E-learningový kurz
Modern quantitative methods and shape analysis in archaeology

Tento materiál vznikl v rámci realizace projektu Strategický rozvoj Univerzity Hradec Králové, reg. č. CZ.02.2.69/0.0/0.0/16_015/0002427.
3D landmark analyses
New 3D ICP-based methods of shape analysis
Practice
Fully Automated Approach for Aligning and Comparing Shapes

Fully Automated Approach for Aligning and Comparing Shapes

Why?

(i) Algorithm can reasonably (!) match corresponding points on different specimens

(ii) Possible to estimate shape differences

(iii) allow for the entertainment of different “correspondence hypotheses” based on the morphocline/“path” that is assumed to connect shapes in the dataset

Demonstration on bones

auto3dgm package for R
www.dougmboyer.com
http://www.stat.duke.edu/sayan/
CRAN
Concerns with homology
- Bookstein (1994) – morphometrics must be applied after homology consideration
- Boyer et al. (2015) – *auto3dgm* can identify an “operational homology” or “biological correspondence” without consideration *a priori*
Iterative Closest Point algorithm (ICP)
- similar to Procrustes - minimize distances between several objects by changing their position, size and rotation
- generalization of Procrustes – can be used to points, but also to lines, splines or surfaces
- difference in the definition of correspondence:
  - Do not use Landmark-to-Landmark…
  - …but Point-to-Closest-Point
- pseudolandmarks
(A) **3D Data preparation**
- Low-resolution models for initial alignment
- High-resolution models for final alignment

**Down-sampling points on meshes**
(1) Randomly pick a point on the surface
(2) Pick the farthest point
(3) Pick a third point which is farthest from these two
(B) Pre-alignment by PCA
- ICP is known to be sensible to initial guess
- PCA – assumption that principal axes of variation of many 3D objects will tend to be homologous amongst samples
- By taking first three PC there is 8 possibilities of alignment of two objects
- Calculations are made on Low-resolution models

(C) Initial alignment by ICP
- These 8 alignments are taken as initial guesses for ICP
- Calculations are made on Low-resolution models
- Resulting comparisons give matrix of Procrustes distances between specimens

Boyer et al., 2015
(D) Check initial alignment by MDS and MST
- both methods are calculated on matrix of Procrustes distances
- Multidimensional Scaling (MDS) – method analogous to PCA, but more suitable for distance matrices
- Minimum Spanning Tree (MST) – connect all specimens by using the shortest edge length possible (nearest neighbors)

(E) Check initial alignment visually
Fixing alignments (*alignFix* protocol)

A) Identification of misaligned specimens (MS)
B) Identification of MS in MST
C) Separation of MST into Base tree and Branches
   - Base tree with well aligned specimens
   - Branches with MS (here Branch A and B)
D) Test mutual alignment of MS to know if they make one coherent branch (here yes)
E) Each MS is aligned with specimens of Base Tree and visually inspected to find joining specimens (here 2 with 4)
F) These two specimens are used for connecting coherent branch (obtained in step D) with Base Tree
G) Recomputing the alignment (now correct result)

not easy with lot of samples…
(F) **Final alignment by ICP**
- Calculations are made on High-resolution models
- Only slight variations of position, size, and rotation are used in ICP
- Resulting comparisons give matrix of Procrustes distances between specimens

Boyer et al., 2015
Parameters

(1) Number of points for low-resolution first alignment
(2) Number of points for high-resolution final alignment
(3) Number of principal alignments
   - 8 by definition
   - but more random principal alignments can be used
Comparison auto3dgm with GPA

Materials and Methods:
- Dataset: 106 bones, 7 groups
- auto3dgm: Initial = 150 pts, Final = 1024 pts,
  Principal alignments = 8
- 3D GPA: 27 landmarks

Results and Discussion
- PCA and correlation between PC showed similarities and coherency
- 3D GPA:
  + more variance kept by less PC
- auto3dgm
  - more sensitive to errors caused by noise
  - large P, small N problem
  + no need to assess homology

Boyer et al., 2015
Visualisation of shape variability of teeth

Question:
- What are main tendencies related to the shape variability of specimens?

Dataset
- 5 or 15 teeth
- dataset and documentation is available at: http://www2.stat.duke.edu/~sayan/auto3dgm/Instructions/index.html

Procedure
- Perform auto3dgm
- Perform Principal Component Analysis (PCA)
- Perform Principal Coordinate Analysis (PCoA)
- Perform Multidimensional Scaling (MDS)
Software
- Meshlab: www.meshlab.net
- R: https://www.r-project.org/
- R Packages: Matrix, clue, lpSolve, linprog, igraph, MASS, geomorph
- PAST: https://folk.uio.no/ohammer/past/
Check folder

auto3dgm: unpacked package
auto3dgm.tar.gz: ‘auto3dgm’ package
auto3dgm_documentation.pdf: package documentation

teeth_dataset: dataset used in analyses
output: folder into which we will save results of alignment
output_original: already calculated results

Web_Example.R: script in R programming language
Check specimens in Meshlab off files in “teeth_dataset” folder

Teeth
Run procedure in R environment
Read (!), edit (!), copy and paste the code from “Web_Example.R” into R console
See “auto3dgm_documentation.pdf” for more information
Run procedure in R environment
Read (!), edit (!), copy and paste the code from “Web_Example.R” into R console
See “auto3dgm_documentation.pdf” for more information
Check results folder
A lot of useful things…
Check results folder
Specimens after initial alignment
Check results folder
Initial and Final alignments
Check results folder
Multidimensional Scaling (MDS) and Minimum Spanning Tree (MST)
Check results folder
Multidimensional Scaling (MDS) and Minimum Spanning Tree (MST)
Check results folder
Coordinates of aligned shapes

morpohologica – initial alignments
morpohologica2 – final alignments
_unscaled – without size adjustment
Check results folder
Coordinates of aligned shapes

cords – the same as morphologica2
Data preparation

1) Open file:
   File >> Open  >> cords.csv

2) Change Separator to Comma
Principal Component Analysis (PCA)

Multivariate >> Ordination >> Principal Components (PCA)

Description and discussion
- how much information we see in graphics?
- how many components are meaningful?
- which changes of shape are represented?
Principal Coordinate Analysis (PCoA)

Multivariate >> Ordination >> Principal Coordinates (PCoA)

Description and discussion
- how much information we see in graphics?
- how many components are meaningful?
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Multidimensional Scaling (MDS)

Multivariate >> Ordination >> Non-metric MDS

Description and discussion
- how much information we see in graphics?
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- which changes of shape are represented?
References

- www.wikipedia.org