Stratigraphic Data

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Introduction

Introduction

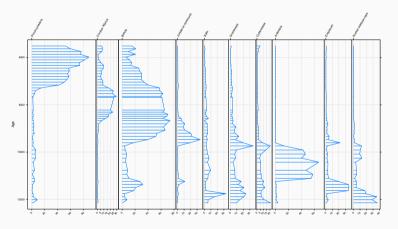
Summarising stratigraphic data

Summarising change in stratigraphic data

- · Ordination commonly used to describe patterns of change in multivariate sediment core data
- PCA, CA, or even DCA axis 1 and 2 scores commonly used
- These methods capture largest patterns of variation in underlying data under assumption of particular model
- · Can be upset by data sets with a dominant gradient
- · Can apply all techniques learned earlier in workshop to stratigraphic data
- \cdot Can we do any better than these methods?

Principal Curves

A single long or dominant gradient in an (palaeo)ecological data set poses particular problems for PCA and CA — horseshoe or arch



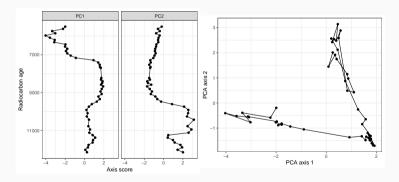
Abernethy Forest pollen data (Birks & Mathewes, 1978)

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Principal Curves

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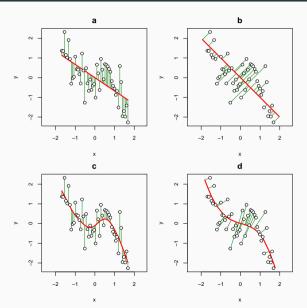
Trend is broken over two or more axes:



Can we generalise the PCA solution to be a smooth, non-linear surface?

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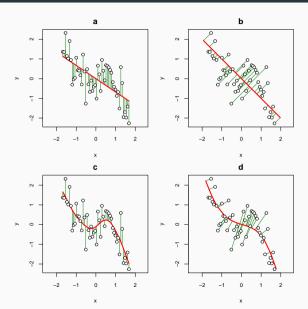
- In OLS regression, y is the response and x is assumed without error
- Errors are minimised in y only sums of squared errors
- \cdot PCA can be seen as a regression of y on x where neither y nor x plays the role of response or predictor
- \cdot In PCA, errors in both x and y are minimised sums of squared orthogonal errors



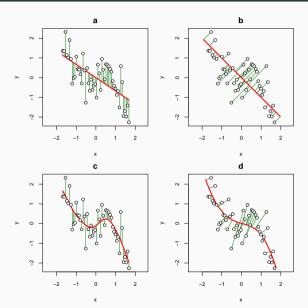
We can generalise the OLS model to a regression of y on x using a smooth function of x, f(x), as the predictor f(x) can be estimated using a multitude of techniques

- Loess smoother
- · Local-linear smooths
- Smoothing splines
- · Regression splines
- ...

f(x) is usually estimated from the data, with smoothness determined by minimising a penalised sums of squares criterion under CV (or GCV): Errors are still assessed in y only



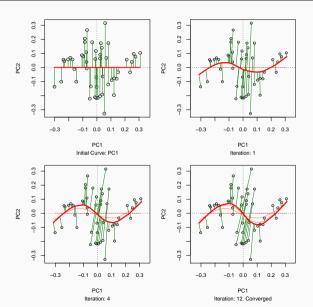
- Ideally we would generalise PCA to find non-linear manifolds in the same way as we went from OLS to semi-parametric regression using smoothers
- This is exactly what is done in the method of principal curves
- Our aim is to estimate as the principal curve, a 1-d manifold that passes through the data in high-dimensions that minimises the sum of squared orthogonal errors
- · We bend the principal component (for example) towards the data to achieve a better fit to the data
- How far and how flexibly we can bend the curve towards the data is determined from the data to minimise a penalized criterion during fitting



Principal Curves — Fitting algorithm

- Start with any smooth curve the first or second PCA or CA axis
- Begin the Projection Step
 - · All objects are projected onto a point on the smooth curve that they are closest too
 - · The distances of the points along the curve that each object projects onto are determined
- Begin the Local Averaging Step
 - · Bend the current smooth curve towards the data so that the sum of squared orthogonal distances is reduced
 - Taking each species (variable) in turn as the response, fit a smoother to predict the response using distance along the current curve as the predictor variable
 - Repeat for all species (variables) and collect the fitted values of the individual smoothers into a matrix that described the new location of the curve in high dimensions
- If the new curve is sufficiently similar to the current curve, declare convergence
- · If algorithm has not converged, iterate the projection and local averaging steps until convergence

Principal Curves — Fitting algorithm



Principal Curves — How Smooth?

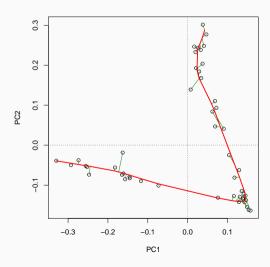
- The smoother fitted to produce the principal curve is a plug-in element of the algorithm
- · Can use any smoother; here used cubic regression splines
- · Important to not over fit the data by allowing too-complex a curve
- · Several options
 - Fit PCs with a large span (few df), note error, then reduce span (increase df), note error, etc. Use screeplot to determine optimal span
 - Fit smoothers to each species using starting curve, allowing (G)CV to choose optimal smoothness for each species. Fit the PC using the median of the smoothness values over all species
 - Allow the optimal degree of smoothness to be determined for each species individually during each local averaging step
- Advantage of latter is that those species that vary along the curve more strongly can use more degrees of freedom than those species that only vary lineally

Principal Curves — Abernethy Forest

```
> aber.pc <- prcurve(abernethy2, trace = FALSE, vary = TRUE, penalty = 1.4)
> aber.pc
    Principal Curve Fitting
Call: prcurve(X = abernethy2, vary = TRUE, trace = FALSE, penalty
= 1.4)
Algorithm converged after 6 iterations
           SumSq Proportion
Total
          103234
                     1.000
Explained 98864
                    0.958
Residual 4370
                     0.042
Fitted curve uses 218.3391 degrees of freedom.
> varExpl(aber.pc)
     PrC
0.9576693
```

Principal Curves — Abernethy Forest

Visualise the fitted curve in PCA space



Principal Curves — Comparison with PCA and CA

- The PC describes the long, sequential gradient in vegetation in a single variable
- The PC explains 96% of the variance in the absolute pollen data
- PCA axis 1 explains 47% and CA axis 1 31% of the variance in the data
- We need at least 2 PCA axes to fully capture the single gradient (80.2%)
- · Distance along the curve between adjacent time points is a measure of compositional change
- Can be expressed as a rate of compositional change highlights the periods of rapid compositional change in the Abernethy sequence

- · Stratigraphic sequences record changes over time
- · How quickly do these changes take place?
- · Rate of change analysis aims to answer this
- Two general approaches:
 - · change in ordination units
 - · change measured in dissimilarity
- · Could also use
 - derivatives of splines from principal curve
 - · derivatives of GAM(s) fitted to variables of interest

- · Jacobsen & Grimm (1988) method involves
 - smooth the data
 - · interpolate to constant time intervals
 - · ordinate smoothed, interpolate data (e.g.~using DCA)
 - · calculate change in ordination/axis score units as measure of RoC
- Dissimilarity-based approach can be performed two ways
 - · Smooth the data & interpolate, then compute dissimilarity between interpolated levels
 - Compute dissimilarity between adjacent samples directly, then standardise dissimilarity by time interval between samples.

TODO - needs an example

Chronological clustering (zonation)

Chronological clustering

- Chronological (or constrained) clustering commonly used to partition a sediment sequence into 2 or more zones
- Useful for, inter alia
 - · delineating periods of similar species composition
 - · identifying discontinuities or periods of rapid change
 - · to facilitate description of a stratigraphic sequence
- · As with standard cluster analysis, plethora of methods available
 - · Optimal partitioning
 - · Binary (divisive) splitting
 - · Agglomerative partitioning
- · Can be used with any dissimilarity (in theory), but common ones are
 - · Cluster sums of squares (within-group Euclidean distance)
 - · Cluster-wise information statistic

Chronological clustering

- · Optimal partitioning
 - · Identifies optimal locations for splits to form k zones
 - · Non-hierarchical, 3 zone solution not found by splitting one of the zones from the two zone solution
 - · Split placed to minimise within-cluster sum of squares or information content
- · Binary (divisive) splitting
 - · Similar to optimal method but is hierarchical
 - · Split sequence into two zones, then split one of the 2 resulting zones, repeat
 - $\cdot\,$ Zone that is split is the one that would reduce within-group SS or IC the most
- · Agglomerative partitioning
 - · Start with all samples in separate zones and fuse the most similar adjacent samples
 - · Repeat, each time fusing most similar samples or zones

CONISS

es the long, sequential gradient in vegetation in a single variable - The PC explains 96% of the variance in the absolute pollen data - PCA axis 1 explains 47% and CA axis 1 31% of the variance in the data - We need at least 2 PCA axes to fully capture the single gradient (80.2%) - Distance along the curve between adjacent time points is a measure of compositional change - Can be expressed as a rate of compositional change — highlights the periods of rapid compositional change in the Abernethy sequence

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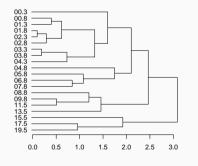
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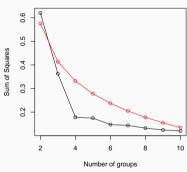
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Chronological clustering

TODO insert HJBB's figure from chpt 11 DPER5 $\,$





Binary splitting via MRT

