Geometric morphometrics

Landmark analyses

Manuel F. G. Weinkauf

Univerzita Karlova, Prague, Czech Republic

26–27 August 2022

Section 1

Introduction

Describe the true overall shape

- We use the x- and y-coordinates of well-defined elements of the structure as they are
- The coordinates of different structures are superimposed to make them comparable

Describe the true overall shape

- We use the x- and y-coordinates of well-defined elements of the structure as they are
- The coordinates of different structures are superimposed to make them comparable
- **Advantage:** Great for structures with many morphologically homologue features

Describe the true overall shape

- We use the x- and y-coordinates of well-defined elements of the structure as they are
- The coordinates of different structures are superimposed to make them comparable
- **Advantage:** Great for structures with many morphologically homologue features
- **Disadvantage:** Not all structures have good landmarks (and some issues with phylogenetic studies because landmarks are not independent of each other)

The types of landmarks

- Landmarks are points that are well defined in all specimens
- Three types of landmarks can be distinguished
  1. **Type I landmarks/anatomical landmarks:** Well defined and biologically homologous points, for instance points where bones meet, nerve canal openings, tubercles
  2. **Mathematical landmarks:** Defined on the basis of geometric properties
     1. **Type II landmarks:** Points that are defined by a local property, such as maximum curvature of the shell
     2. **Type III landmarks:** Landmarks at extremal points of a structure (e.g. the tip of the finger bone) or at constructed points (e.g. the centroid of the eye cavity)

We extract coordinates of well-defined points

We extract coordinates of well-defined points

- **Type I**

We extract coordinates of well-defined points

• **Type I** • **Type II**

We extract coordinates of well-defined points

- **Type I**
- **Type II**
- **Type III**

Hospitality in ancient Greece

- We now have x- and y-coordinates of corresponding (morphological homologous) points $\Rightarrow$ in contrast to outline semi-landmarks we could analyse them as they are

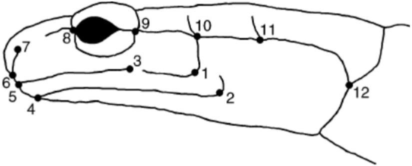
Hospitality in ancient Greece

- We now have x- and y-coordinates of corresponding (morphological homologous) points $\Rightarrow$ in contrast to outline semi-landmarks we could analyse them as they are
- But first, we need to talk about an old Greek fella named Procrustes

Who is Procrustes, and what did he do to my data?

- We extract landmarks from different individuals
  - They may be from different sexes
  - They may be from different ontogenetic stages

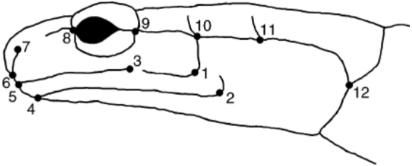
Adams (2004) Ecology 85 (10): 2664–70

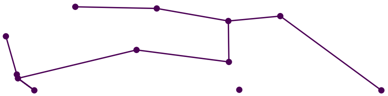


Who is Procrustes, and what did he do to my data?

- We extract landmarks from different individuals
  - They may be from different sexes
  - They may be from different ontogenetic stages

Adams (2004) Ecology 85 (10): 2664–70

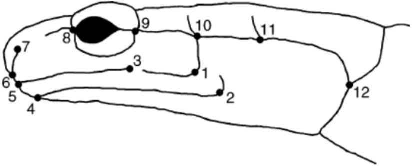


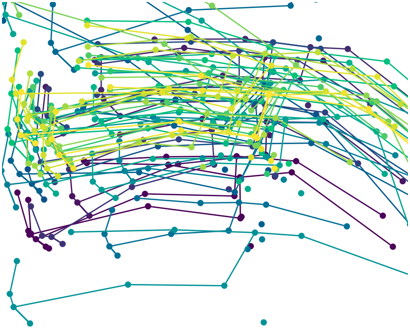


Who is Procrustes, and what did he do to my data?

- We extract landmarks from different individuals
  - They may be from different sexes
  - They may be from different ontogenetic stages
- $\Rightarrow$ Specimen size and image cropping are factors that influences landmark position

Adams (2004) Ecology 85 (10): 2664–70

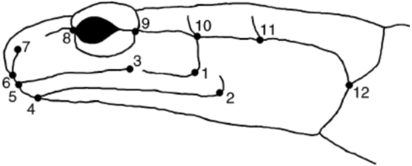


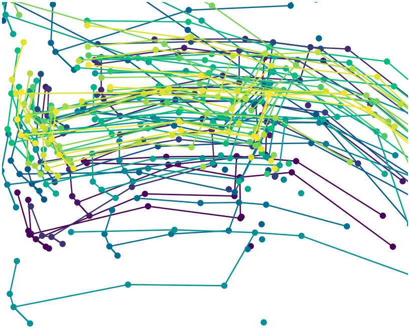


Who is Procrustes, and what did he do to my data?

- We extract landmarks from different individuals
  - They may be from different sexes
  - They may be from different ontogenetic stages
- ⇒ Specimen size and image cropping are factors that influences landmark position
- **We only want pure shape information, without noise**

Adams (2004) Ecology 85 (10): 2664–70





Procrustes superimposition

- Centres all shapes in the dataset at the origin $\{0, 0, [0]\}$

Procrustes superimposition

- Centres all shapes in the dataset at the origin $\{0, 0, [0]\}$
- Scales all shapes to unit size

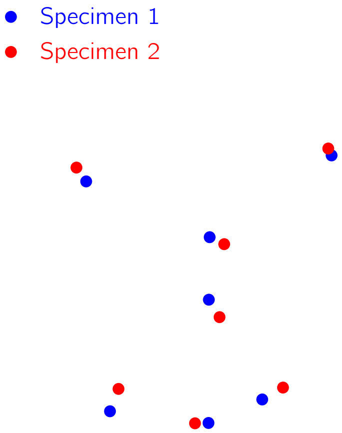
Procrustes superimposition

- Centres all shapes in the dataset at the origin $\{0, 0, [0]\}$
- Scales all shapes to unit size
- Rotates all shapes to similar orientation

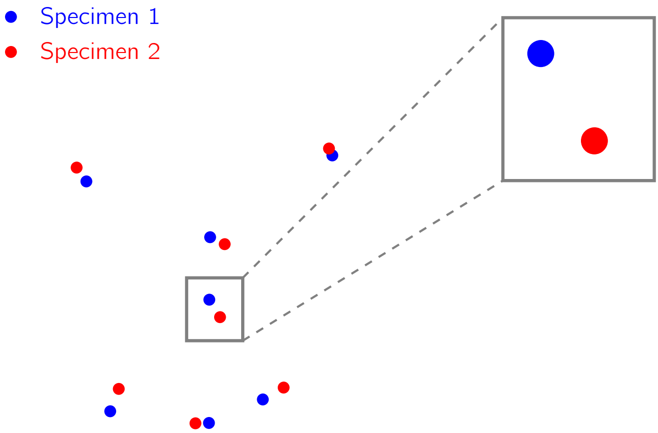
Procrustes superimposition

- Centres all shapes in the dataset at the origin $\{0, 0, [0]\}$
- Scales all shapes to unit size
- Rotates all shapes to similar orientation
- $\Rightarrow$ **Removes arbitrary shape and size information, only pure shape information remains**

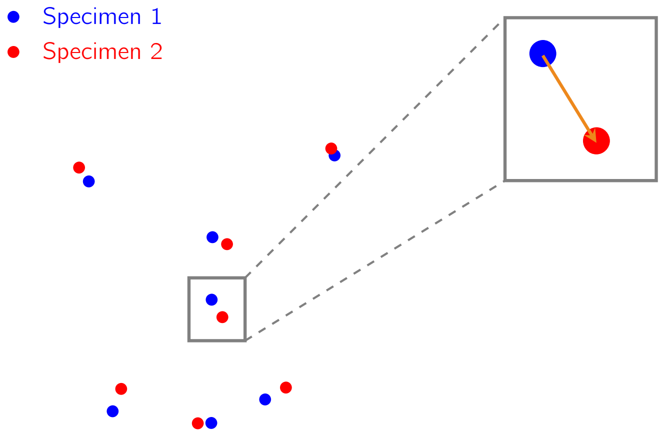
Procrustes distances



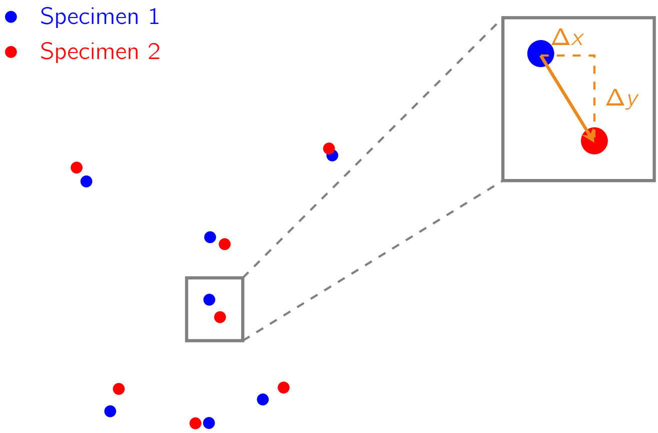
Procrustes distances



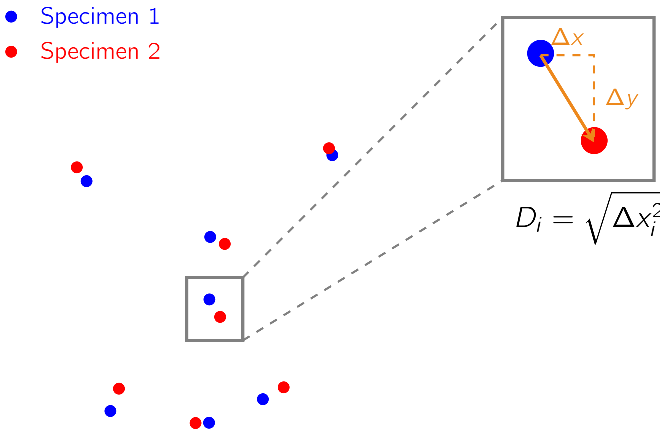
Procrustes distances



Procrustes distances

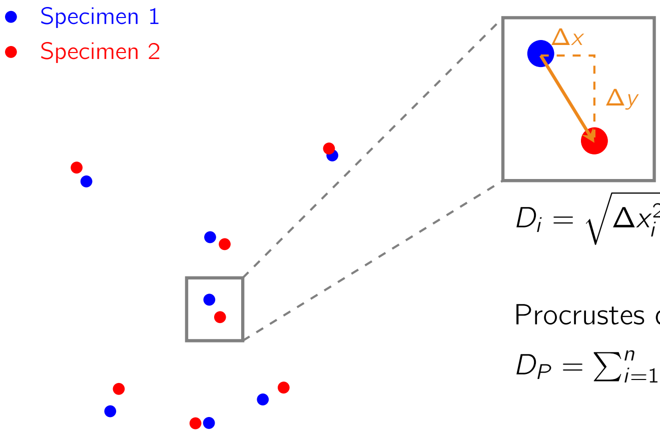


Procrustes distances



$$D_i = \sqrt{\Delta x_i^2 + \Delta y_i^2}$$

Procrustes distances



$$D_i = \sqrt{\Delta x_i^2 + \Delta y_i^2}$$

Procrustes distance D_P:

$$D_P = \sum_{i=1}^{n} D_i$$

Procrustes superimposition

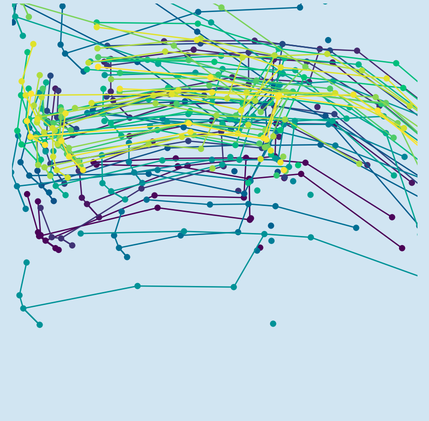
- Scales, translates, and rotates all shapes until the total of all Procrustes distances is minimized

Procrustes superimposition

- Scales, translates, and rotates all shapes until the total of all Procrustes distances is minimized
- All remaining Procrustes distances between landmark configuration are **true shape differences** between specimens
- Procrustes distances are the **major measurement of differences between shapes** in landmark analyses in further analyses

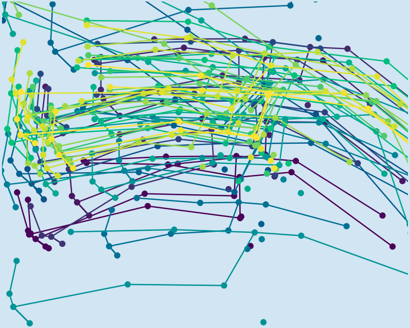
An example: Salamander heads

Before superimposition

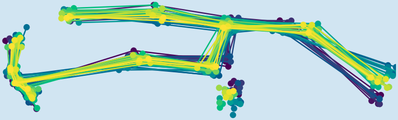


An example: Salamander heads

Before superimposition



After superimposition



But beware!

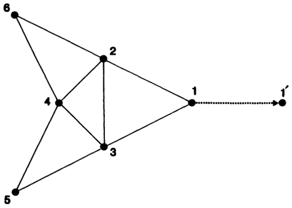
- Procrustes superimposition removes degrees of freedom from the data
  1. $-4\,\mathrm{df}$ for 2 D-data
  2. $-7\,\mathrm{df}$ for 3 D-data
- $\Rightarrow$ Standard methods must be adapted for this

But beware!

- Procrustes superimposition removes degrees of freedom from the data
  1. $-4\,\mathrm{df}$ for 2 D-data
  2. $-7\,\mathrm{df}$ for 3 D-data
- $\Rightarrow$ Standard methods must be adapted for this
- The superimposition is applied to the entire shape as a whole
- $\Rightarrow$ Procrustes-superimposed landmarks are collinear
  1. Only allows to investigate variation in entire shape, not compare individual parts of the shape
  2. Strong variation in one part of the shape is re-distributed across entire shape

The Pinocchio Effect

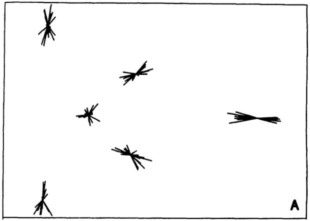
- Shape variation can be strongly localized in small part of the organism
- For instance sauropod dinosaur's neck length

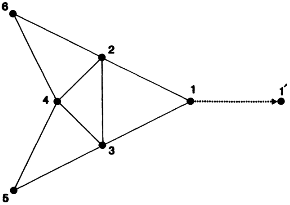


Rohlf and Slice (1990) Syst. Zool. 39 (1): 40–59

The Pinocchio Effect

- Shape variation can be strongly localized in small part of the organism
- For instance sauropod dinosaur's neck length

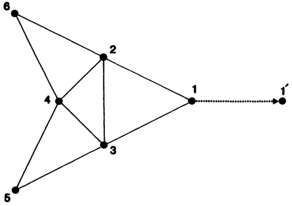


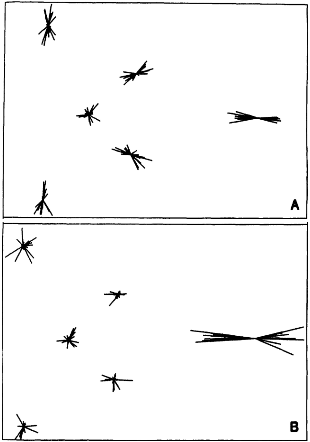


Rohlf and Slice (1990) Syst. Zool. 39 (1): 40–59

The Pinocchio Effect

- Shape variation can be strongly localized in small part of the organism
- For instance sauropod dinosaur's neck length
- Solution: **Generalized resistant fit**





Rohlf and Slice (1990) Syst. Zool. 39 (1): 40–59

R

Example of landmark data preparation

For a look at landmark data preparation in R, we move on to exercise № 4

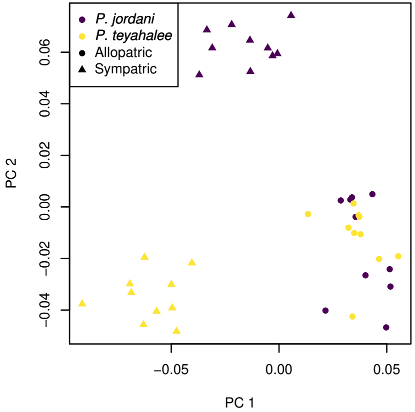
Open the exercise sheet for instructions and code examples

Section 2

Landmark data analysis

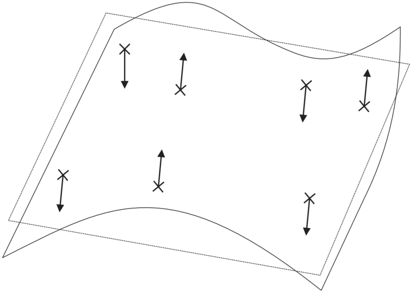
We now have a multivariate dataset

- After superimposition, we can do the usual things with the landmark data
  1. PCA to visualize differences
  2. Cluster analyses to define groups
  3. LDA/CVA to distinguish *a priori* defined groups
  4. MANOVA to test for between-group differences



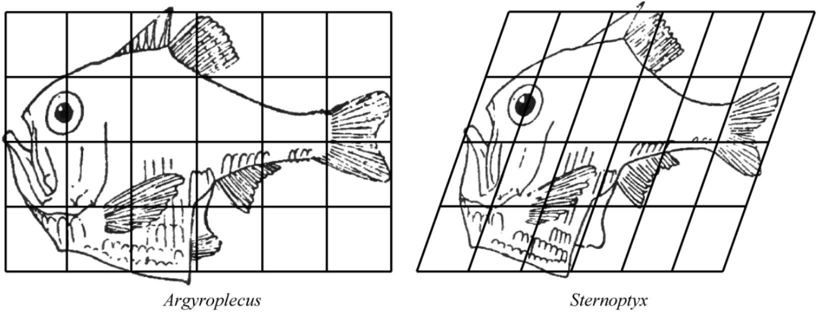
We can also visualize shape changes

- Suppose we have two shapes (e.g. two species)
- We can imagine the landmarks of one shape to be drawn on a thin, flat, stiff, yet flexible plate
- We can then bend and deform that shape until the landmarks fit those of the other shape



Hammer and Harper (2006) Paleontological Data Analysis (Blackwell: Malden, Oxford, Carlton)

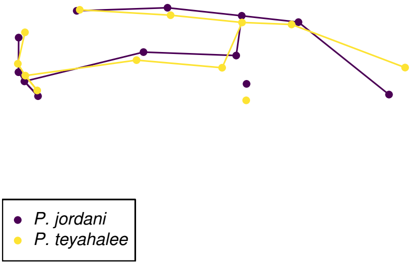
The principal of the thin-plate spline



Thompson (1917) On Growth and Form (Cambridge University Press: Cambridge)

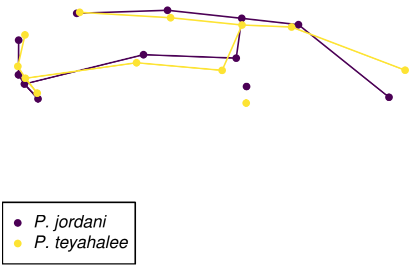
The principal of the thin-plate spline

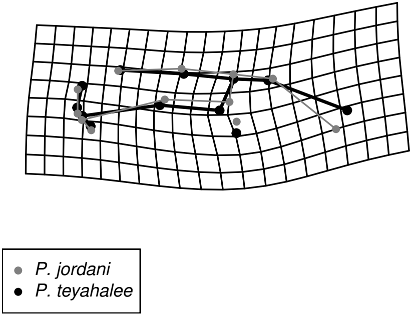
Example: Our salamanders



The principal of the thin-plate spline

Example: Our salamanders

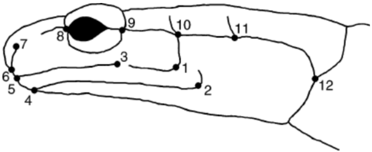


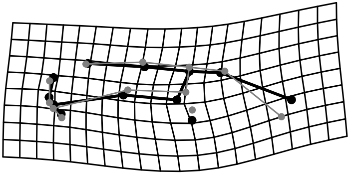


How to interpret the thin-plate spline

Example: Our salamanders

- From *P. jordani* to *P. teyahalee* . . .



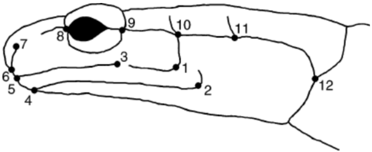


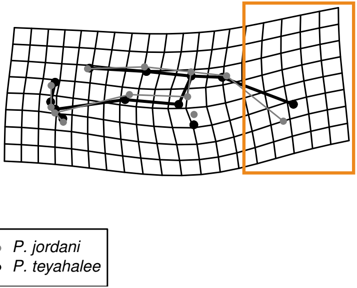
- *P. jordani*
- *P. teyahalee*

How to interpret the thin-plate spline

Example: Our salamanders

- From *P. jordani* to *P. teyahalee* . . .
  1. . . . the posterior skull lifted up

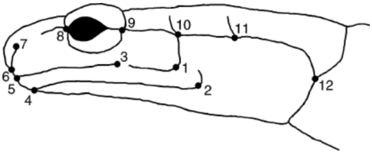


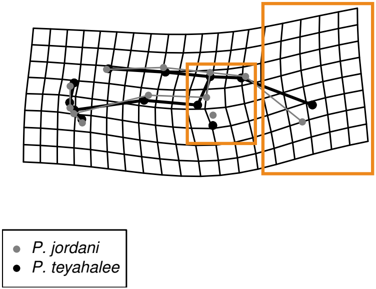


How to interpret the thin-plate spline

Example: Our salamanders

- From *P. jordani* to *P. teyahalee* . . .
  1. . . . the posterior skull lifted up
  2. . . . the mid-skull became thicker

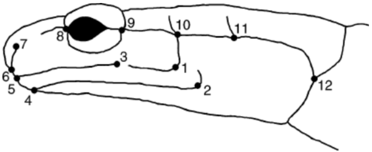


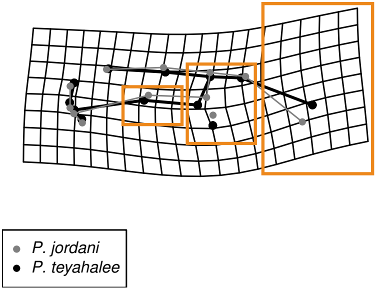


How to interpret the thin-plate spline

Example: Our salamanders

- From *P. jordani* to *P. teyahalee* . . .
  1. . . . the posterior skull lifted up
  2. . . . the mid-skull became thicker
  3. . . . the snout became shorter in expense of the posterior skull



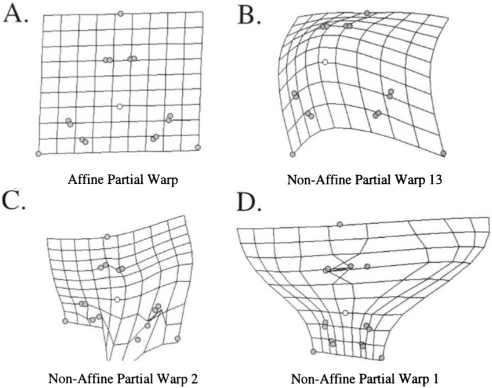


Going further with thin-plate splines

- Thin-plate splines are the basis for a lot of techniques in geometric morphometrics
  1. Principal and partial warps to decompose morphological change
  2. Relative warps to find groupings by comparing all specimens with the mean shape
  3. Disparity analyses to quantify morphological variation

Partial warps

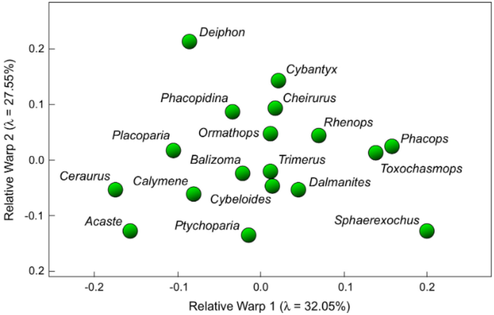
- Separates morphological deformation into
  1. **Affine component** of uniform shape deformation
  2. **Non-affine components** of localized deformation on different scales



MacLeod (2001) in: Adrain et al., Fossils, Phylogeny, and Form (Springer: Boston)

Relative warps

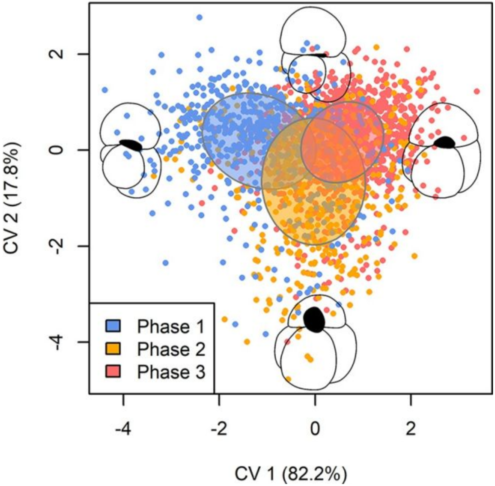
- PCA of the bending energy matrix for transformation between each shape and the mean shape
- Allows to separate groups amongst dataset



MacLeod (2010) Palaeontology Newsletter 75: PaleoMath101–21

Disparity analysis

- Measure of morphological variation within a taxonomic or morphological group
- Usually based on Riemannian shape variation within groups



Weinkauf et al. (2019) PLoS ONE 14 (10): e0223490

R

Example of landmark data analysis

For a look at landmark data analysis in R, we move on to exercise № 5

Open the exercise sheet for instructions and code examples