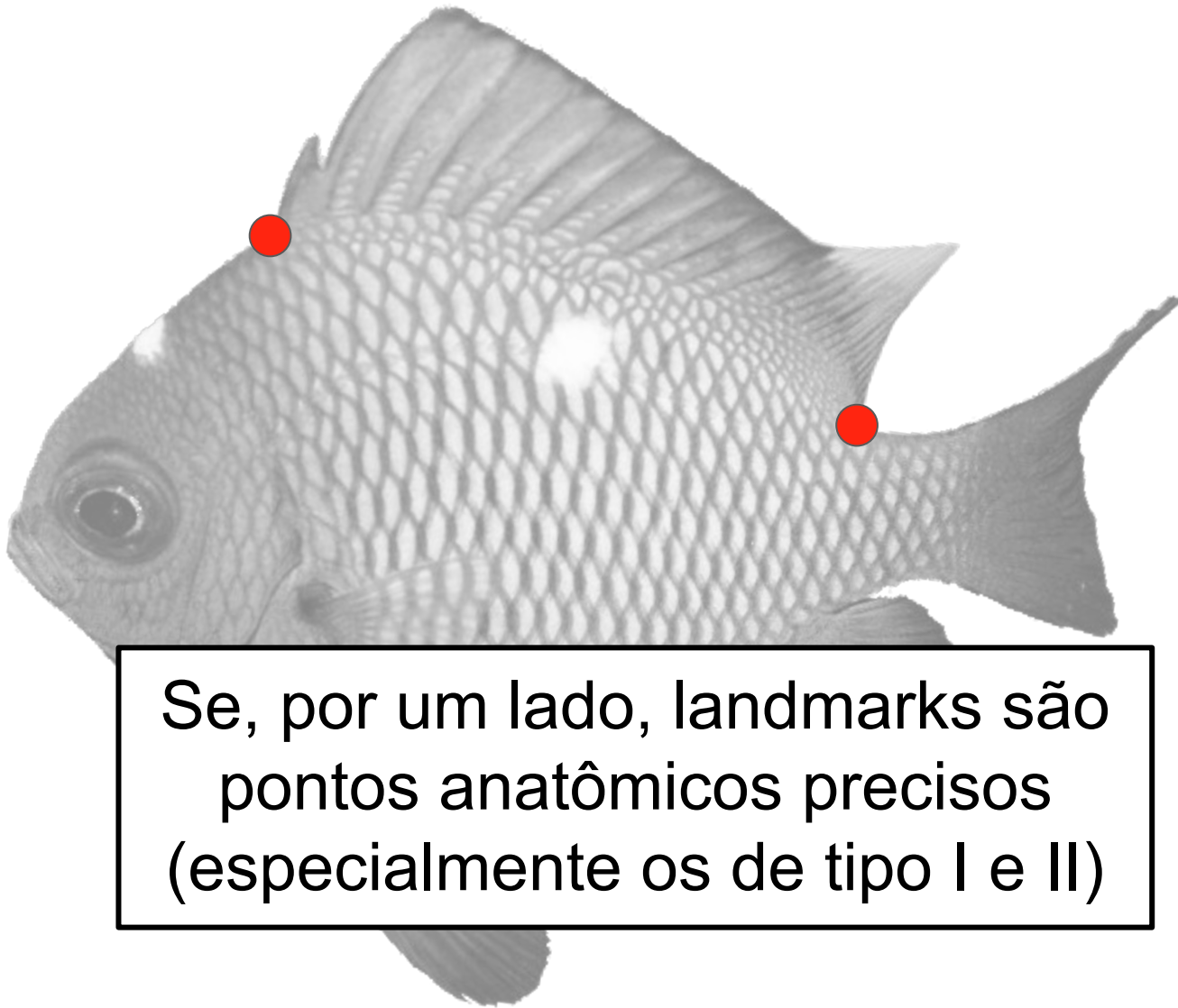




# Tópicos I – Morfometria Geométrica

Diego de Almeida da Silva

Aula 6: Tutorial



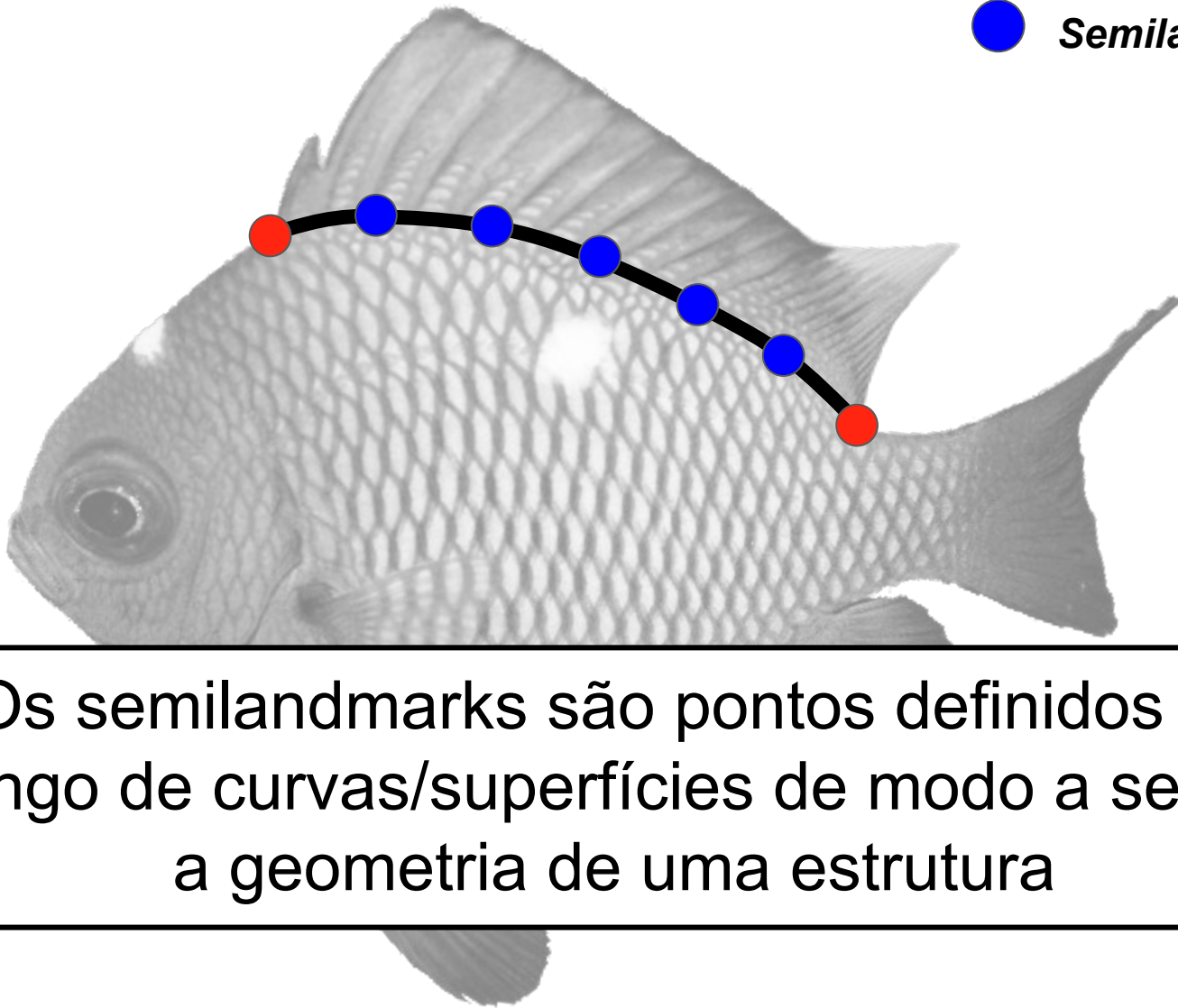
Se, por um lado, landmarks são pontos anatômicos precisos (especialmente os de tipo I e II)



*Landmarks*

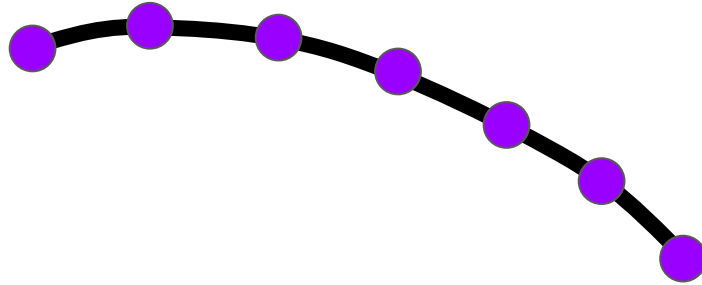


*Semilandmarks*



Os semilandmarks são pontos definidos ao longo de curvas/superfícies de modo a seguir a geometria de uma estrutura

# *Curvas*



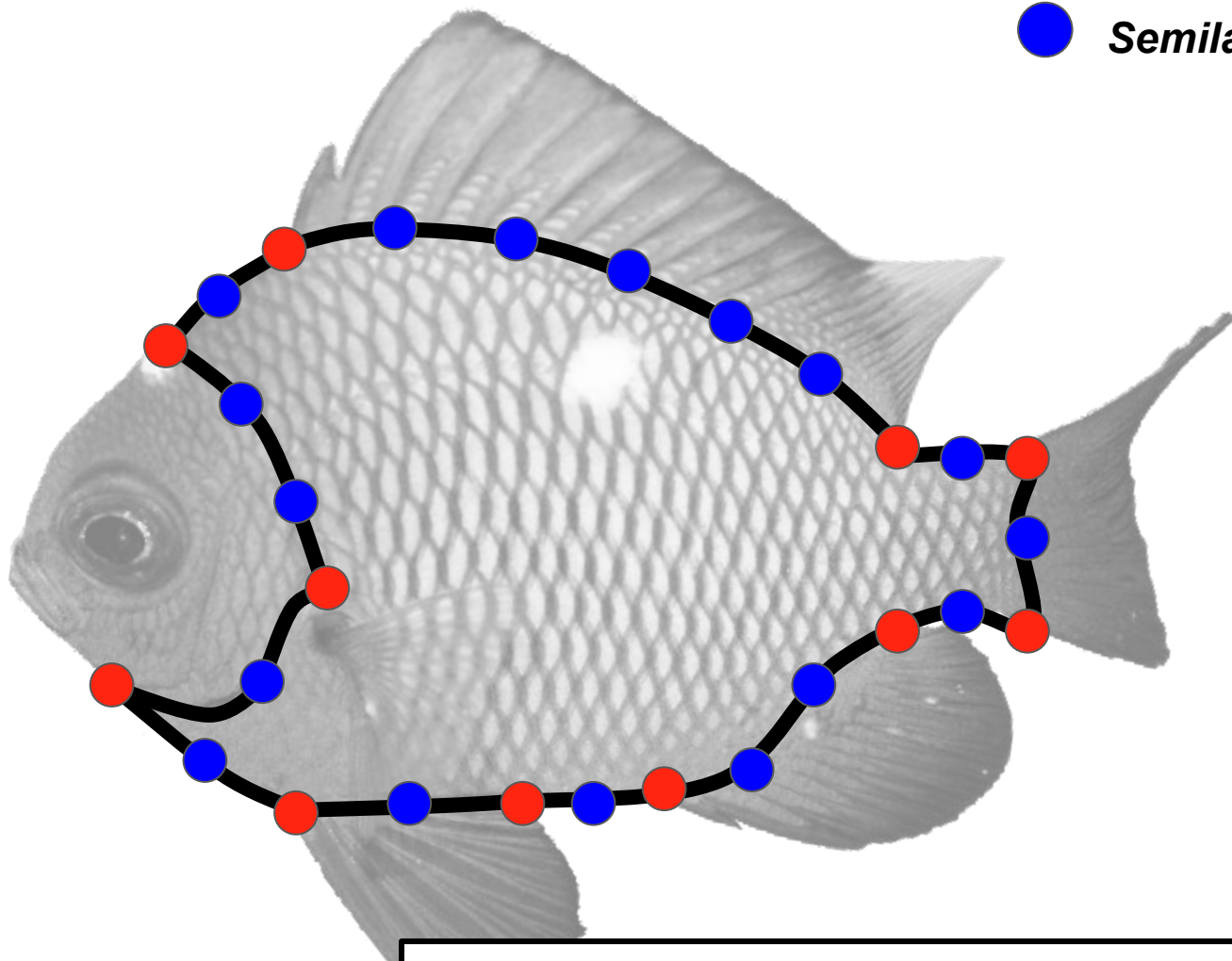
*Tipo mais simples de distribuição de  
semilandmarks*



*Landmarks*



*Semilandmarks*



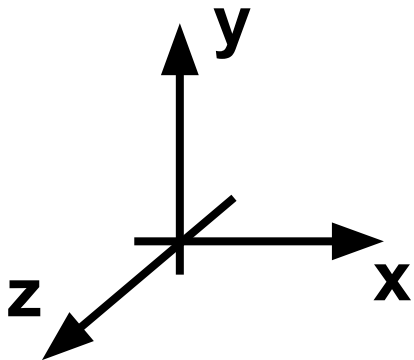
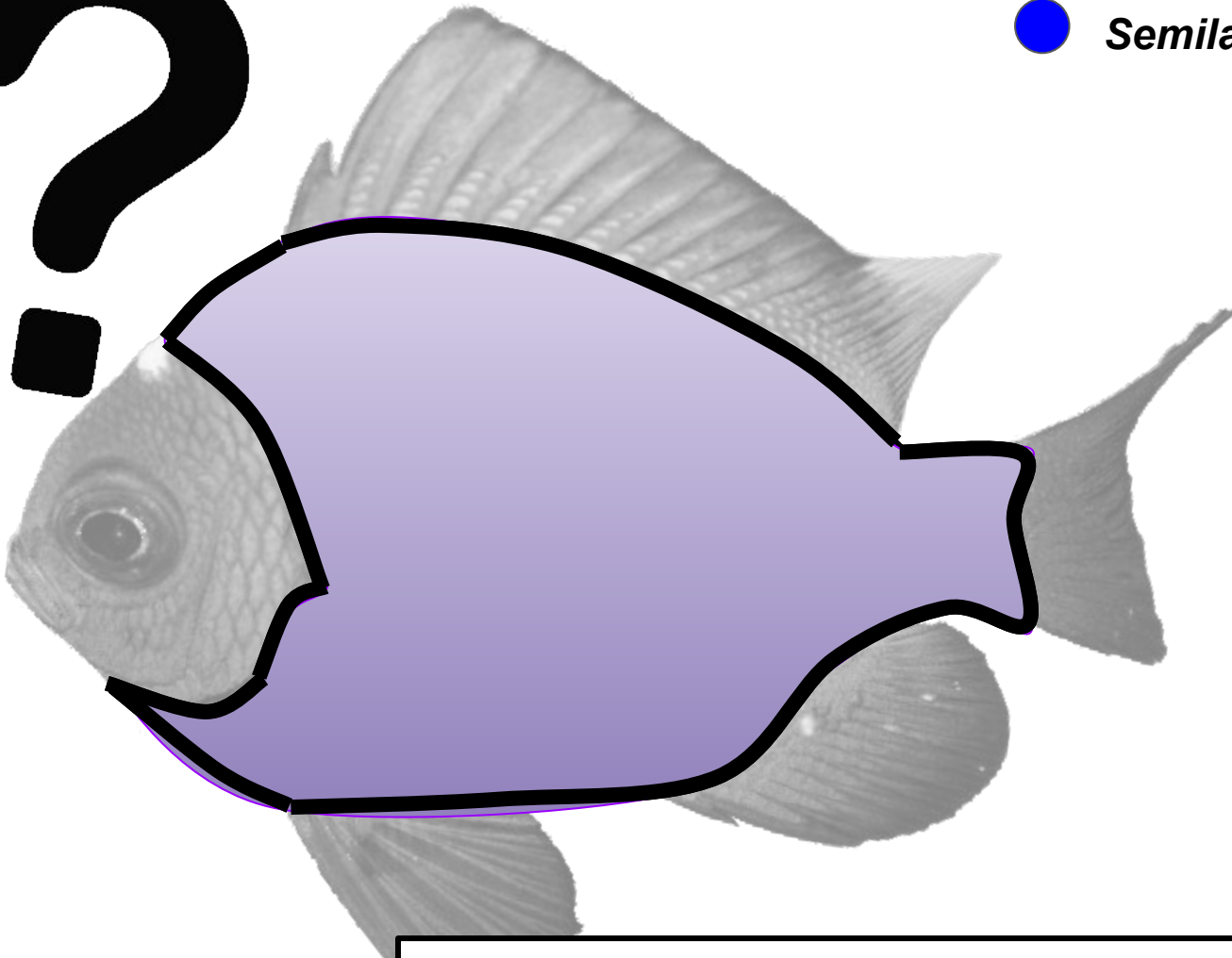
E podemos adaptá-lo a um  
número indefinido de curvas



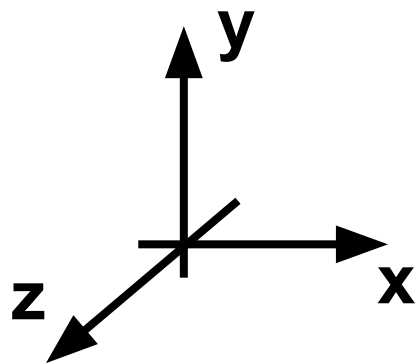
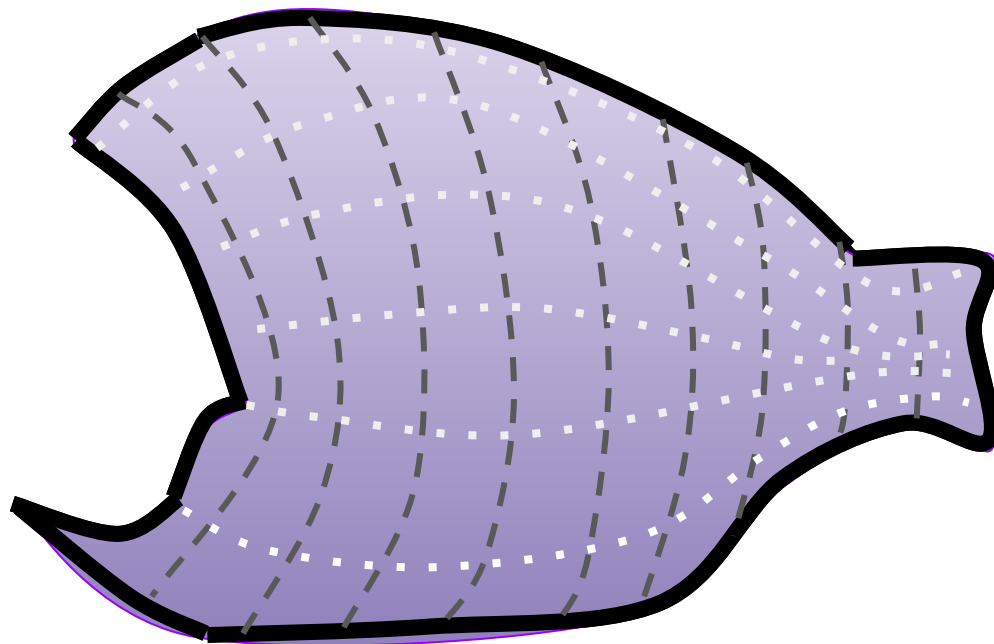
*Landmarks*



*Semilandmarks*



E se nos interessa toda uma  
superfície?



Principalmente a  
*tridimensionalidade* dela

# *Por que utilizar **dados 3D**?*

Research Article

## **Missing the third dimension in geometric morphometrics: how to assess if 2D images really are a good proxy for 3D structures?**

Andrea CARDINI<sup>a,b,\*</sup>

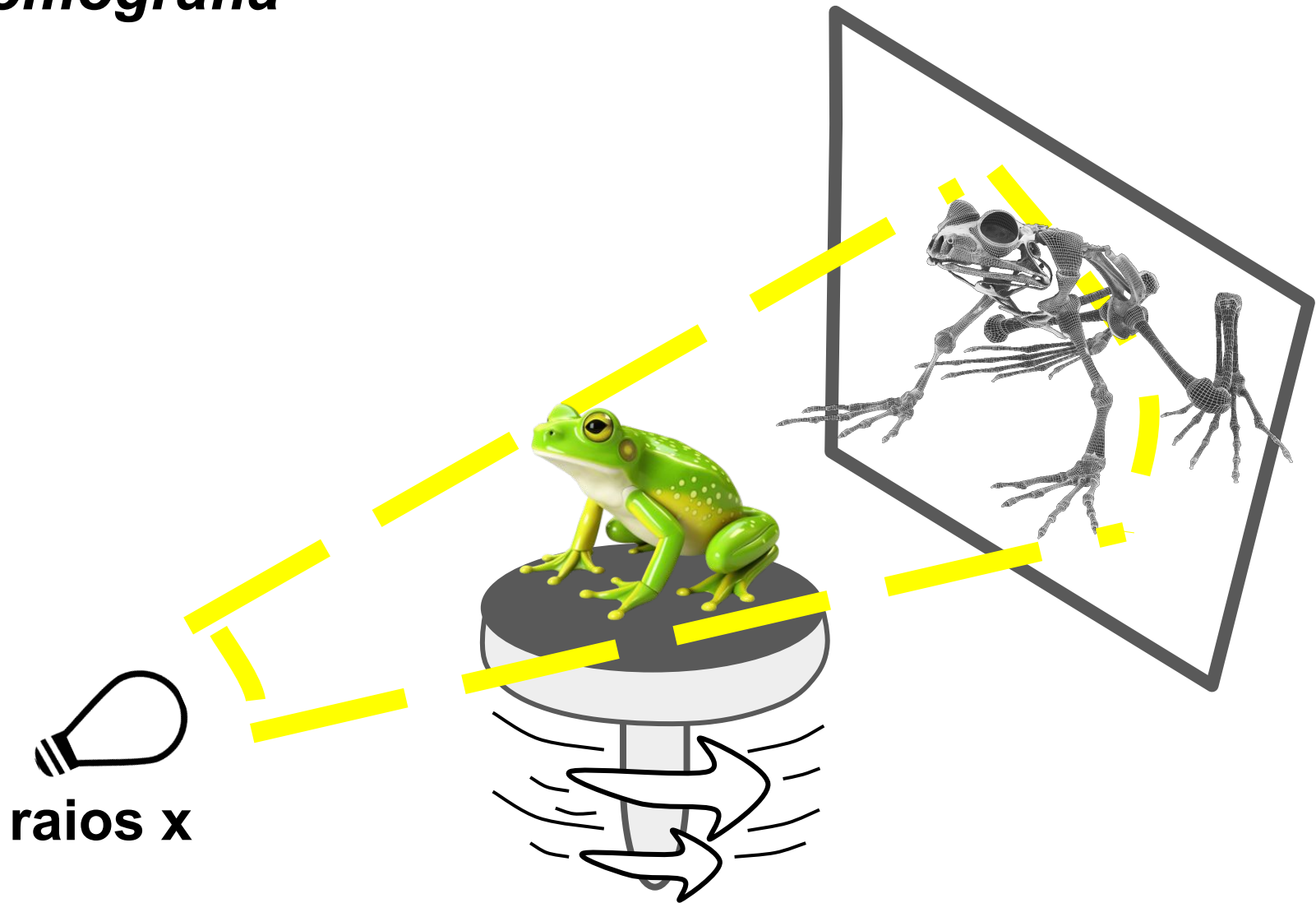
<sup>a</sup>*Dipartimento di Scienze Chimiche e Geologiche, Università di Modena e Reggio Emilia, l.go S. Eufemia 19, 41121 Modena, Italy*

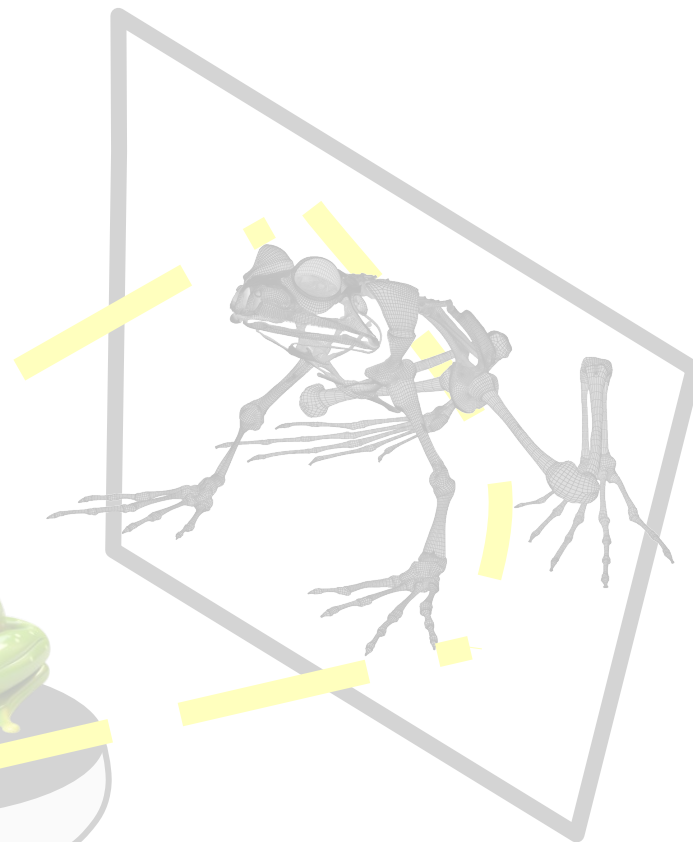
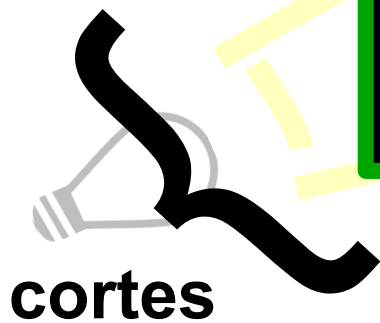
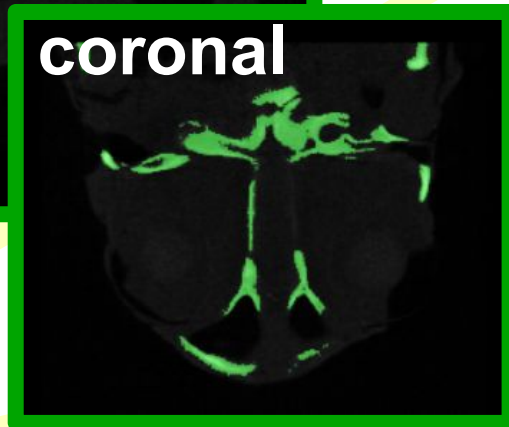
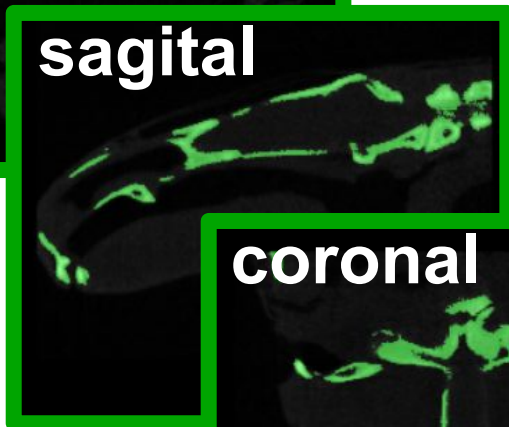
<sup>b</sup>*Centre for Forensic Science, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia*

<https://dx.doi.org/10.4404/hystrix-25.2-10993>

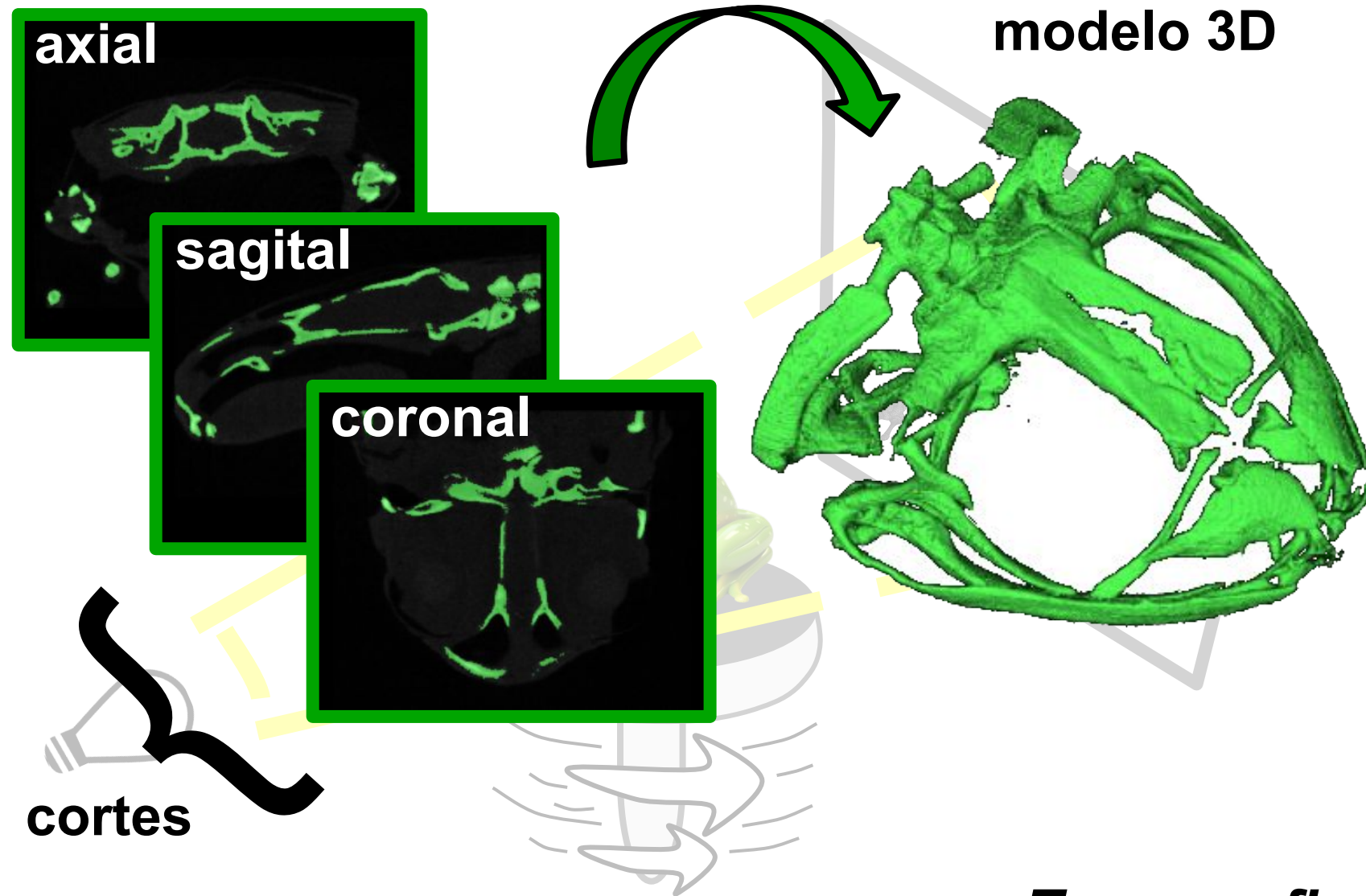


# Tomografia



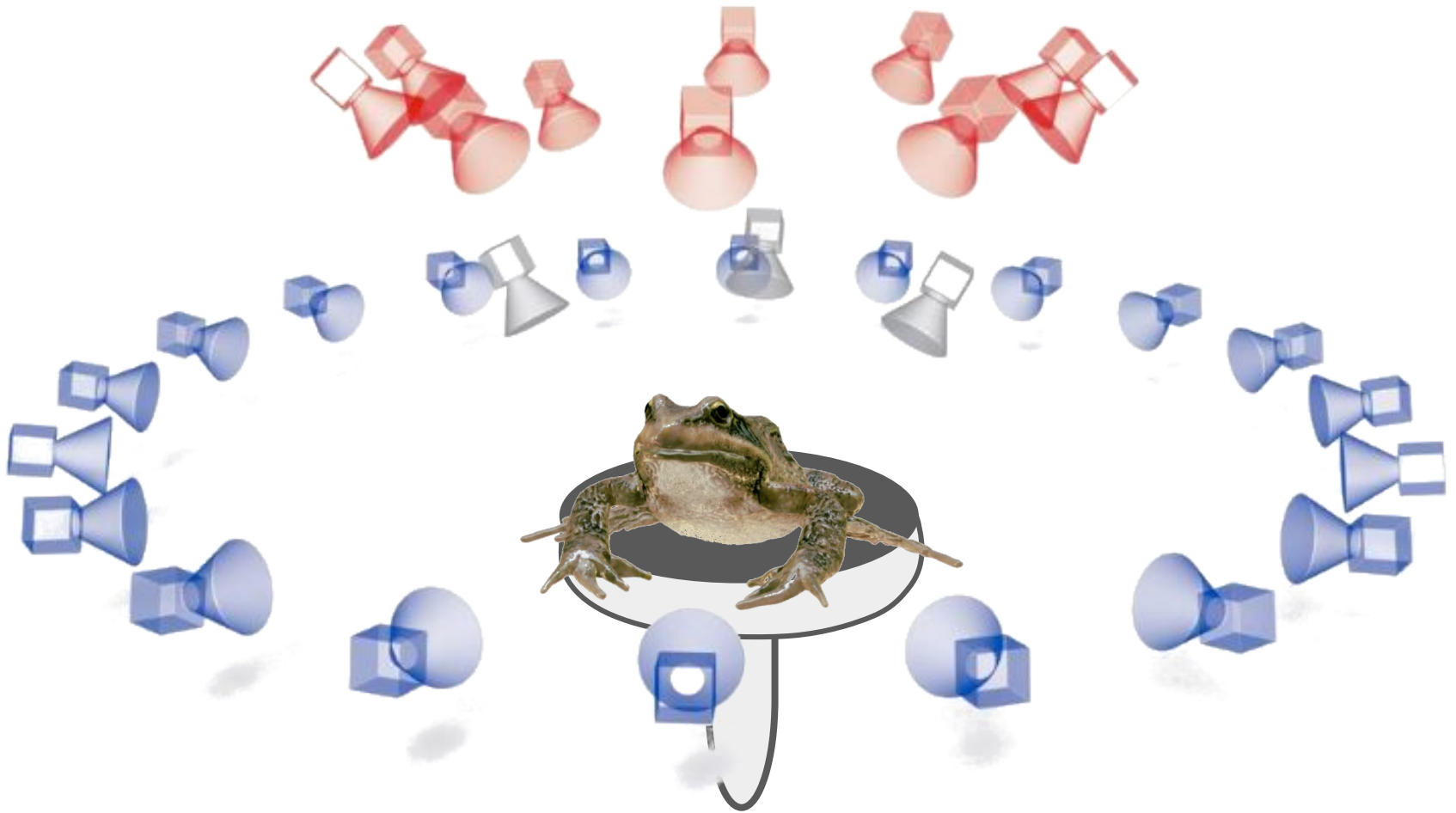


***Tomografia***



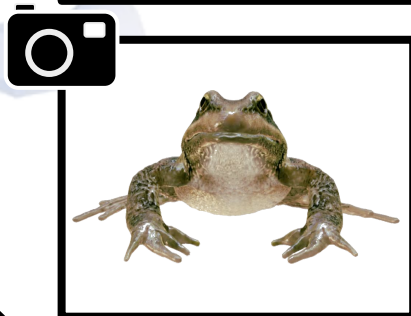
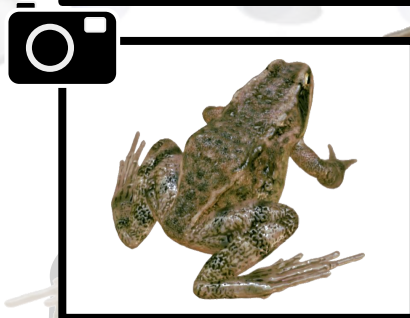
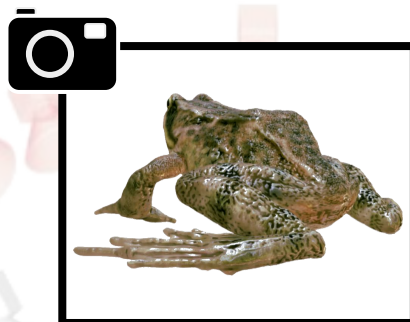
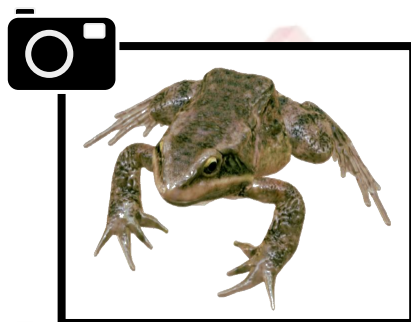
***Tomografia***

# ***Fotogrametria***





**modelo 3D**



**fotos**

***Fotogrametria***








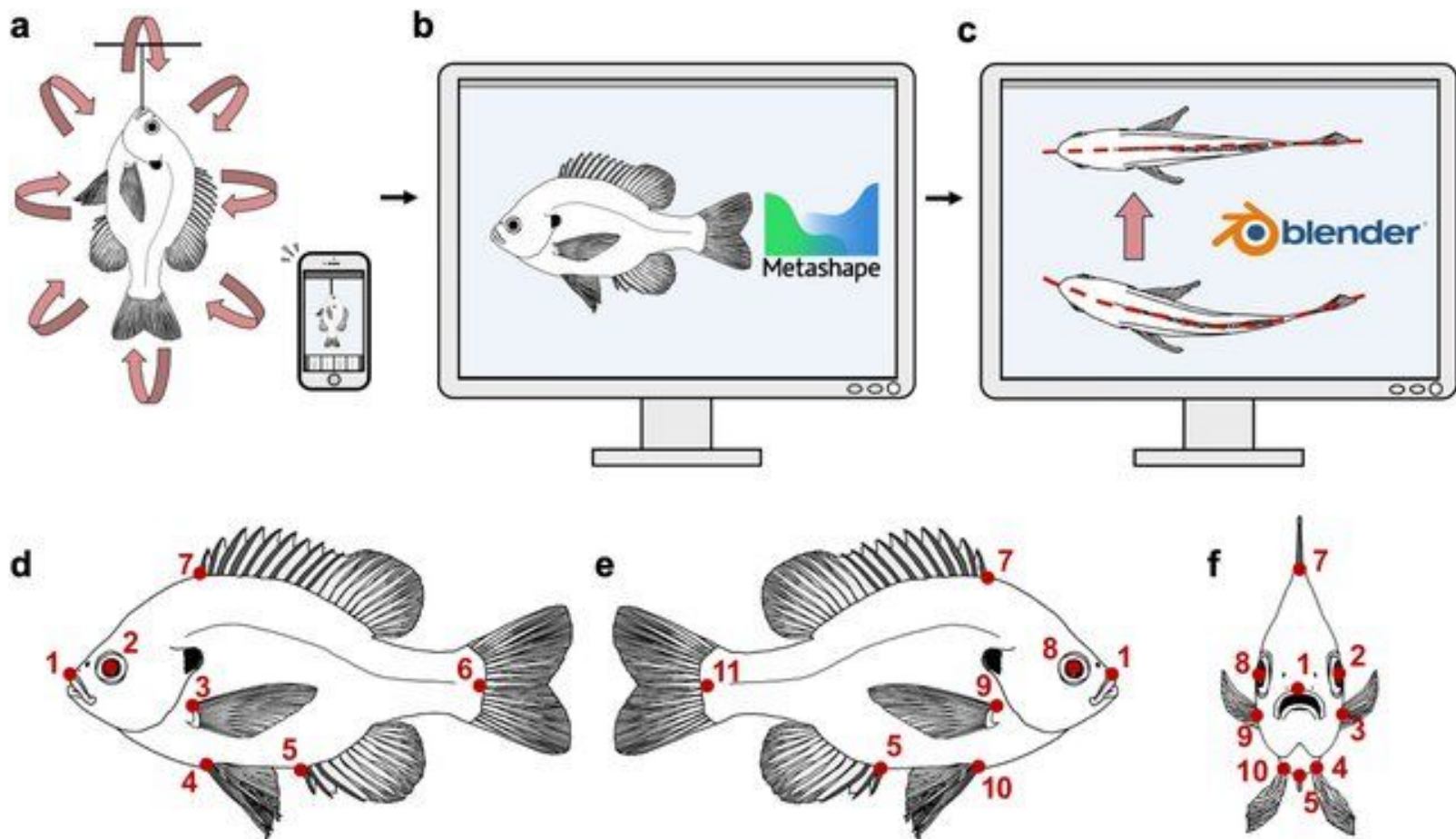
## scientific reports

OPEN

### Water constraints drive allometric patterns in the body shape of tree frogs

Kathleen M. S. A. Castro<sup>1,6</sup>, Talita F. Amado<sup>2,6</sup>, Miguel Á. Olalla-Tárraga<sup>2</sup>, Sidney F. Gouveia<sup>4,6</sup>, Carlos A. Navas<sup>3</sup> & Pablo A. Martinez<sup>5,6</sup>

 Check for updates



## scientific reports

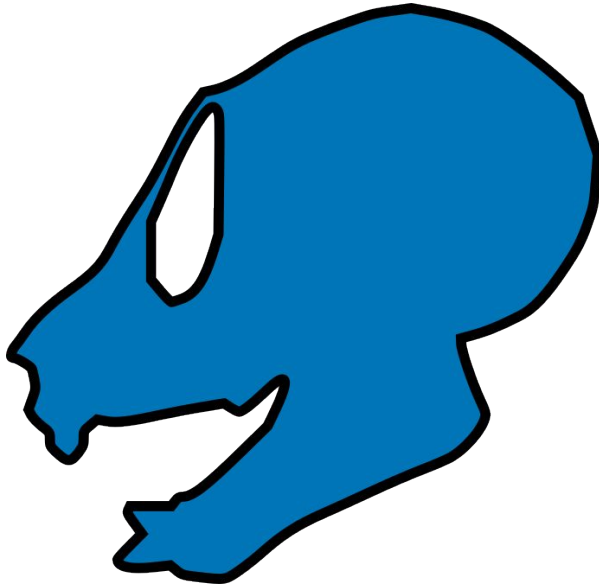
### OPEN Phylogenetic structure of body shape in a diverse inland ichthyofauna

Kevin T. Torgersen<sup>1,2</sup>, Bradley J. Bouton<sup>1</sup>, Alyx R. Hebert<sup>1</sup>, Noah J. Kleyla<sup>1</sup>, Xavier Plasencia II<sup>1</sup>, Garrett L. Rolfe<sup>1</sup>, Victor A. Tagliacollo<sup>2</sup> & James S. Albert<sup>1</sup>



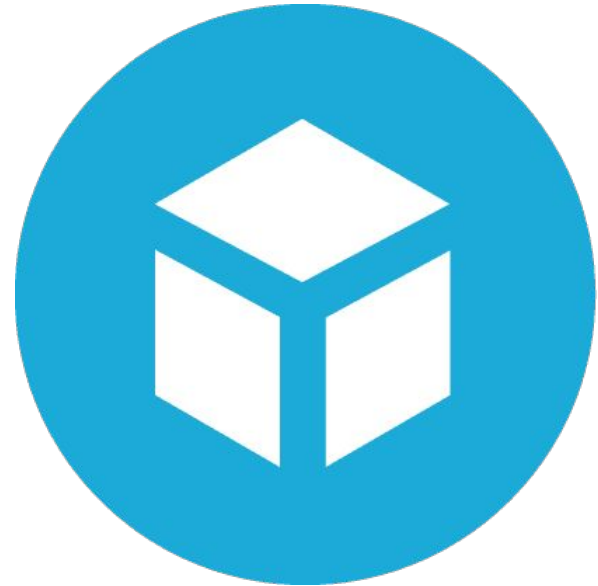


*Fontes de dados online:*



**MorphoSource**

<https://www.morphosource.org/>



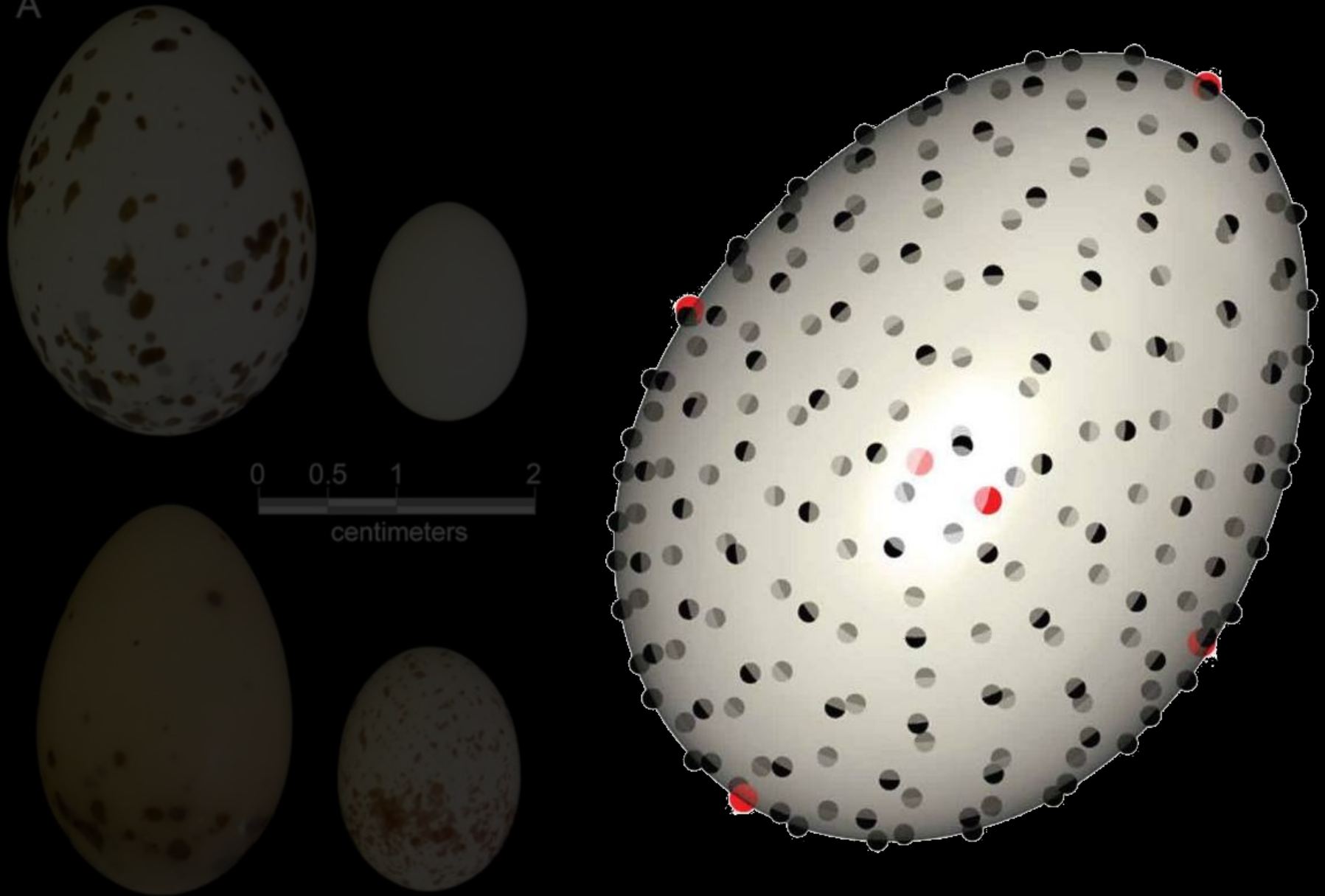
**Sketchfab**

<https://sketchfab.com/>

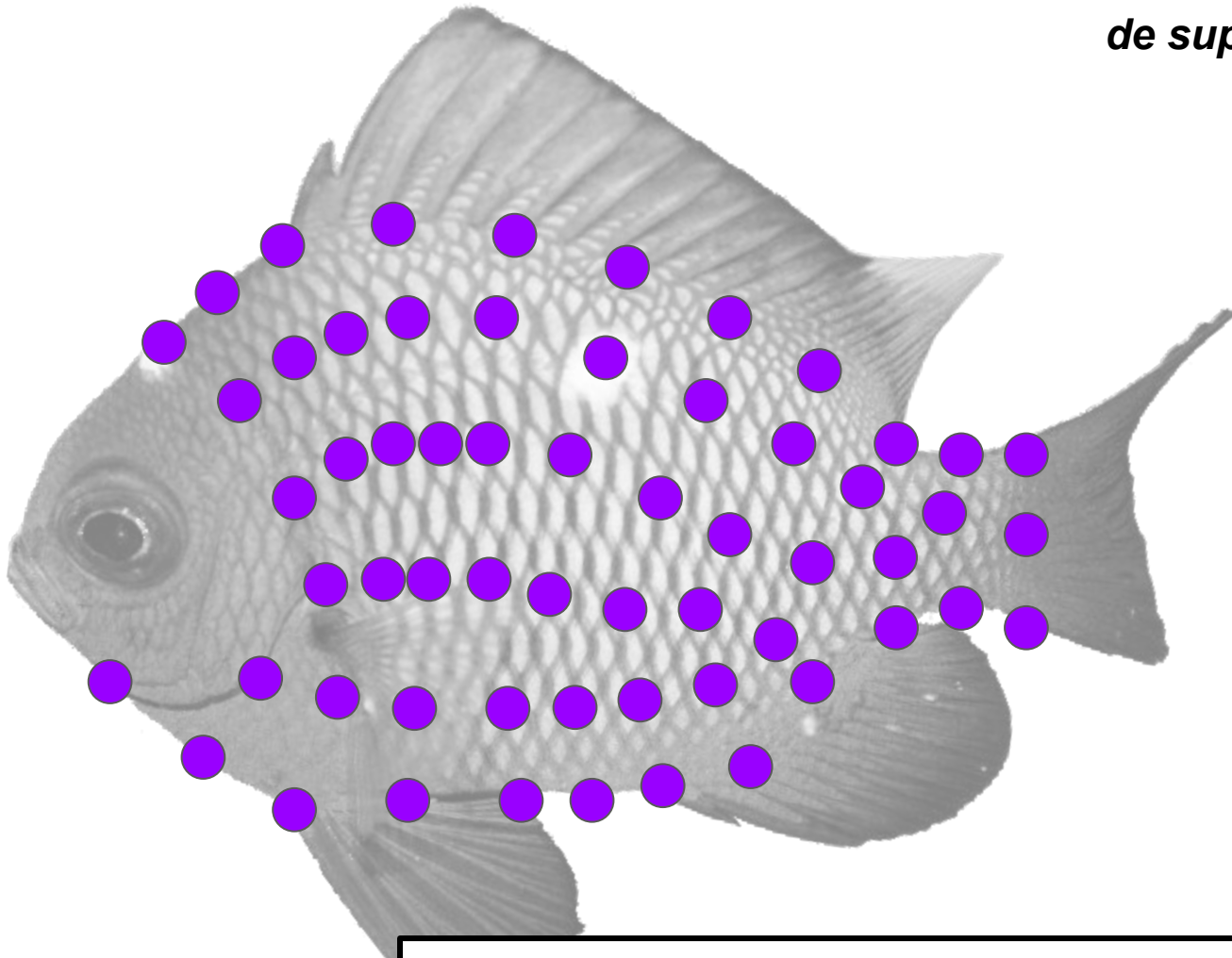
A



A

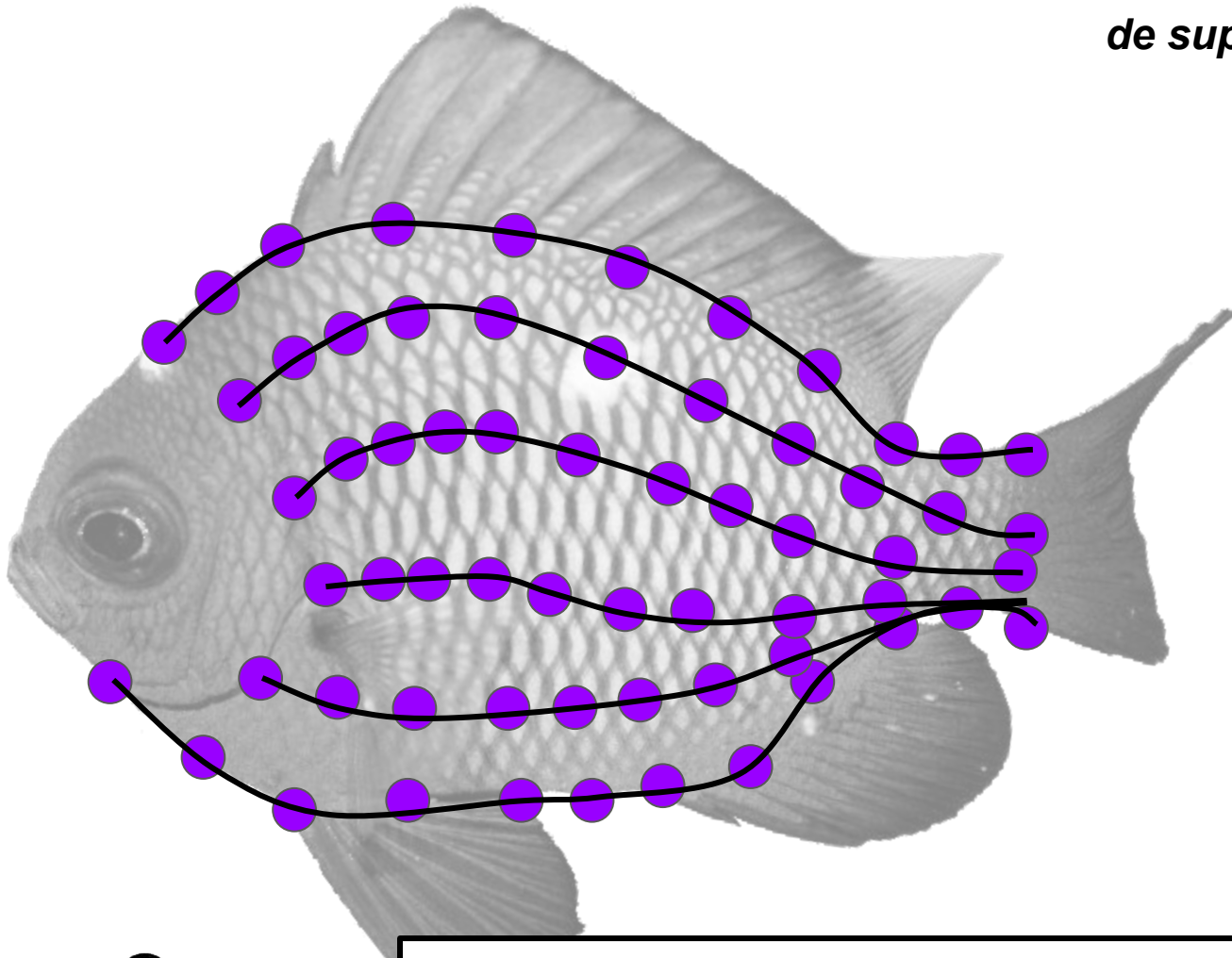


● *Semilandmarks*  
*de superfície*



Trata-se de uma extrapolação  
das curvas habituais

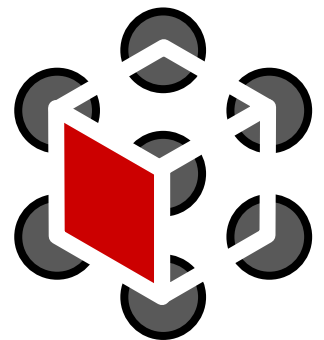
● **Semilandmarks**  
*de superfície*

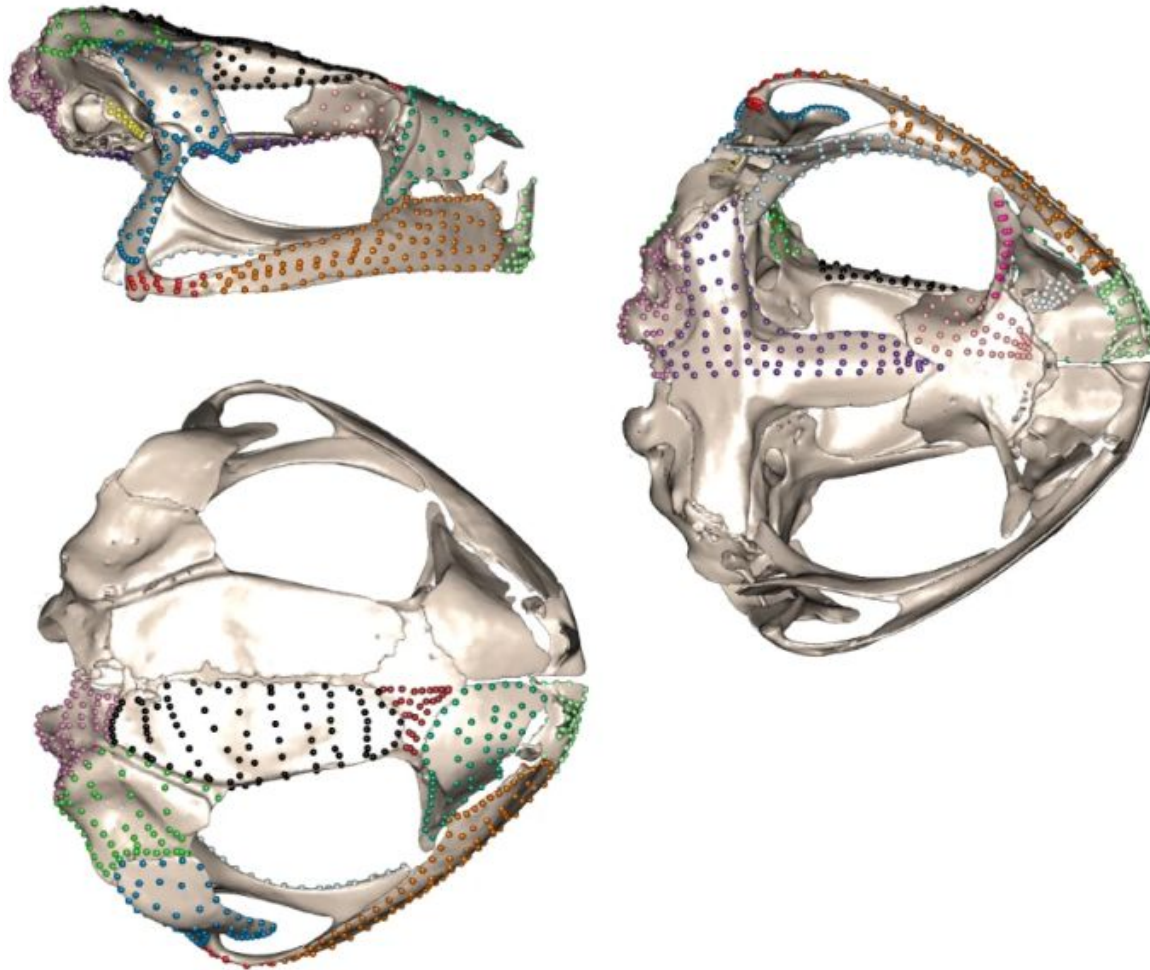


Que também deve passar por  
deslizamento (*sliding*)

*O método tem aplicações importantes  
para diversas perguntas*

*Vide “Aula 6 - Tutorial” para um exemplo de  
posicionamento dos landmarks*

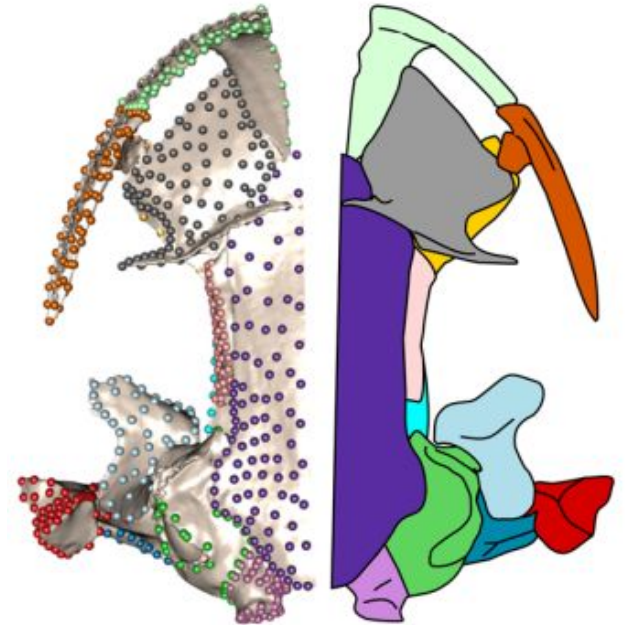
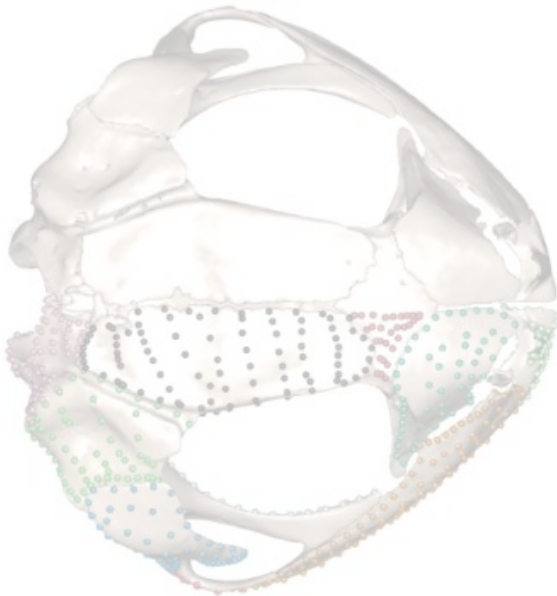
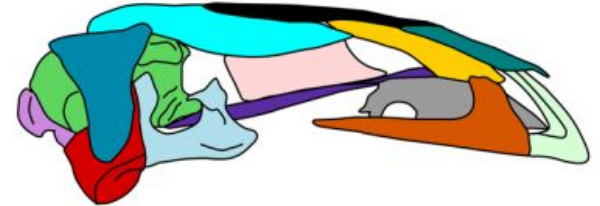
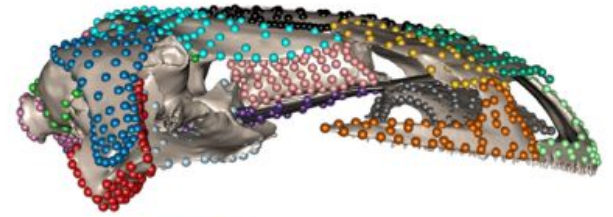
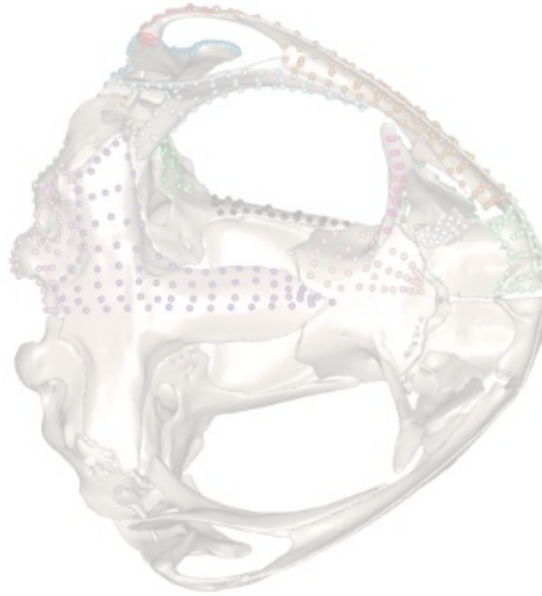
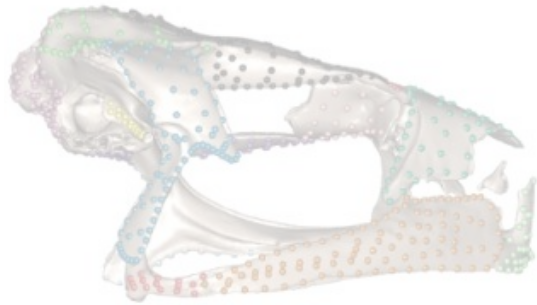




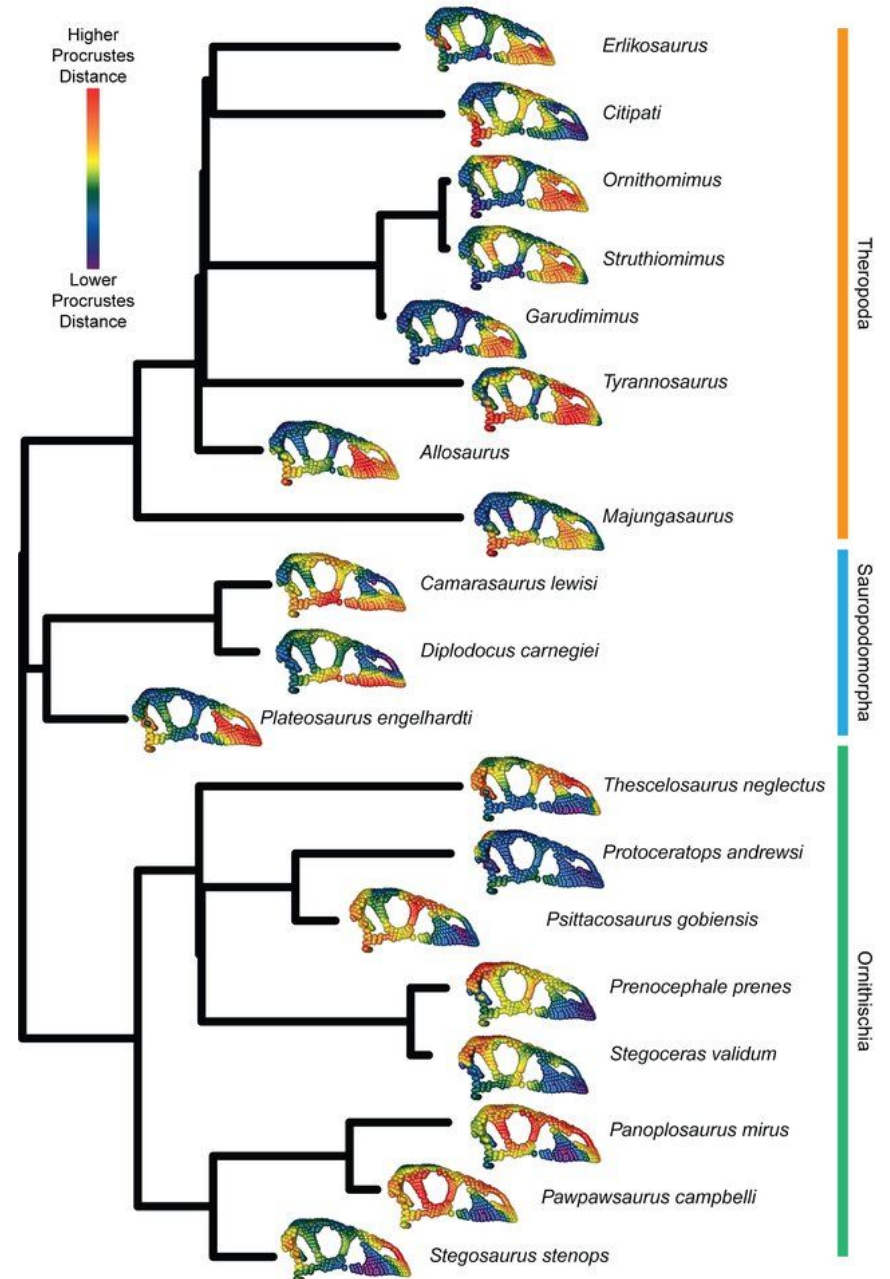
***Variação da forma,  
alometria***



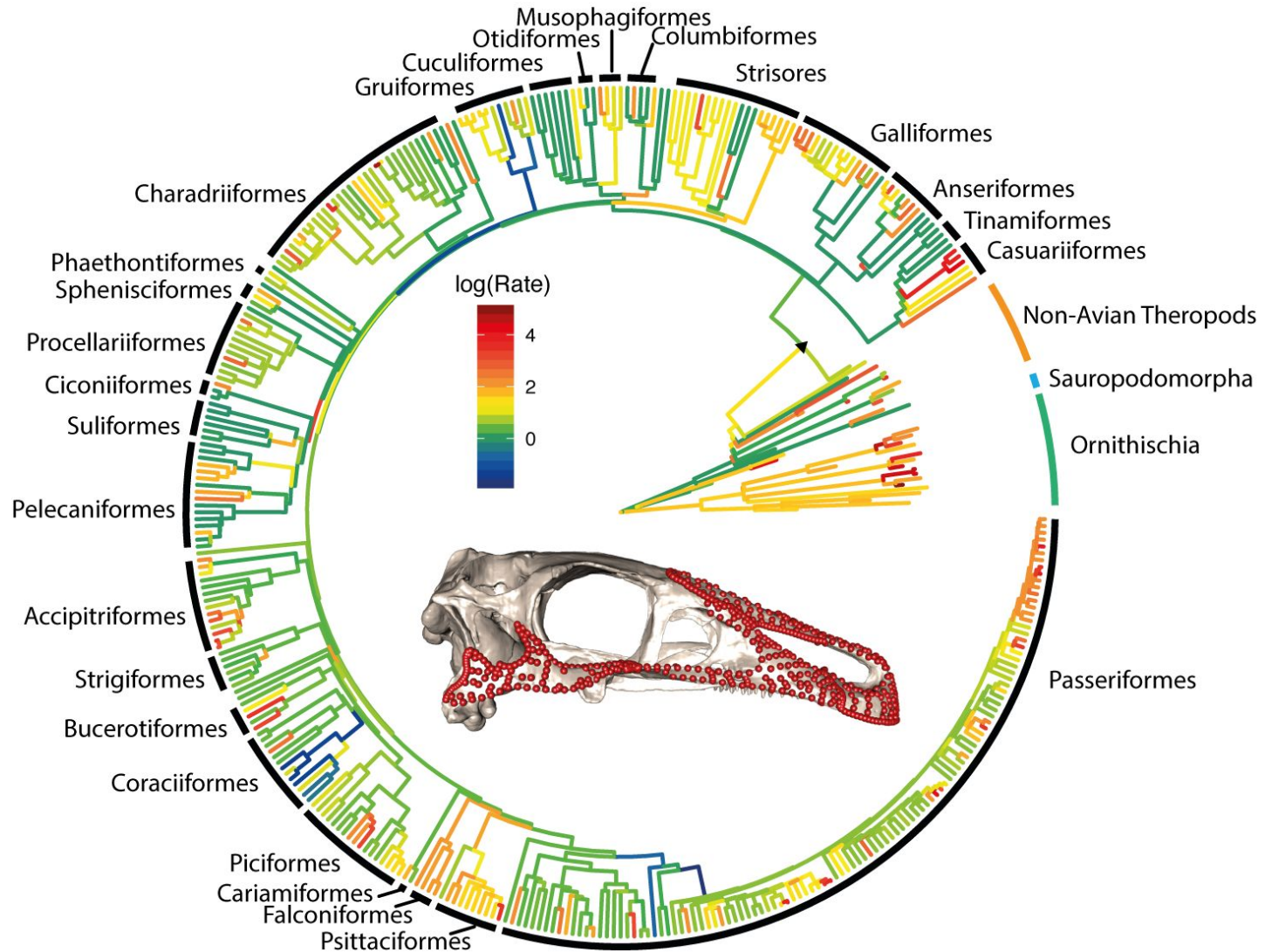
# ***Modularidade***







**Reconstrução**



***Taxas evolutivas***

**Ponto importante: a relação de simetria entre pontos que formam um patch**



*Especialmente  
nos fósseis*

*Taxas evolutivas*

# Retrodeformação

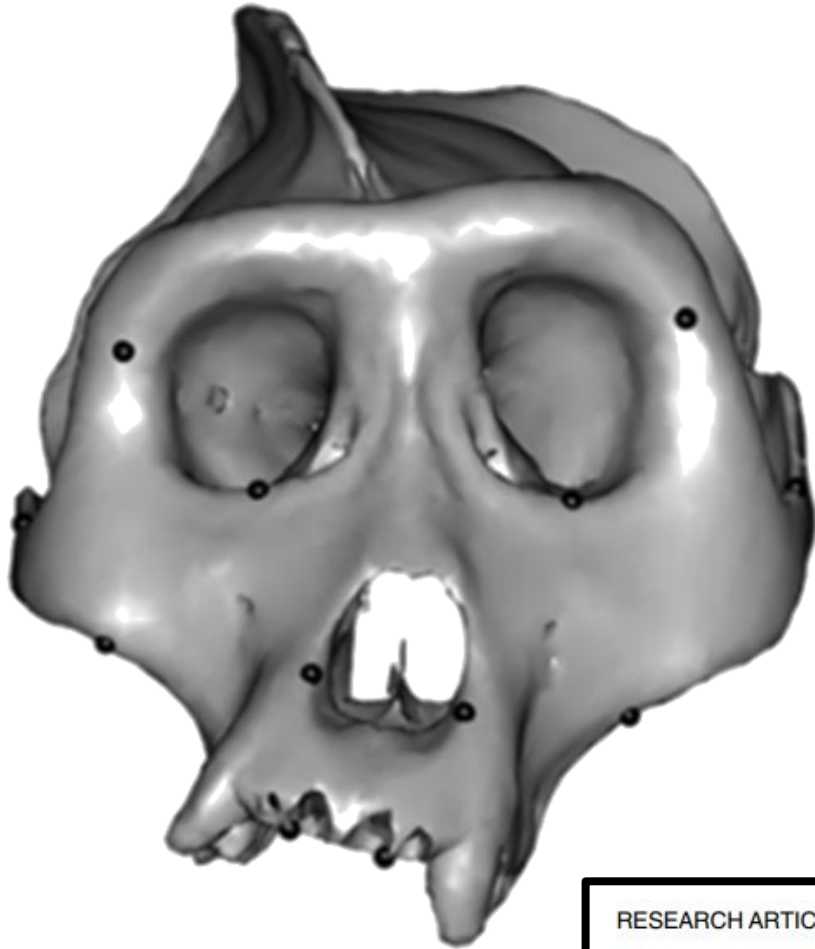
*Processo de correção da forma a partir  
da presumida **simetria bilateral***

*Especialmente  
nos fósseis*

# Retrodeformação

*Processo de correção da forma a partir da presumida **simetria bilateral***

*É gerada uma **interpolação** da forma através do **espelhamento** dos landmarks e **cálculo da média** entre a posição dos pontos espelhados e os originais*

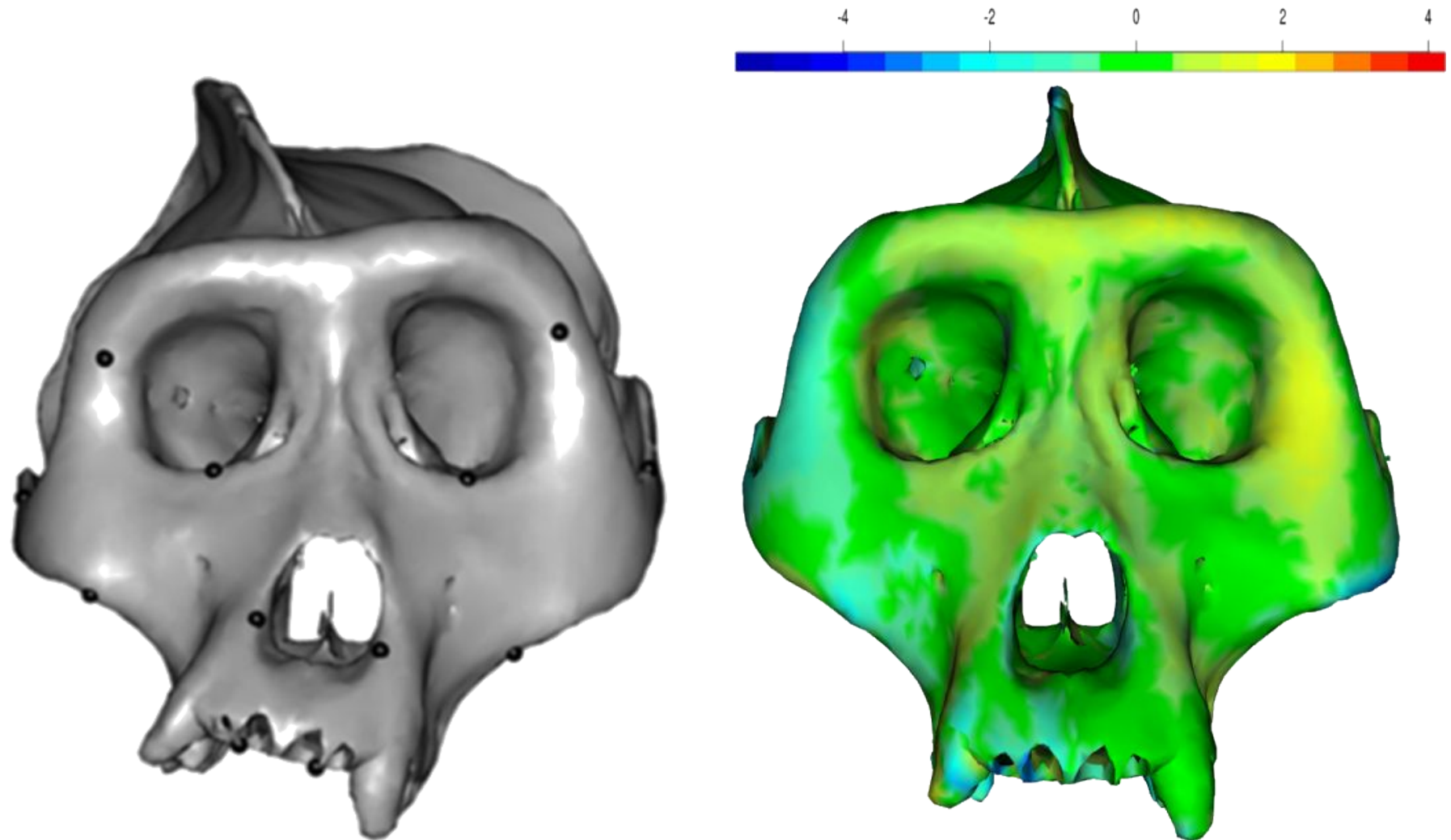


RESEARCH ARTICLE

Retrodeformation of fossil specimens based  
on 3D bilateral semi-landmarks:  
Implementation in the R package “Morpho”

Stefan Schlager<sup>1\*</sup>, Antonio Profico<sup>2</sup>, Fabio Di Vincenzo<sup>2</sup>, Giorgio Manzi<sup>2</sup>

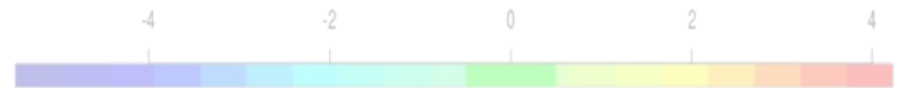




RESEARCH ARTICLE

Retrodeformation of fossil specimens based  
on 3D bilateral semi-landmarks:  
Implementation in the R package “Morpho”

Stefan Schlager<sup>1\*</sup>, Antonio Profico<sup>2</sup>, Fabio Di Vincenzo<sup>2</sup>, Giorgio Manzi<sup>2</sup>



*Ainda a respeito de fósseis, e se **falta** algum landmark na nossa amostra?*

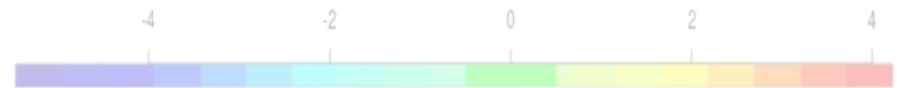
*= **missing data***

RESEARCH ARTICLE

Retrodeformation of fossil specimens based on 3D bilateral semi-landmarks: Implementation in the R package “Morpho”

Stefan Schlager<sup>1\*</sup>, Antonio Profico<sup>2</sup>, Fabio Di Vincenzo<sup>2</sup>, Giorgio Manzi<sup>2</sup>





*Ainda a respeito de fósseis, e se **falta** algum landmark na nossa amostra?*

*= **missing data***

*\*não é um problema exclusivo da paleontologia*

RESEARCH ARTICLE

Retrodeformation of fossil specimens based on 3D bilateral semi-landmarks: Implementation in the R package “Morpho”

Stefan Schlager<sup>1\*</sup>, Antonio Profico<sup>2</sup>, Fabio Di Vincenzo<sup>2</sup>, Giorgio Manzi<sup>2</sup>

# Electrorana\_limoae

-5.0621209e+000	-3.8099505e-003	-3.9463415e+000
-5.0898237e+000	-1.9331388e-001	-3.9927847e+000
-4.7747393e+000	1.7115210e+000	-3.5873501e+000
-4.8440871e+000	-1.7103398e+000	-4.0063615e+000
-5.4061427e+000	5.8428979e-001	-2.2647359e+000
-5.3439765e+000	-1.2857398e+000	-2.4291258e+000
9999	9999	9999
-4.8955784e+000	-1.6598980e+000	-3.7135680e+000
9999	9999	9999
-3.2296526e+000	-1.4744456e+000	-1.1801982e+000
-2.8094277e+000	2.4354935e+000	-1.7785830e+000
-2.9339211e+000	-2.5582156e+000	-2.1103020e+000
-4.4382401e+000	2.3665370e-001	-1.3000946e+000
-4.6391826e+000	-7.8523791e-001	-1.5487530e+000
-1.7757404e+000	4.0609388e+000	-2.2161775e+000
-1.5853300e+000	-4.0948052e+000	-3.0658708e+000
1.5491557e+000	2.8890617e+000	-8.8229084e-001
9999	9999	9999
1.4104303e+000	5.0453706e+000	-2.4375682e+000
1.8109424e+000	-4.1751618e+000	-3.4826241e+000
-3.1773655e+000	-1.5936130e-001	-1.2884459e+000
1.1637151e+000	5.0049825e+000	-2.4350321e+000

Electrorana\_limoae

-5.0621209e+000	-3.8099505e-003	-3.9463415e+000
-5.0898237e+000	-1.9331388e-001	-3.9927847e+000
-4.7747393e+000	1.7115210e+000	-3.5873501e+000
-4.8440871e+000	-1.7103398e+000	-4.0063615e+000
-5.4061427e+000	5.8428979e-001	-2.2647359e+000
-5.3439765e+000	-1.2857398e+000	-2.4291258e+000

9999	9999	9999
------	------	------

-4.8955784e+000	-1.6598980e+000	-3.7135680e+000
-----------------	-----------------	-----------------

9999	9999	9999
------	------	------

-3.2296526e+000	-1.4744456e+000	-1.1801982e+000
-2.8094277e+000	2.4254025e+000	1.7205020e+000
-2.9339211e+000	-2.4254025e+000	-1.7205020e+000
-4.4382401e+000	2.4254025e+000	1.7205020e+000
-4.6391826e+000	-7.4254025e+000	-1.7205020e+000
-1.7757404e+000	4.4254025e+000	1.7205020e+000
-1.5853300e+000	-4.4254025e+000	-1.7205020e+000
1.5491557e+000	2.4254025e+000	1.7205020e+000

9999	9999	9999
------	------	------

1.4104303e+000	5.0453706e+000	-2.4375682e+000
1.8109424e+000	-4.1751618e+000	-3.4826241e+000
-3.1773655e+000	-1.5936130e-001	-1.2884459e+000
1.1637151e+000	5.0049825e+000	-2.4350321e+000

*Cada landmark faltante  
deve ser indicado com NA  
(ou 9999, a depender do  
formato do arquivo)*

# Estimando landmarks

*Existem métodos diversos:*

- *Simetria*
- *Substituição média*
- *Interpolação através do TPS*
- *Interpolação por regressão*

*Métodos de interpolação  
analisam **toda** a sua amostra*

# Estimando landmarks

*Existem métodos diversos:*

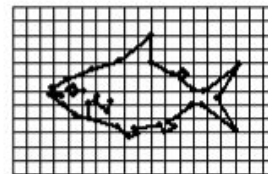
- *Simetria*
- *Substituição média*
- *Interpolação através do TPS*
- *Interpolação por regressão*

*Métodos de interpolação  
analisam **toda** a sua amostra*

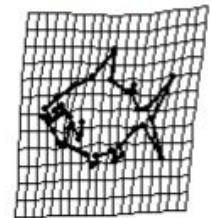
# Estimando landmarks

*Interpolação a partir da grade para os landmarks completos, estimando o landmark ausente através da menor distorção possível*

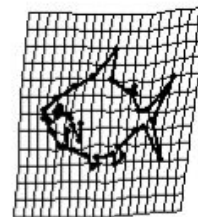
Reference



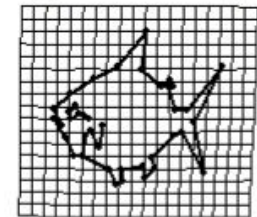
TPS: Reference --> Original



TPS: Ref --> Estimated Specimen



TPS: Original --> Estimated Specimen



method="TPS"

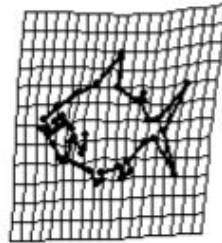


# Estimando landmarks

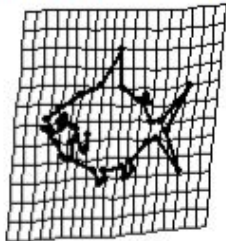
Reference



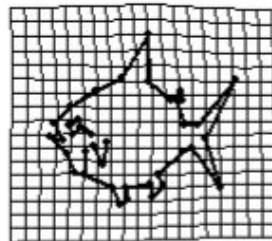
TPS: Reference --> Original



TPS: Ref --> Estimated Specimen



TPS: Original --> Estimated Specimen



*Prevê a posição dos landmarks ausentes usando um modelo de regressão baseado nos espécimes que possuem todos os landmarks*

method="Reg"

## Exemplo

*Conhecendo o **Morpho**, outro dos  
pacotes do R para morfometria  
geométrica*

Agora, vamos pro

