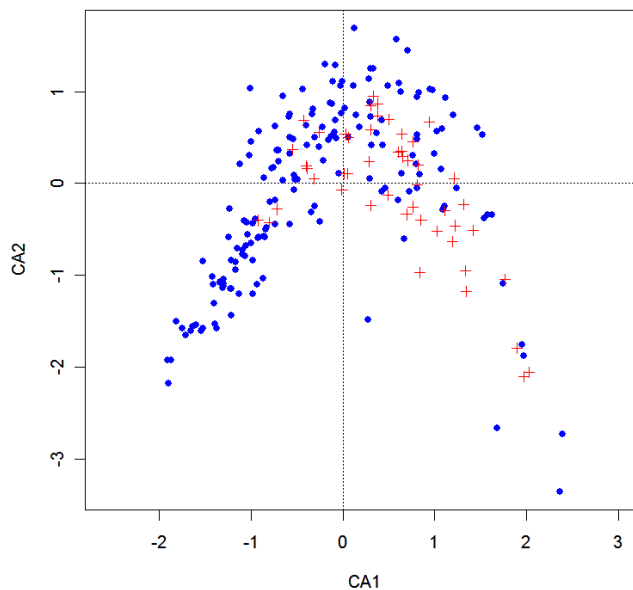


# Correspondence Analysis (CA)

*“Arch” and “Compression” Effects*



Correspondence Analysis of Oregon Streamside Birds



## Correspondence Analysis (CA and DCA)

### *From CA to DCA*

Hill and Gauch (1980) proposed DCA to overcome the major faults of CA:

- Single long gradients appear as curves or arcs in ordination: the solution is to *detrend the later axes* by making their means equal along segments of previous axes or via fitting polynomials.
- Sites are packed more closely at gradient extremes than at the center: the solution is to *rescale the axes* to equal variances of species scores.
- Rare species seem to have an unduly high influence on the results: the solution is to *downweight rare species*.

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## Correspondence Analysis ( DCA)

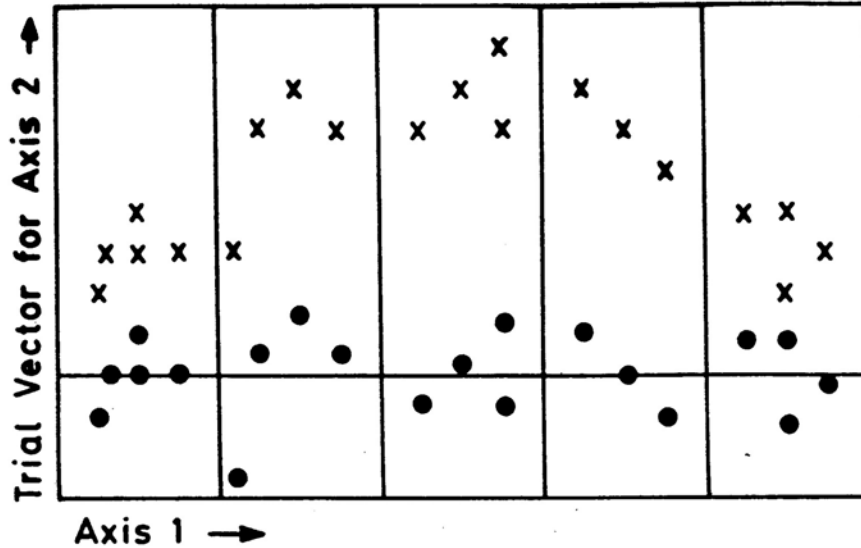
### *Reciprocal Averaging Algorithm*

- Assign arbitrary weights to samples.
- ■ Compute species scores as weighted averages.
- Compute sample scores as weighted averages.
- For subsequent axes, orthogonalize site scores.
- Rescale (standardize) sample scores.
- “Detrend” and “rescale” subsequent axes in DCA.
- Stop on convergence.

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## Correspondence Analysis ( DCA )

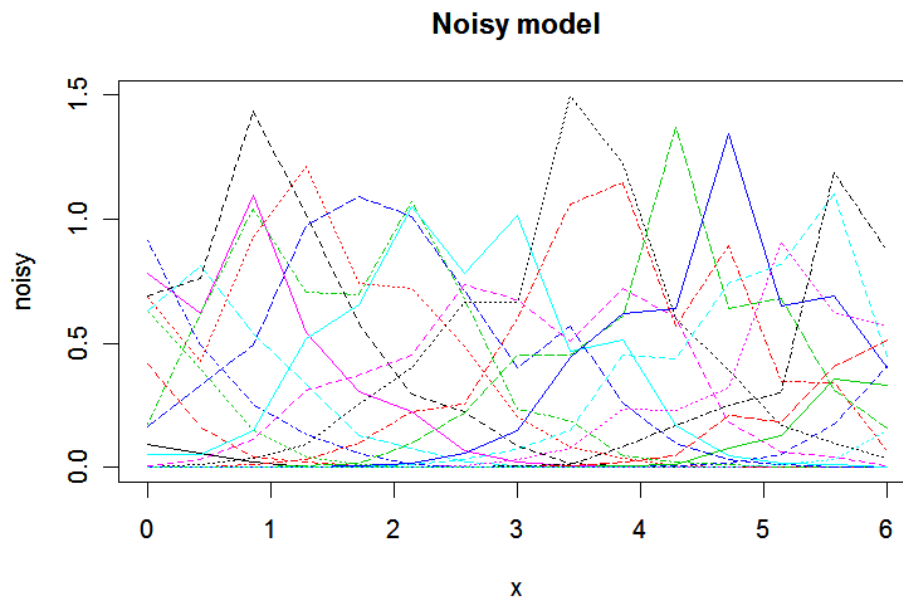
*Detrending and decompressing to remove  
arch and compression effects*



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## Comparison of Ordination Techniques

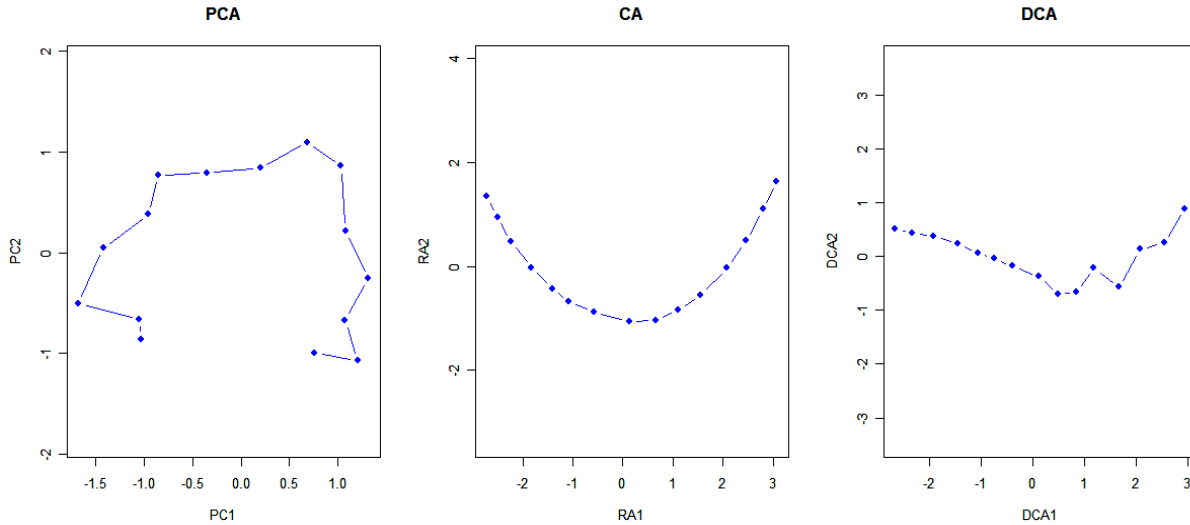
*Simulated noisy unimodal data set*



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# Comparison of Ordination Techniques

*Simulated noisy unimodal data set*



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## Correspondence Analysis (DCA)

*DCA Axis ("Gradient") Length*

After rescaling, the axis is supposed to be scaled by 'SD' units, so that the average width of Gaussian species responses is supposed to be 1 over whole axis (although this is only true under the ideal species packing model).

Thus, an axis length of 4 SD's theoretically is "long" enough to exhibit the complete rise and fall of species along the "gradient".

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

	DCA1	DCA2	DCA3	DCA4
Eigenvalues	0.2385	0.11455	0.04909	0.06909
Decorana values	0.2422	0.08748	0.04097	0.03287
Axis lengths	2.0907	1.50667	0.96230	1.16767

Rule of Thumb:

length < 2 : linear

length 2-3: possibly linear

length 3-4: probably unimodal

length > 4 : unimodal

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## Correspondence Analysis (CA and DCA)

### *Strengths of CA and DCA*

- Dual ordination of samples and species; maximizes correspondence; intuitive for community data sets.
- Complete summary of the data dimensions when dual ordination makes sense and underlying Gaussian model is valid.
- For most suitable community data sets, CA is equal or superior to PCA.
  - ▶ Less vulnerable than PCA to the "arch" and "compression" effects.
  - ▶ Better than PCA at handling long ecological gradients.
- DCA is not subject to the arch and compression effects.

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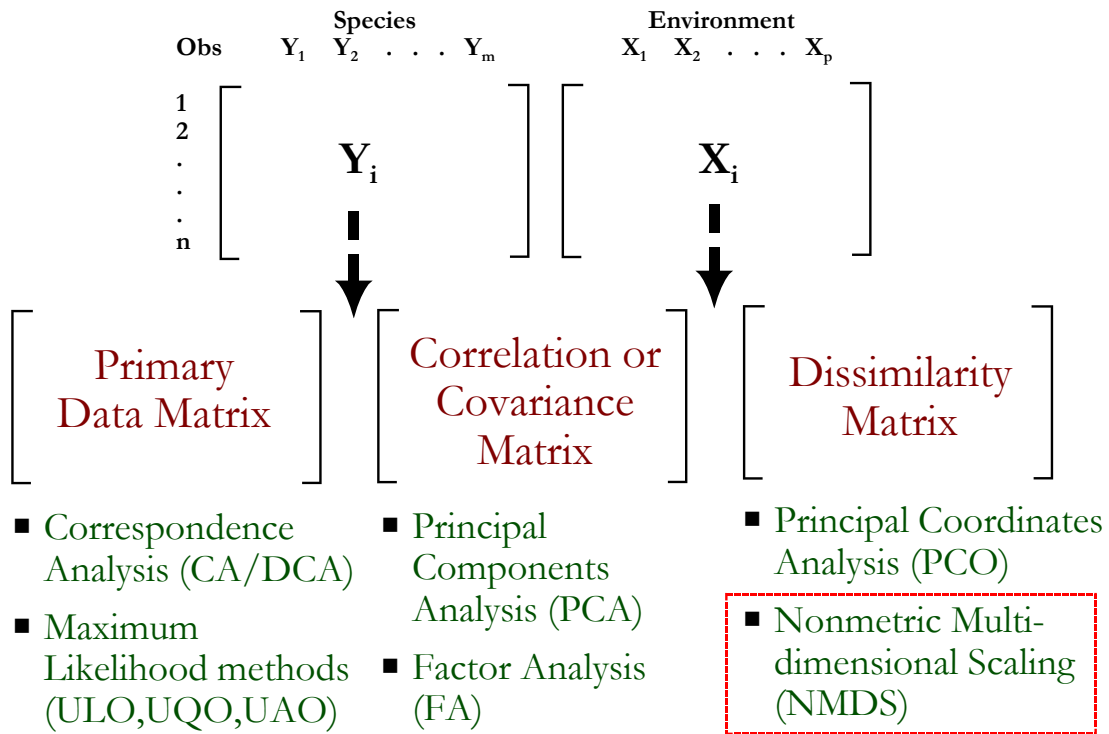
## Correspondence Analysis (CA and DCA)

### *Limitations of CA and DCA*

- Only appropriate when dual ordination makes sense (i.e., community data sets).
- Performs poorly if species response is not unimodal and all species are not similarly scaled (maxima and dispersions) – common in most data sets.
- CA subject to “arch” and “compression” effects.
- DCA heavily criticized for arbitrary detrending and rescaling which may obscure underlying “true” structure.
- Underlying chi-square distance metric heavily criticized for use with community data.

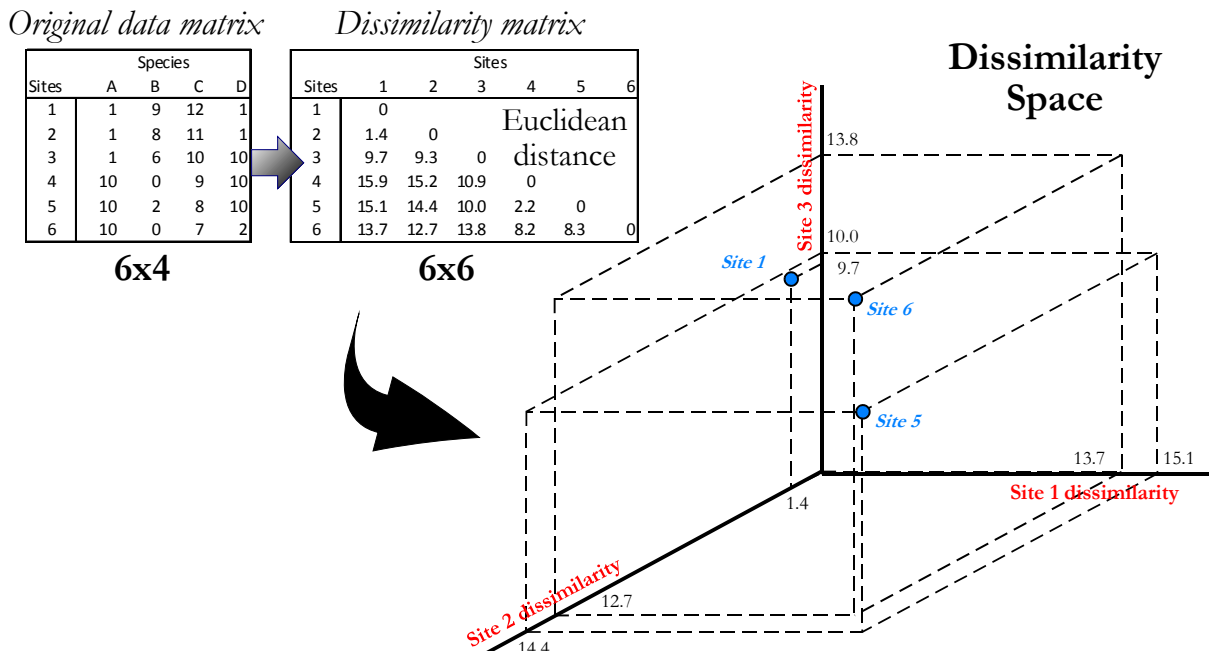
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# Indirect (Unconstrained) Ordination Techniques



# Indirect (Unconstrained) Ordination Techniques

## *Distance-based Ordinations*



## Multidimensional Sclaing (MDS) [also Principal Coordinates Analysis (PCO)]

### *Key Features and Considerations*

- Eigenanalysis (PCA) of a dissimilarity matrix.
- Any dissimilarity measure can be used.
- Identical to PCA if a Euclidean distance matrix used.
- Linear mapping like PCA, but based on non-Euclidean metrics.
- Probably should be used more often because of flexibility in measuring non-Euclidean dissimilarities.
- PCA after certain row standardizations may accomplish the same thing.
- Probably better than PCA and CA/DCA with binary data.

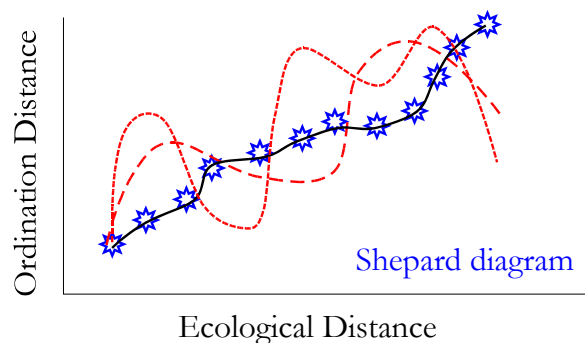
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## Nonmetric Multidimensional Sclaing (NMDS)

### *Key Features and Considerations*

- Avoids assumption of linear relationships among variables.
- No assumption of linear or unimodal response function.
- Allows the use of any dissimilarity measure or standardization.

Goal: Map samples into reduced ordination space such that ecological distances among samples are preserved in ordination.

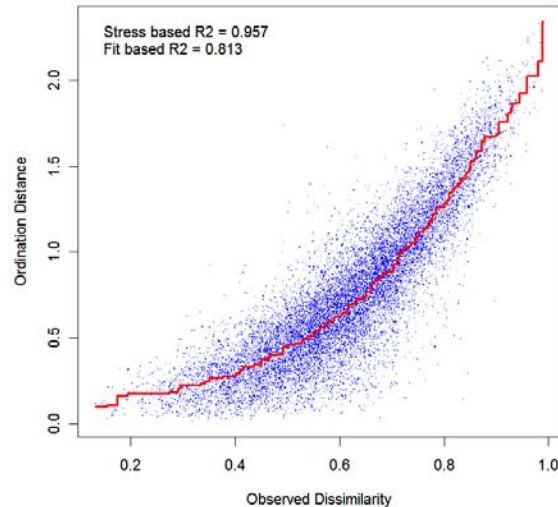


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# Nonmetric Multidimensional Scaling (NMDS)

## *How it Works*

- Iterative search for the best positions of  $n$  samples on  $k$  dimensions (axes) that minimizes the stress of the  $k$ -dimensional configuration.
- “Stress” is a measure of departure from monotonicity in the relationship between the distance in original  $p$ -dim space and distance in reduced  $k$ -dim ordination space.

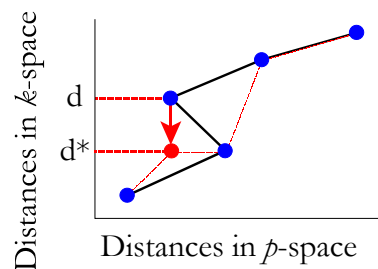


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# Nonmetric Multidimensional Scaling (NMDS)

## *How it Works*

1. Calculate dissimilarity matrix ( $\Delta$ ), i.e., distances between samples in  $p$ -dim space.
2. Assign samples to starting configuration (random; MDS solution) in  $k$ -dim space ( $\mathbf{X}$ ).
3. Normalize  $\mathbf{X}$  (subtract axis means and divide by overall sd of scores).
4. Calculate Euclidean distances between samples in  $k$ -dim space ( $\mathbf{D}$ ).
5. Rank elements of  $\Delta$ .
6. Put elements of  $\mathbf{D}$  in same order.
7. Calculate  $\mathbf{D}^*$  (replacing  $d_{ij}$  with  $d_{ij}^*$  to achieve monotonicity constraint).



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# Nonmetric Multidimensional Scaling (NMDS)

## *How it Works*

8. Calculate raw stress ( $S^*$ );  
goodness-of-fit statistic.

9. Standardize (normalize) stress ( $S$ ).

10. Try to minimize stress ( $S$ ) by  
changing the best configuration  
of samples in  $k$ -space (e.g.,  
steepest-descent algorithm).

11. Iterate steps 3-10 until stable  
solution is achieved.

$$S = \sqrt{\frac{\sum_{i=1}^{n-1} \sum_{j=i+1}^n (d_{ij} - d_{ij}^*)^2}{\sum_{i=1}^{n-1} \sum_{j=i+1}^n d_{ij}^2}}$$

$d_{ij}$  = original distance in  $k$ -dim  
space

$d_{ij}^*$  = adjusted distance in  $k$ -dim  
space

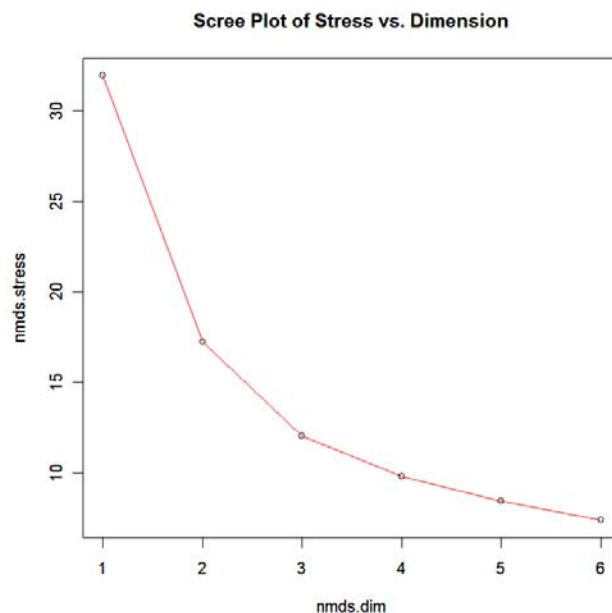
12. Conduct several runs and  
keep the solution with  
minimum stress [ $\min(S)$ ].

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# Nonmetric Multidimensional Scaling (NMDS)

## *Choosing the Right Number of Dimensions*

- NMDS solution (axes scores) depends on the number of axes selected.
- For a given number of dimensions, the solution for a particular axis is unique.
- Axis numbers are arbitrary, so that the percent of variance on an axis does not necessarily decrease sequentially.



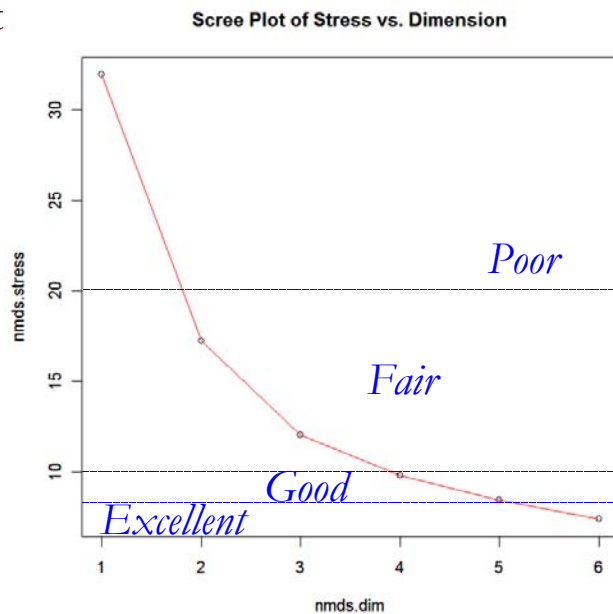
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# Nonmetric Multidimensional Scaling (NMDS)

## *Evaluating Goodness-of-Fit*

- Low stress (in %) = good fit of ordination configuration to original dissimilarities.

<5%	Excellent representation with no risk of misinterpretation
5-10%	Good ordination with no real risk of false inferences
10-20%	Fair ordination; need cautious interpretation
>20%	Unreliable

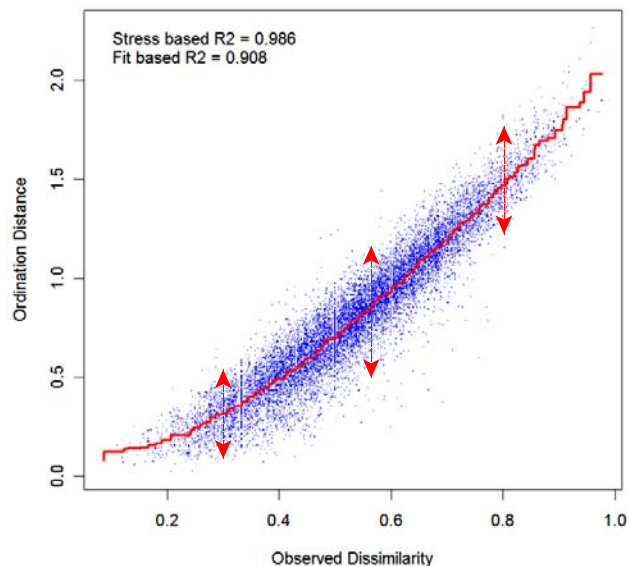


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# Nonmetric Multidimensional Scaling (NMDS)

## *Evaluating Goodness-of-Fit*

- Stress (=GOF) can be reported as an  $R^2$ :
  - ▶ *Stress-based*  $R^2 = 1 - S^2$
  - ▶ *Fit-based*  $R^2 =$  correlation between the fitted values and ordination distances, or between the step line and the points.
- Final stress depends on the dimensions of the original data set:
  - ▶ If  $N > 4P$ , stress insensitive to dimensionality

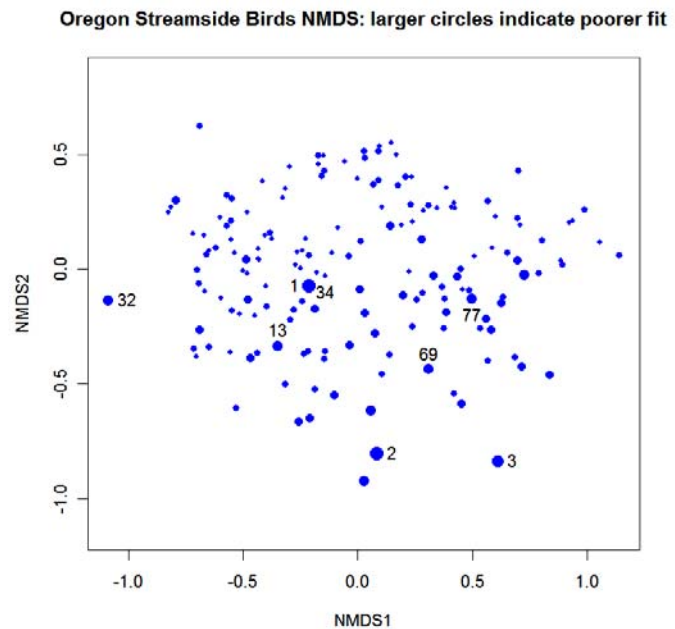


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# Nonmetric Multidimensional Scaling (NMDS)

## *Evaluating Goodness-of-Fit*

- Final stress is sensitive to high leverage points with particularly poor fit.
- Goodness-of-fit statistic for each point (i.e., its stress) can reveal influential samples.

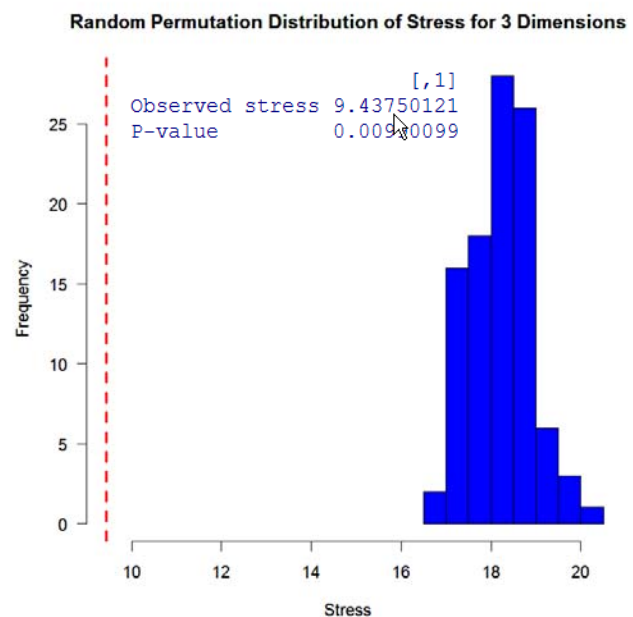


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# Nonmetric Multidimensional Scaling (NMDS)

## *Monte Carlo Test of Significance*

- Based on stress values from randomized versions of the data set (column shuffle).
- Strong outliers or a single super-abundant species can result in randomizations with stress similar to real data.
- Too conservative for small data sets ( $N < 10$ ).
- Too many zeros can produce empty samples, making some distance measures impossible.

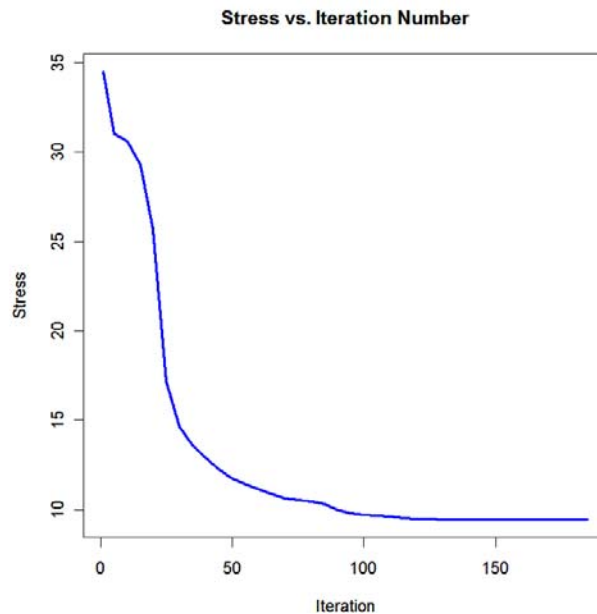


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## Nonmetric Multidimensional Scaling (NMDS)

### *Evaluating the Stability of the Solution*

- For a stable solution, the iterative search to minimize stress should decline steeply and then stabilize.
- Unstable solution can be caused by overfitting the data (using a dim too high given N), or where 2 or more local minima are equal competitors for the global minimum.



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## Nonmetric Multidimensional Scaling (NMDS)

### *Strengths of NMDS*

- No assumptions about linearity or Gaussian species responses to environmental gradients.
- Unbiased summary of the data as faithful as possible to the full multivariate structure.
- Allows the use of any dissimilarity measure or relativization.
- For most suitable community data sets, NMDS has proven equal to or superior to PCA and CA/DCA.
  - ▶ Less vulnerable than PCA and CA to the "arch" and "compression" effects.

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# Nonmetric Multidimensional Scaling (NMDS)

## *Limitations of NMDS*

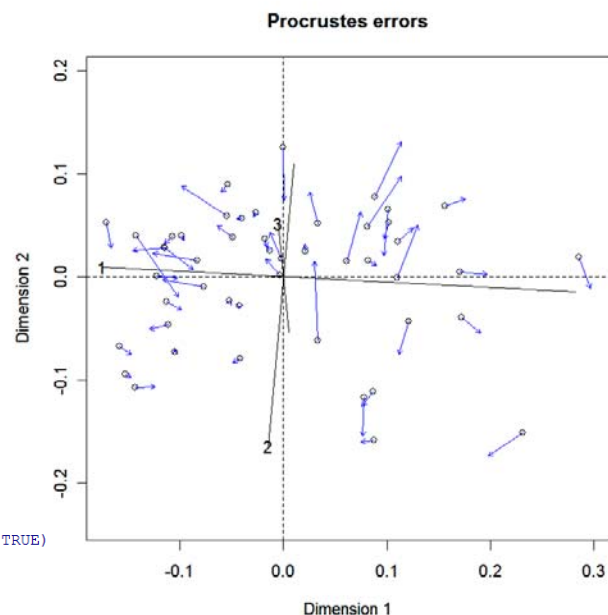
- Not based on any underlying theoretical model (e.g., Gaussian responses to environmental gradients).
- Solution depends on the dimensionality and is sensitive to “incorrect” specification.
- No inherent ordering of axes.
- Concept of variance explained by axes not clearly resolved, so it is difficult to compare performance with other techniques.
- Computationally demanding; e.g., can be time-consuming to do Monte Carlo tests on large data sets.

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# Indirect (Unconstrained) Ordination Techniques

## *Comparison of Ordinations*

- Procrustes rotation uses uniform scaling (expansion or contraction) and rotation to minimize the squared differences between two ordinations.



```
Call:
protest(X = rip.veg.nmds3, Y = rip.veg.nmds3a, symmetric = TRUE)
Correlation in a symmetric Procrustes rotation: 0.9458
Significance: < 0.001
Based on 1000 permutations.
```

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## Indirect (Unconstrained) Ordination Techniques

### *Comparison of Ordinations*

<u>Technique</u>	<u>Data matrix</u>	<u>Metric</u>	<u>Mapping</u>
PCA	Covariance	Euclidean	Linear
CA DCA	Primary	Chi-square	Weighted linear (unimodal)
MDS	Distance	Any	Linear
NMDS	Distance	Any	Nonlinear

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## Indirect (Unconstrained) Ordination Techniques

### *Comparison of Ordinations*

<u>Technique</u>	<u>When to use</u>
PCA	Not for community data; with short gradients; when <i>linear model</i> is appropriate
CA DCA	For community data when <i>unimodal</i> assumption met well (i.e., long gradients)
DCA	As above when arch and compression effect is severe
MDS	When Euclidean metric and linear mapping desirable but PCA assumptions not met (e.g., binary data)
NMDS	When other models not suitable

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