

# How to build an average model when samples are variably incomplete? Application to fossil data

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**AMIS**  
UMR 5288 du CNRS

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ET  
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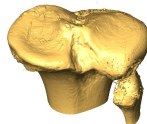
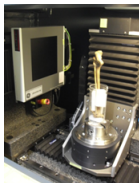


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# INTRODUCTION

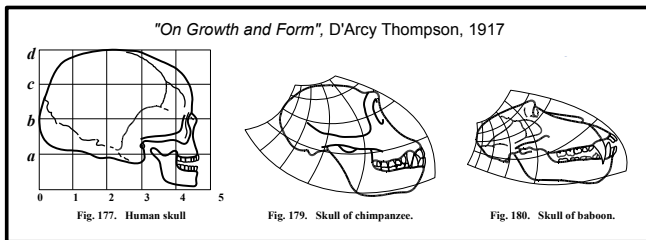
Paleontology :

- ▶ Study of morphology and morphometry.



3D reconstruction of a bone by tomographic acquisition

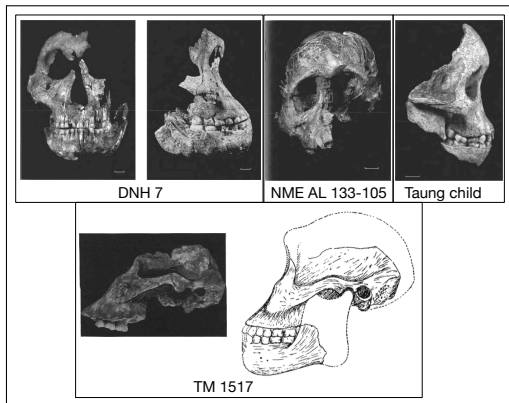
- ▶ Taxonomy: naming and classifying organisms.





# INTRODUCTION

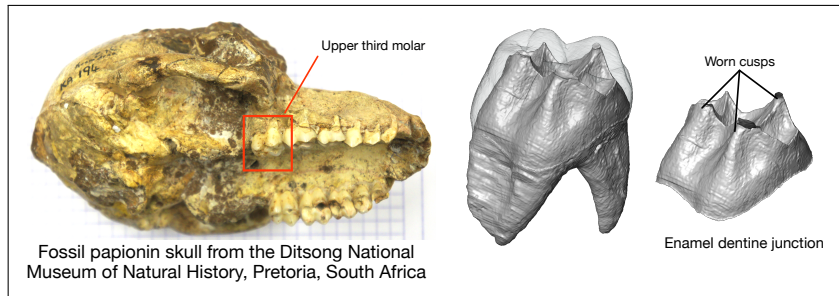
- ▶ Alteration of the geometry of the samples by biological modifications or post-mortem taphonomic processes.
- ▶ How to deal with **missing parts** ?



# INTRODUCTION

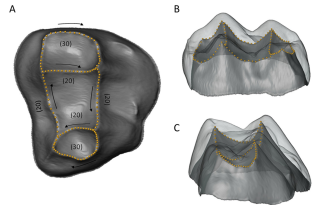
An example of missing data

- ▶ Material : enamel-dentine junction of fossil teeth ( $\approx 2$  million years) to be compared to living baboon teeth.
- ▶ Analysis of the enamel dentine junction which characterizes the tooth shape.
- ▶ Problem of enamel and dentine loss due to dental wear  $\Rightarrow$  **Missing parts** problem.

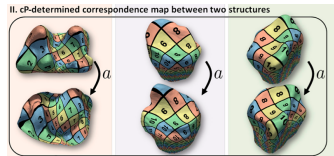


# MORPHOMETRIC METHODS

- ▶ Geometric Morphometrics based on a limited set of landmark positions.
- ▶ Surface-based morphometrics which implies to find automatically the correspondences all over the surface.



Beaudet 2015



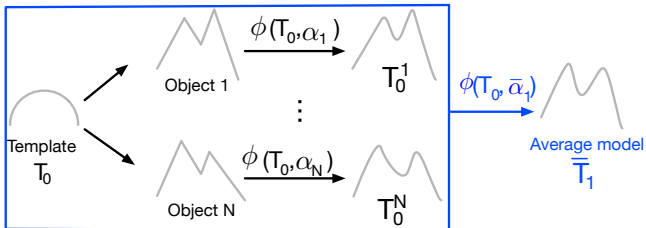
Boyer et al. 2011

# REGISTRATION METHODOLOGY

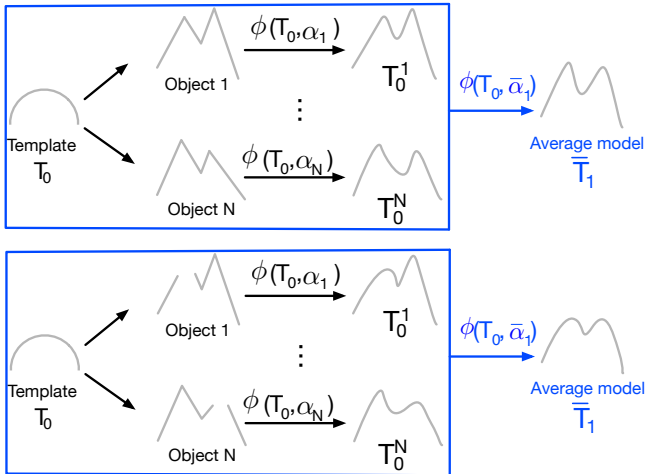
Based on Deformetrica (<http://www.deformetrica.org>),  
Durrleman et al. 2014.

(Registration)

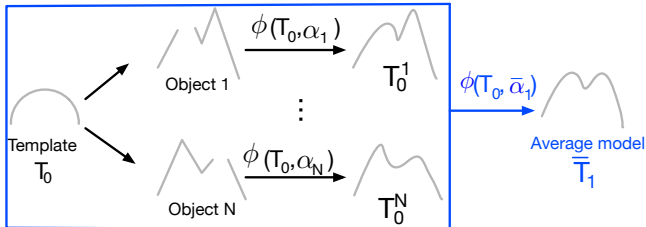
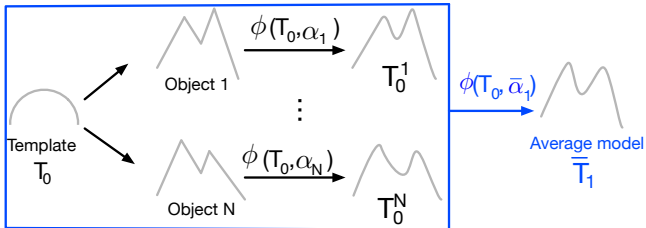
# 1. STANDARD AVERAGE



# 1. STANDARD AVERAGE

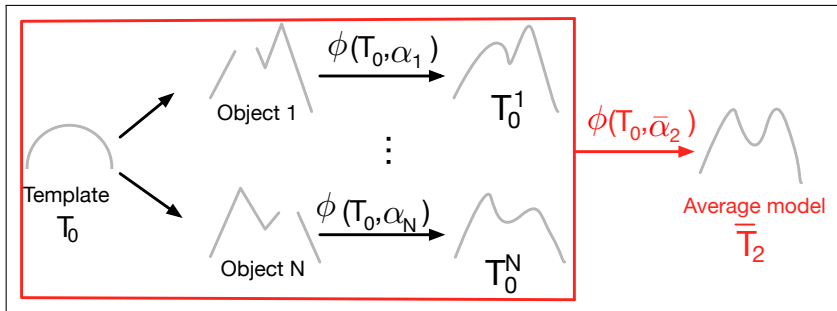


# 1. STANDARD AVERAGE



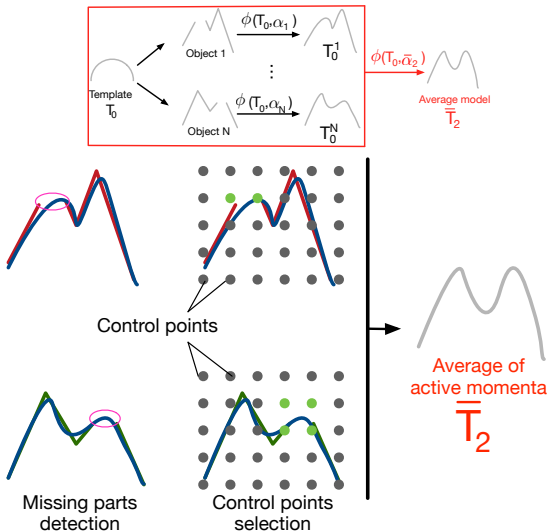
How can the optimum average be evaluated when samples present missing parts ?

## 2. NOT TAKING INTO ACCOUNT THE MISSING PARTS

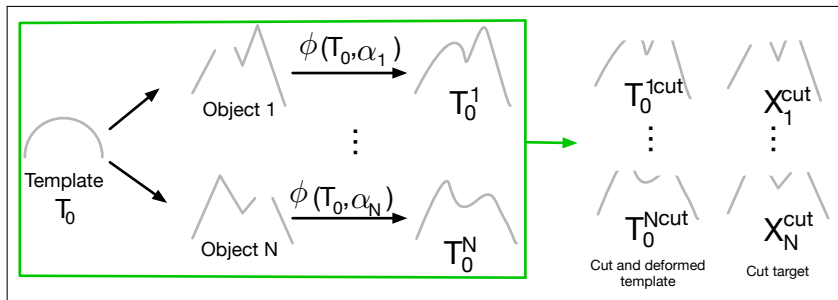




## 2. NOT TAKING INTO ACCOUNT THE MISSING PARTS

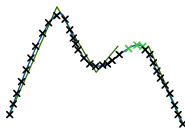
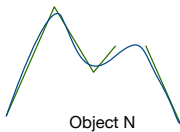
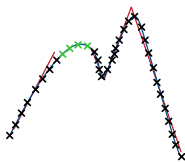
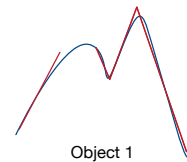
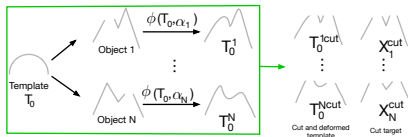


### 3. COMMON PARTS ONLY





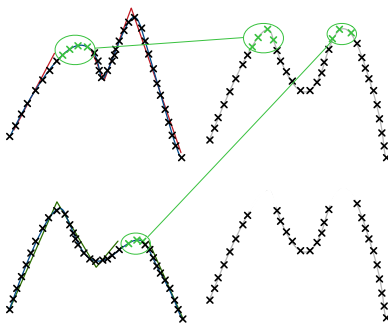
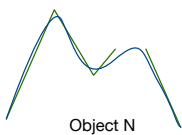
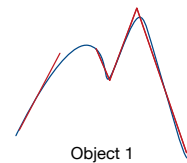
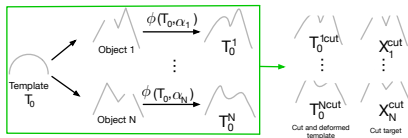
### 3. COMMON PARTS ONLY



Registration

Detection of  
missing parts

### 3. COMMON PARTS ONLY

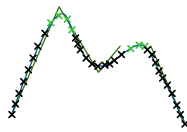
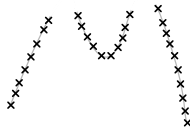
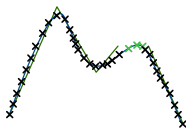
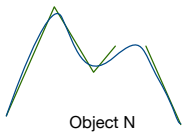
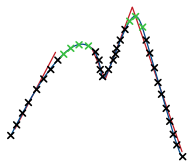
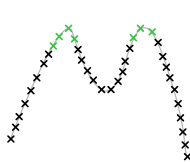
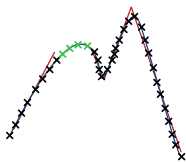
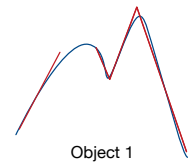
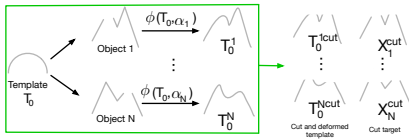


Registration

Detection of  
missing parts

Average shape

### 3. COMMON PARTS ONLY

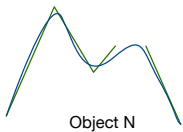
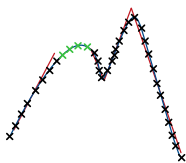
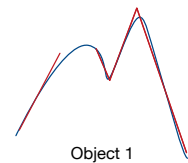
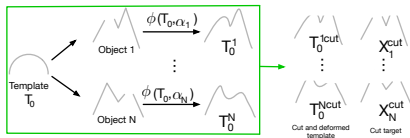


Registration

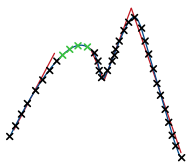
Detection of missing parts

Average shape

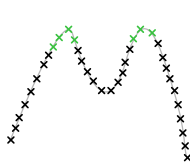
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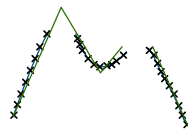
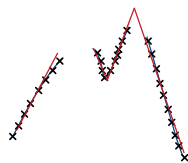
Registration



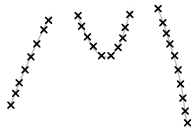
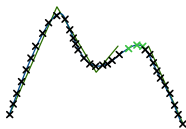
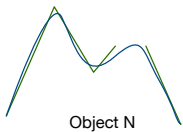
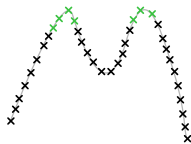
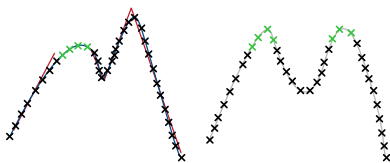
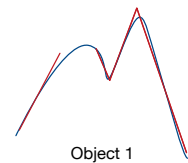
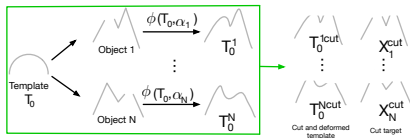
Detection of missing parts



Average shape



### 3. COMMON PARTS ONLY



Registration

Detection of  
missing parts

Average shape

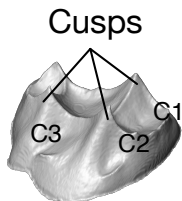
Cut objects



# DATABASE

- ▶  $\mu$ -CT acquisitions performed at Necsa (South Africa) and CIRIMAT (France).
- ▶ Resolution:  $\simeq 70\mu\text{m}$ .
- ▶ Study of the missing part influence on 3 cusps.

(EDJ segmentation)



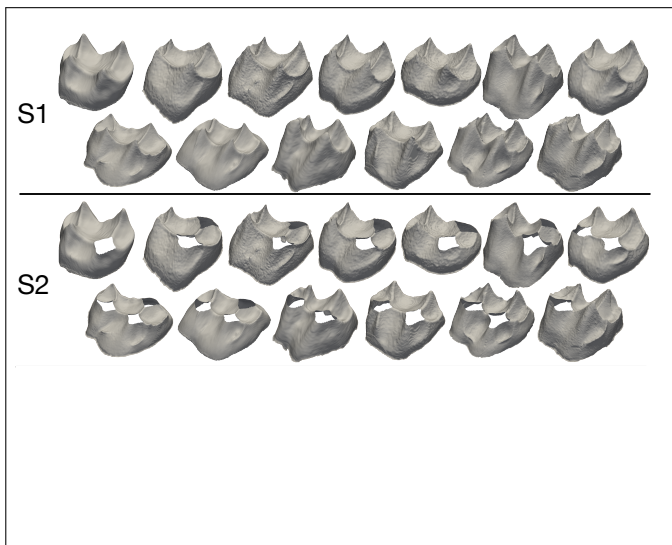
# DATABASE

First sample : 13 complete surfaces



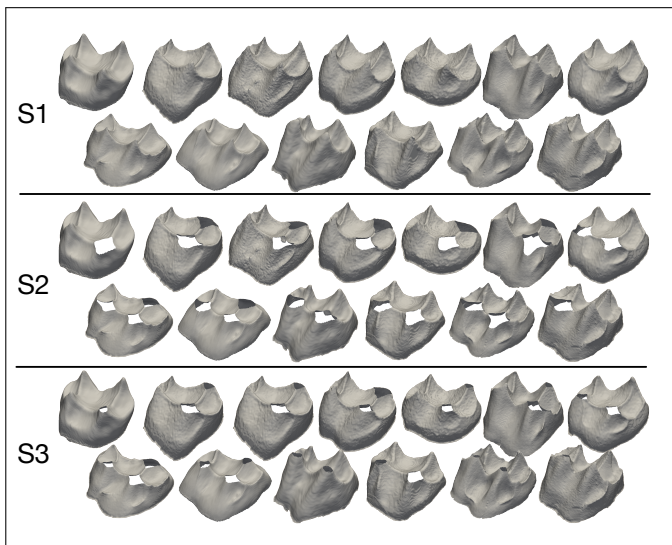
# DATABASE

Second sample : 13 manually cut surfaces





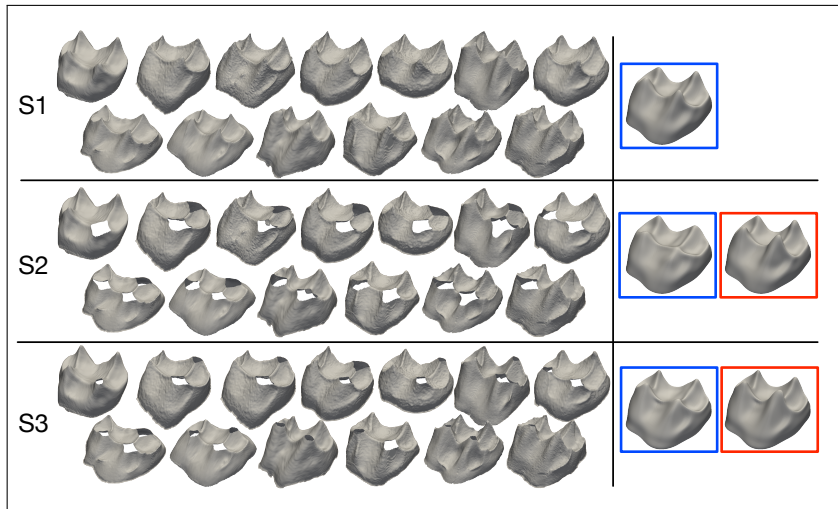
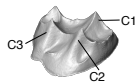
# DATABASE

Third sample : 13 manually cut surfaces



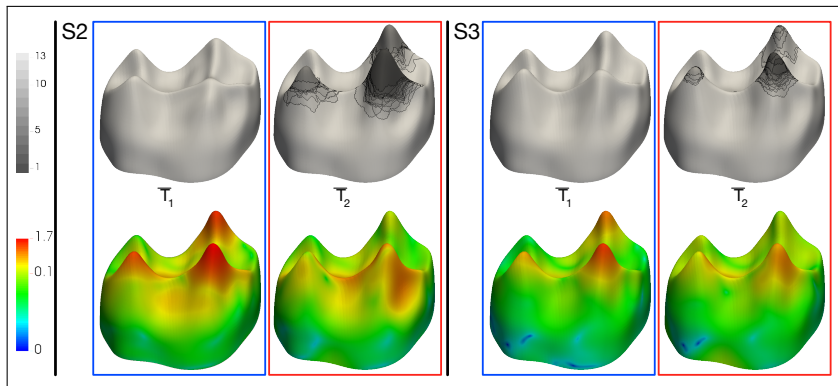
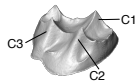
## RESULTS

-  Result with standard average
-  Result with our average procedure



# COMPARISON WITH THE GROUND-TRUTH COMPLETE DATASET

- Result with standard average
- Result with our average procedure

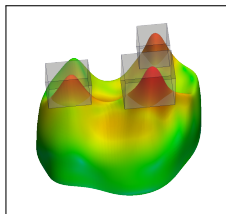
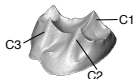


Top: Number of samples used to compute the average shape.

Bottom: distance maps between the ground-truth shape and the average shapes with incomplete samples.

# COMPARISON WITH THE GROUND-TRUTH COMPLETE DATASET

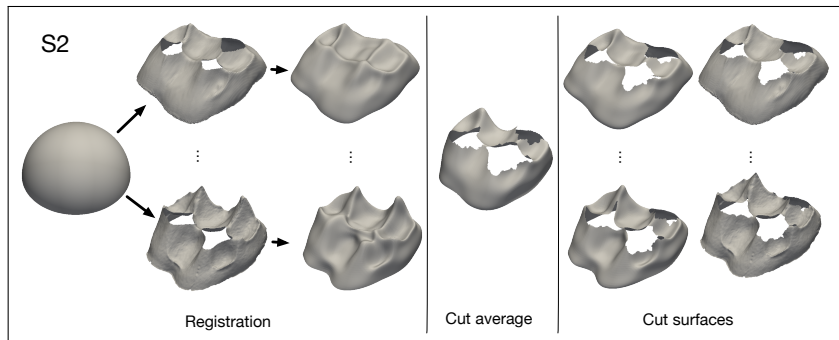
- Result with standard average
- Result with our average procedure



		All	Cusp 1	Cusp 2	Cusp 3
S2	<input type="checkbox"/>	0.11 (0.21)	0.47 (0.18)	0.81 (0.38)	0.58 (0.23)
	<input type="checkbox"/>	0.10 (0.13)	0.18 (0.09)	0.42 (0.17)	0.06 (0.03)
S3	<input type="checkbox"/>	0.05 (0.10)	0.15 (0.07)	0.40 (0.22)	0.25 (0.11)
	<input type="checkbox"/>	0.05 (0.07)	0.15 (0.08)	0.24 (0.12)	0.05 (0.02)

The mean (and standard deviation) of the distances between the average shape of S1 and the average shapes of S2 and S3

# ELIMINATION OF NON-COMMON PARTS





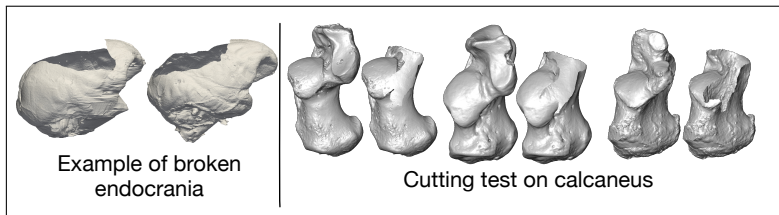
# CONCLUSION

Our method contributes to:

- ▶ the inclusion of damaged specimens in morphometrical analyses.
- ▶ a more accurate evaluation of the paleobiodiversity.

Perspectives:

- ▶ anatomical variant.
- ▶ influence of the parameters.
- ▶ application on endocrania and bones (calcaneus).



# THANK YOU FOR YOUR ATTENTION!

## Acknowledgments:

- ▶ Didier Ginibriere, G. Fleury, B. Duployer, and C. Tenailleau (Toulouse), S. Potze (Pretoria), B. Zipfel (Johannesburg), E. Gilissen and W. Wendelen (Tervuren), L. Bam, J. Hoffman, and F. de Beer (Pelindaba), and the four WBIR anonymous reviewers.

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