

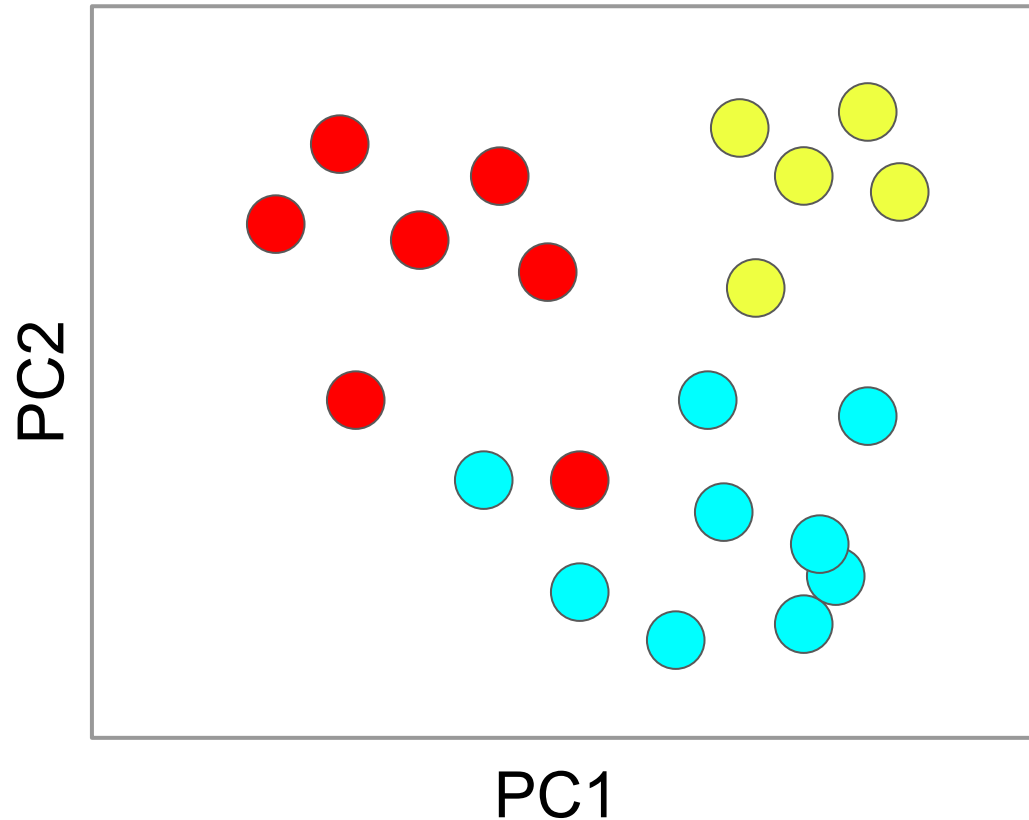


# Tópicos I – Morfometria Geométrica

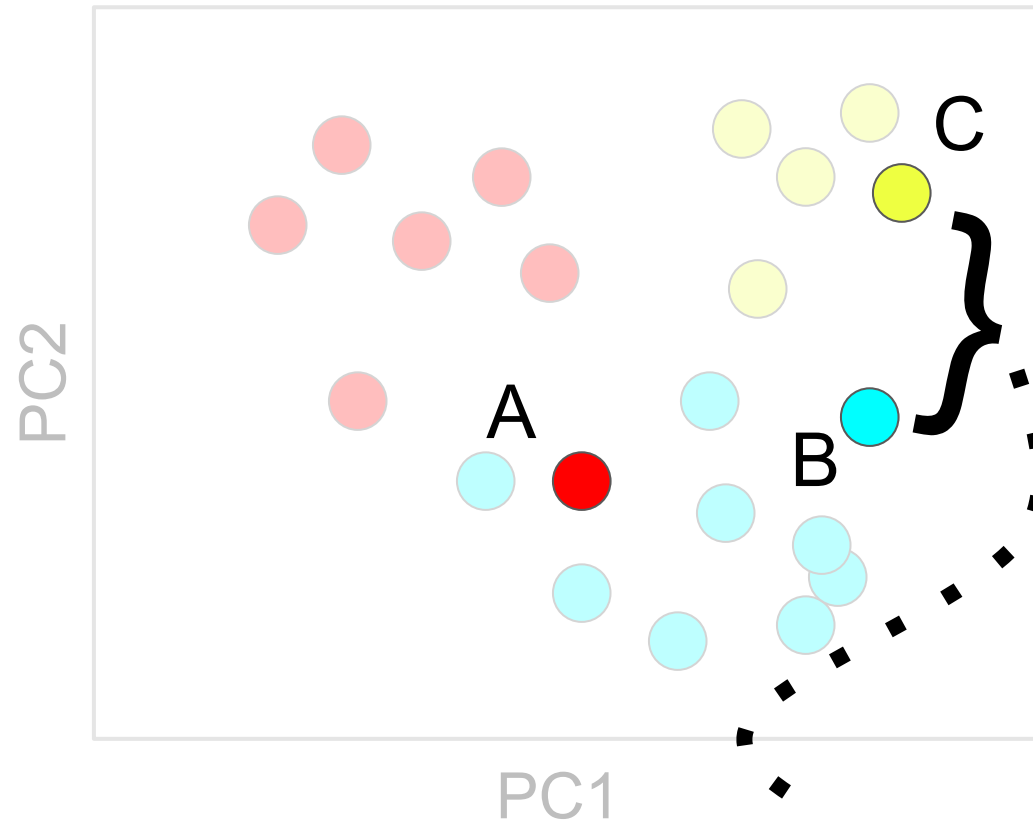
Diego de Almeida da Silva

Aulas 7 e 8

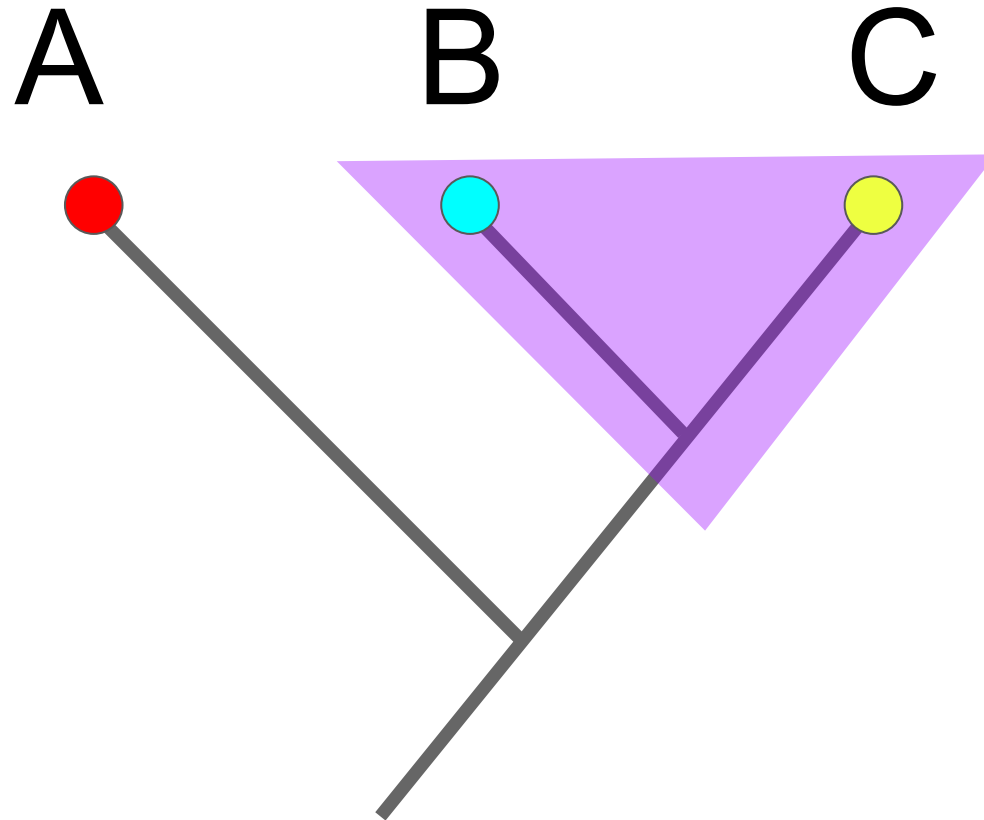
*A disposição no morfoespaço pode ser interpretada a partir de uma perspectiva biológica*



*A disposição no morfoespaço pode ser interpretada a partir de uma perspectiva biológica*



$$D_{Proc} = \sqrt{\sum_{i=1}^K \sum_{j=1}^M (\mathbf{z}_{1,ij} - \mathbf{z}_{2,ij})^2}$$



*Bastante razoável presumir similaridade  
relacionada à proximidade filogenética*

A

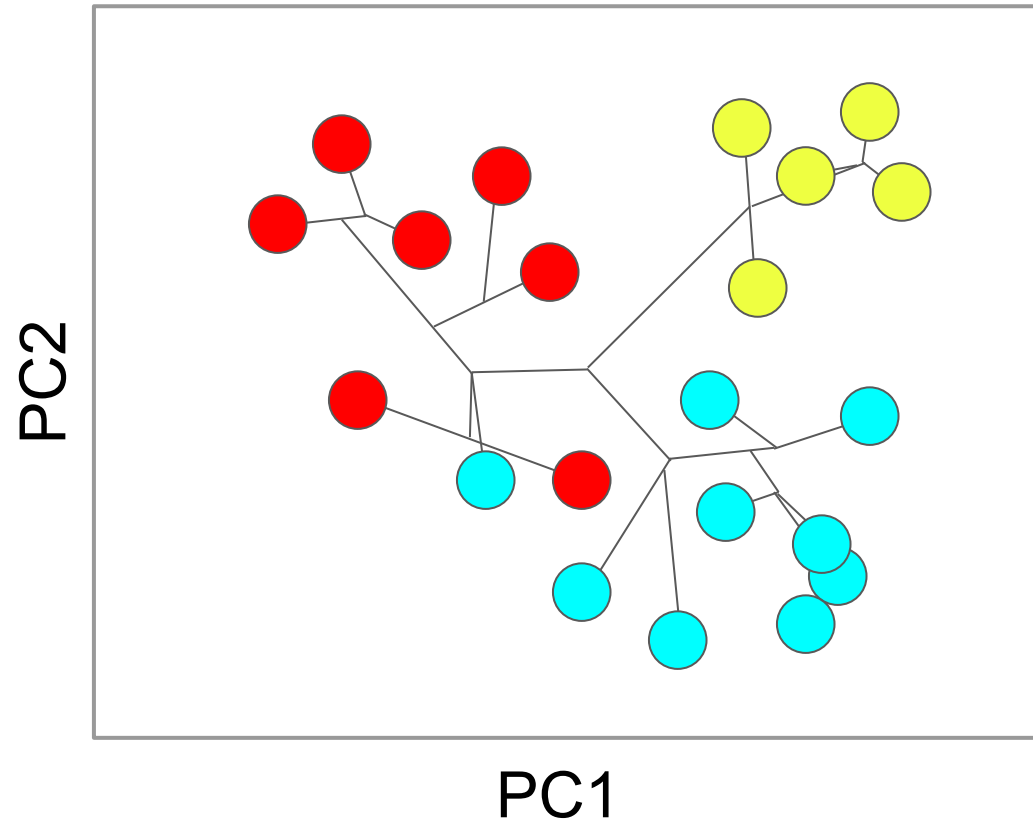
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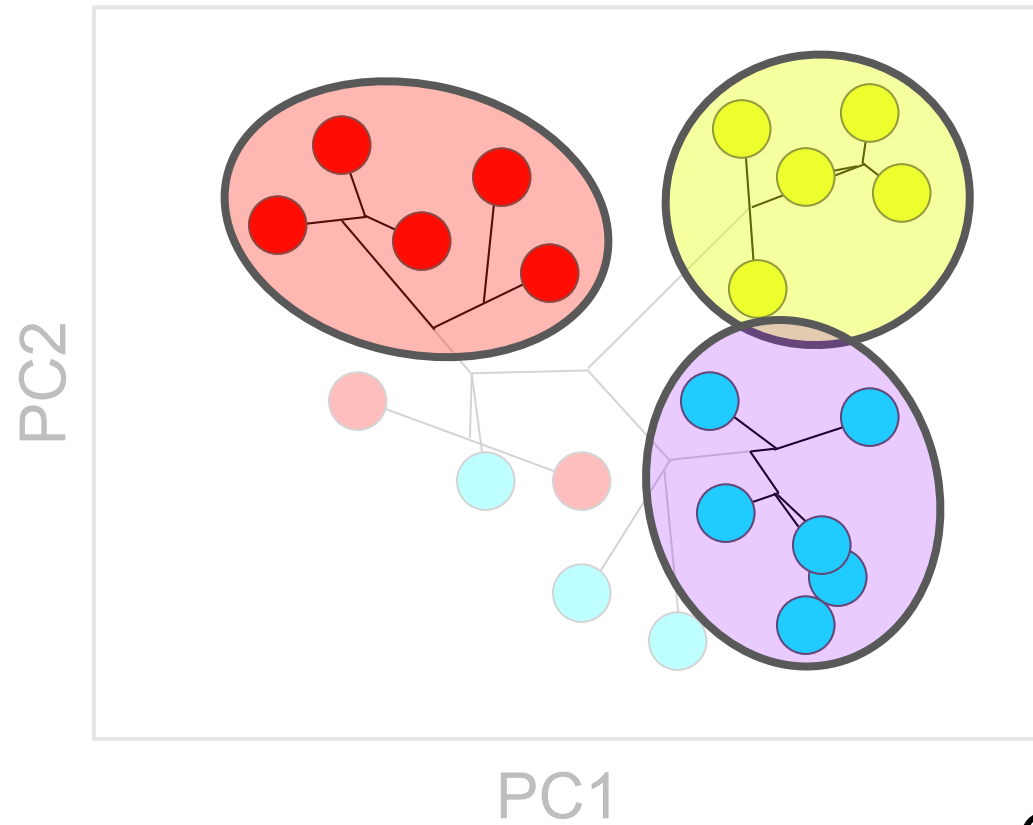
C

**Filomorfoespaço: projeção da filogenia  
sobre o espaço da forma**

*Bastante razoável presumir similaridade  
relacionada à proximidade filogenética*

*Filomorfoespaço: projeção da  
filogenia sobre o espaço da forma*





*Clados bem definidos*

→ *forma **conservada** na filogenia*



PC2

*Como quantificar a  
associação com a  
filogenia?*

PC1

*Clados bem definidos*

→ *forma **conservada** na filogenia*



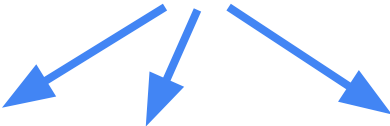
# Sinal Filogenético

*Medida da tendência de características ou traços biológicos de **espécies relacionadas evolutivamente** ser **mais semelhantes** entre si do que com espécies não relacionadas*


## ***K de Blomberg***


$$K = \frac{\text{Var}_{\text{filogenia}}}{\text{Var}_{\text{terminais}}}$$

Comparação entre os  
valores para duas espécies


$$K = \frac{\text{Var}_{\text{filogenia}}}{\text{Var}_{\text{terminais}}} = \frac{\sum_{i,j} (x_i - \bar{x})(x_j - \bar{x}) C_{i,j} / n}{\sum_i (x_i - \bar{x})^2 / (x_j - \bar{x})}$$

Matriz de covariância  
filogenética

$$K = \frac{\text{Var}_{\text{filogenia}}}{\text{Var}_{\text{terminais}}} = \frac{\sum_{i,j} (x_i - \bar{x})(x_j - \bar{x}) C_{i,j} / n}{\sum_i (x_i - \bar{x})^2 / (x_j - \bar{x})}$$


$$K = \frac{\text{Var}_{\text{filogenia}}}{\text{Var}_{\text{terminais}}} = \frac{\sum_{i,j} (x_i - \bar{x})(x_j - \bar{x}) C_{i,j} / n}{\sum_i (x_i - \bar{x})^2 / (x_j - \bar{x})}$$


Como os valores se relacionam **sem** a ponderação filogenética

# *Movimento Browniano*



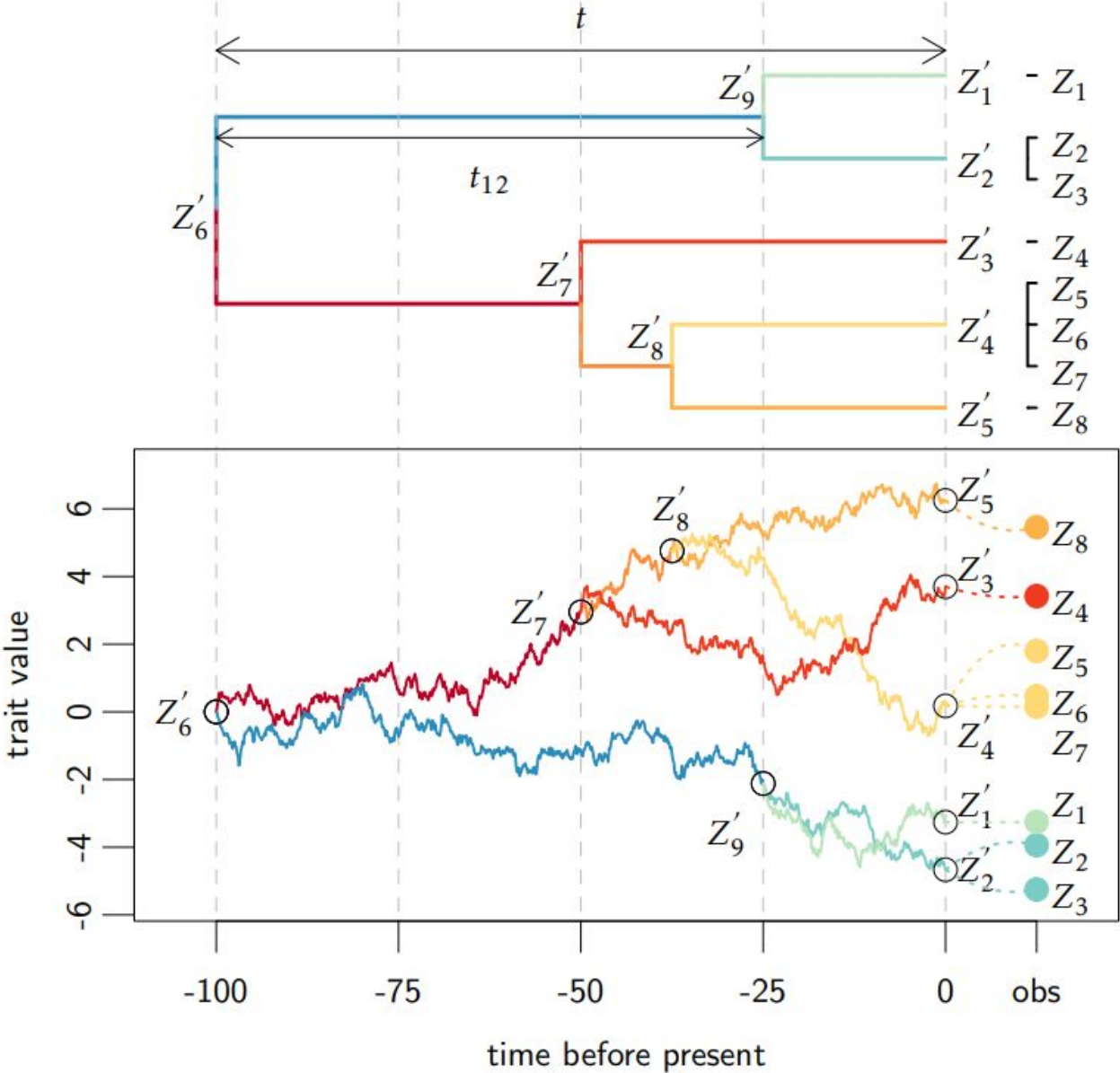
[youtu.be/SWaanGJDh2c](https://youtu.be/SWaanGJDh2c)

# *Movimento Browniano*

*Acúmulo de mudanças guiado por  
processos **estocásticos***



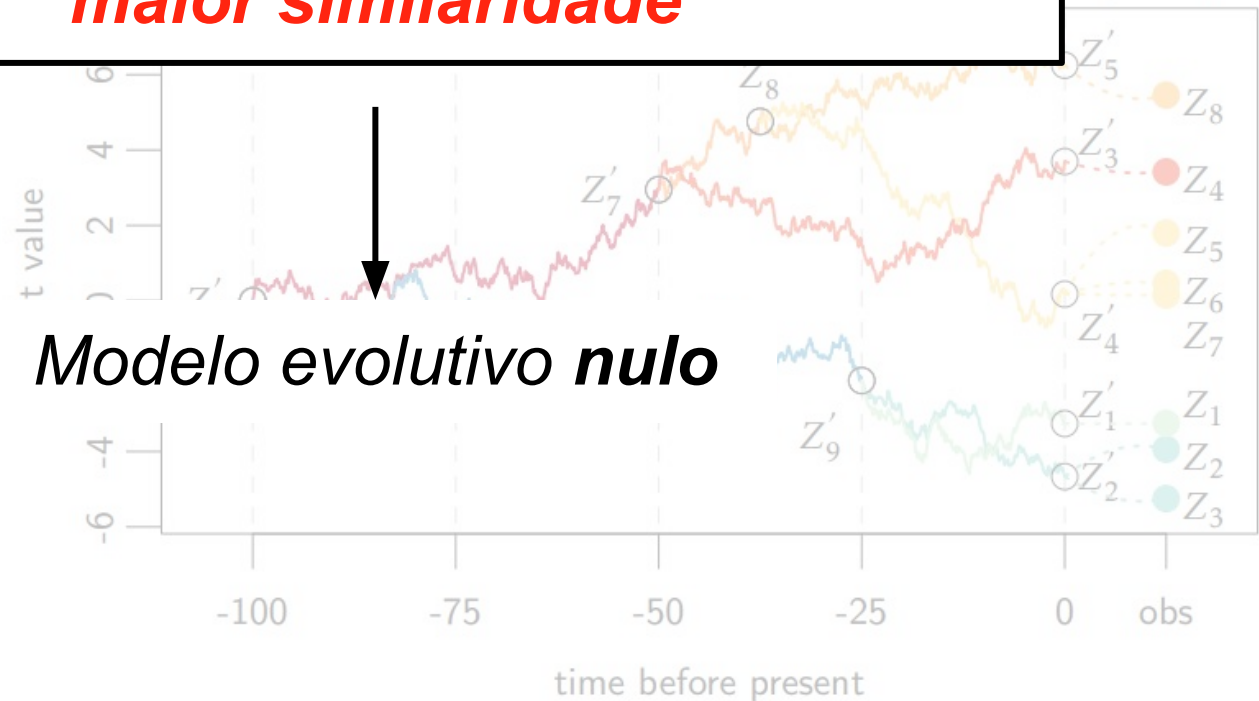
[youtu.be/SWaanGJDh2c](https://youtu.be/SWaanGJDh2c)



*Movimento Browniano*



**Menor tempo desde a cladogênese,  
menos processos estocásticos sofridos,  
*maior similaridade***



**Modelo evolutivo *nulo***

*Movimento Browniano*

- $K = 1$  → *estrutura exata esperada por BM*
- $K > 1$  → *conservação filogenética*
- $K < 1$  → *baixo sinal filogenético*

# Exemplo

No pacote *phylocurve* há uma extensão multivariada para o *K*, o *K.mult*

*Syst. Biol.* 63(5):685–697, 2014

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Advance Access publication April 30, 2014

## A Generalized *K* Statistic for Estimating Phylogenetic Signal from Shape and Other High-Dimensional Multivariate Data

DEAN C. ADAMS\*

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\*Correspondence to be sent to: Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, IA 50011, USA;


E-mail: dcadams@iastate.edu.



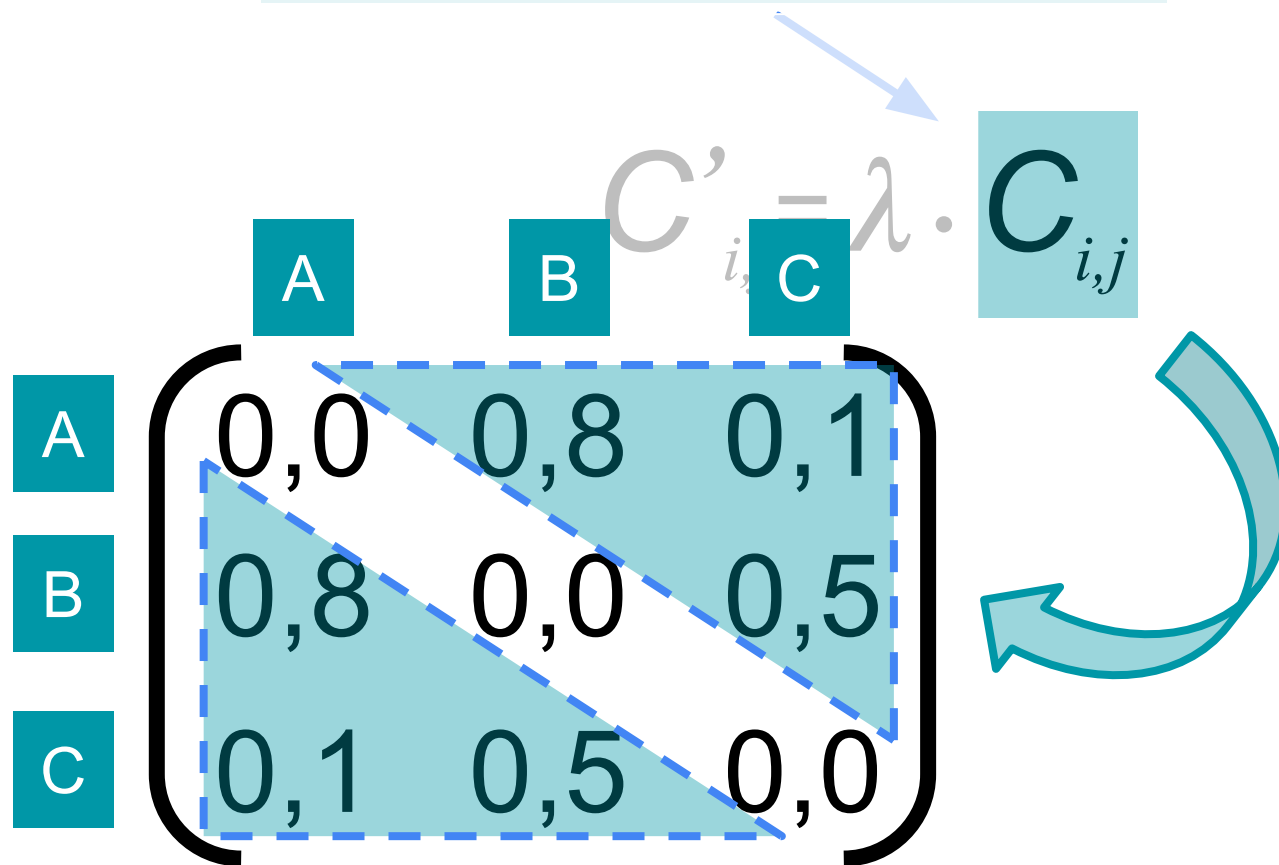
***$\lambda$  de Pagel***

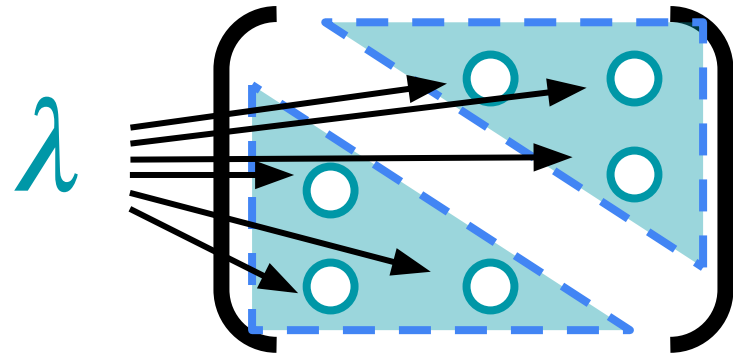
$$C'_{i,j} = \lambda \cdot C_{i,j}$$


## Matriz de covariância filogenética


$$C'_{i,j} = \lambda \cdot C_{i,j}$$




# Matriz de covariância filogenética





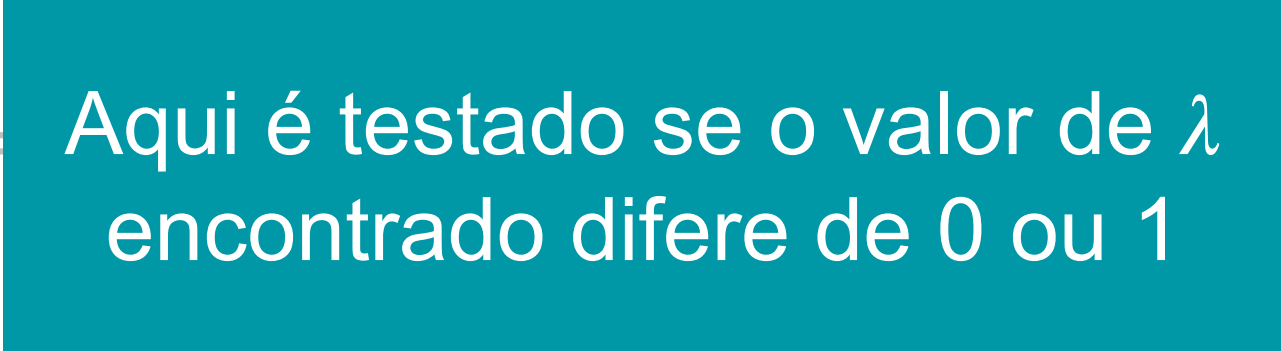
$$C'_{i,j} = \lambda \cdot C_{i,j}$$


Valor estimado, para maximizar  
a verossimilhança

- $\lambda = 1$   *conservação  
filogenética por BM*
- $\lambda = 0$   *independência  
filogenética*
- $\lambda > 1$   *restrição evolutiva  
(lento)*

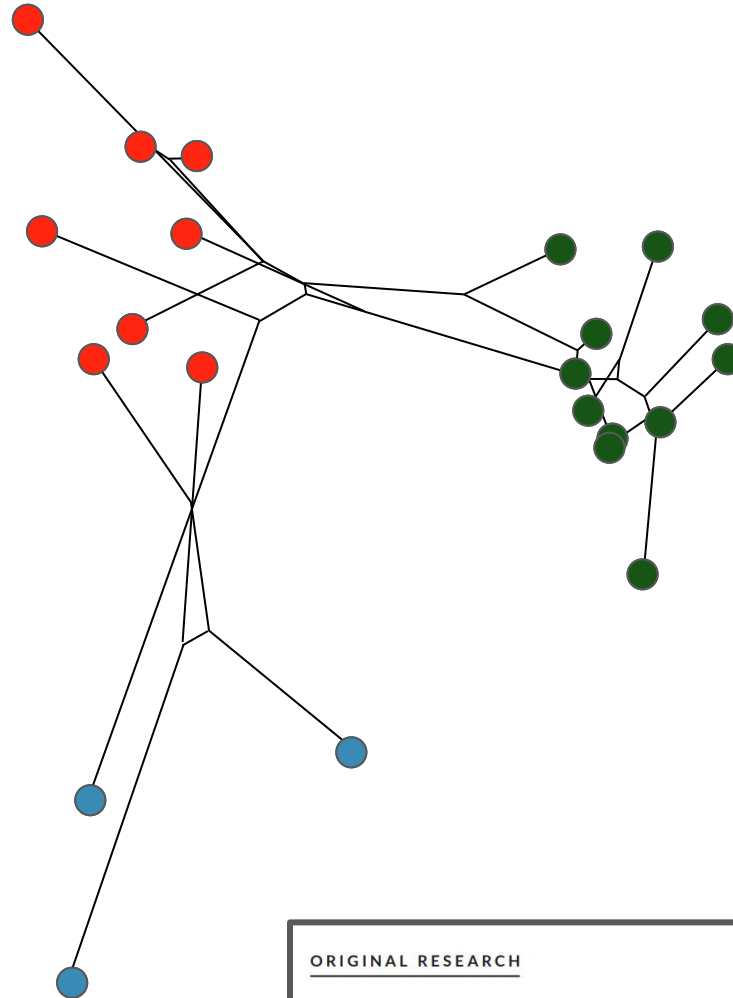


- $\lambda = 1$   *conservação  
filogenética por BM*

- $\lambda =$   *cia  
ica*

- $\lambda > 1$   *restrição evolutiva  
(lento)*

- dieta 1
- dieta 2
- dieta 3



## ORIGINAL RESEARCH

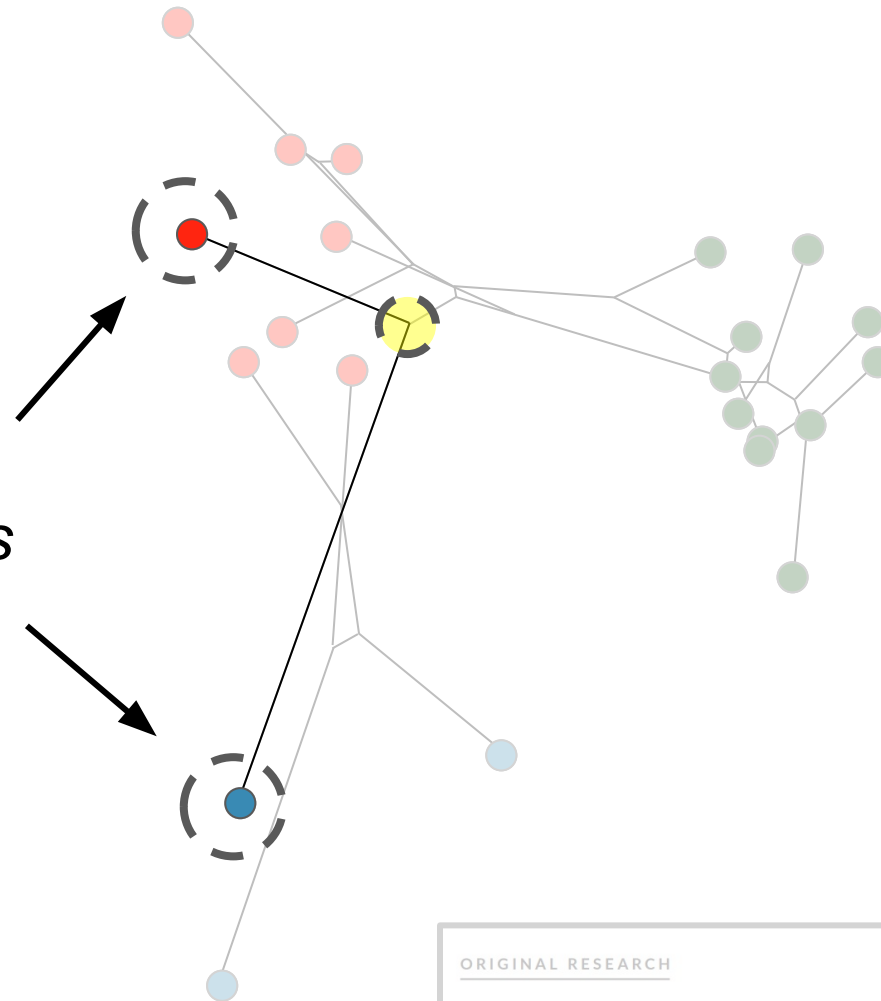
Ecology and Evolution Open Access WILEY

### Convergent evolution of specialized generalists: Implications for phylogenetic and functional diversity of carabid feeding groups

Dennis Baulechner<sup>1</sup>  | Frank Jauker<sup>1</sup>  | Thomas A. Neubauer<sup>1,2</sup>  |  
Volkmar Wolters<sup>1</sup> 

- dieta 1
- dieta 2
- dieta 3

*spp irmãs  
em grupos  
distintos*



## ORIGINAL RESEARCH

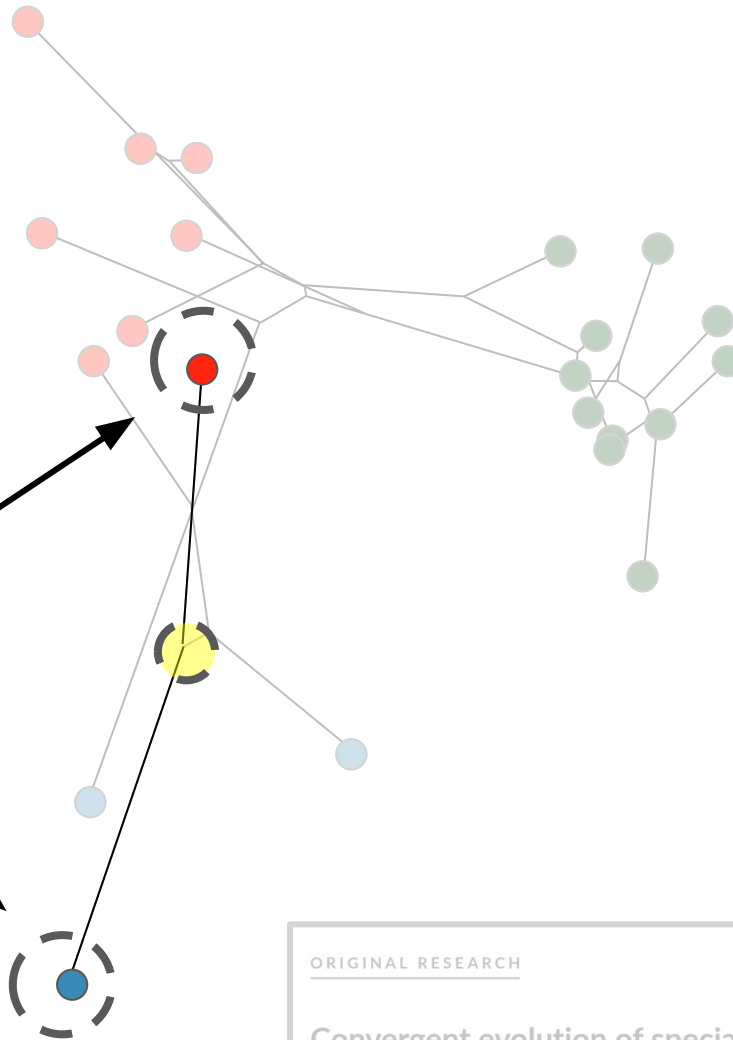
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*spp irmãs  
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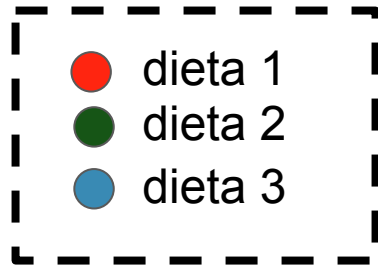


## ORIGINAL RESEARCH

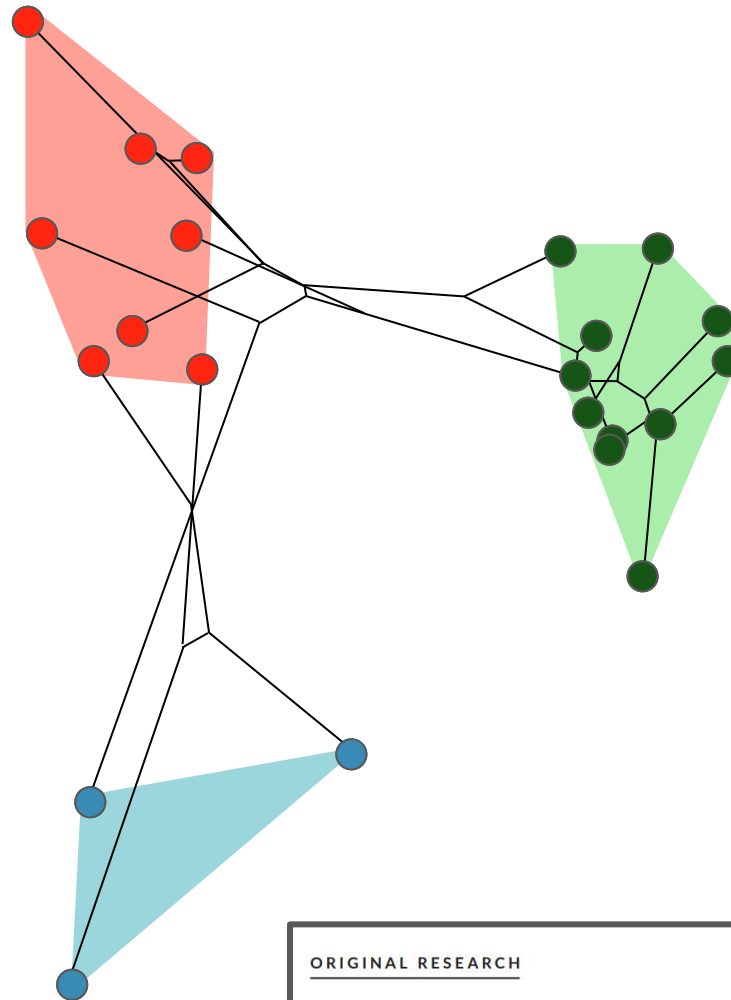
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*Convergência na  
ocupação do  
morfoespaço*



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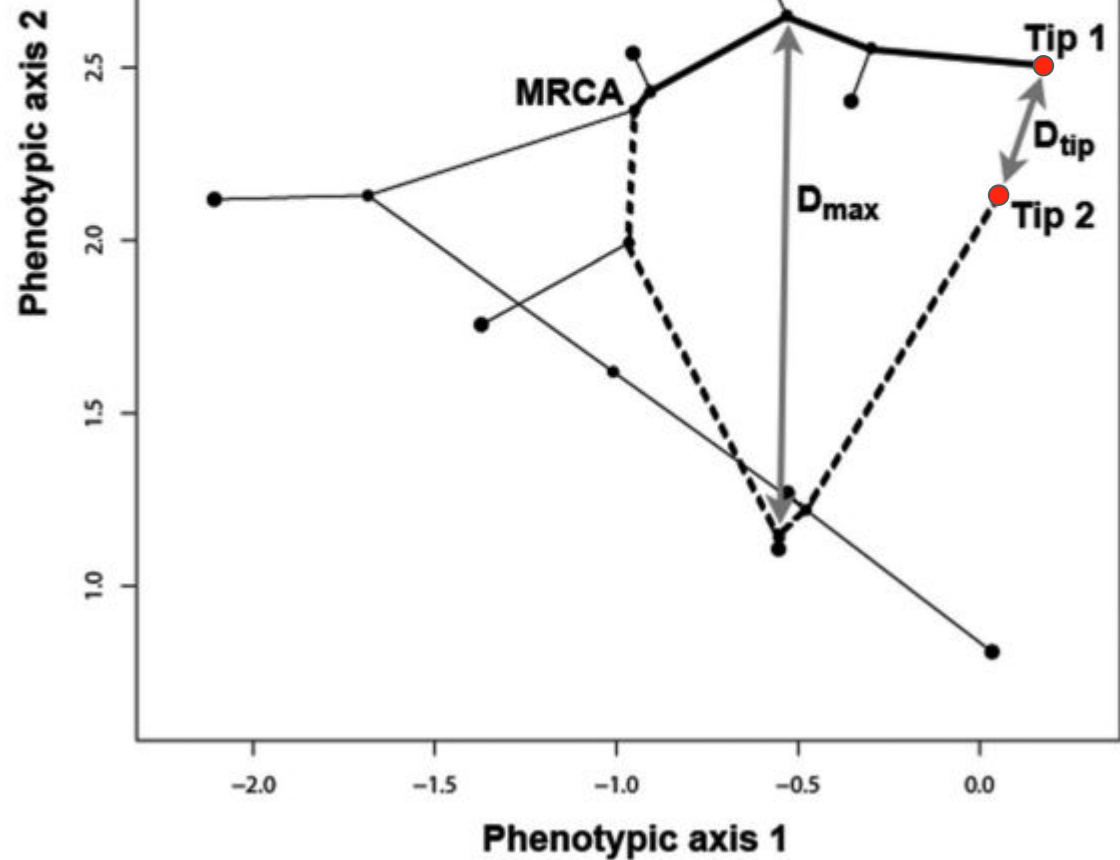
**The definition, recognition,  
and interpretation of convergent  
evolution, and two new measures  
for quantifying and assessing  
the significance of convergence**

C. Tristan Stayton<sup>1,2</sup>

<sup>1</sup>Department of Biology, Bucknell University, 337 Biology Building, Lewisburg, Pennsylvania 17837

<sup>2</sup>E-mail: tstayton@bucknell.edu

*Stayton 2015:  
índices de  
convergência*





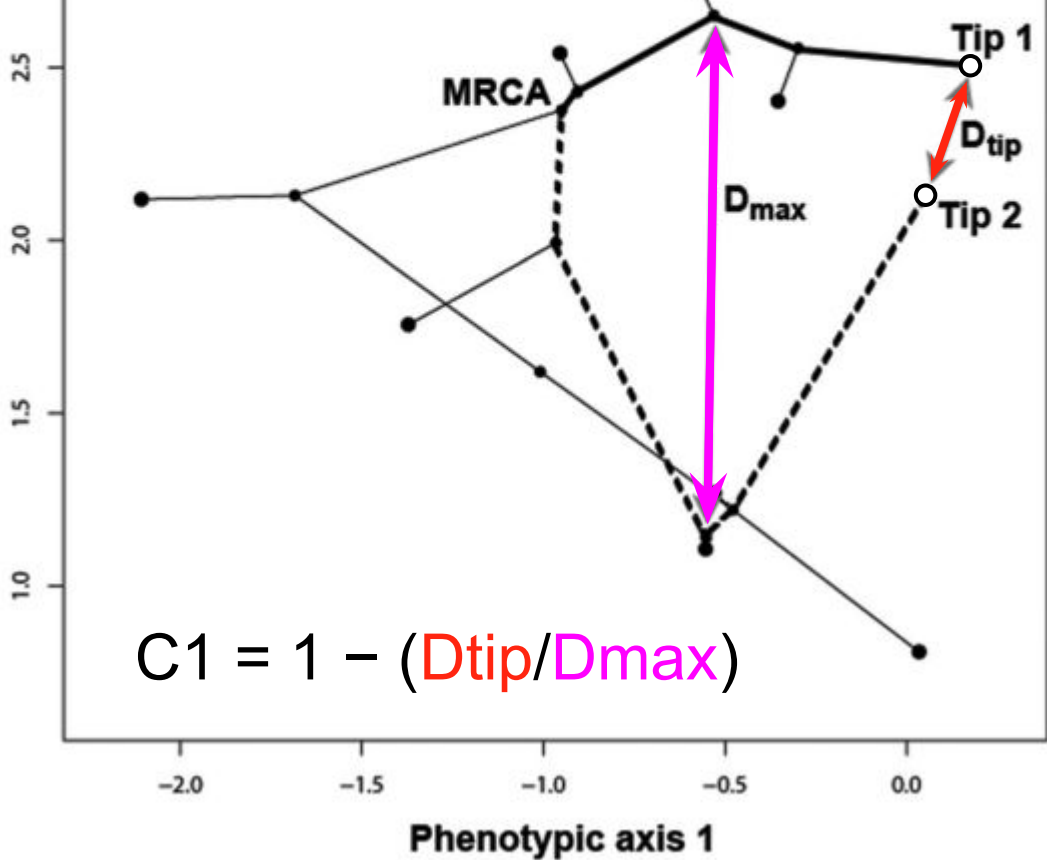
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C. Tristan Stayton<sup>1,2</sup>

<sup>1</sup>Department of Biology, Bucknell University, 337 Biology Building, Lewisburg, Pennsylvania 17837

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Phenotypic axis 2



*C1: similaridade morfológica entre os táxons convergentes*



# The definition, recognition, and interpretation of convergent evolution, and two new measures for quantifying and assessing the significance of convergence

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Phenotypic axis 2

2.5  
2.0  
1.5  
1.0

MRCA

$D_{max}$

Tip 1

$D_{tip}$

Tip 2

$$C2 = D_{tip} - D_{max}$$

Phenotypic axis 1

-2.0

-1.5

-1.0

-0.5

0.0

*C2: distância percorrida pelos taxa convergentes*





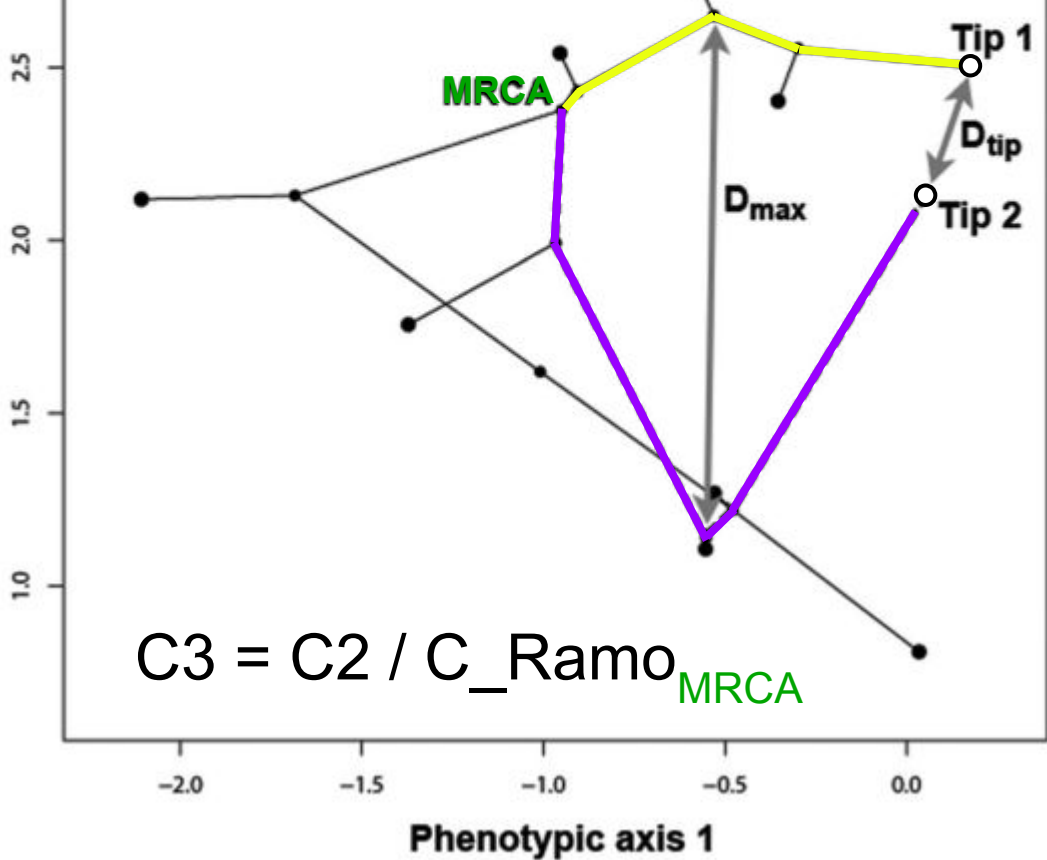
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Phenotypic axis 2



*C3: distância percorrida pelos taxa convergentes, em função do tempo do clado*



# The definition, recognition, and interpretation of convergent evolution, and two new measures for quantifying and assessing the significance of convergence

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<sup>1</sup>Department of Biology, Bucknell University, 337 Biology Building, Lewisburg, Pennsylvania 17837

<sup>2</sup>E-mail: tstayton@bucknell.edu

Phenotypic axis 2

2.5  
2.0  
1.5  
1.0

MRCA

$D_{max}$

Tip 1

$D_{tip}$

Tip 2

$$C3 = C2 / C\_Ramo_{Todos}$$

Phenotypic axis 1

-2.0

-1.5

-1.0

-0.5

0.0

C4: distância percorrida pelos taxa convergentes, em função do tempo da árvore

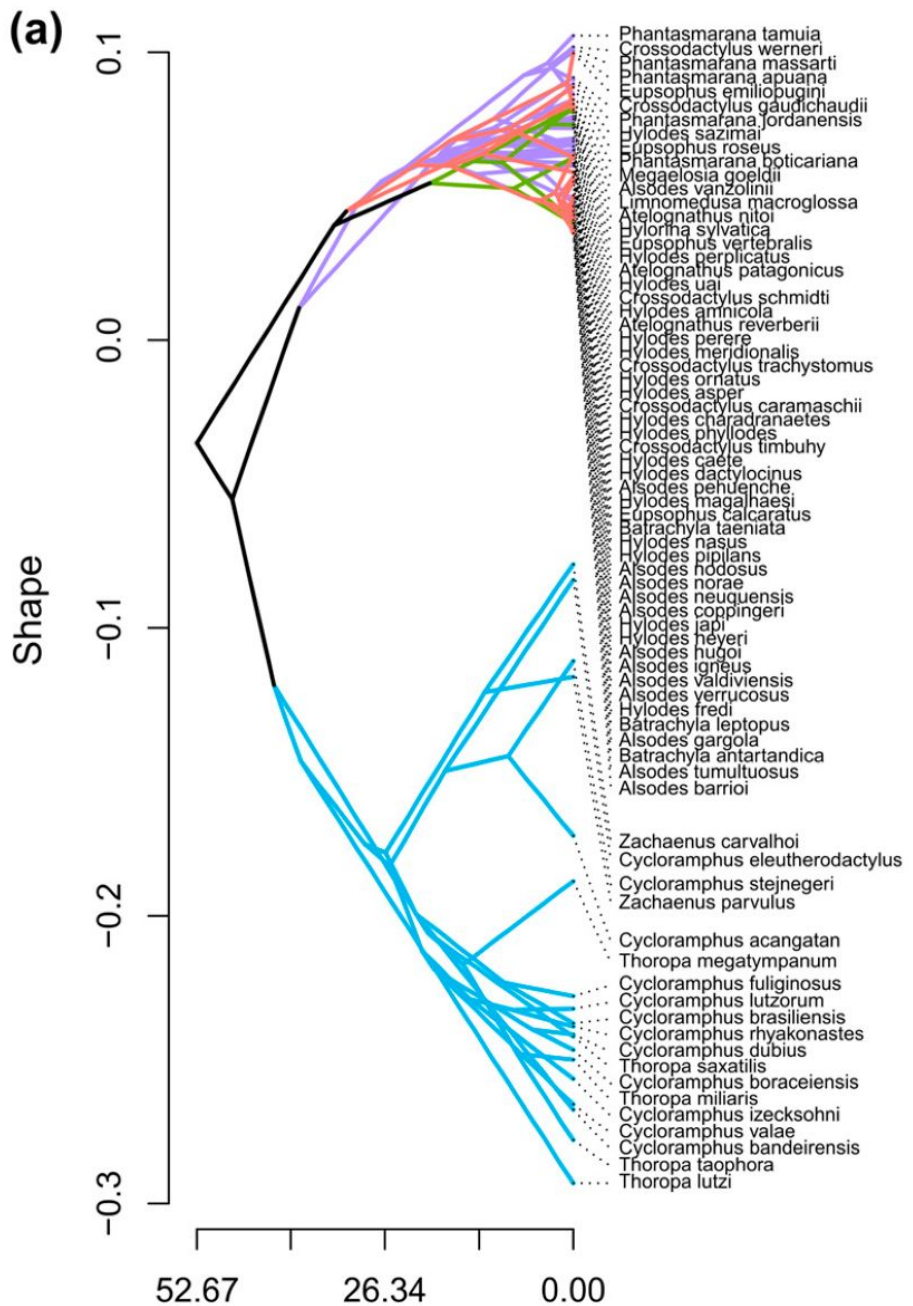
**Atenção:** K de Blomberg,  $\lambda$  de Pagel, C3 e C4 de Stayton

*Todos levam em consideração os comprimentos de ramos*

**Atenção:** K de Blomberg,  $\lambda$  de Pagel, C3 e C4 de Stayton

*Todos levam em consideração os comprimentos de ramos*

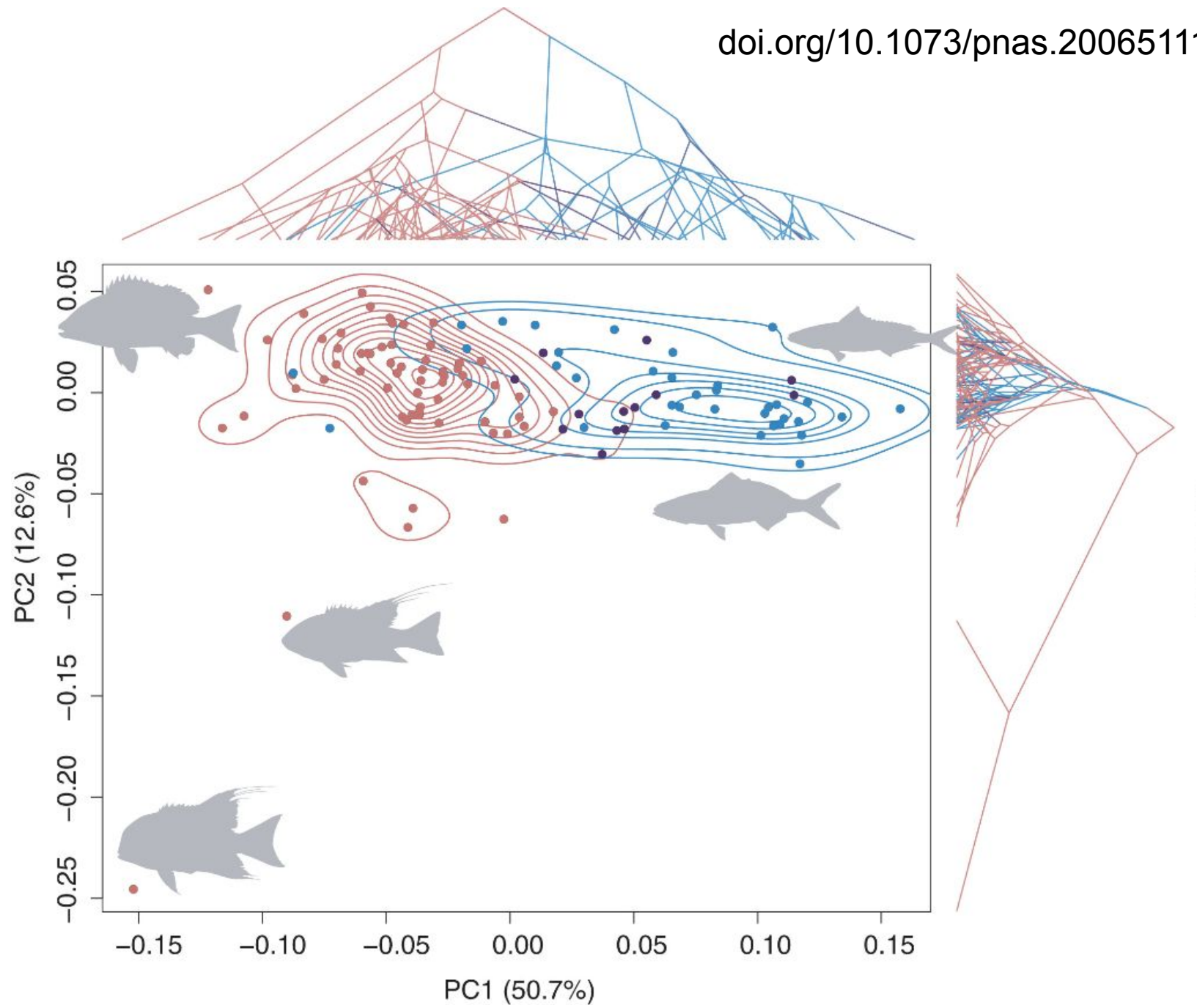
***O tempo é importante***



*Fenograma\*: a mudança da forma ao longo do tempo*

Diversificação na ocupação do morfoespaço ao longo do tempo

*\*Traitgram*

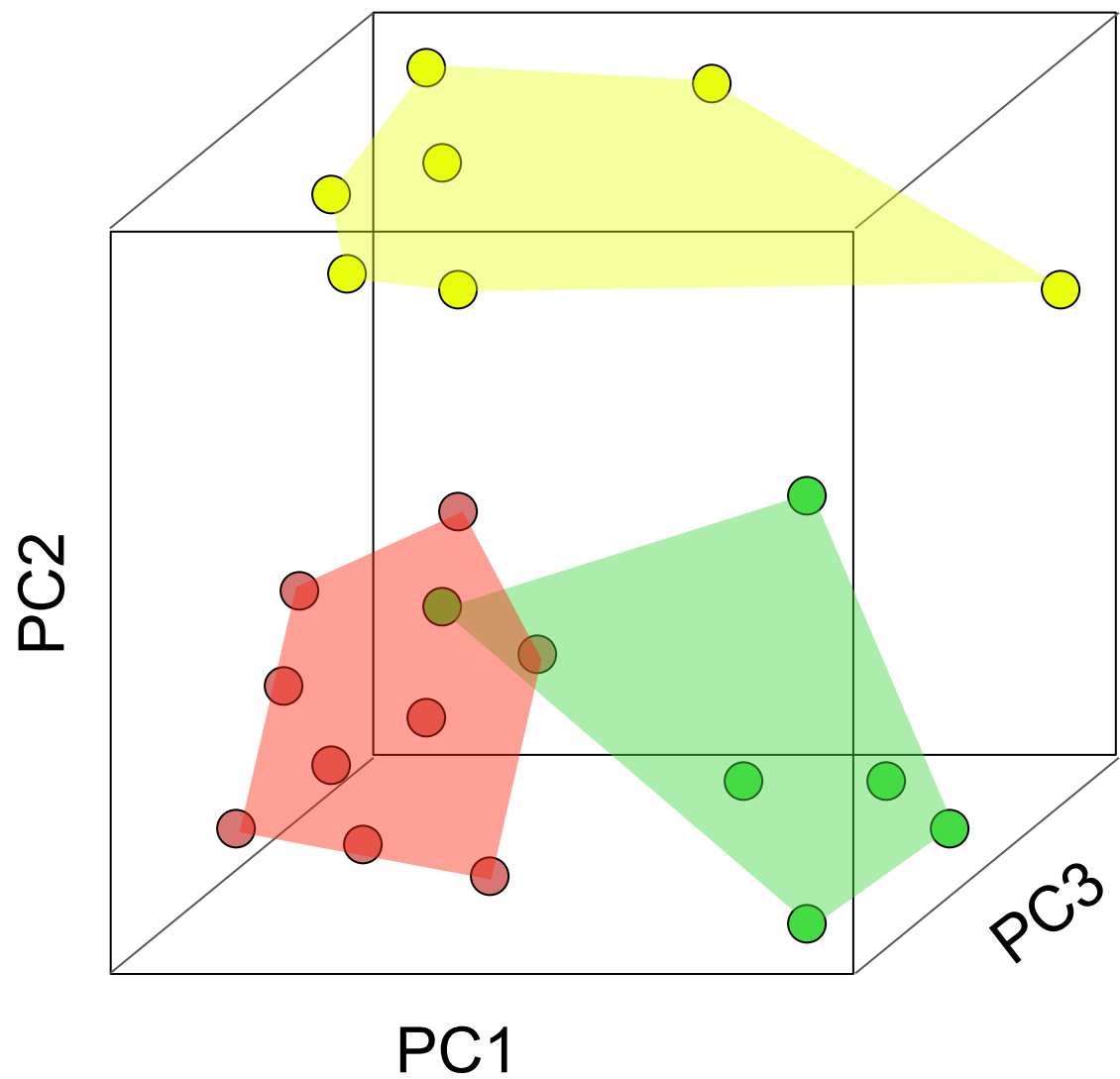


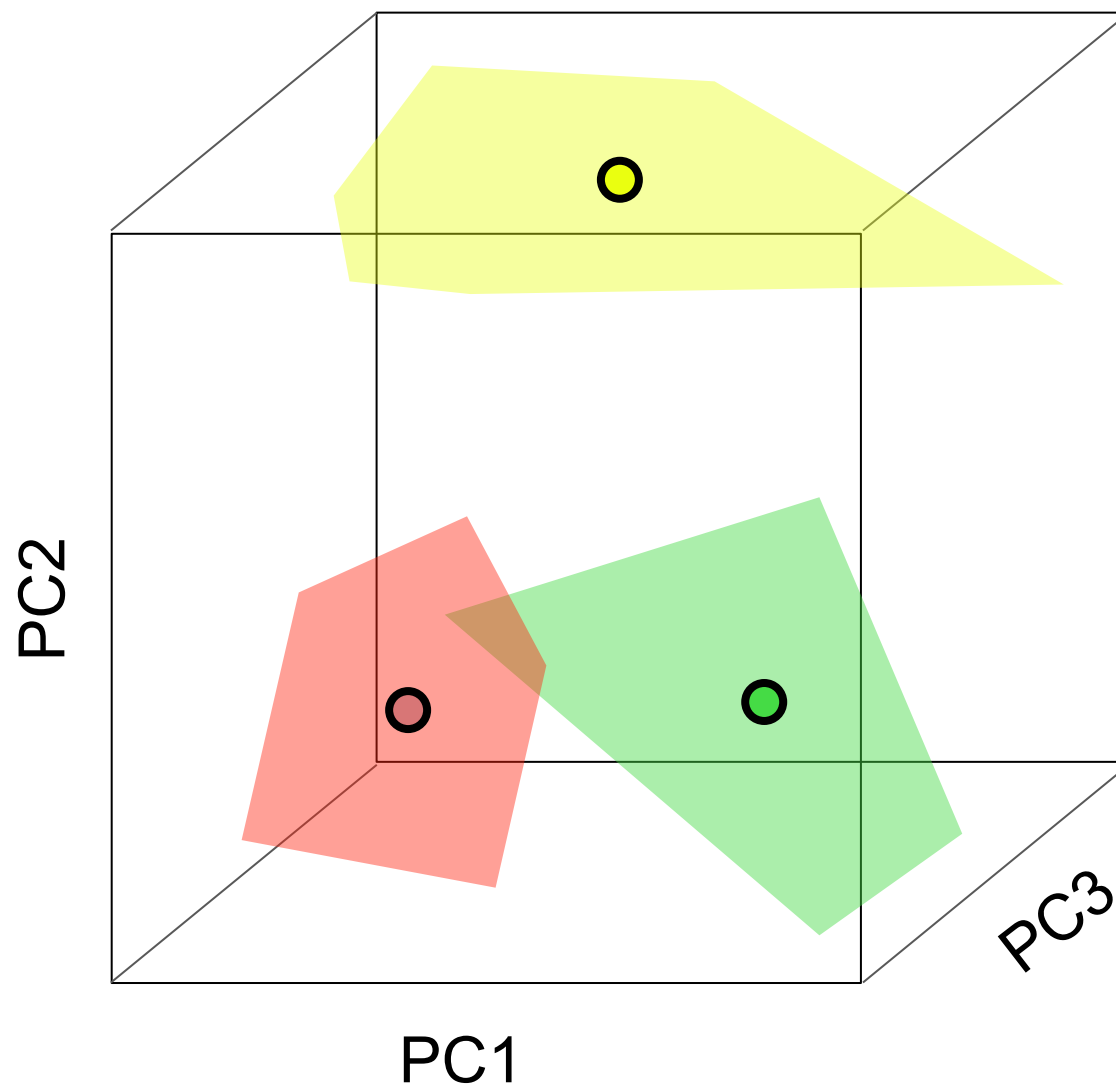
***A ocupação do morfoespaço permite a  
exploração de significado biológico em  
diversos sentidos***

*A ocupação do morfoespaço permite a  
exploração de significado biológico em  
diversos sentidos*

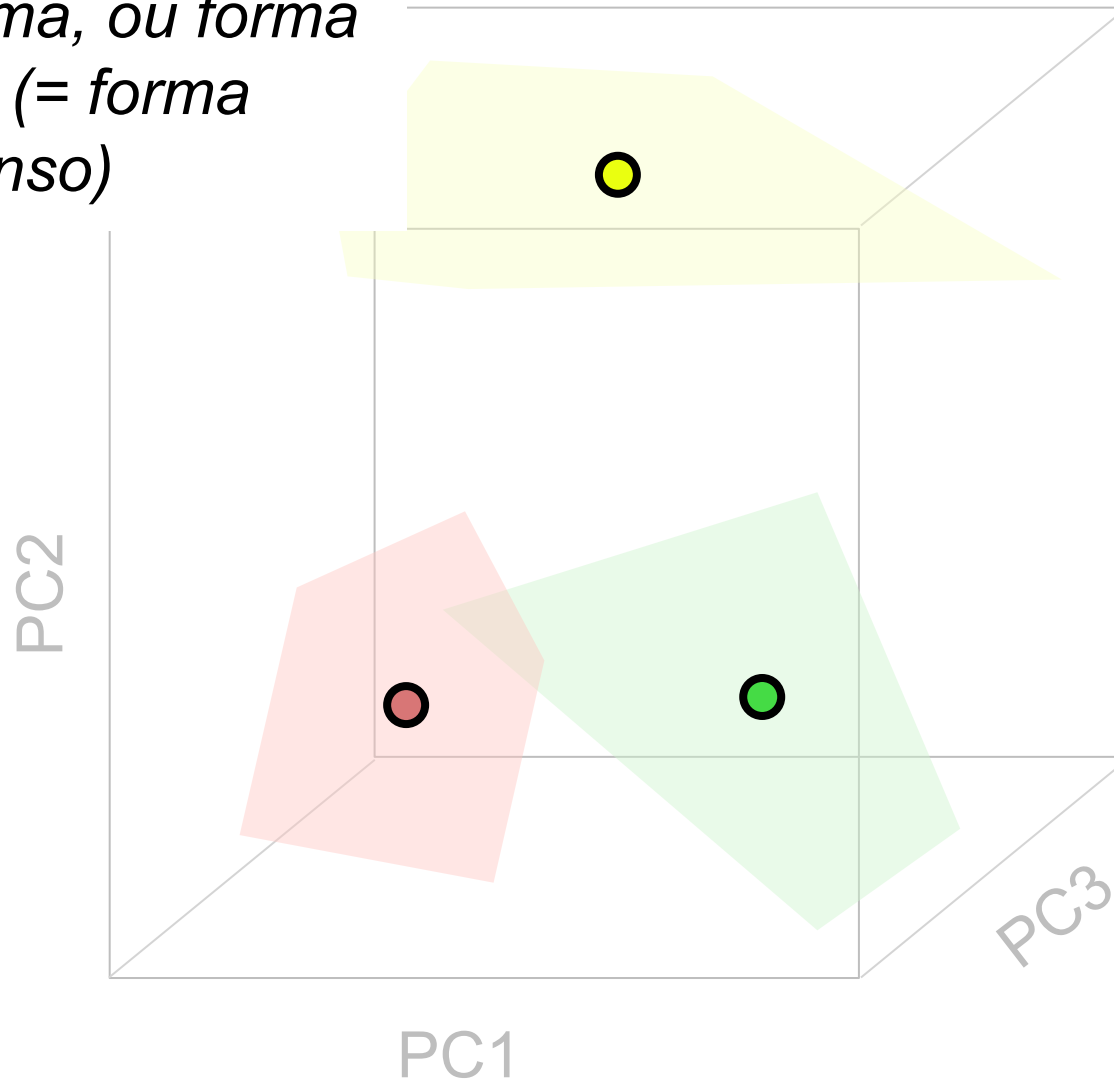
*Inclusive por consequência estatística*





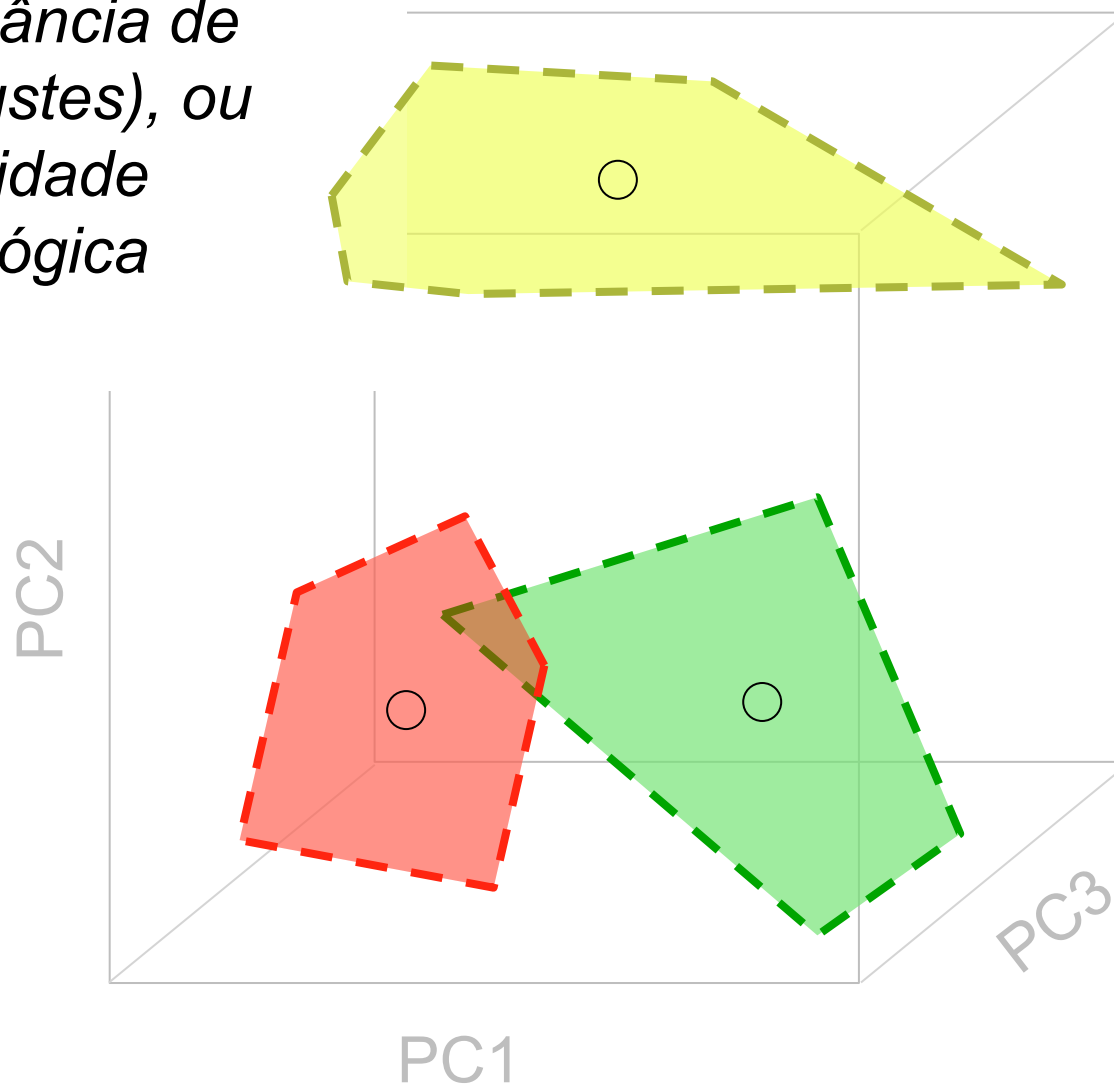


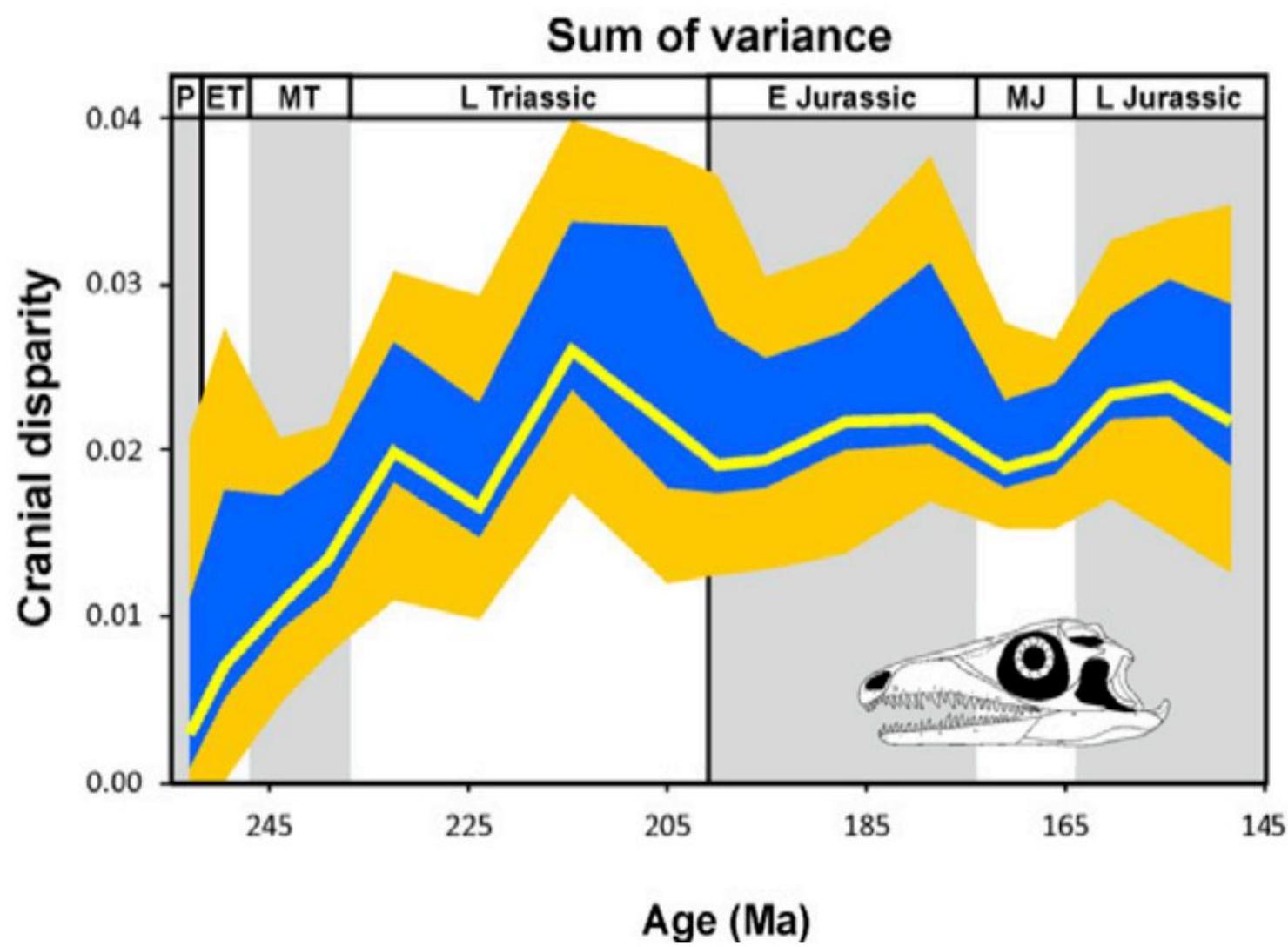
***Tendência central  
da forma, ou forma  
média (= forma  
consenso)***

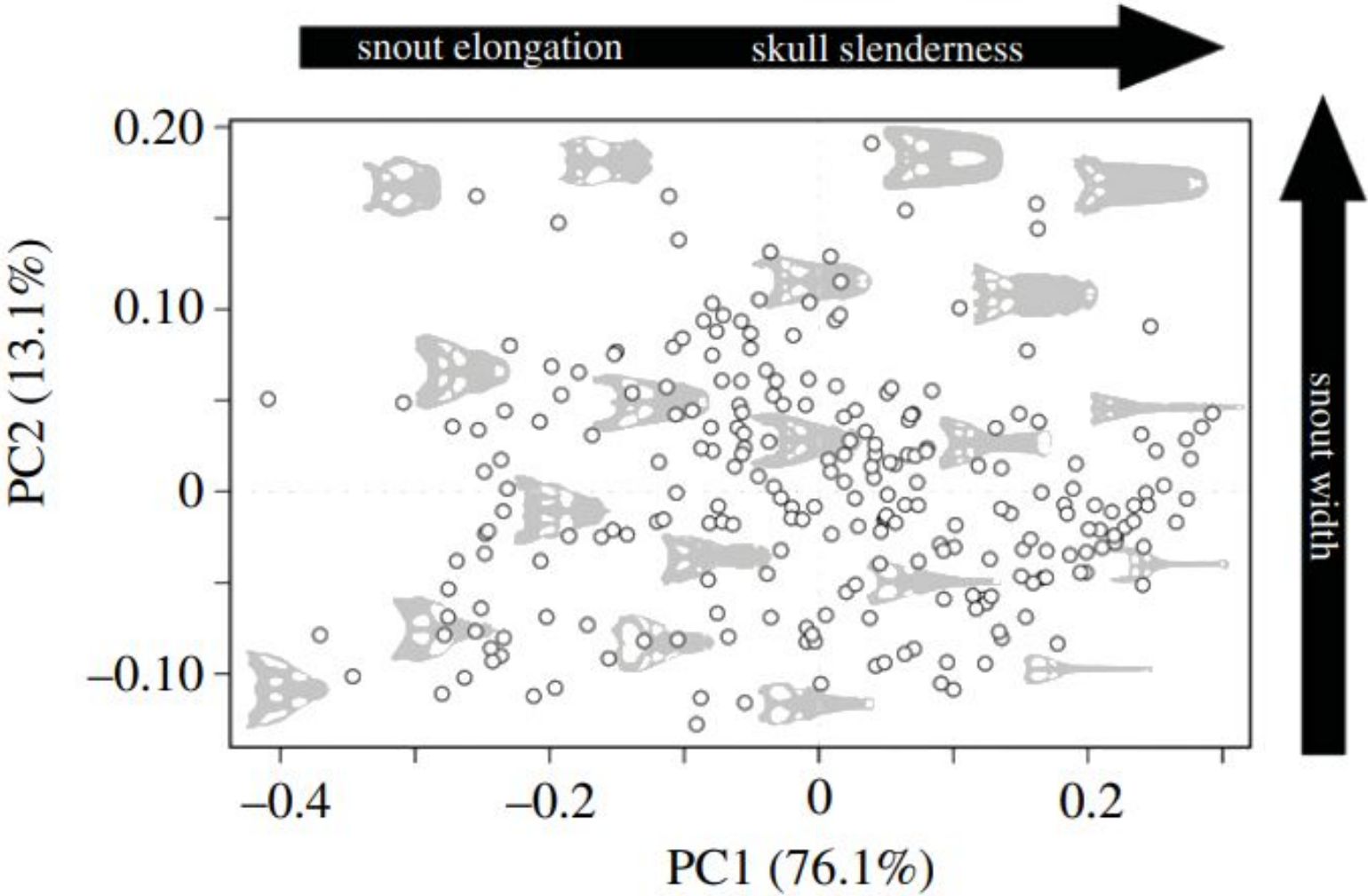


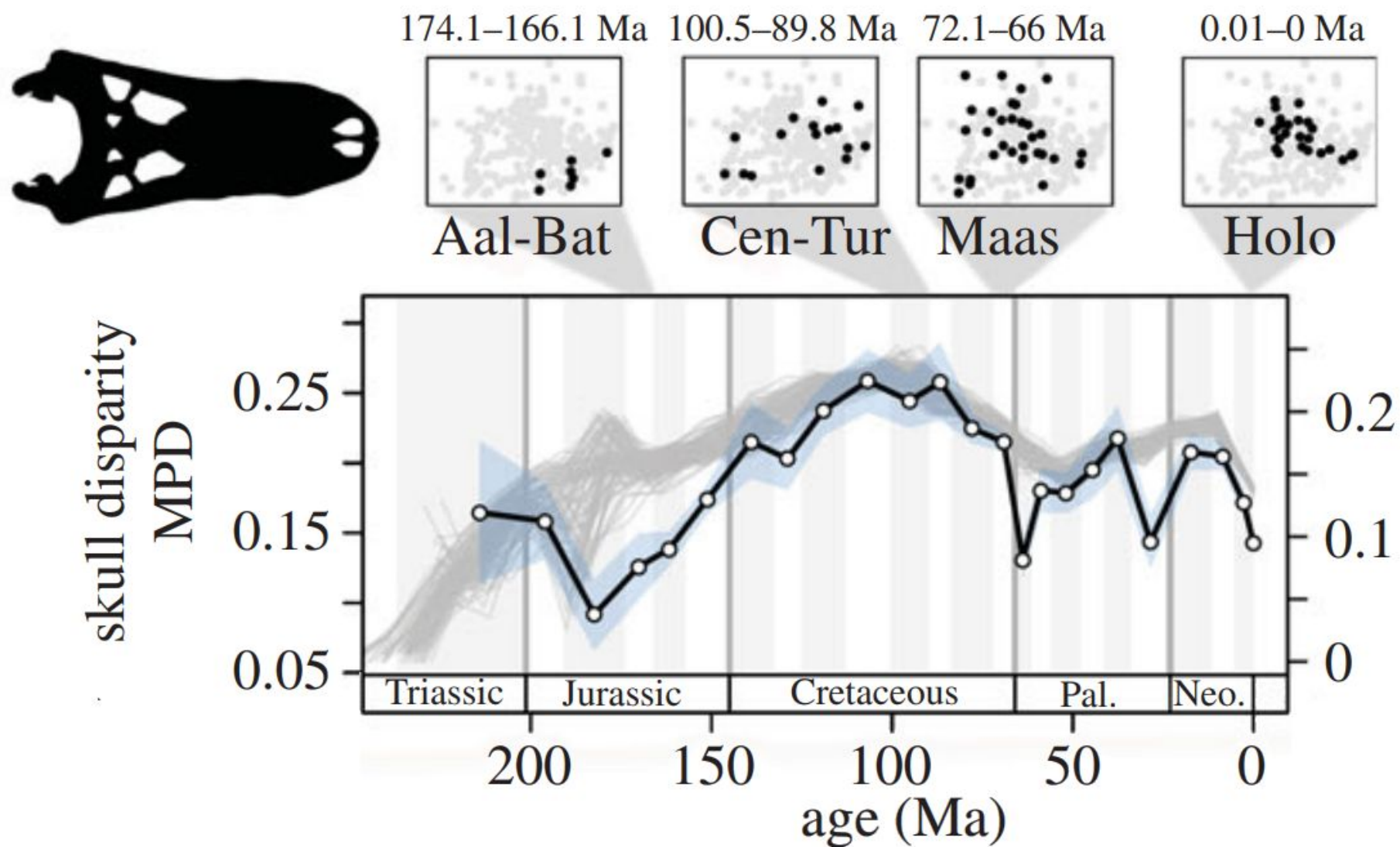
## ***Variação da forma***

*(= variância de Procrustes), ou  
disparidade  
morfológica*







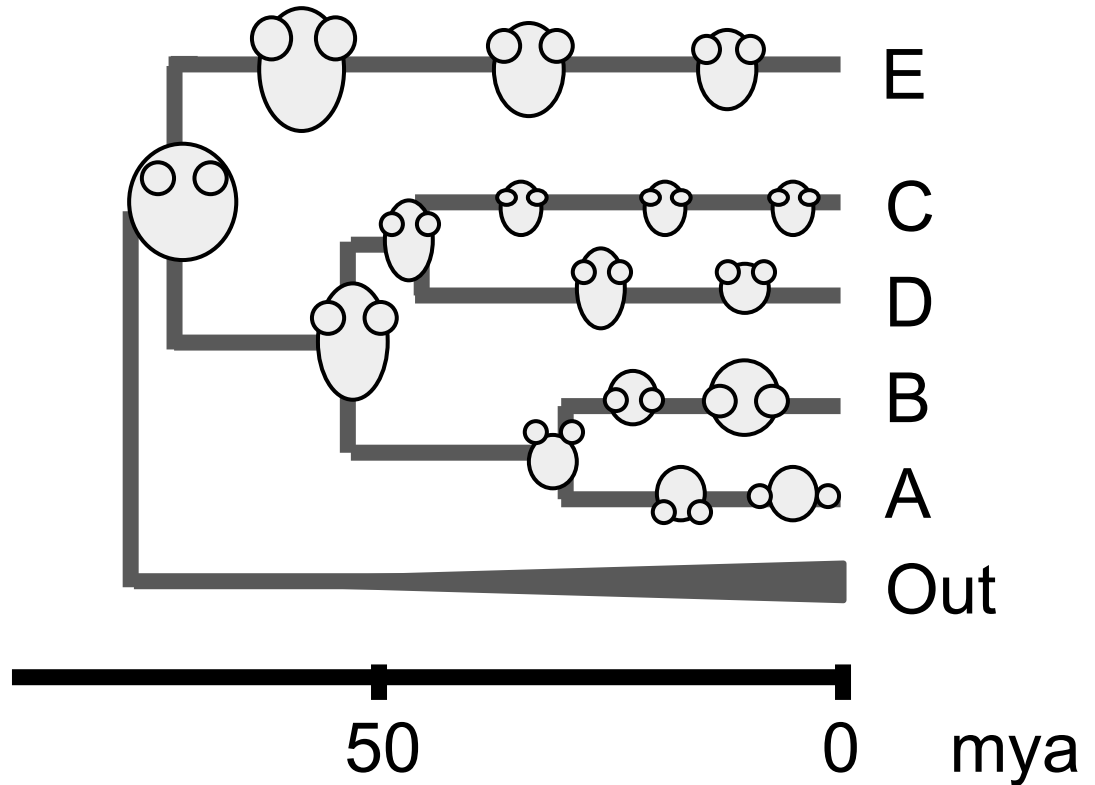


*Além da ocupação do morfoespaço, a **variação da forma** também pode ser mais ou menos acelerada ao longo do tempo*



## *Taxas evolutivas*

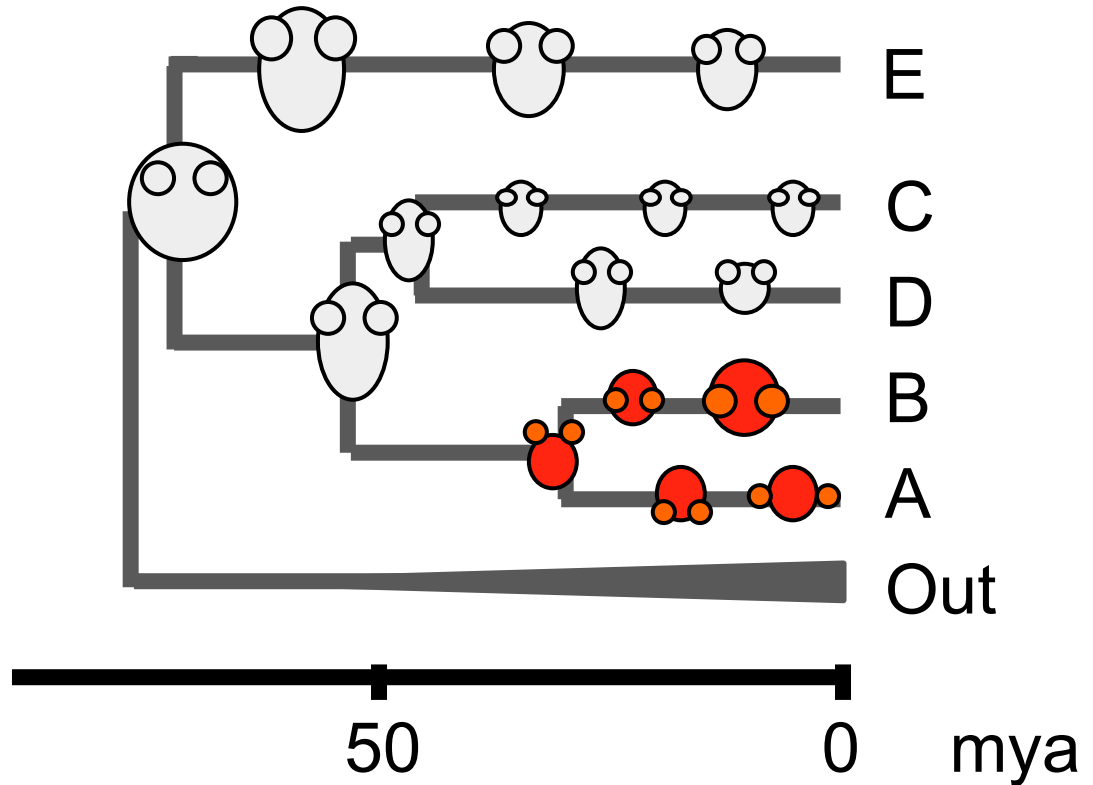
Medida da **mudança acumulada** ao longo dos ramos de uma filogenia



## *Taxas evolutivas*

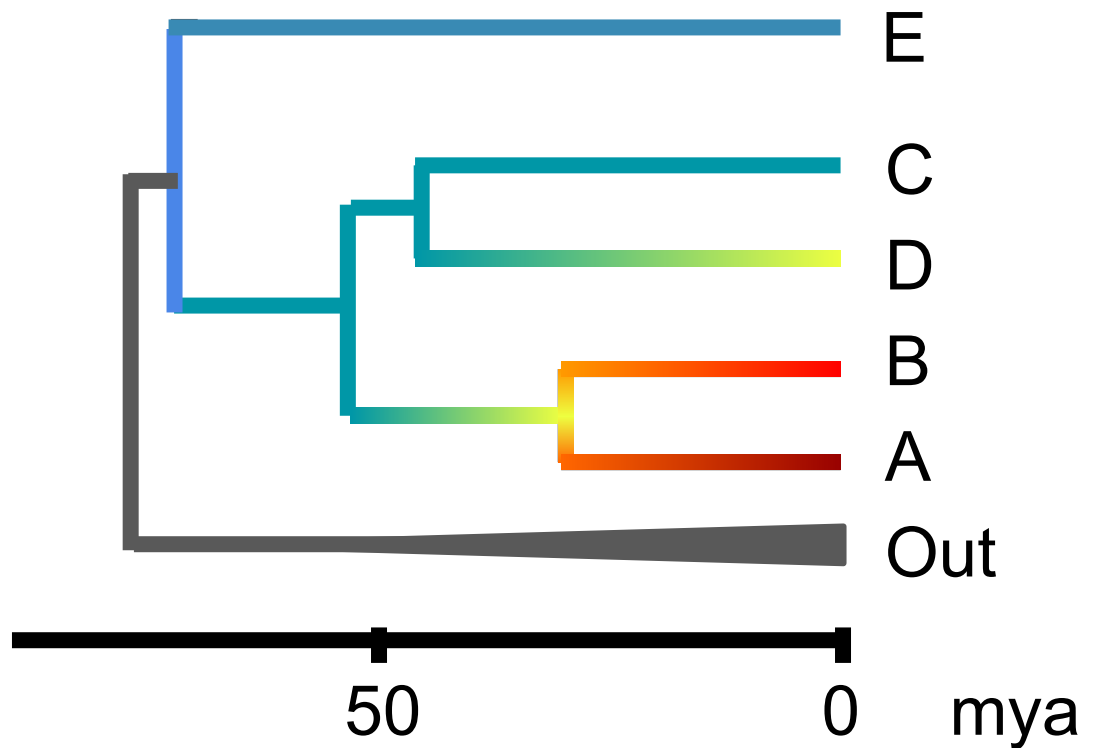
*Pode ser usada para identificar pontos de **quebra**, sugerindo processos evolutivos distintos*

- *aceleração;*
- *estase...*



*Taxas evolutivas*

*Permitindo **mapear**  
como variou a  
mudança  
morfológica na  
filogenia*



## Exemplo

*Prática de evolução da forma, aplicando  
**phytools**, **geiger** e diversos outros  
pacotes do R na morfometria  
geométrica*

Agora, vamos pro

