Two “non-standard” methods to analyze 2D/3D shapes

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2D SHAPE ANALYSIS BASED ON PLANAR MECHANISM DESIGN

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In general, based on Fourier descriptors:

- Is it well adapted to the shape?
  20 harmonics gives 4x20=80 coefficients to explain the positions of 84 points
- EEF parameters are not directly related to local geometry
- May be sensitive to the definition of the origin point.

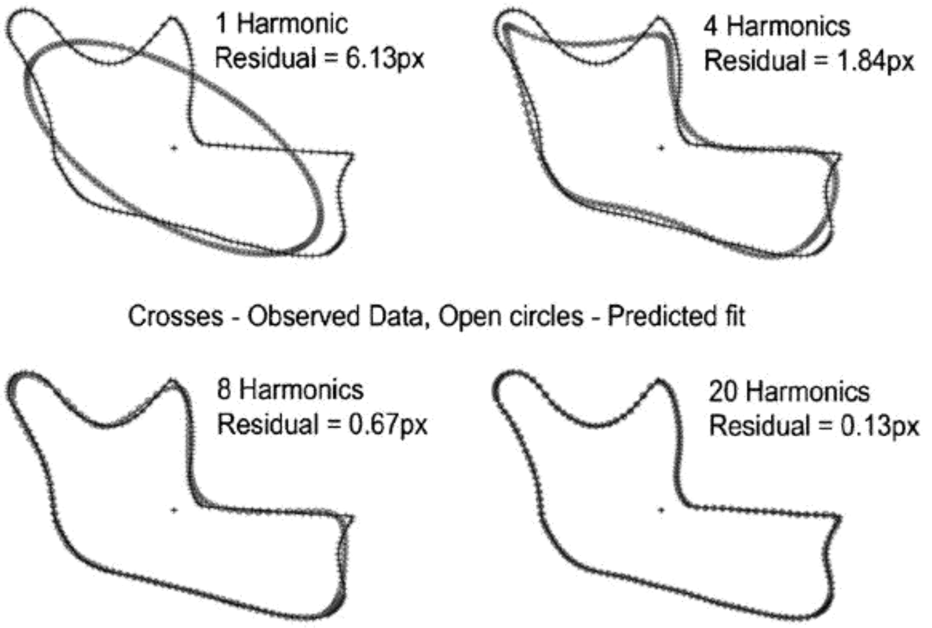


Fig. 6. Convergence of the EFF fit to the mandible outline.

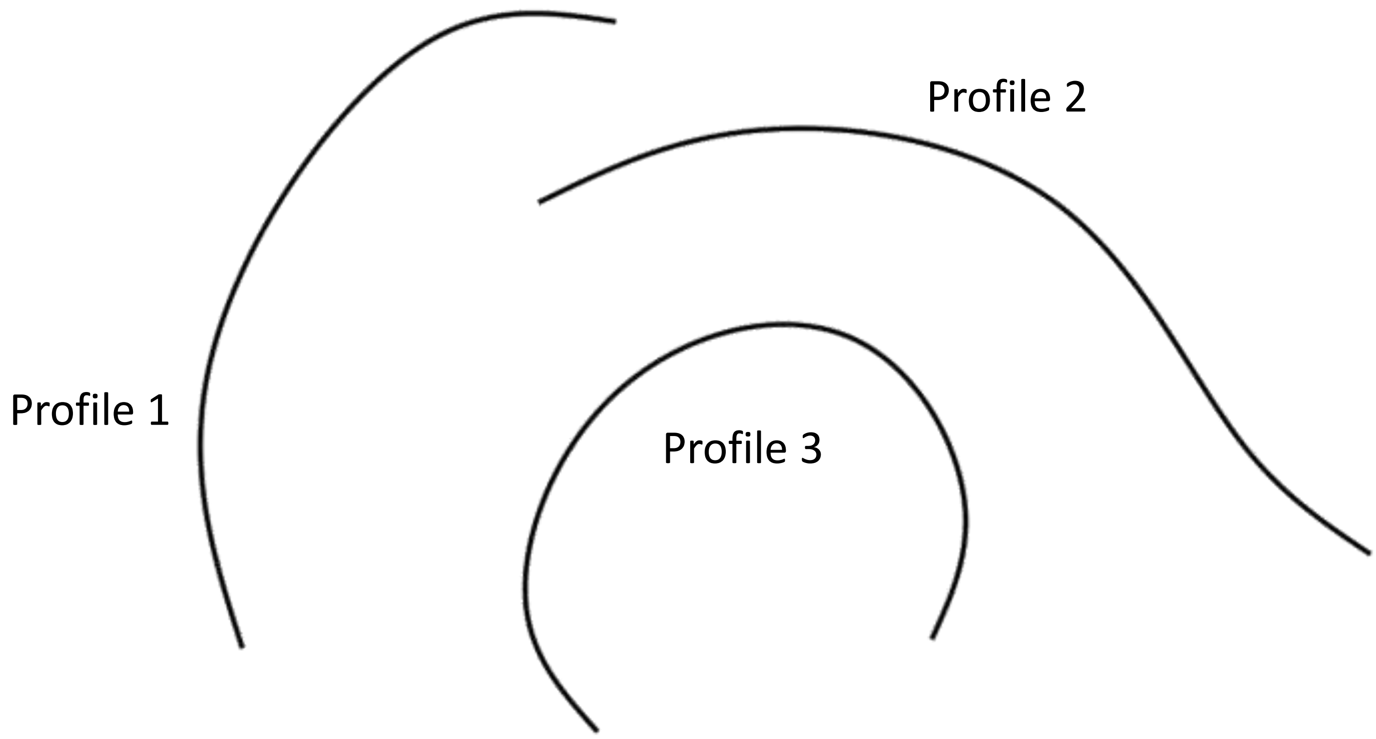
A New Method

- New method based on mechanical considerations…..
- Shape changing rigid-body mechanisms
- Mechanism: revolute joints (pivot) / prismatic joints (glissière) which parameters are easy to understand.

B. Li, A.P. Murray, D.H. Myszka, G. Subsol. "Synthesizing Planar Rigid-Body Chains for Morphometric Applications". ASME International Design Engineering Technical Conferences & Computers and Information in Engineering Conference, Charlotte (U.S.A.), August 2016.

The Goal

Different profile shapes



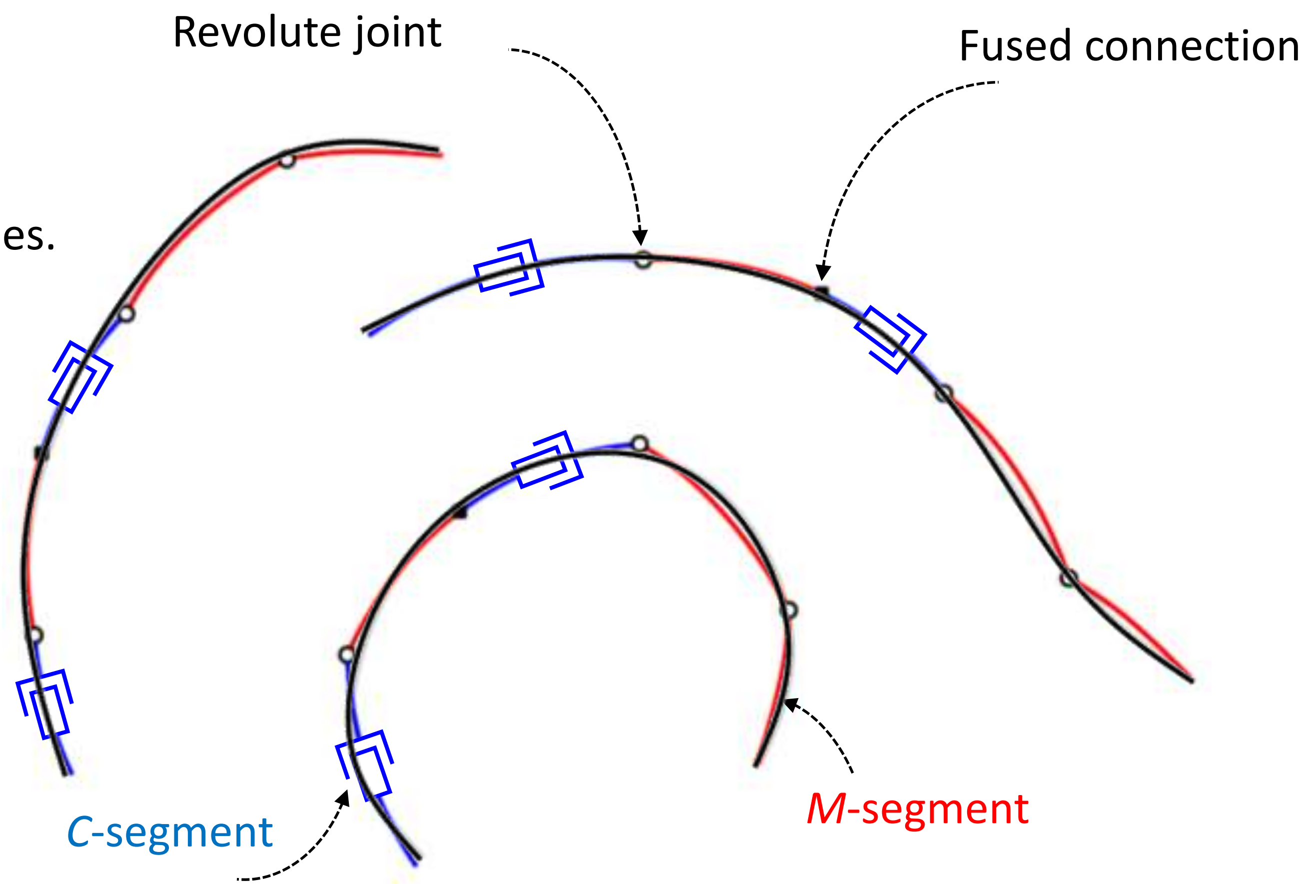
Find a chain of rigid bodies composed of:

- **C**onstant-curvature segments (slide)
- **M**ean fixed segments

connected by:

- **F**used connections
- **R**evolute joints

which fits with all the profiles.



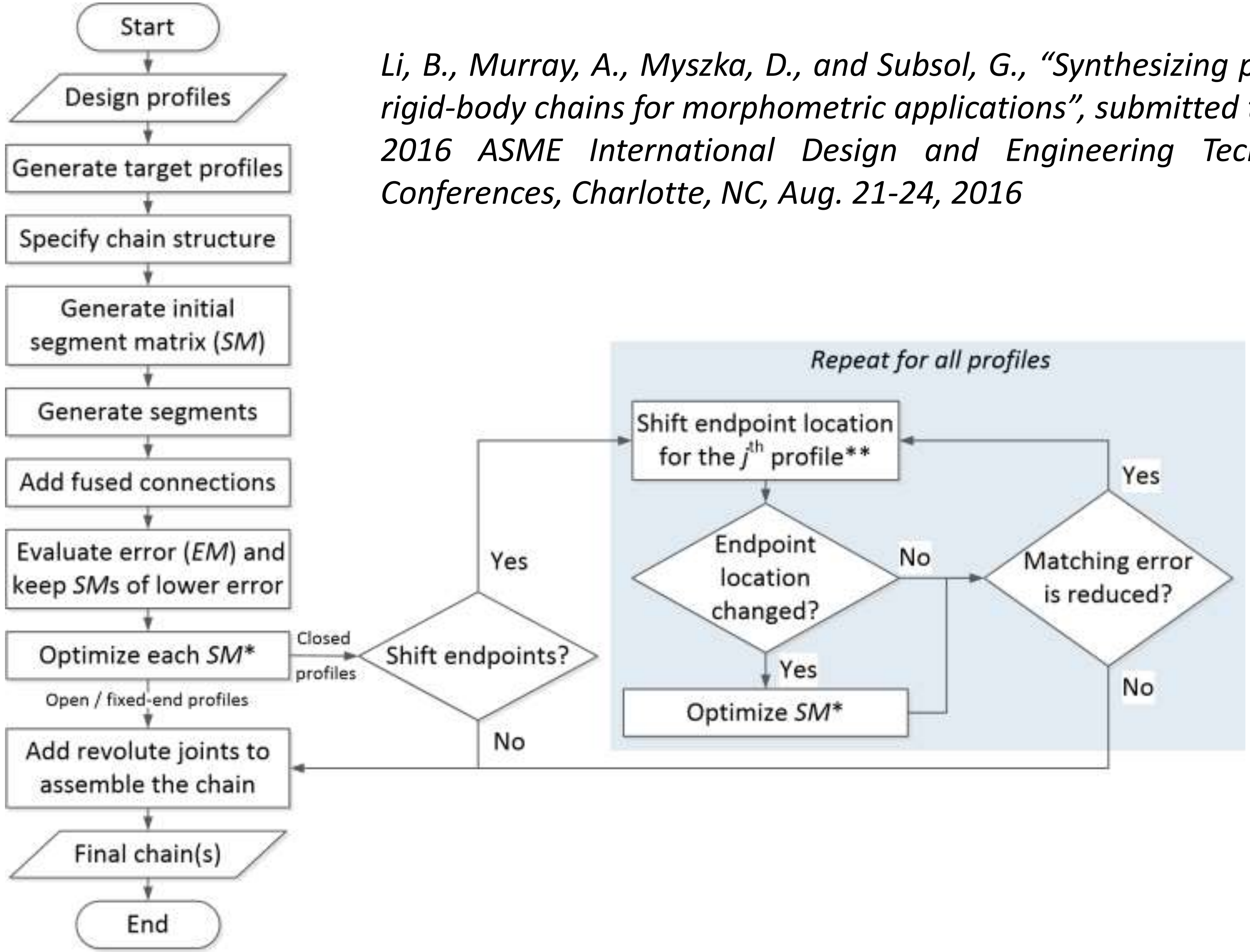
C / **R** / M / **F** / C / **R** / M / **R** / M

The Goal

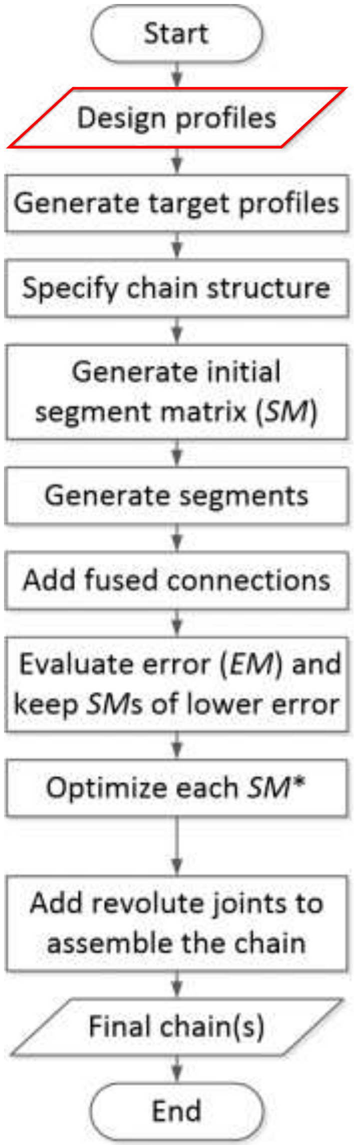
2 C segments + 3 **R joints** = 5 scalar parameters (angles) only by profile!

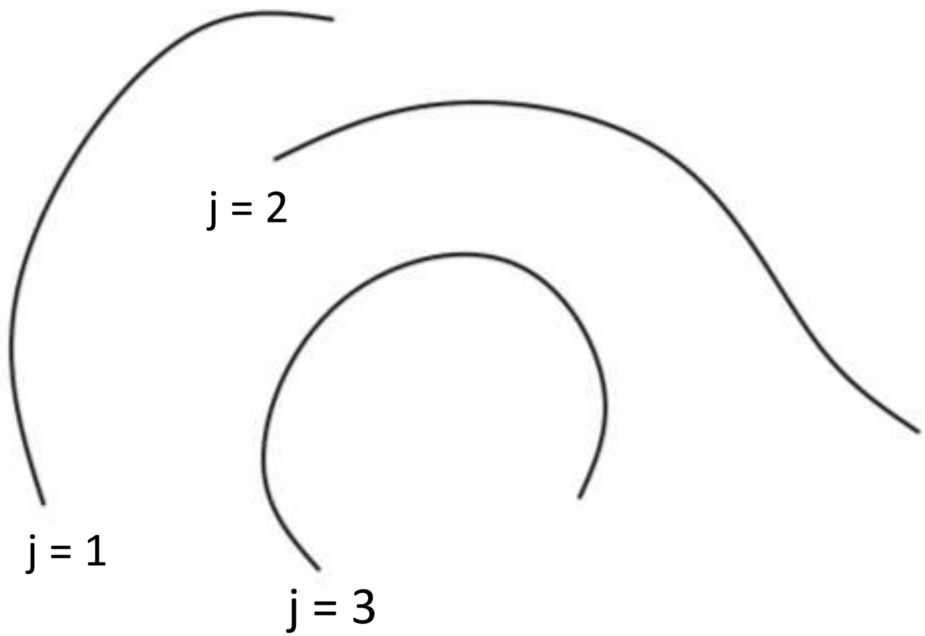
General Procedure

Li, B., Murray, A., Myszka, D., and Subsol, G., "Synthesizing planar rigid-body chains for morphometric applications", submitted to the 2016 ASME International Design and Engineering Technical Conferences, Charlotte, NC, Aug. 21-24, 2016



Design Profiles

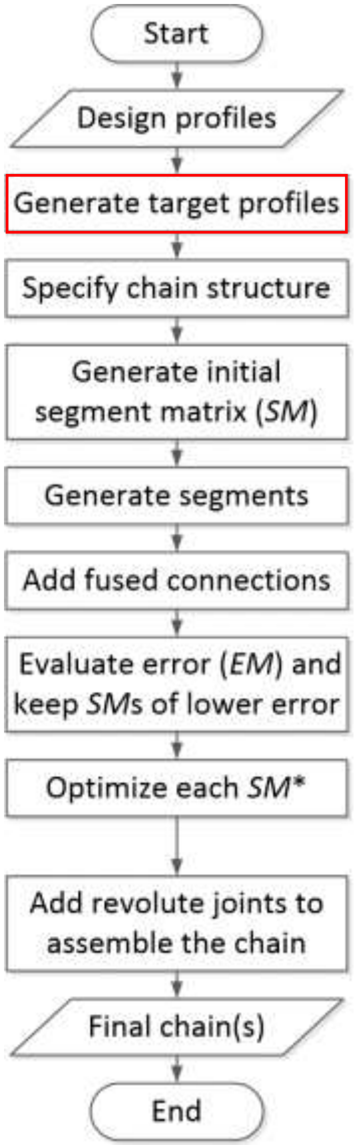


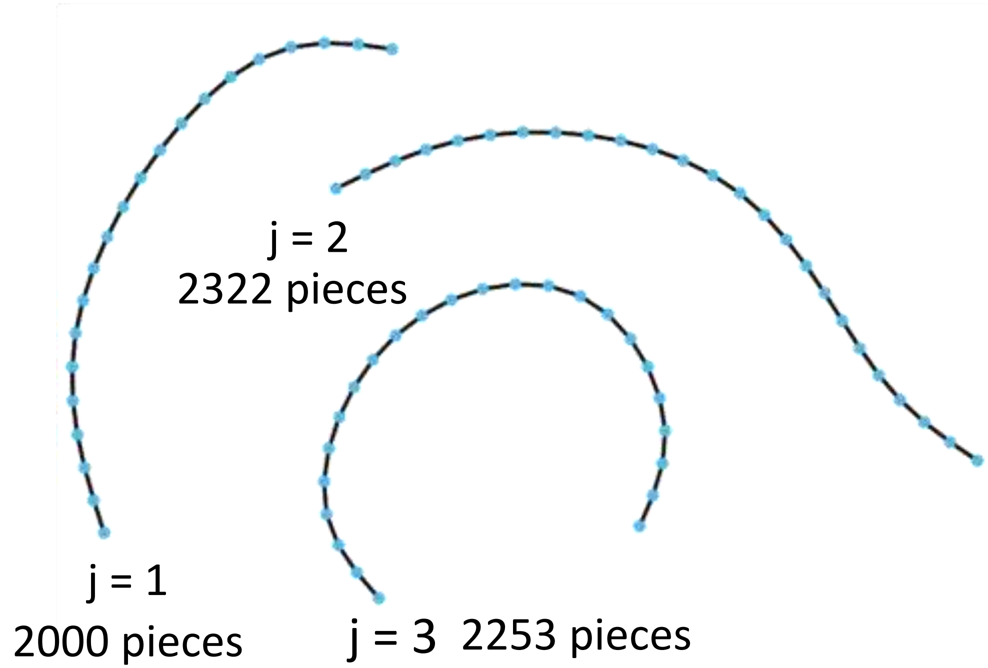


Can be generated from:

- Mathematical functions
- Point coordinates
- Line drawings

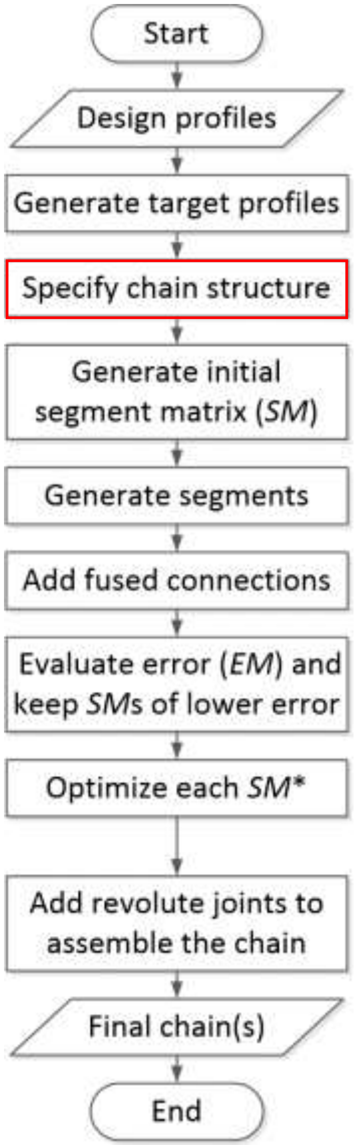
Target Profiles

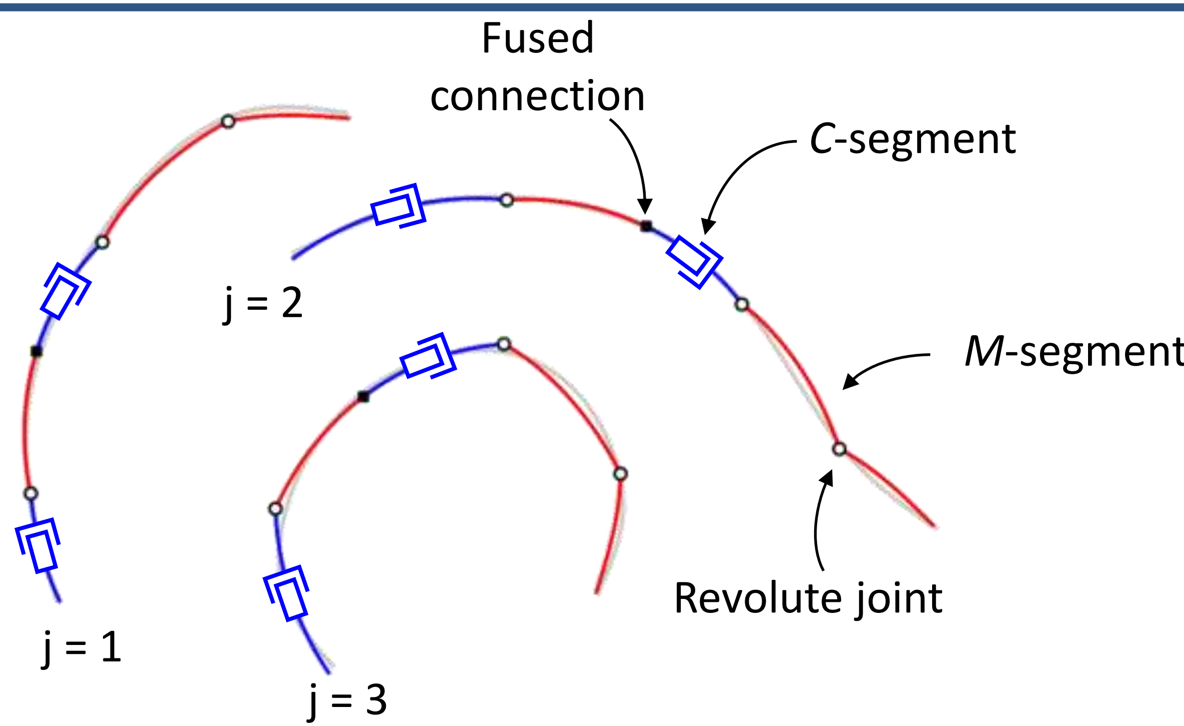




1. Compute the arc length of each design profile $C_j = \sum_{i=1}^{N_j - 1} c_{j_i}$
2. Determine the number of pieces should be in each target profile $m_j = \left\lceil \frac{C_j}{C_{\min}} m_d \right\rceil$
3. Desired piece length of target profile $s_j = \frac{C_j}{m_j}$

Specify Chain Structure



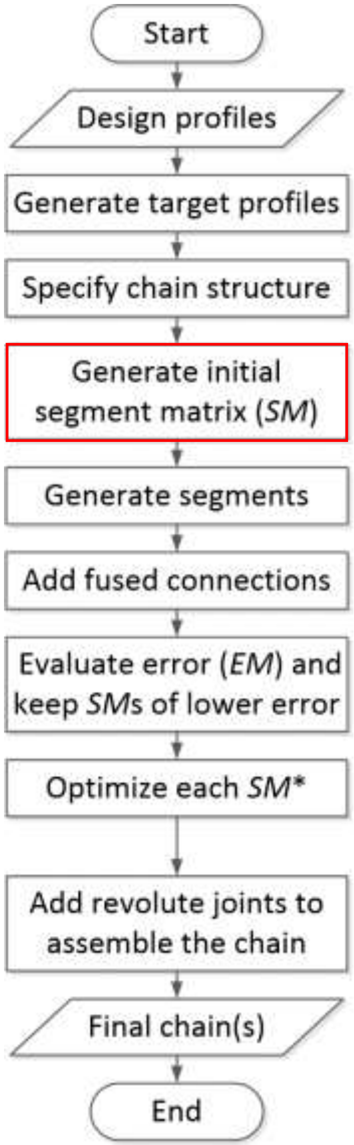


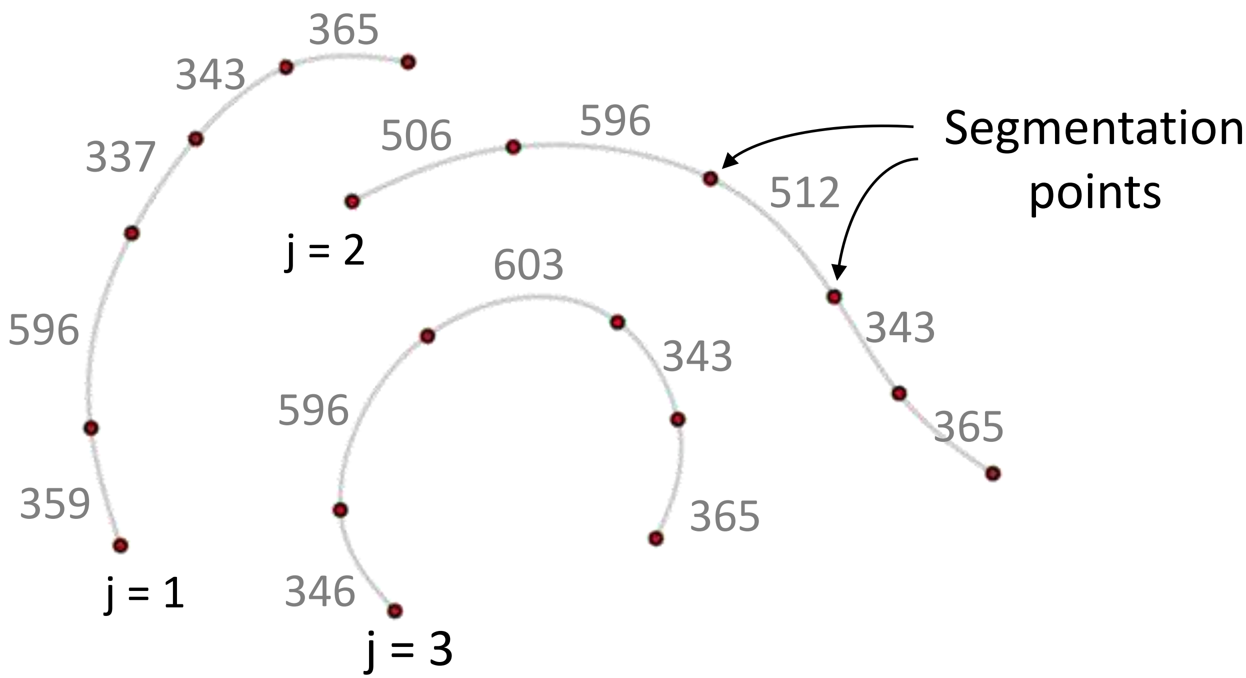
Segment vector, $\mathbf{V} = [C\ M\ C\ M\ M]$

Connection vector, $\mathbf{W} = [R\ F\ R\ R]$

Minimum number of pieces in a segment, α

Initial Segment Matrices (*SM*)

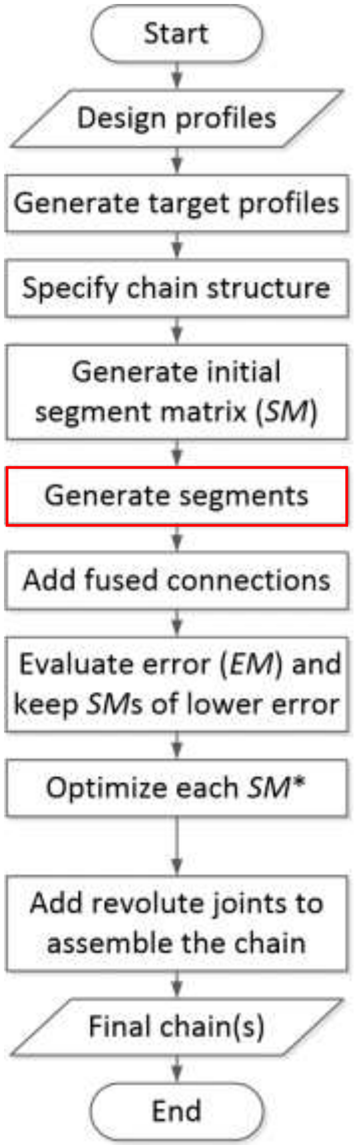




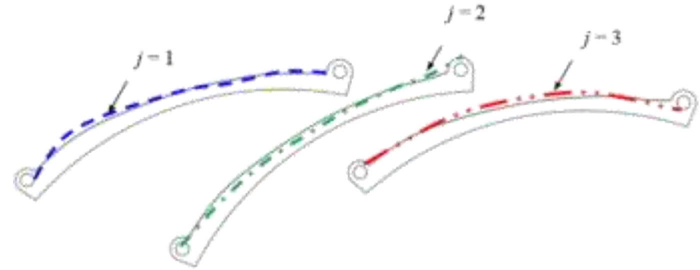
$$\mathbf{V} = [\ C \quad M \quad C \quad M \quad M\ ]$$

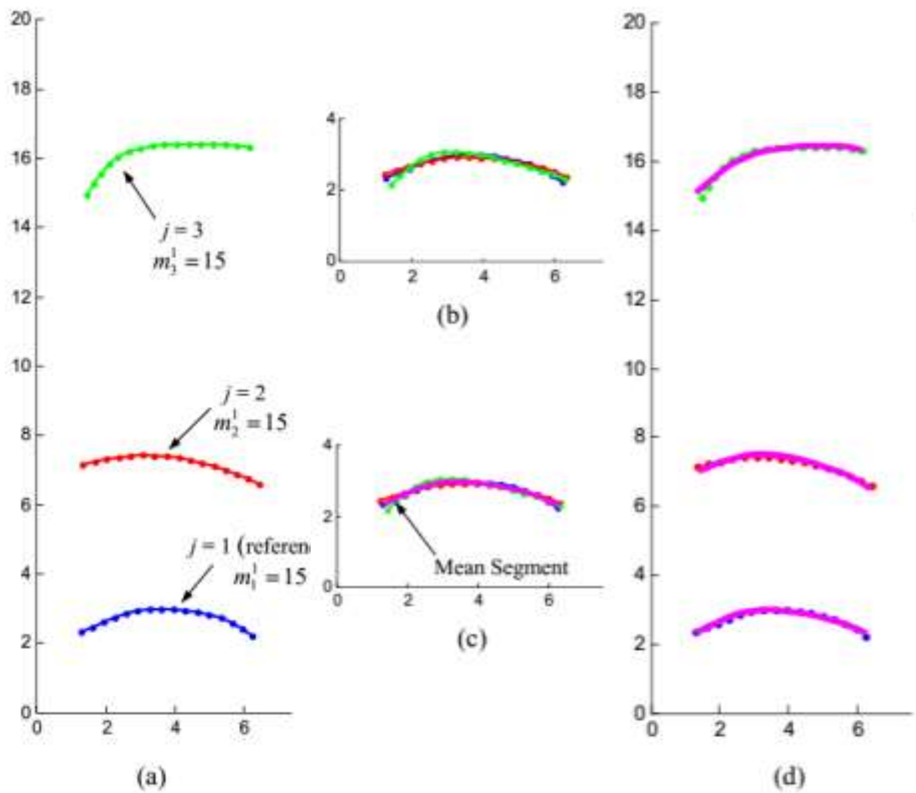
$$SM = \begin{bmatrix} 359 & 596 & 337 & 343 & 365 \\ 506 & 596 & 512 & 343 & 365 \\ 346 & 596 & 603 & 343 & 365 \end{bmatrix} \begin{matrix} j = 1 \\ j = 2 \\ j = 3 \end{matrix}$$

Generating Segments



M-Segments





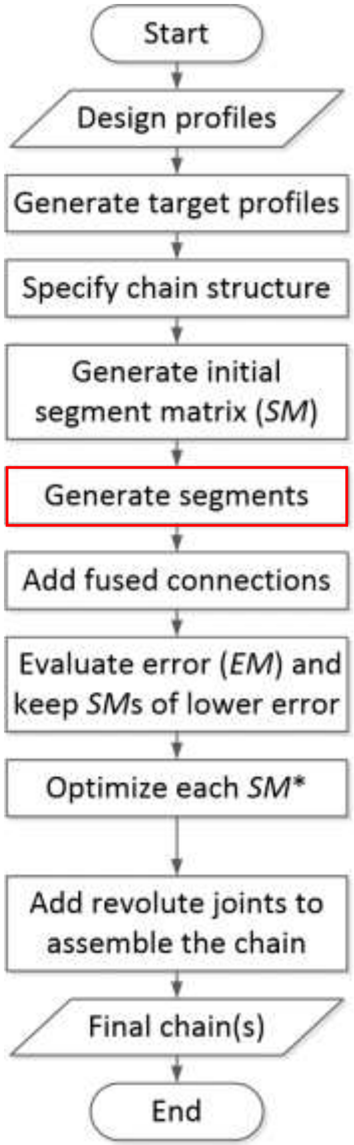
Finding average geometry

$$\mathbf{Z}_{m_i} = \frac{1}{p}\left(\mathbf{z}_{1_i} + \sum_{j=2}^{p} \mathbf{Z}_{j_i}\right)$$

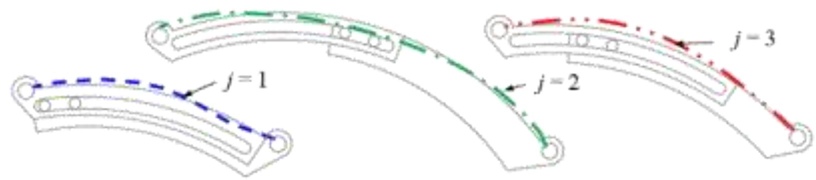
Actual segment point coordinates

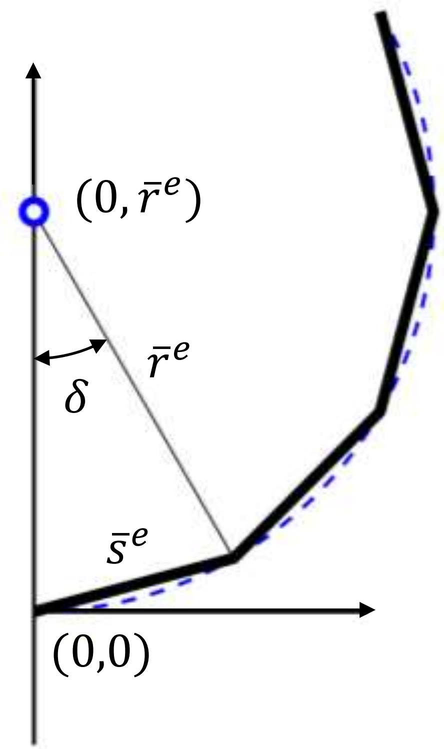
$$\bar{\mathbf{z}}^e_{j_i} = \left(\hat{\mathbf{A}}^e_j\right)^{-1}\left(\mathbf{Z}_{m_i} - \hat{\mathbf{d}}^e_j\right)$$

$$i = k^e_j, \ldots, k^{e+1}_j \qquad j = 2, \ldots, p.$$



C-Segments





Average radius (reciprocal of curvature)

$$\bar{r}^e = \frac{1}{\sum_{j=1}^{p} m_j^e - 1}\left(\sum_{j=1}^{p}\left(\sum_{i=k_j^e+1}^{k_j^{e+1}-1} r_{j_i}\right)\right)$$

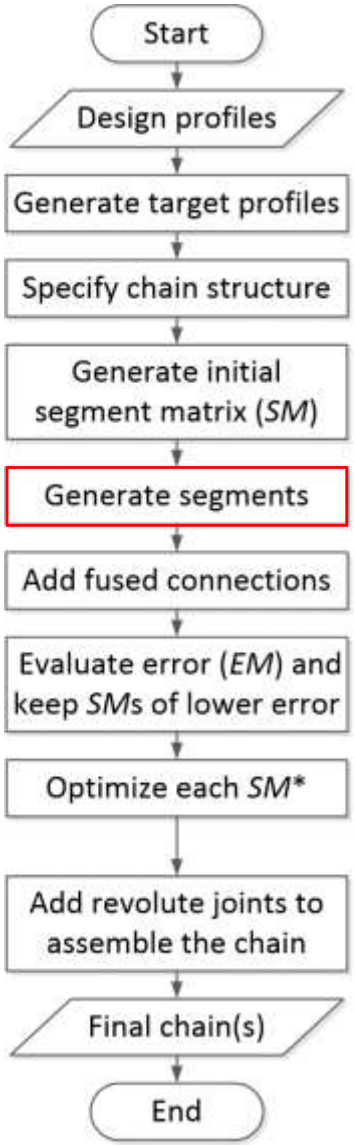
Segment arc length

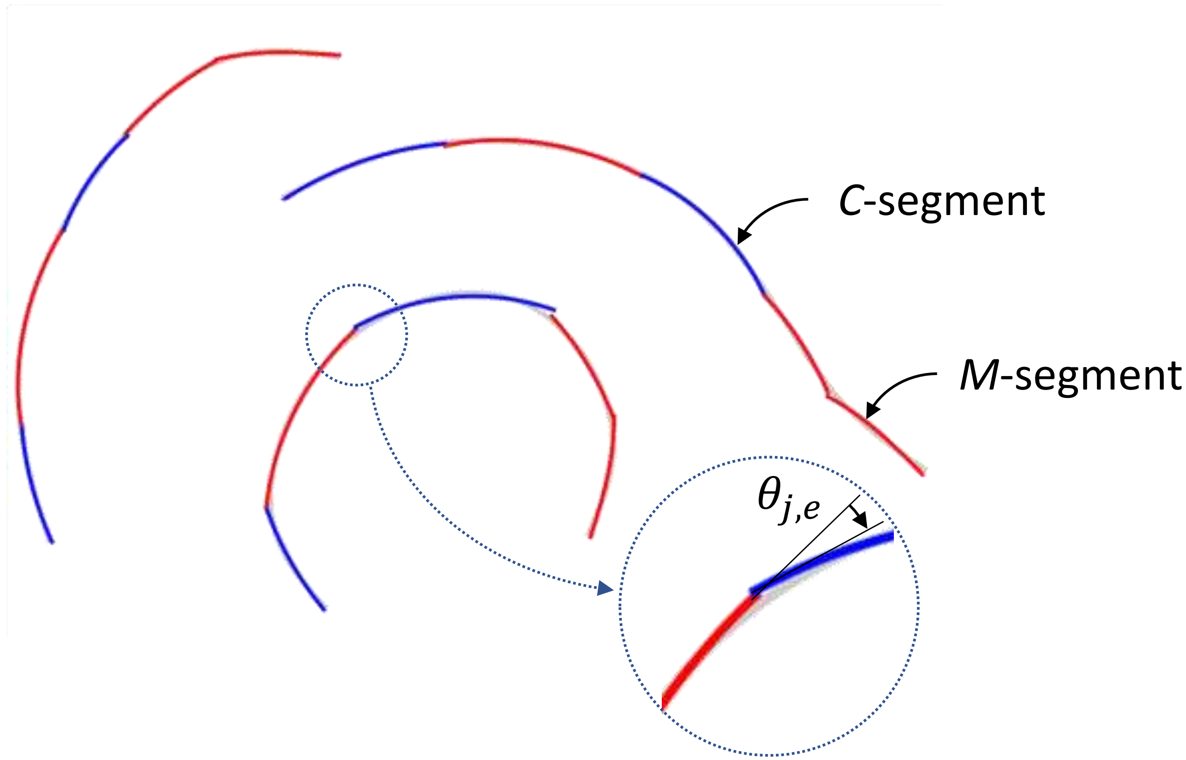
$$L_j^e = m_j^e\,\bar{s}^e$$

Average piece length

$$\bar{s}^e = \sum_{j=1}^{p}\left(\frac{1}{m_j^e}\left(\sum_{i=k_j^e+1}^{k_j^{e+1}-1} s_{j_i}\right)\right)$$

Generate Segments

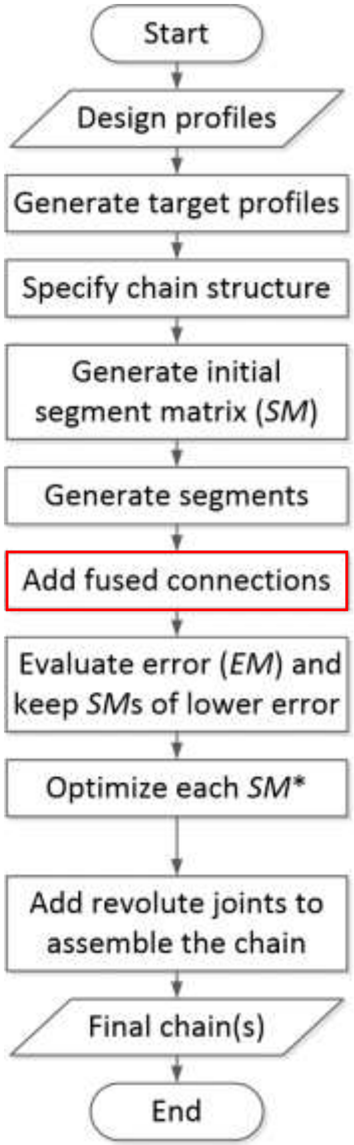


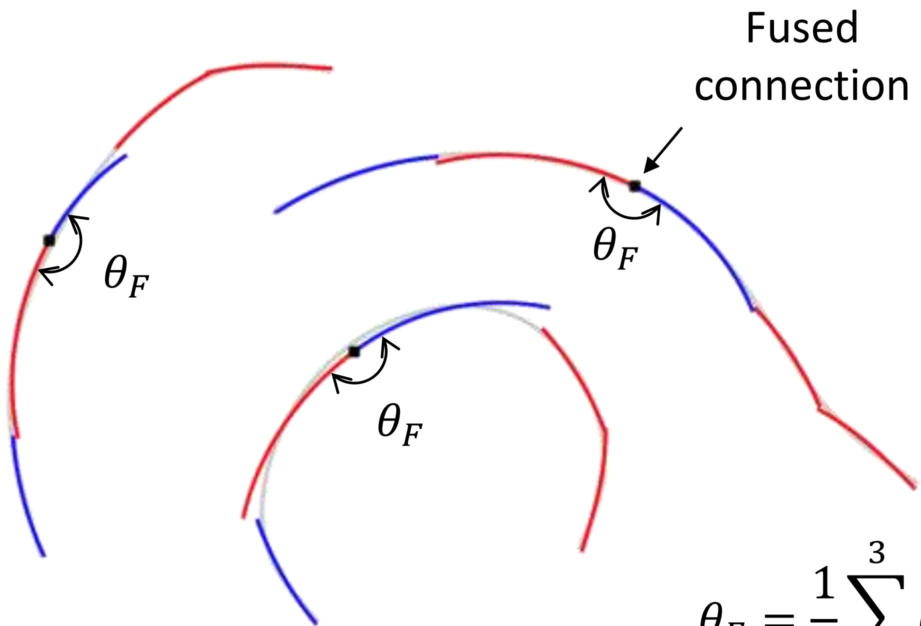


$$\mathbf{V} = [\; C \quad M \quad C \quad M \quad M \;]$$

$$SM = \begin{bmatrix} 359 & 596 & 337 & 343 & 365 \\ 506 & 596 & 512 & 343 & 365 \\ 346 & 596 & 603 & 343 & 365 \end{bmatrix} \begin{matrix} j = 1 \\ j = 2 \\ j = 3 \end{matrix}$$

Fused Connections

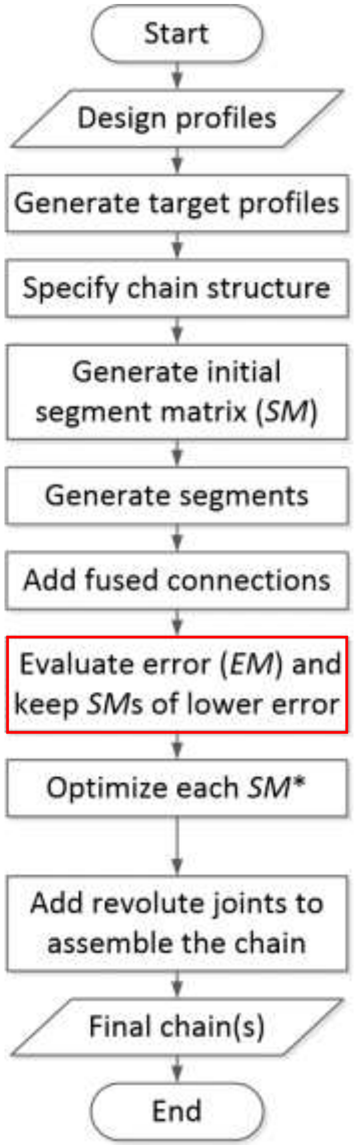




$$\theta_F = \frac{1}{3}\sum_{j=1}^{3} \theta_{j,2}$$

$$\mathbf{W} = [R\ F\ R\ R]$$

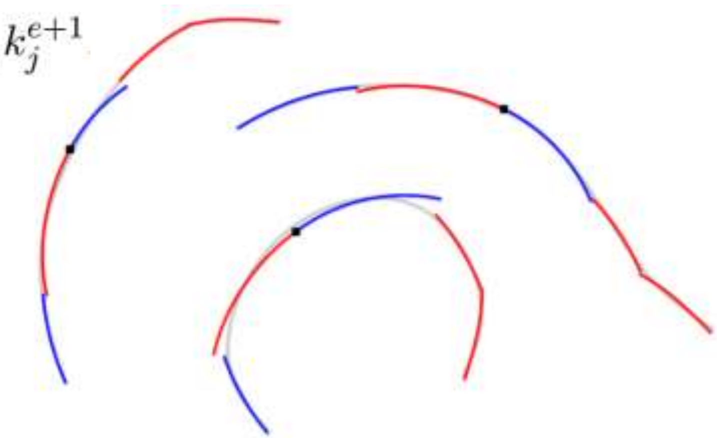
Error Evaluation



$$E_j^e = \max\left|\bar{\mathbf{z}}_{j_i}^e - \mathbf{z}_{j_i}\right| \qquad i = k_j^e, \dots, k_j^{e+1}$$

$$\bar{E} = \frac{1}{q}\sum_{e=1}^{q}\left(\frac{1}{p}\sum_{j=1}^{p} E_j^e\right)$$

$$\bar{E}^e = \sum_{j=1}^{p} E_j^e$$



$$\begin{matrix} & \text{C} & \text{M} & \text{C} & \text{M} & \text{M} \end{matrix}$$

$$EM = \begin{bmatrix} 0.35 & 1.00 & 1.96 & 0.27 & 0.52 \\ 0.46 & 1.19 & 1.19 & 0.78 & 1.27 \\ 0.81 & 3.23 & 4.31 & 0.55 & 0.76 \end{bmatrix}$$

Segment to be elongated

Segment to be shorted

Overall mean error,

$$\bar{E} = 1.24$$

Mean error of each M-segment:

$$\bar{E}^2 = 1.81, \qquad \bar{E}^4 = 0.53, \qquad \bar{E}^5 = 0.86$$

SM Optimization

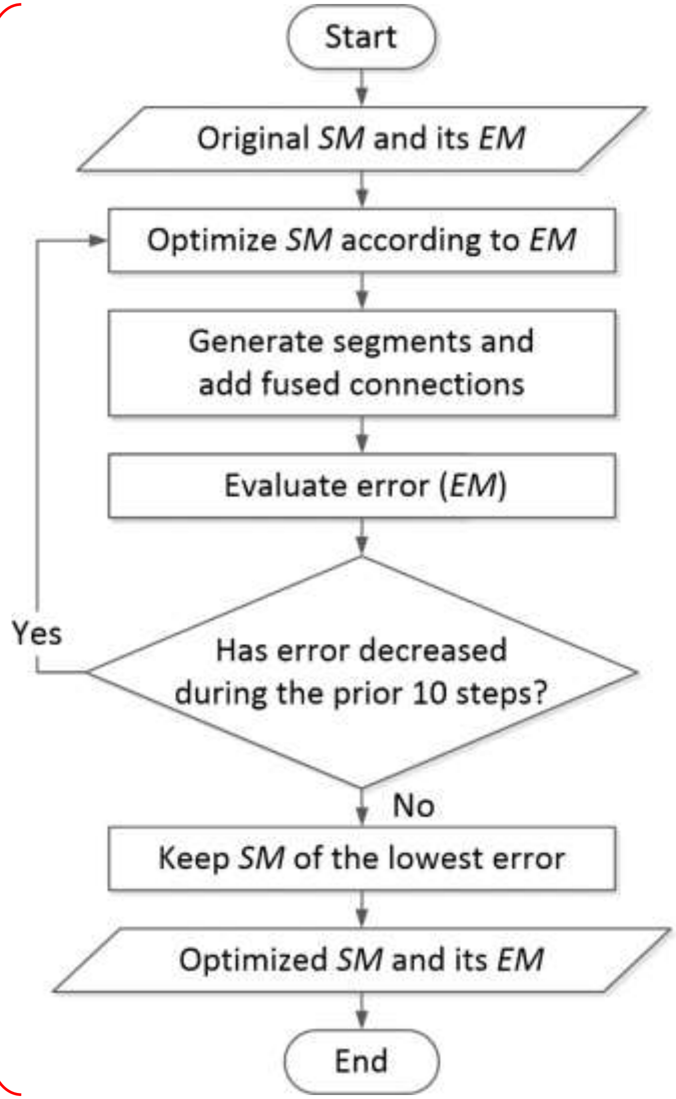
$$
\begin{array}{ccccc} C & M & C & M & M \end{array}
$$

$$SM_0 = \begin{bmatrix} 359 & 596 & 337 & 343 & 365 \\ 506 & 596 & 512 & 343 & 365 \\ 346 & 596 & 603 & 343 & 365 \end{bmatrix}$$

$$SM_1 = \begin{bmatrix} 360 & 595 & 335 & 344 & 366 \\ 507 & 595 & 510 & 344 & 366 \\ 346 & 595 & 602 & 344 & 366 \end{bmatrix}$$

⋮

$$SM_f = \begin{bmatrix} 326 & 420 & 376 & 522 & 356 \\ 660 & 420 & 364 & 522 & 356 \\ 509 & 420 & 446 & 522 & 356 \end{bmatrix}$$



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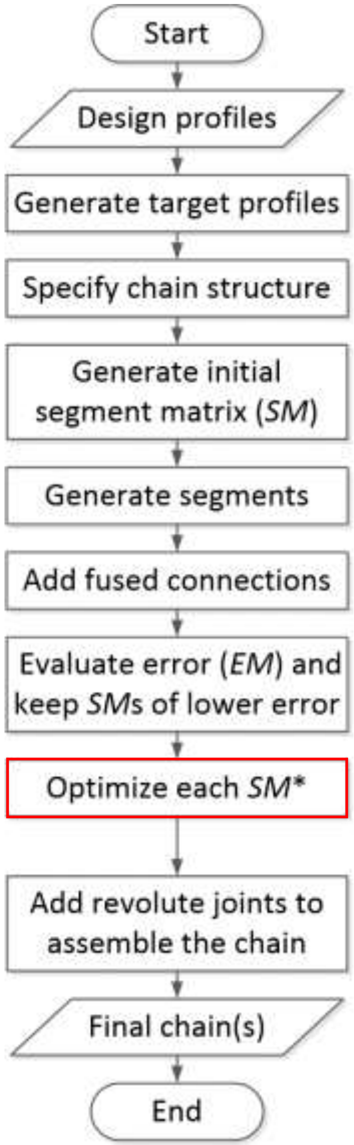
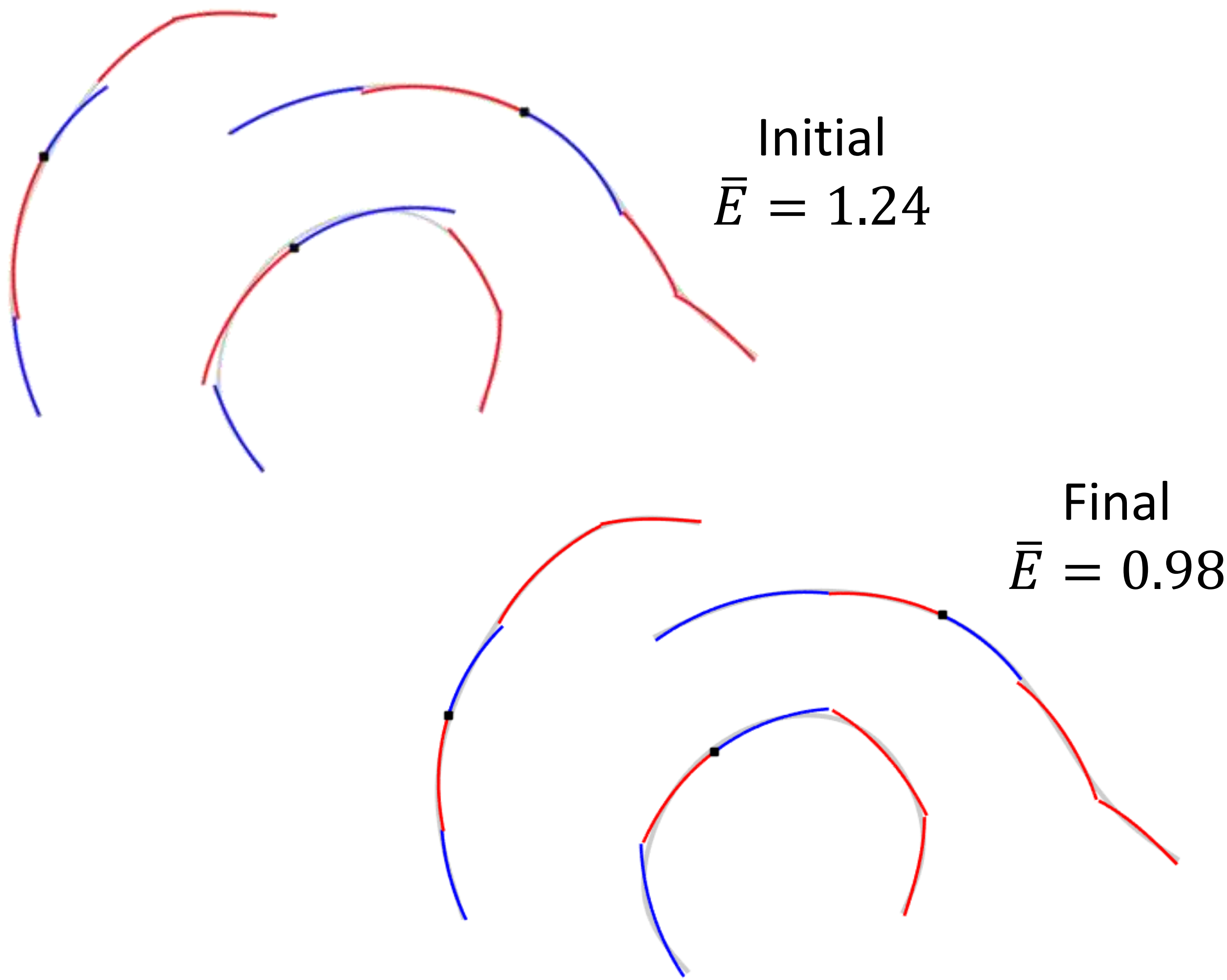
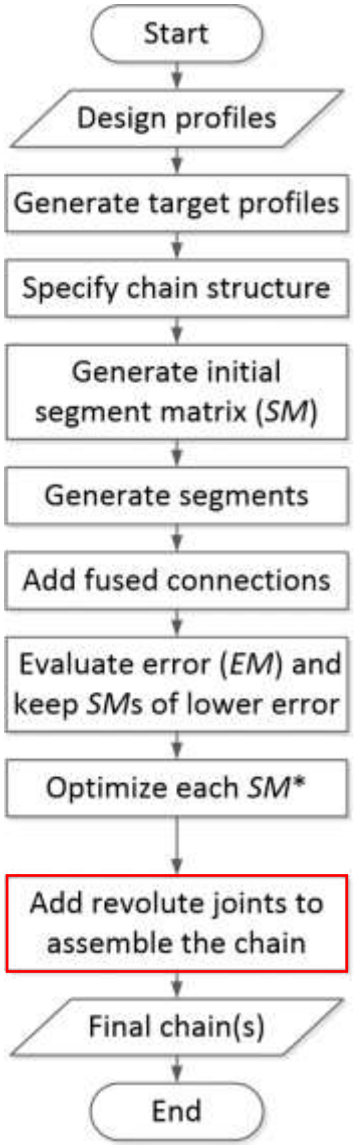


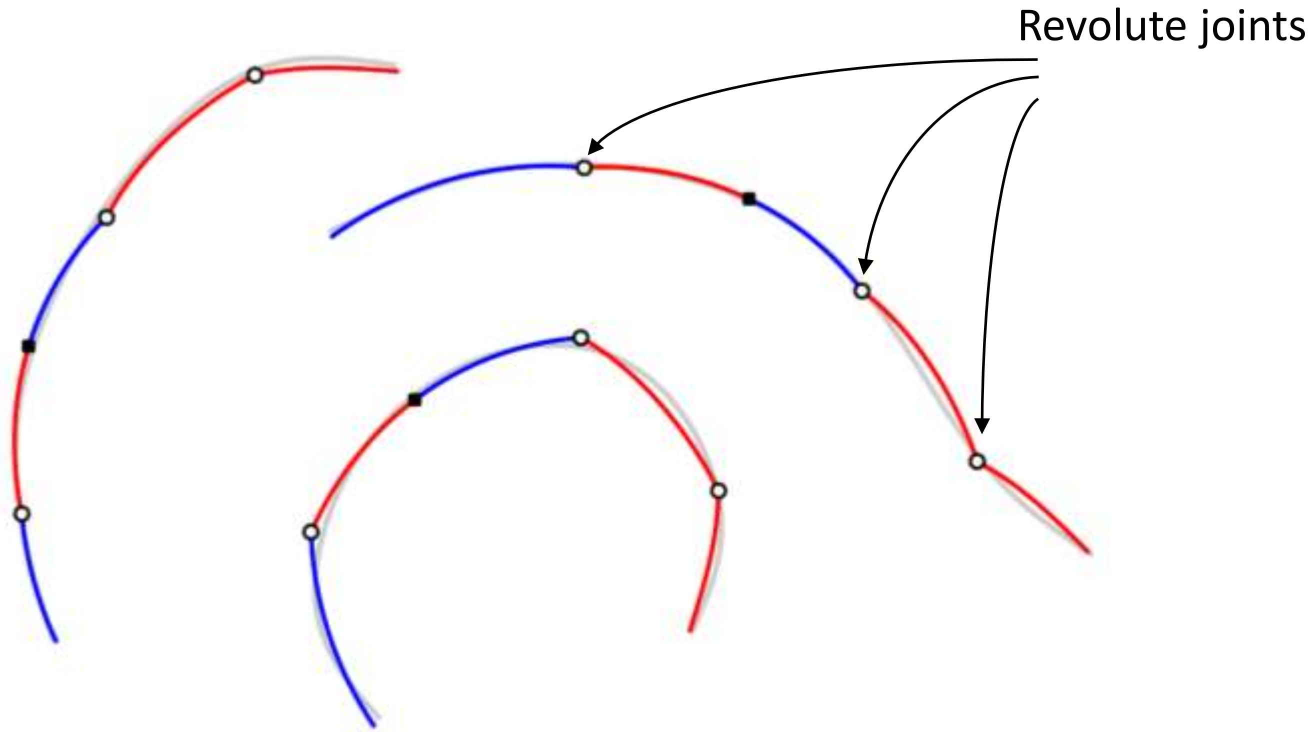
Start
Design profiles
Generate target profiles
Specify chain structure
Generate initial segment matrix (*SM*)
Generate segments
Add fused connections
Evaluate error (*EM*) and keep *SMs* of lower error
Optimize each *SM**
Add revolute joints to assemble the chain
Final chain(s)
End



Initial
$\bar{E} = 1.24$
Final
$\bar{E} = 0.98$

Assembling with Revolute Joints

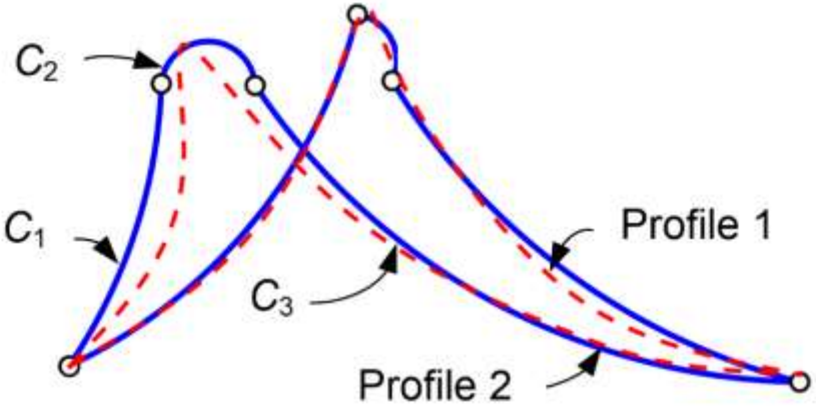


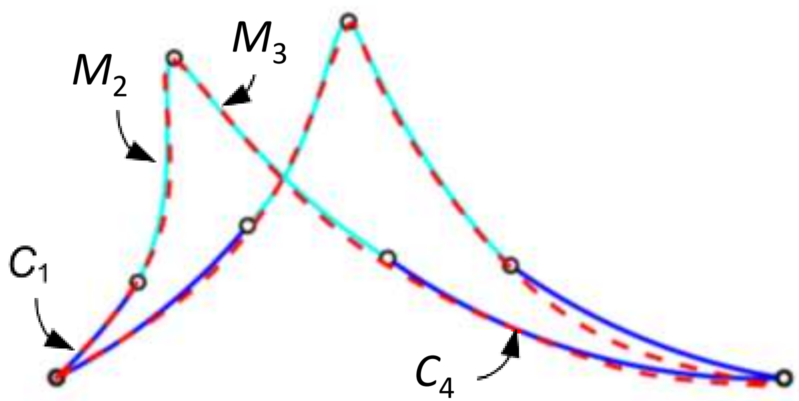


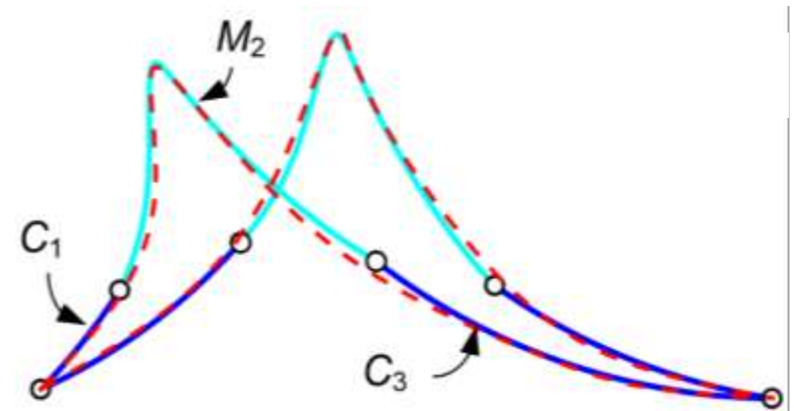
$$\mathbf{X} = \mathrm{fmincon}(f, \mathbf{X}_0, \mathbf{C})$$

By multivariate optimization

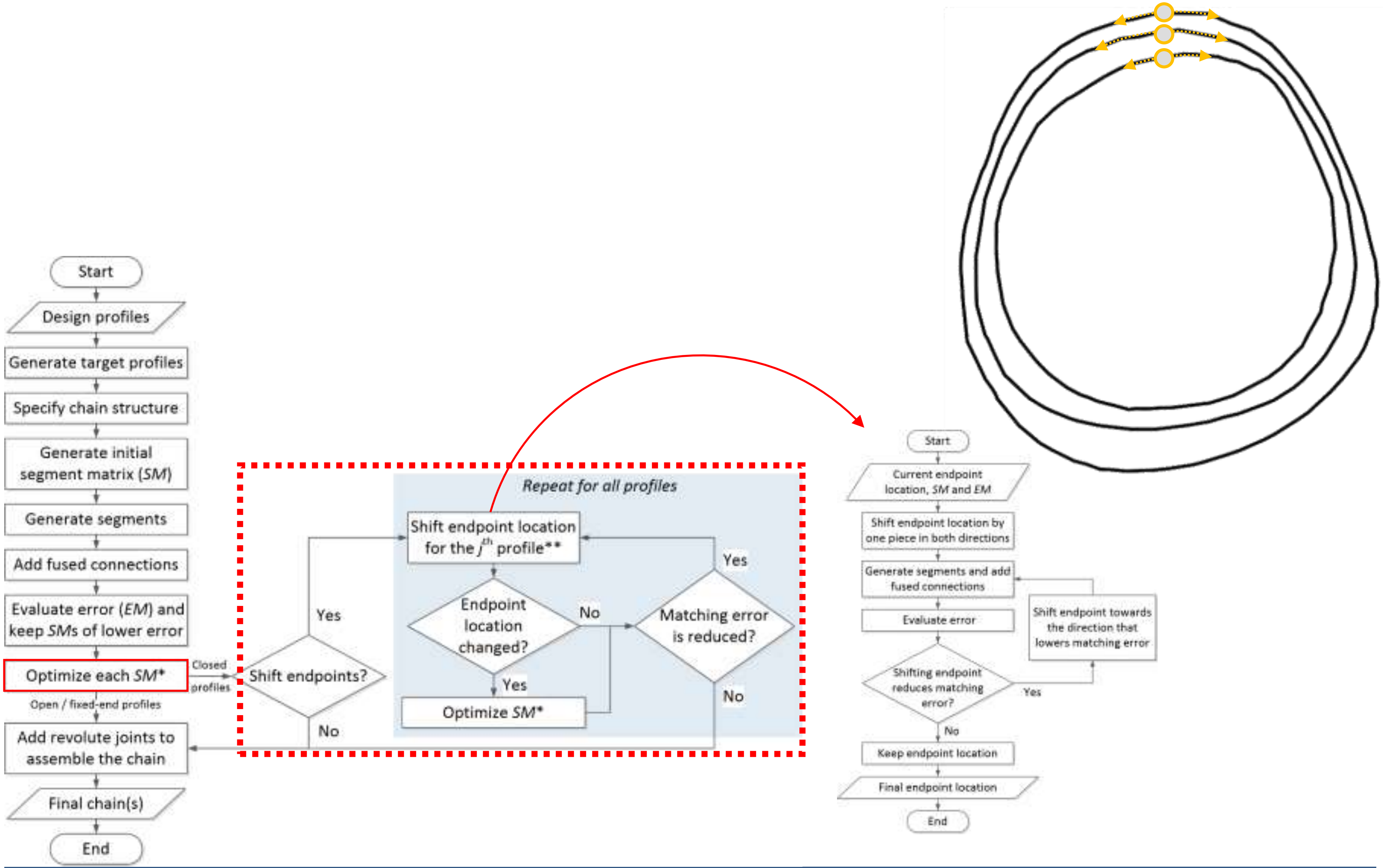
High-Curvature Regions



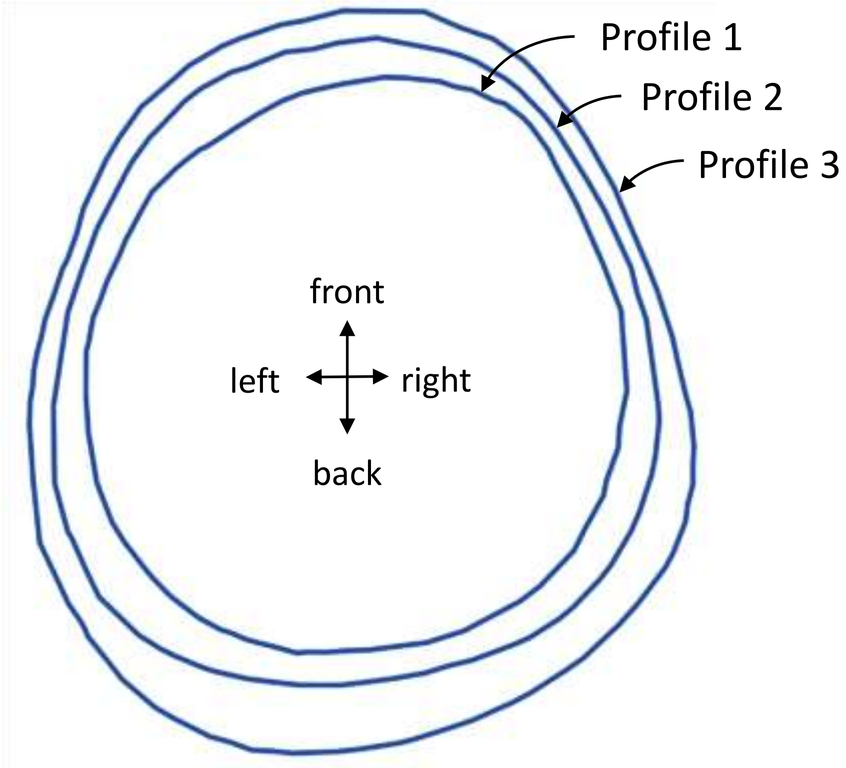


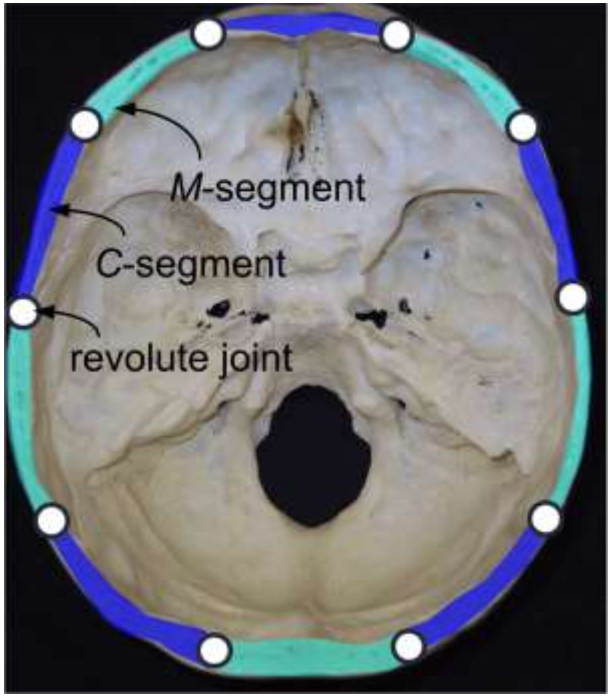


Shifting Endpoints for Closed Profiles



Head Circumference





Head Circumference

Fused connection between endpoints

V = [*C M C M C M C M C M C*]

W = [*F R F R F F R F R F*]

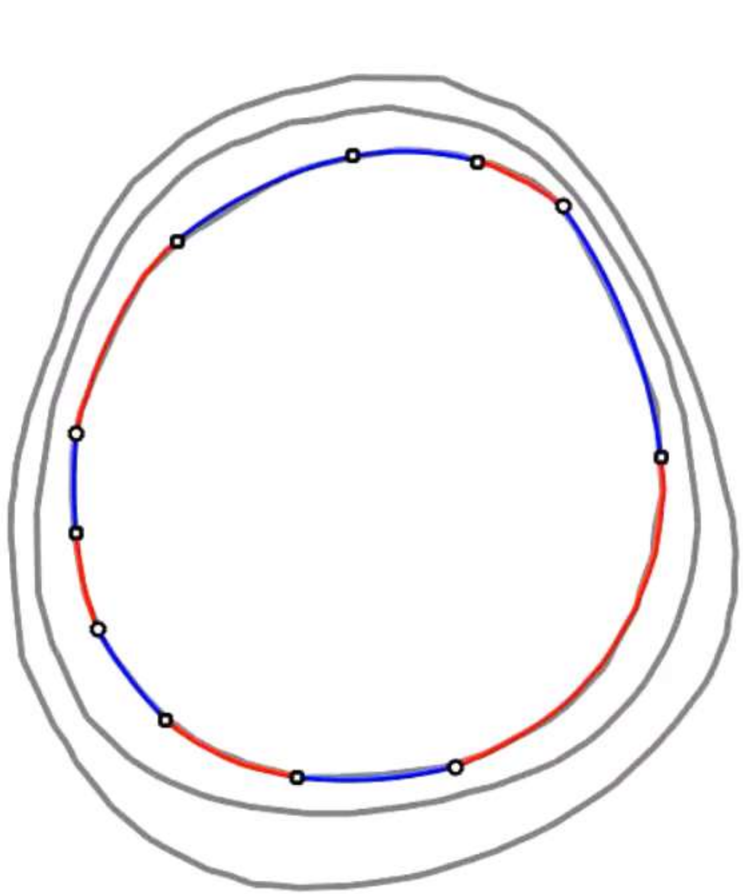
10 parameters to characterize the shape

(4 R joints & 6 C segments)

Max diameter = 877.17,

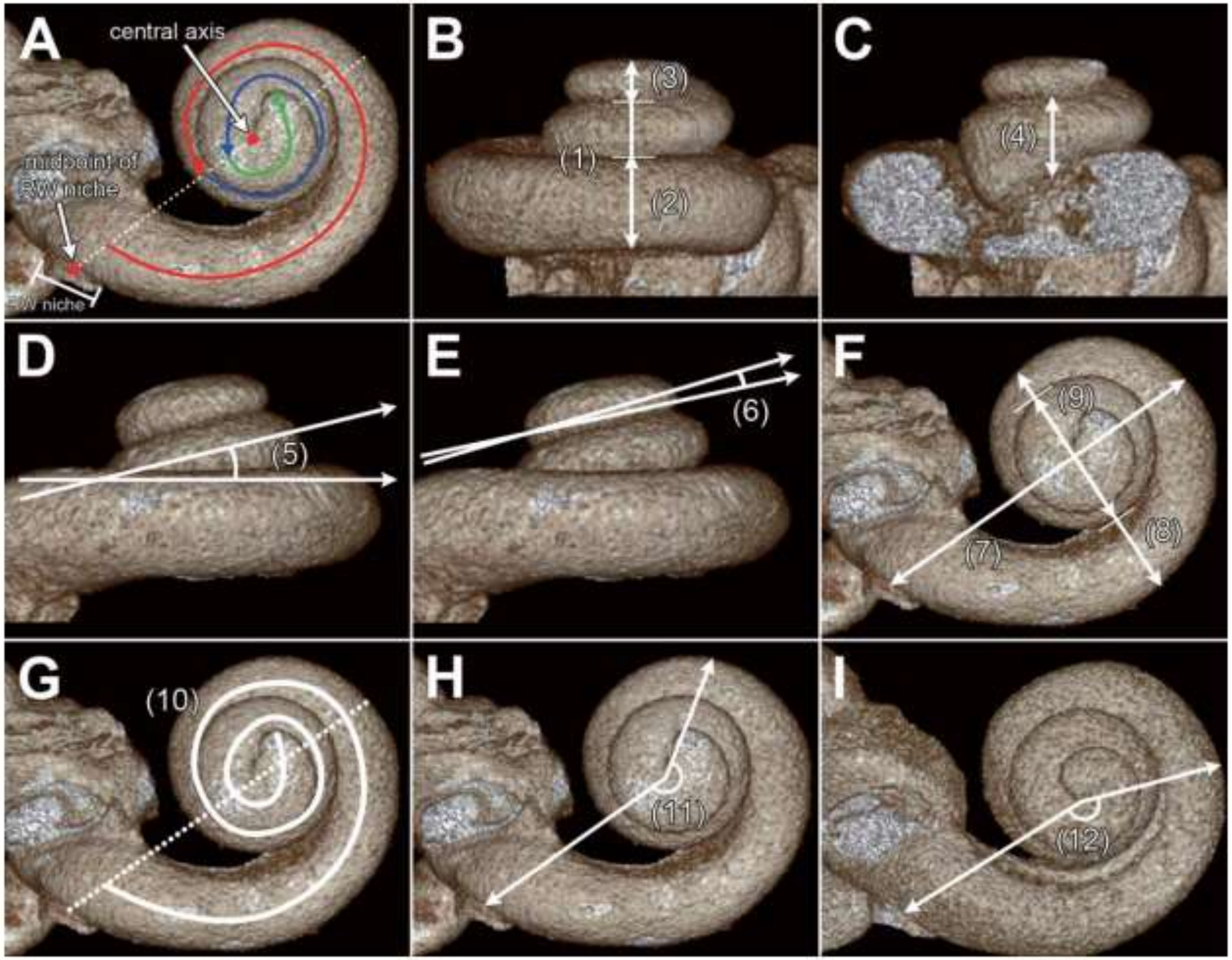
mean matching error = 6.90

(0.79% of max diameter)

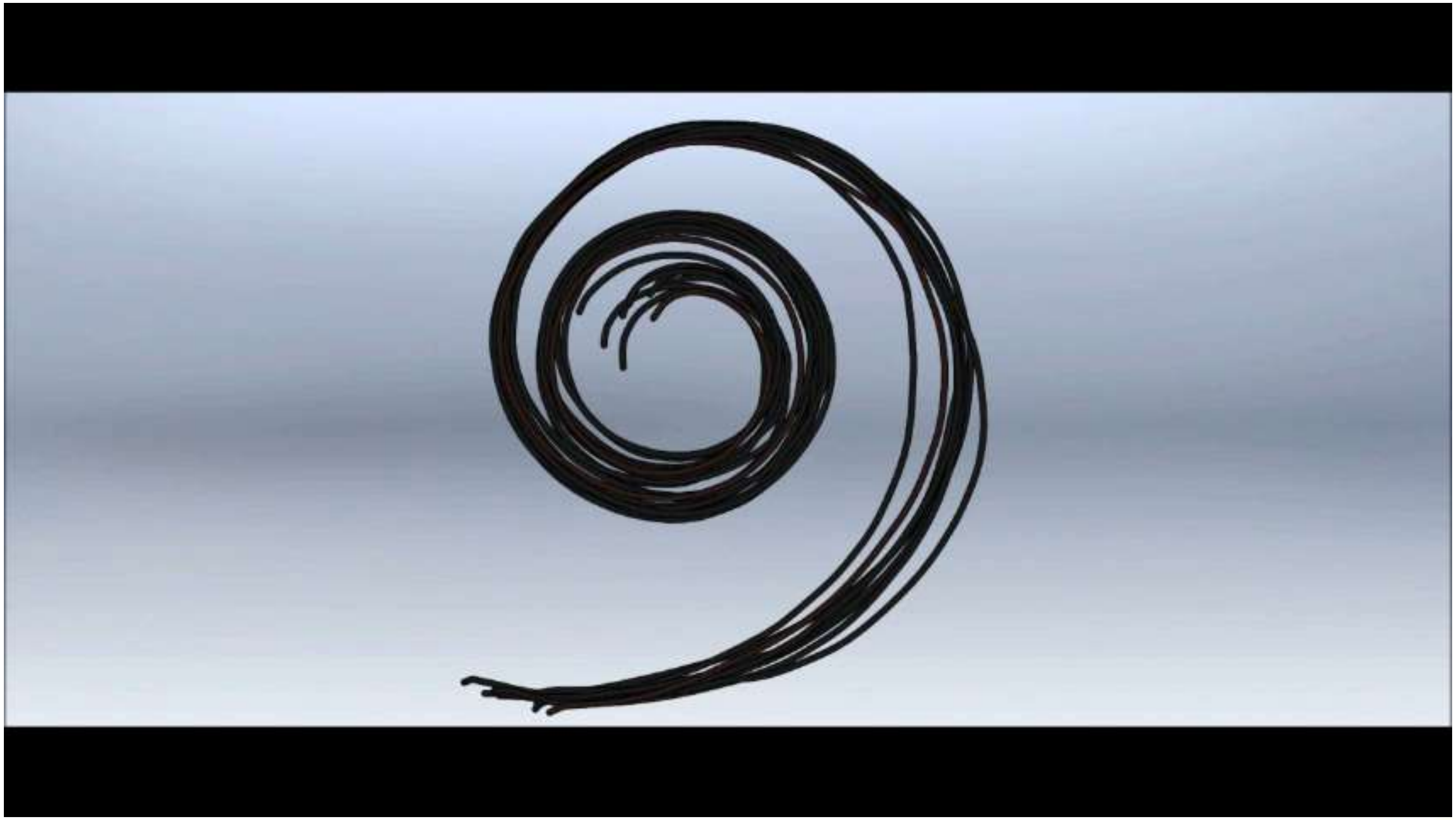


	C1	C2	C3	C4	C5	C6	R1	R2	R3	R4
Profile1	0.44	0.49	0.38	0.28	0.17	0.46	-0.27	-0.09	-0.08	-0.11
Profile 2	0.96	0.37	0.70	0.16	0.28	0.50	0.21	0.03	-0.05	0.09
Profile 3	0.68	0.73	0.43	0.62	0.46	0.38	0.16	0.26	0.02	0.09

The Cochleae

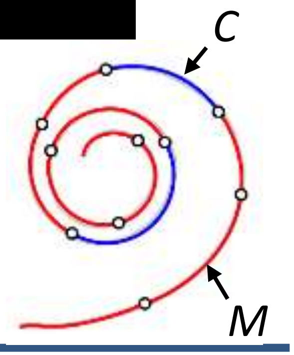


The Cochleae



V = [*M M M M C M M C M M M*]
W = [*R R … R R*] (10 revolute joints)
12 parameters to characterize shapes
(10 R joints + 2 C segments)

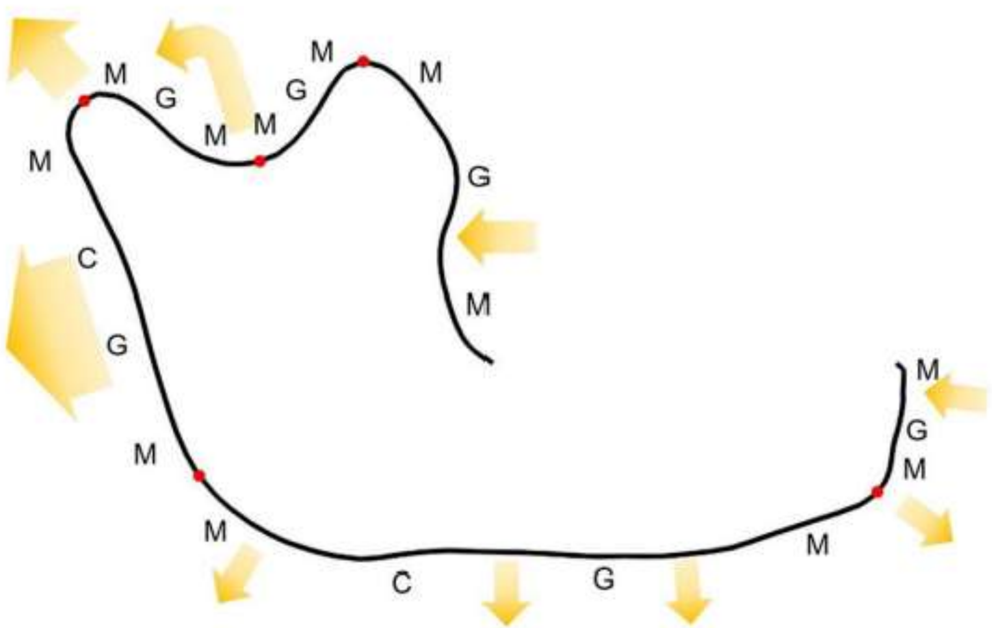
Average profile width = 798.68
Average profile length = 976.40
Mean matching error = 6.91



Extension 1 : Growing segment

20 segments = [M G M M G M M G M M C G M M C G M M G M] and no connection
Based on the growth pattern of the mandible

B. Li, S. Zhou, A.P. Murray, G. Subsol. "Shape-changing chains for morphometric analysis of 2D and 3D, open or closed outlines". Scientific Reports (2021 2-year impact factor: 4.380). 11, article number 21479. November 2021.



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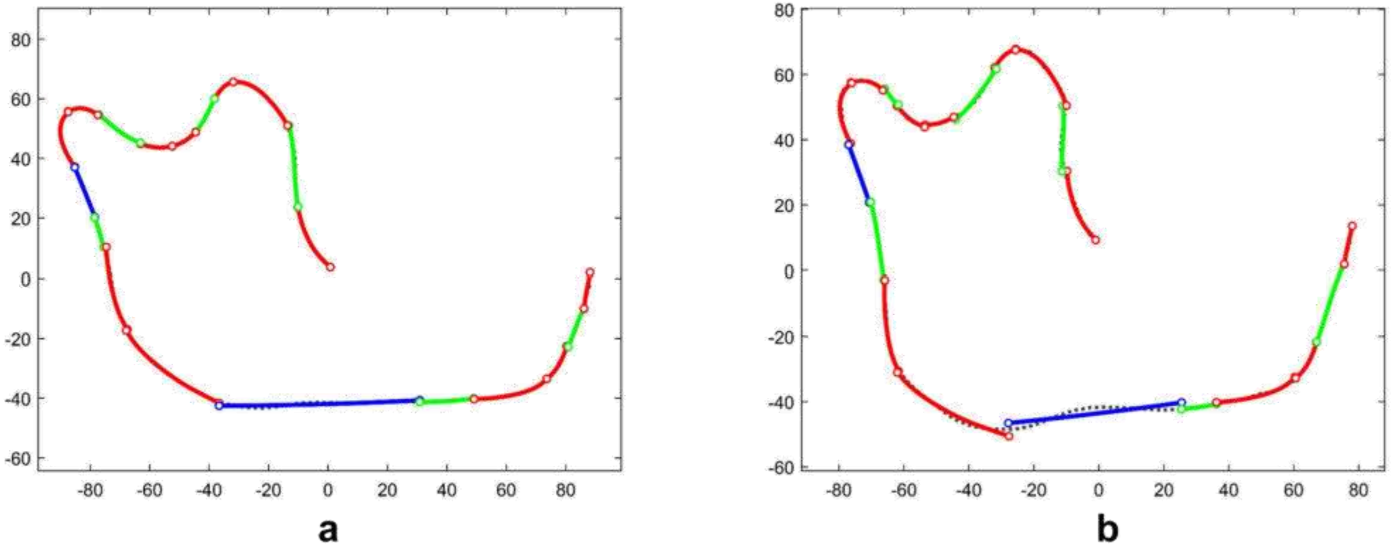


Extension 1 : **G**rowing segment

20 segments = [M G M M G M M G M M C G M M C G M M G M] but no connection
Based on the growth pattern of the mandible

B. Li, S. Zhou, A.P. Murray, G. Subsol. "Shape-changing chains for morphometric analysis of 2D and 3D, open or closed outlines". Scientific Reports (2021 2-year impact factor: 4.380). 11, article number 21479. November 2021.

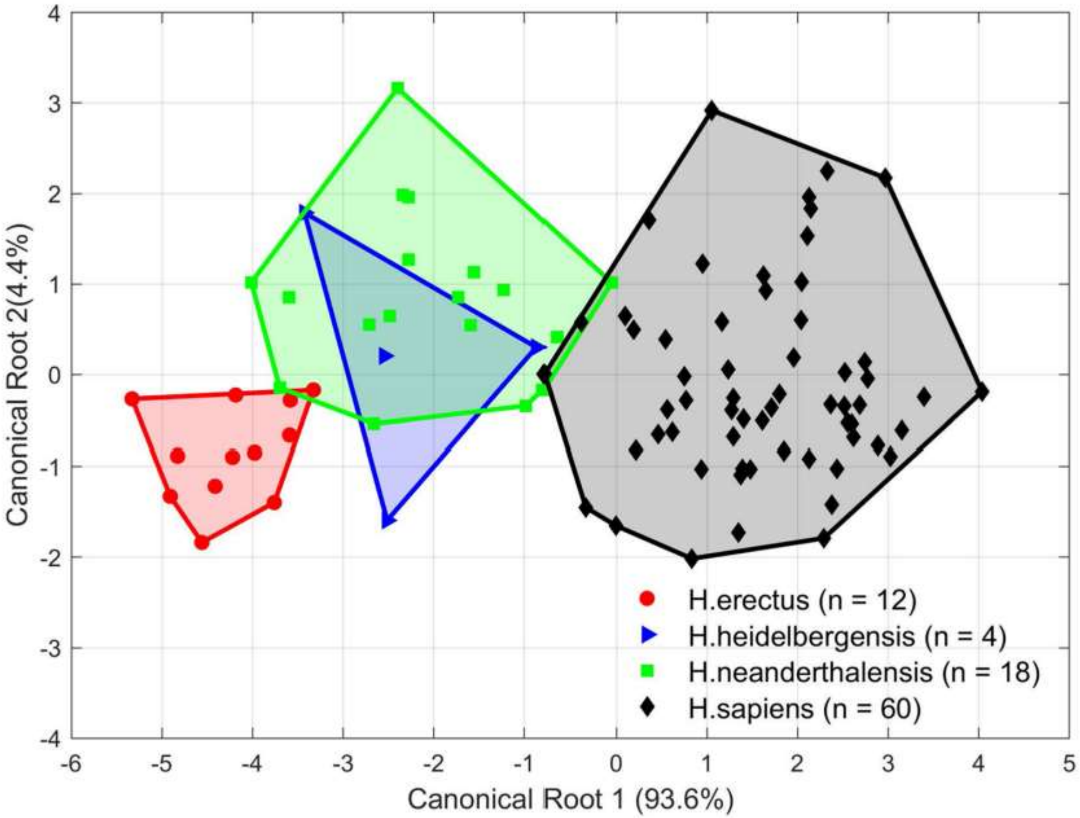
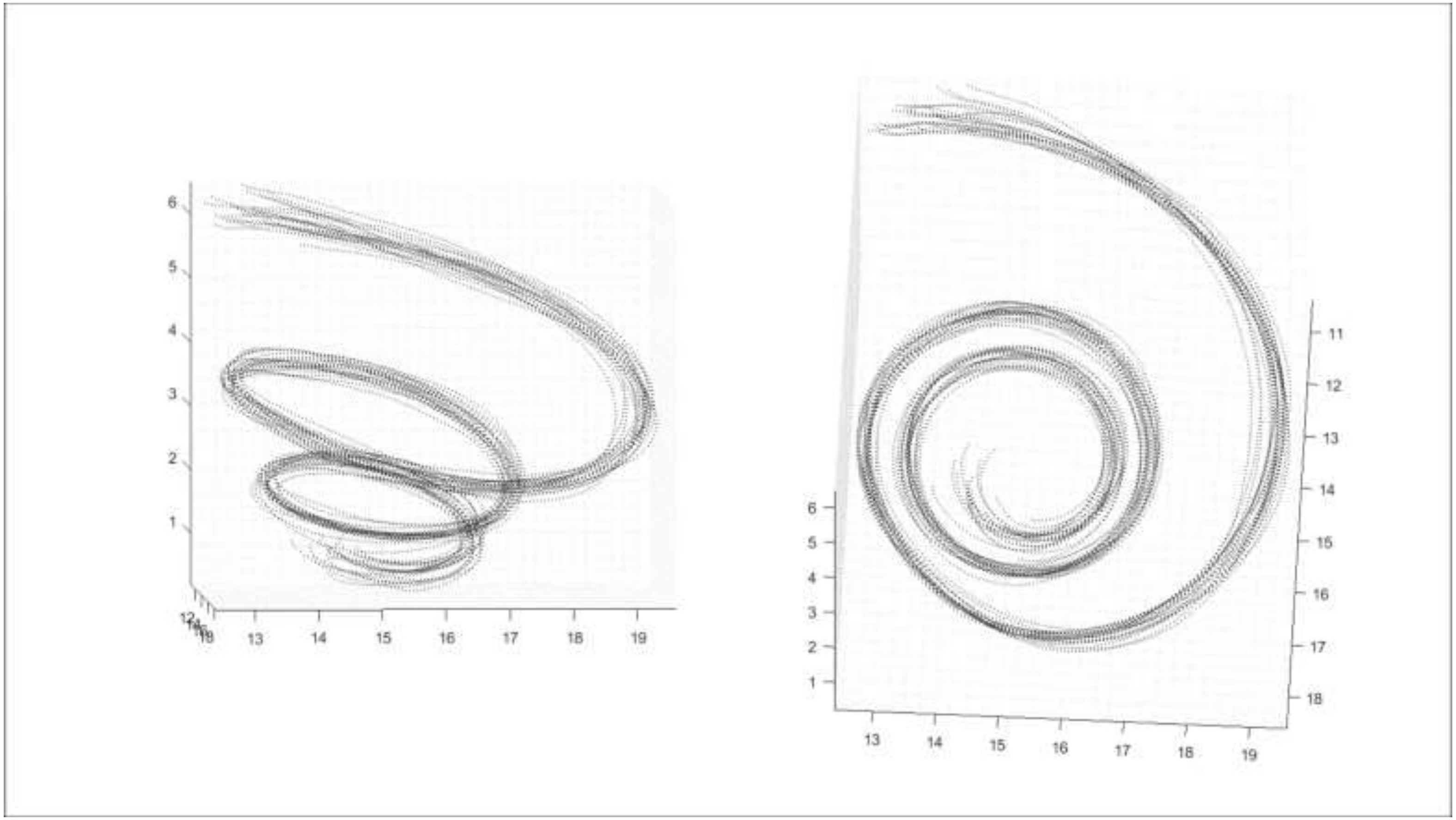


Figure 8. Canonical plot of the 94 human mandibles from four groups (*H. erectus*, *H. heidelbergensis*, *H. neanderthalensis*, and *H. sapiens*) based on the orientation changes between segments (19 variables).

Extension 2: generalization to 3D

Examples: Cochlea in 3D

T= [M M M M H M H M M] and ball joints



A new 3D morphometric method based on a combinatorial encoding of 3D point configurations: application to skull anatomy for clinical research and physical anthropology

Kevin Sol, LIRMM, Montpellier

Emeric Gioan -, AlGCo Research-Team , LIRMM, Montpellier

Gérard Subsol - Research-Team ICAR, LIRMM, Montpellier

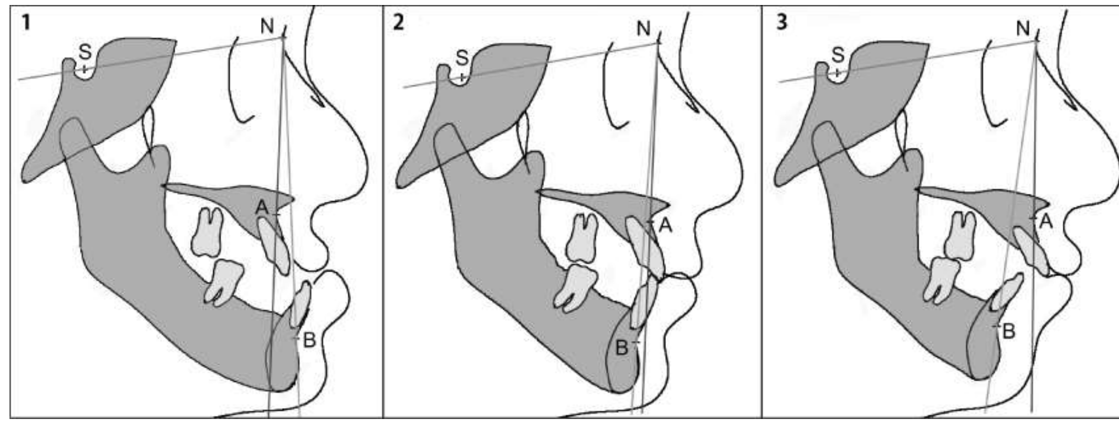
Thanks to Yann Heuzé et Joan Richstmeier - PennState Univ., U.S.A.

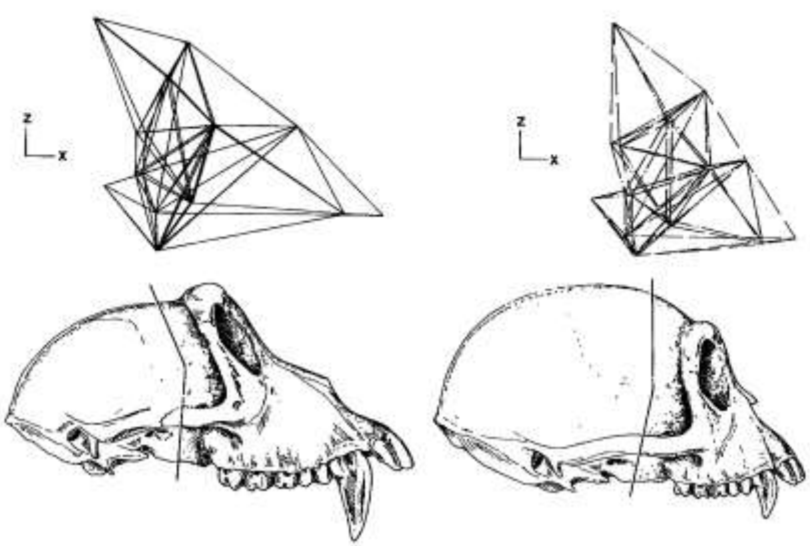
José Braga et Jacques Treil – CAGT, Toulouse

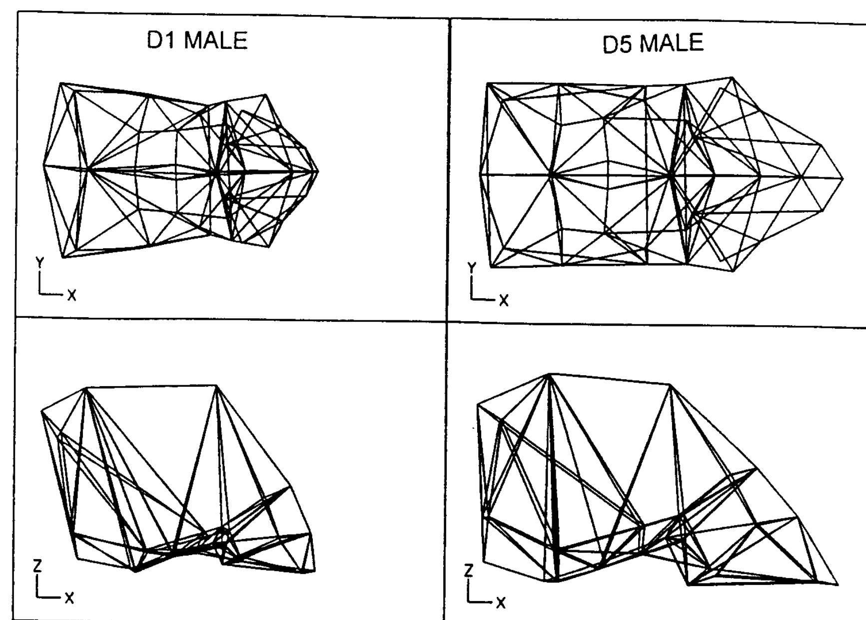
LIRMM

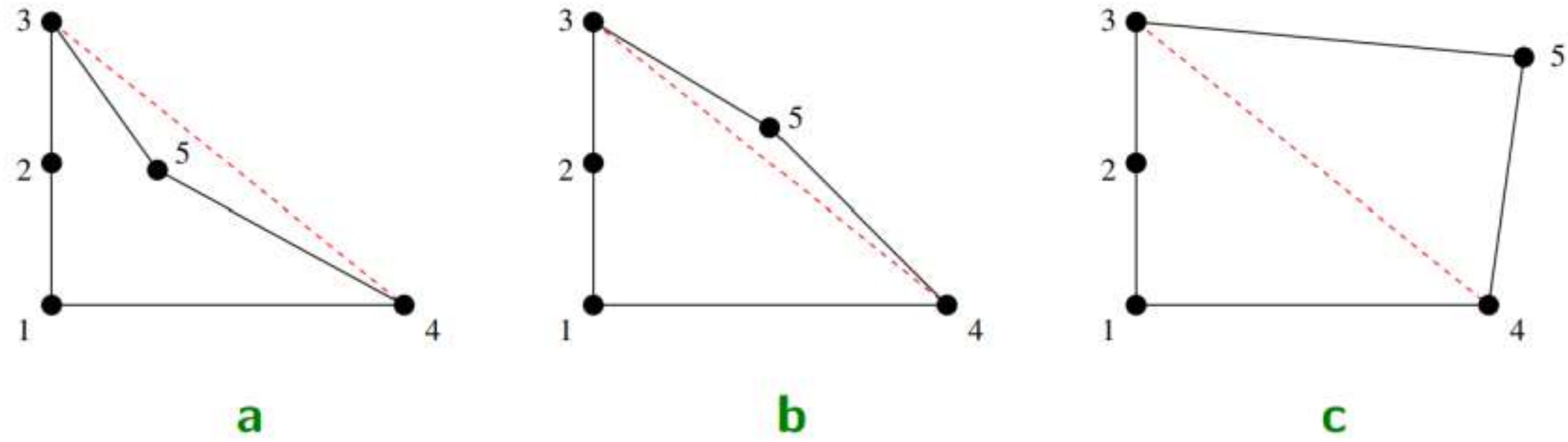
In landmark-based morphometry, shape differences may be not "metric" but rather algebraic (or topological).

Example: a subset of landmarks moves in front of an other subset (e.g. facial pathology)

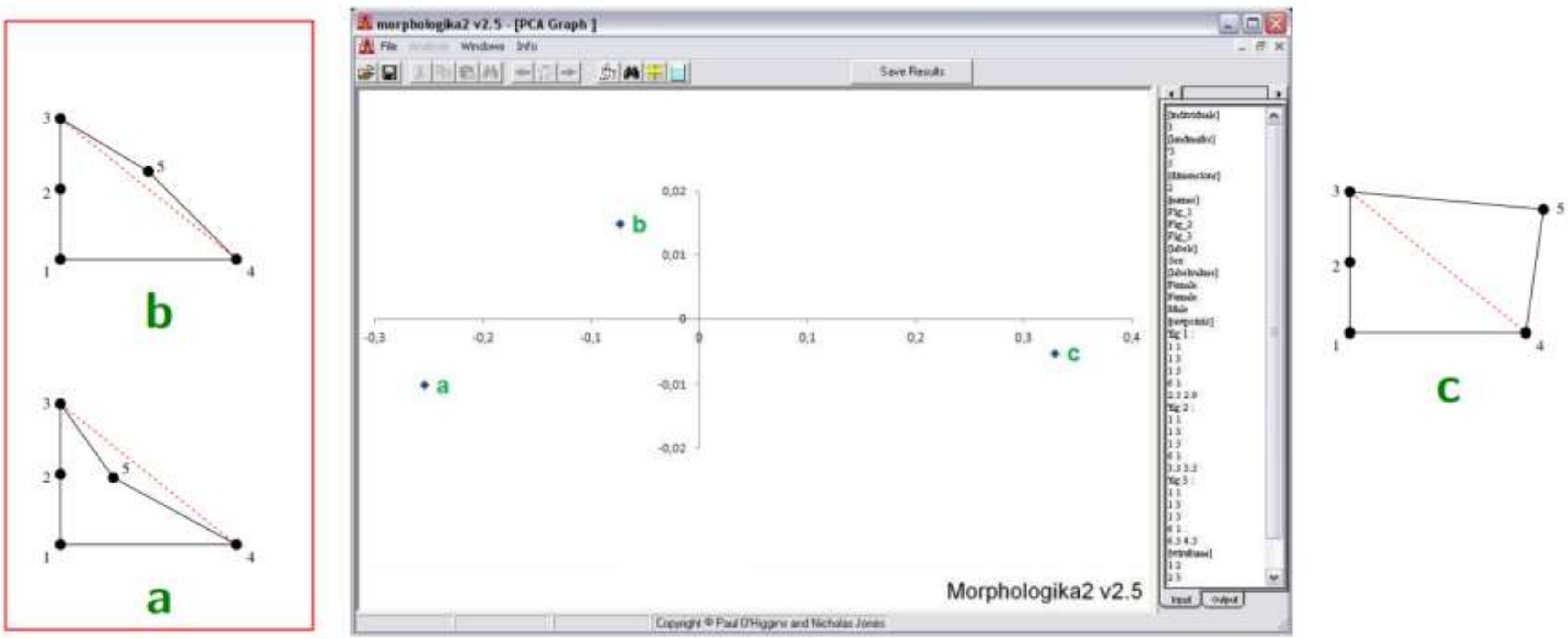




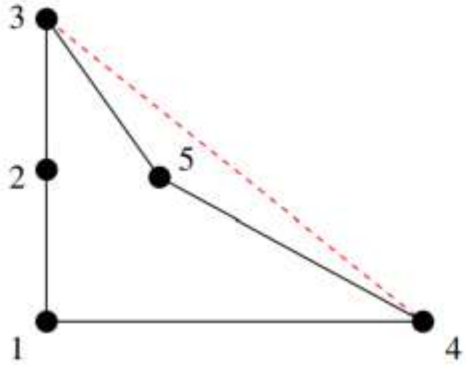




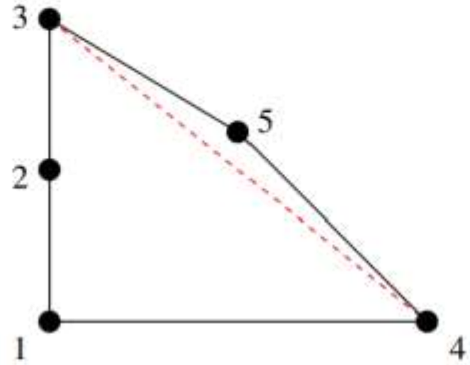
1
2
3
4
5
a
b
c



b
a
morphologika2 v2.5 - [PCA Graph]
File
Windows
Info
Save Results
-0,3
-0,2
-0,1
0
0,1
0,2
0,3
0,4
0,02
0,01
-0,01
-0,02
Morphologika2 v2.5
Copyright © Paul O'Higgins and Nicholas Jones
c



a



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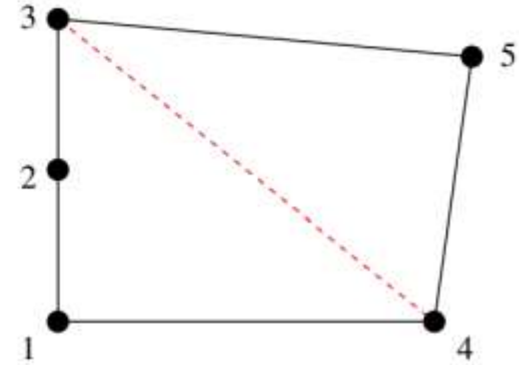

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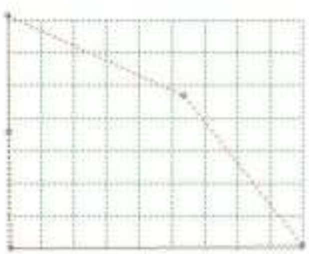
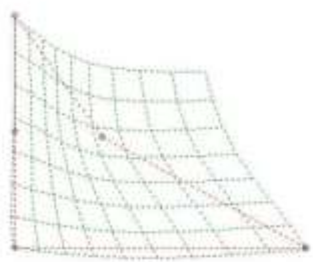
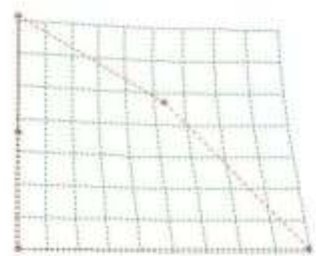


Mean shape



a



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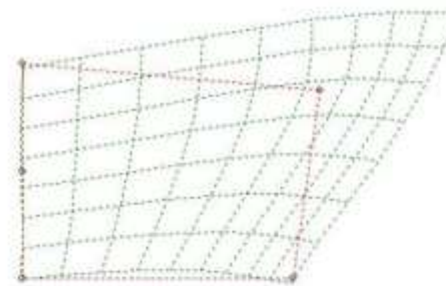
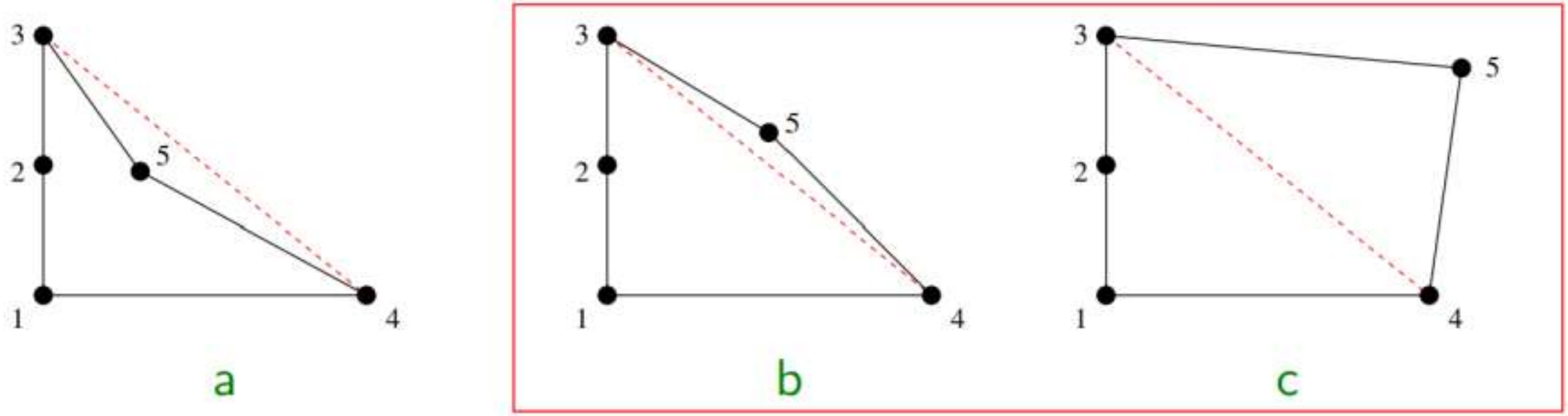
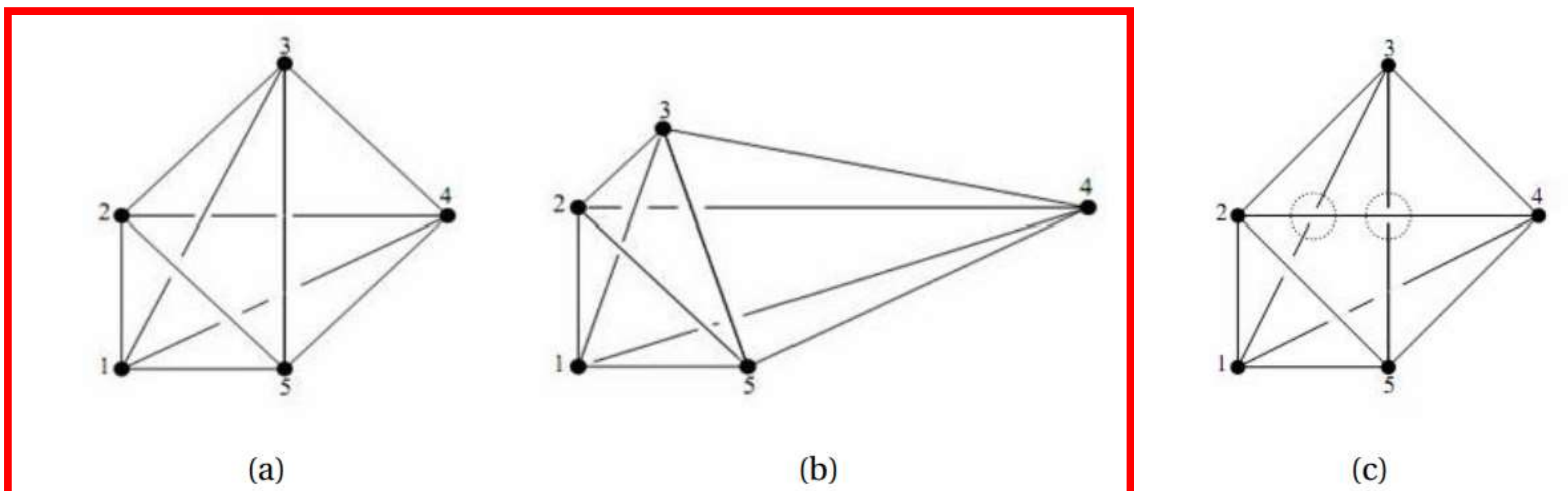


c

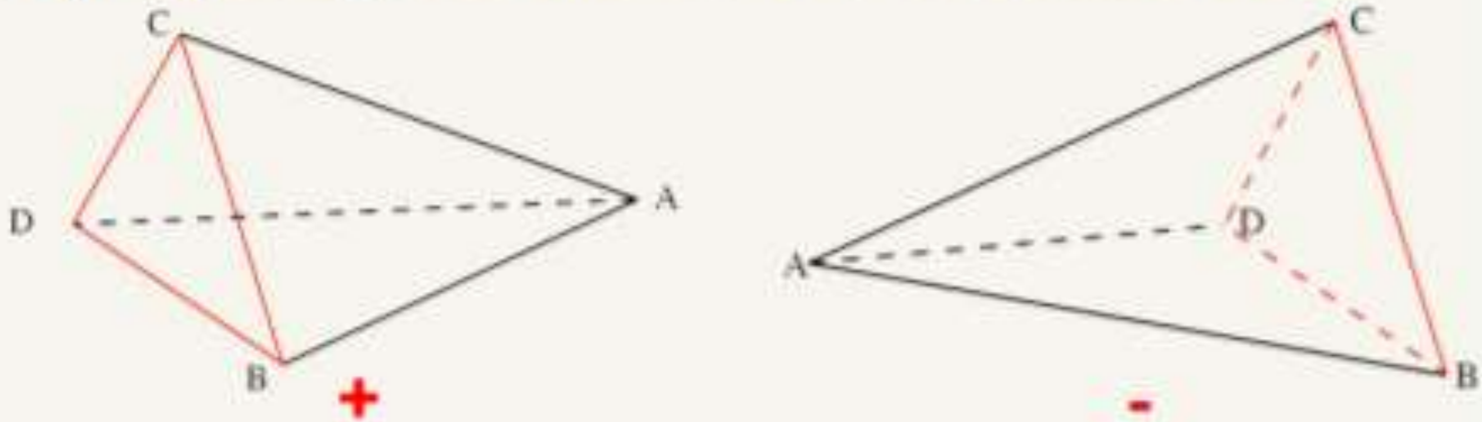
Objective





A new 3D morphometric method

In 3D, each set of 4 landmarks A, B, C, D, can be associated with a sign depending on the orientation of the tetrahedron ABCD.

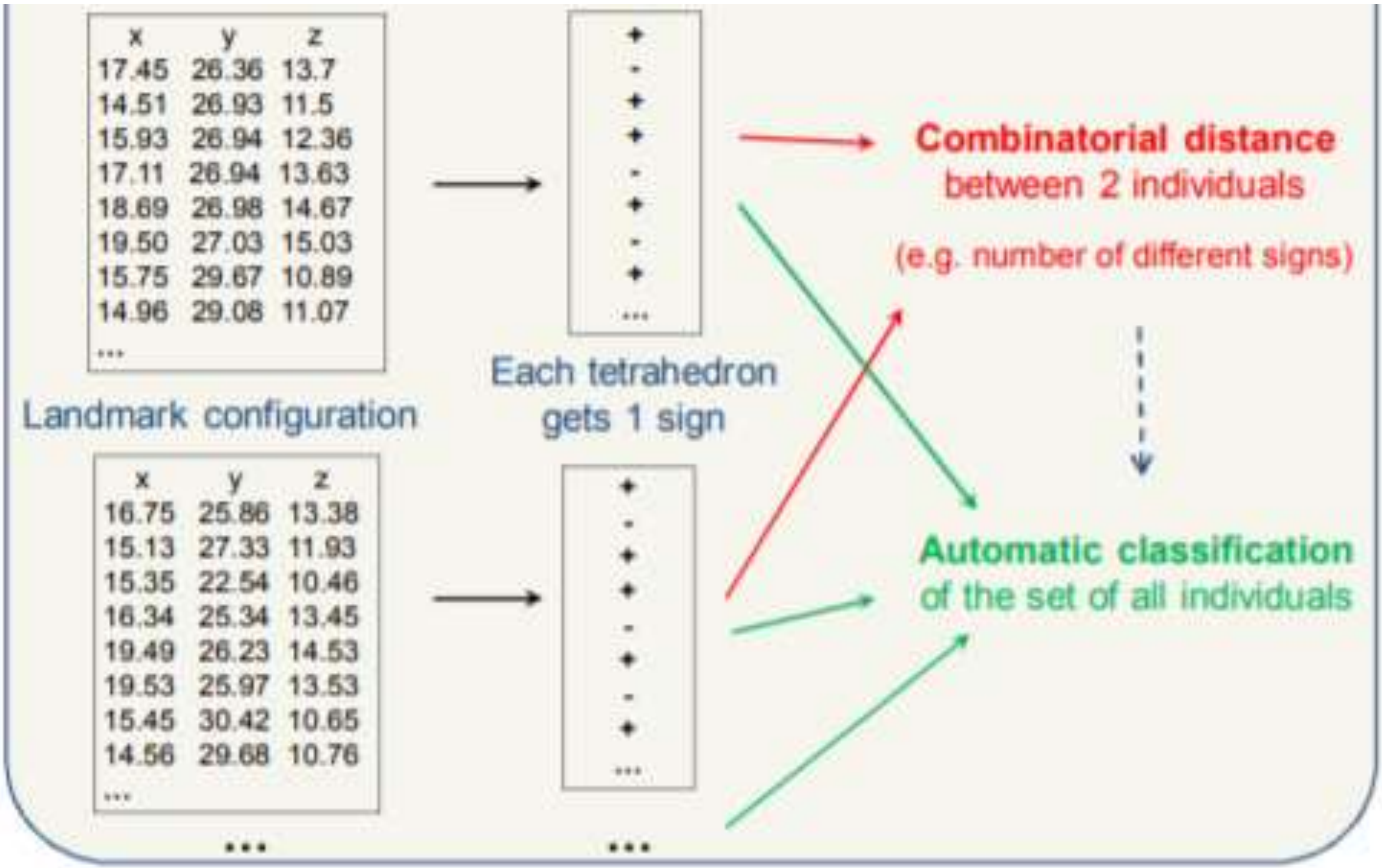


For a configuration composed of *n 3D* landmarks, we consider

$t = \frac{n!}{(n-4)!\cdot 4!}$ tetrahedra and get a vector of *t* signs (+ or -) that encodes the "shape" of the configuration.

This vector defines a *combinatorial mathematical structure* called an ***Oriented Matroid.***

[Björner, Las Vergnas, Sturmfels, White, Ziegler. "Oriented Matroids". Cambridge University Press. 1999]

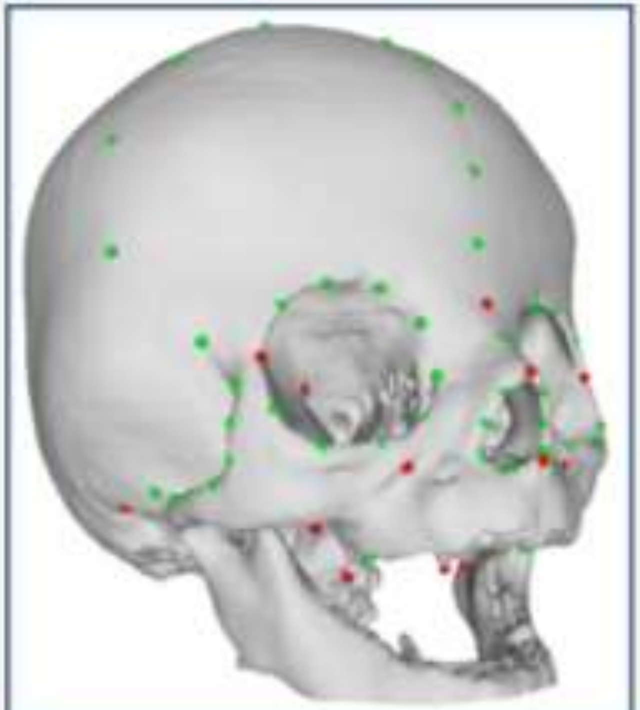


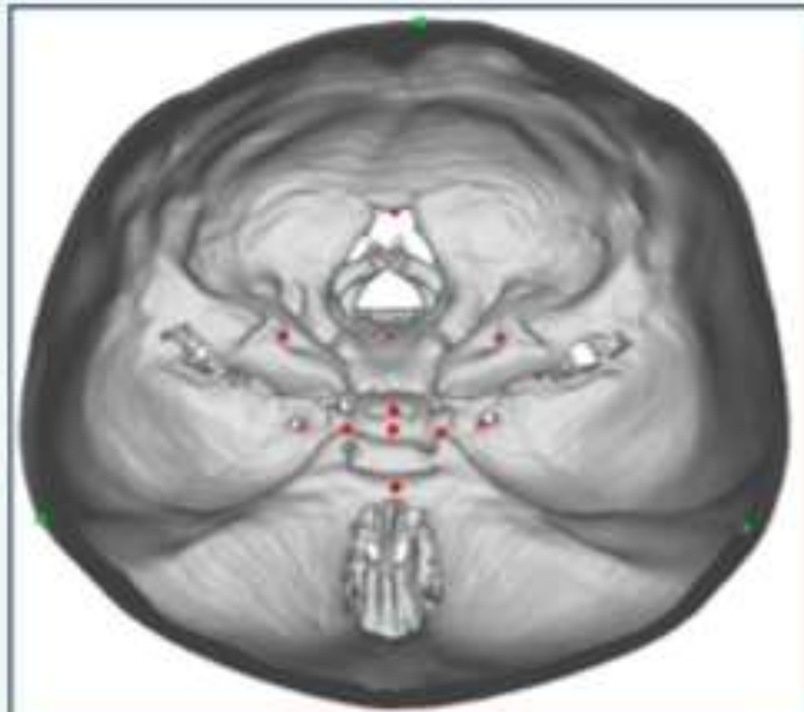
x y z
17.45 26.36 13.7
14.51 26.93 11.5
15.93 26.94 12.36
17.11 26.94 13.63
18.69 26.98 14.67
19.50 27.03 15.03
15.75 29.67 10.89
14.96 29.08 11.07
...
Landmark configuration
x y z
16.75 25.86 13.38
15.13 27.33 11.93
15.35 22.54 10.46
16.34 25.34 13.45
19.49 26.23 14.53
19.53 25.97 13.53
15.45 30.42 10.65
14.56 29.68 10.76
...
...
+ - + + - + - + ...
Each tetrahedron gets 1 sign
+ - + + - + - + ...
...
Combinatorial distance
between 2 individuals
(e.g. number of different signs)
Automatic classification
of the set of all individuals

Data

- 3D CT-images of 40 children (0.1 – 19.9 months) with craniosynostosis, i.e. premature fusion of cranial sutures
- visual evaluation and classification into 3 categories by a clinician:
  - BCS (*bicoronal*): fusions of both lateral sutures (15)
  - LUCS (*left unicoronal*): fusion of only left-side suture (8)
  - RUCS (*right unicoronal*): fusion of only right-side suture(17)
- 133 landmarks defined by an expert:

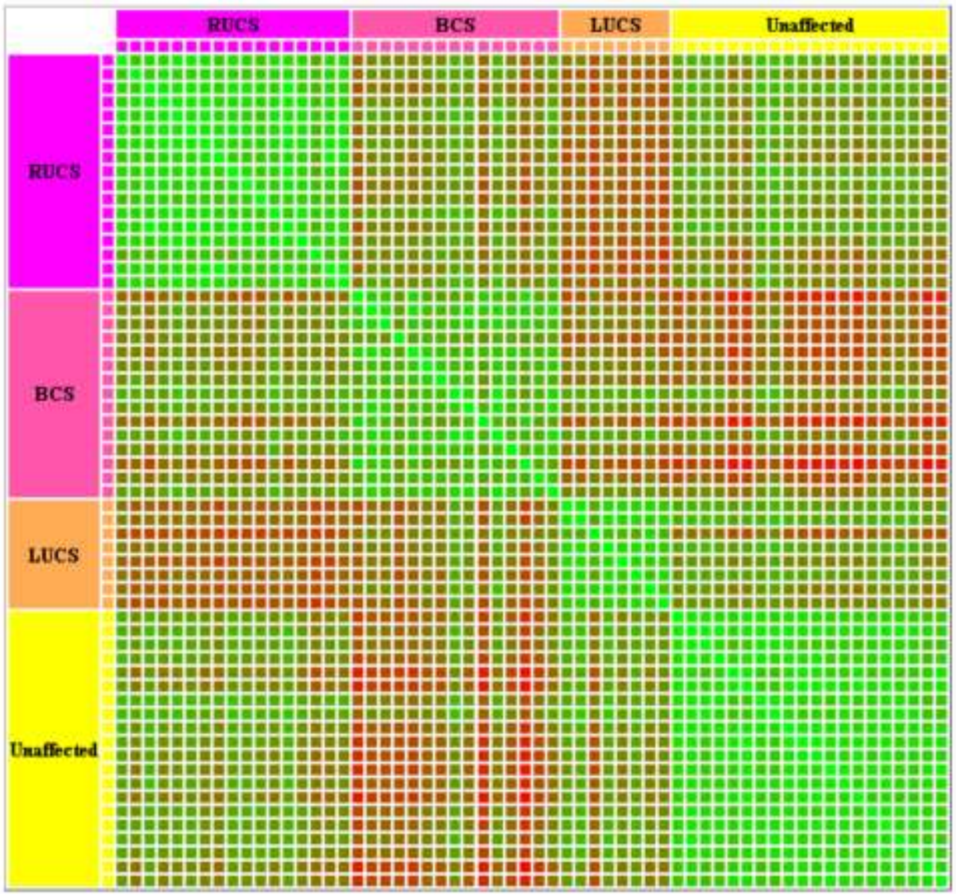
  41 anatomical landmarks / 92 curve semilandmarks.





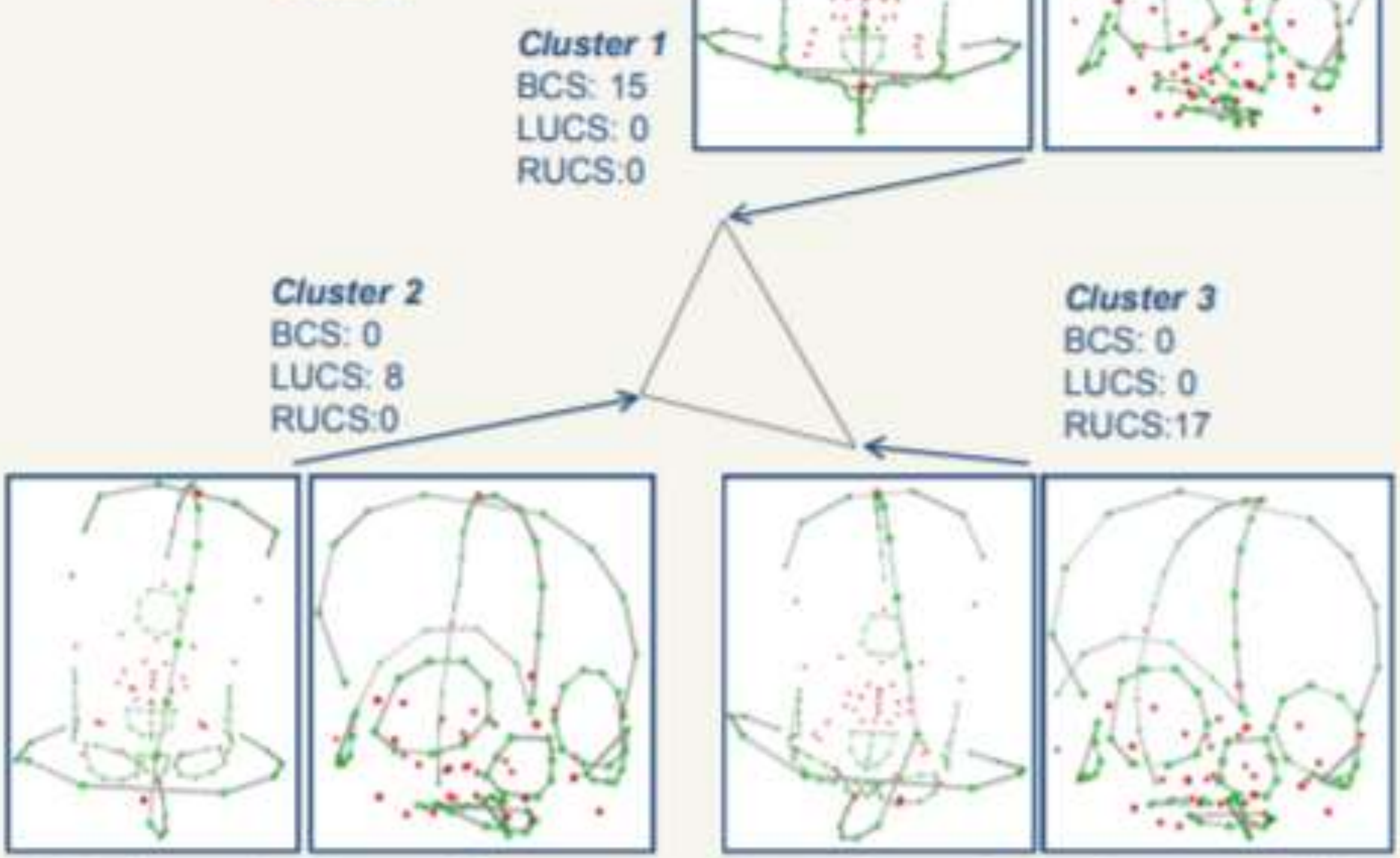
+ 20 Unaffected/Control

	RUCS	BCS	LUCS	Unaffected
RUCS	16.2%	27.6%	34%	25.9%
BCS	27.6%	20.2%	30%	33.4%
LUCS	34%	30%	17.5%	26%
Unaffected	25.9%	33.4%	26%	15.8%



Automatic classification

Cluster analysis by K-means criterion / algorithm using this combinatorial distance.



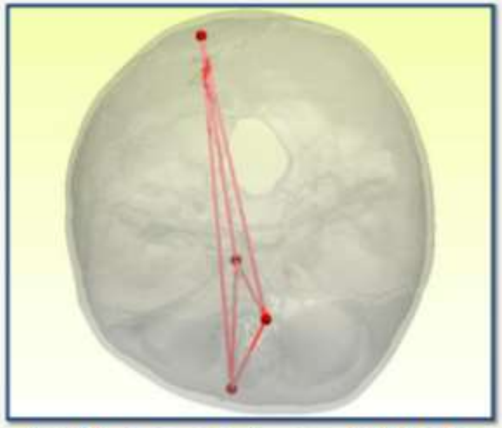
Mathematically, K-means clustering based on this combinatorial distance provides classification matching diagnostic categories.

E. Gioan, K. Sol, G. Subsol. "A combinatorial method for 3D landmark-based morphometry: application to the study of coronal craniosynostosis". 15th International Conference on Medical Image Computing and Computer Assisted Intervention, Nice (France), October 2012, Lecture Notes in Computer Science 7512, p. 533–541, Springer, 2012.

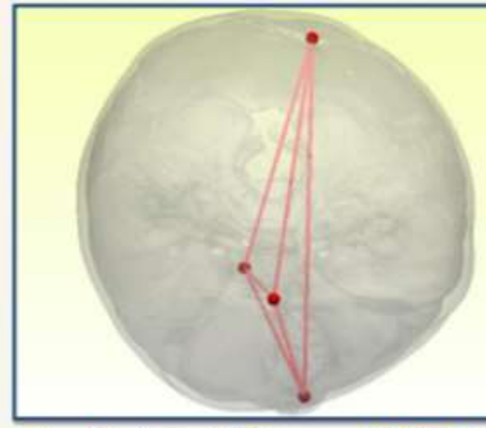
K. Sol. "Une approche combinatoire novatrice fondée sur les matroïdes orientés pour la caractérisation de la morphologie 3D des structures anatomiques". Ph.D. Thesis in Computer Science, University of Montpellier II (France), December 2013.

• Some Characterizations of Classes

(using only the 41 anatomical landmarks)

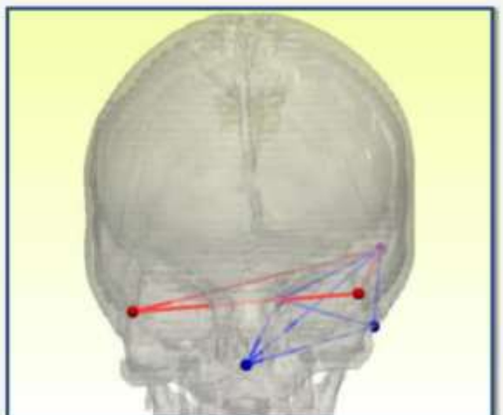


$[\chi(b_1) = +1] \Leftrightarrow$ **RUCS**

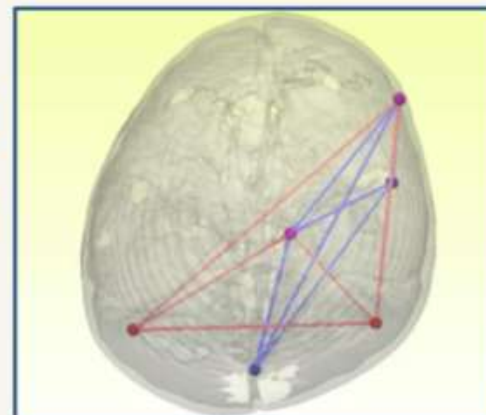


$[\chi(b_2) = +1] \Leftrightarrow$ **LUCS**

- ➢ RUCS and LUCS are characterized by the sign of only 1 basis.
- ➢ The 2 basis b_1 and b_2 are symmetric w.r.t. the median sagittal plan.



$[\chi(b_3) = -1]$ and $[\chi(b_4) = -1]$ $\Leftrightarrow$ **BCS**



- ➢ The signs of 2 bases characterize the category **BCS**.

- ➢ Based on the discriminability, we found a subset $\mathcal{S}$ of 5 bases and a vector x in $\{-1,1\}^{\mathcal{B}}$ such as: ***M*** is **unaffected** if and only if $\boldsymbol{M} \in B(\mathcal{S}, x, 2)$ (i.e. the signs of at least 3 of these 5 bases are the same in x and $\chi_{\mathbf{M}}$).