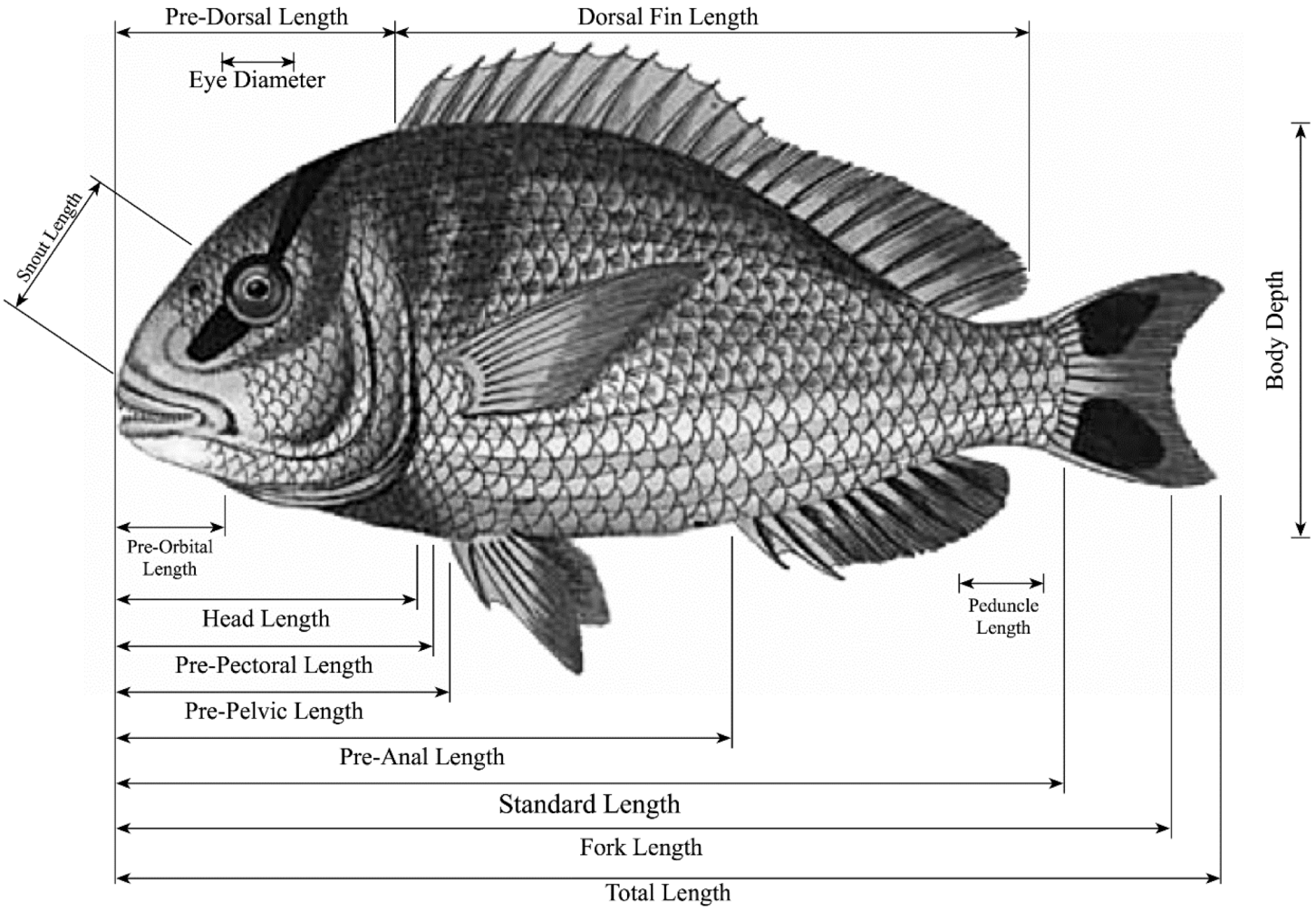
Métodos comparativos para dados multivariados

Outline da aula

- Breve histórico da morfometria geométrica
- “revolução” na morfometria na década de 1980
- Principais conceitos e aplicações
- Principais métodos comparativos para dados multivariados
  - Taxa evolutiva
  - Ajuste de modelos evolutivos levando em conta correlação entre traits
  - Mudança de estado ótimo ao longo da filogenia

Lógica da morfometria tradicional



MacLeod 2017

Problemas com a morfometria tradicional

- Usa várias medidas lineares, razões e ângulos mas que não capturam a *posição* dos marcos anatômicos
- Difícil estabelecer homologia entre estruturas
- Medidas lineares não capturam geometria
- Geram várias variáveis correlacionadas que precisam passar por redução (e.g., PCA) antes de serem usadas
- Confunde **tamanho** e **formato**
- Sempre o PC 1 é relacionado com tamanho

Vantagens da GM

- Consegue separar Tamanho de Formato, além de fornecer técnicas de visualização

- Permite medir formas não só em 2D como em 3D

Definição de forma

“all the geometric information that remains when location, scale and rotational effects are filtered out from an object”

Kendall 1977

David Kendall

Desenvolveu o aparato matemático/geométrico para medir forma

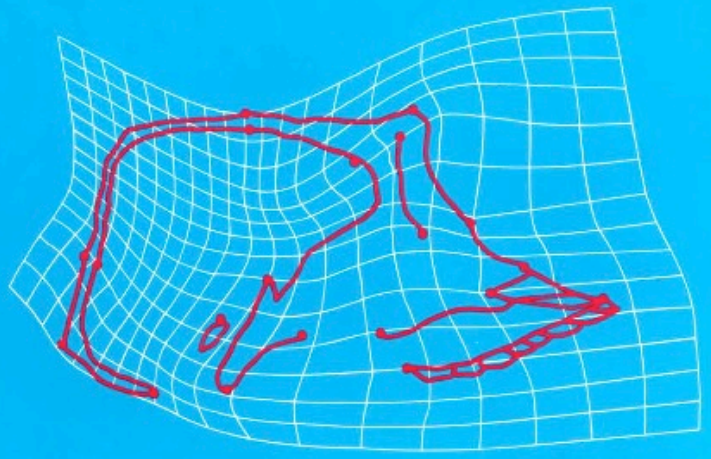
Fred Bookstein

Desenvolveu métodos estatísticos que hoje em dia fazem parte do "catecismo" da GM

James Rholf

Adaptou Procrustes para dados de landmark

Proceedings of the Michigan Morphometrics Workshop

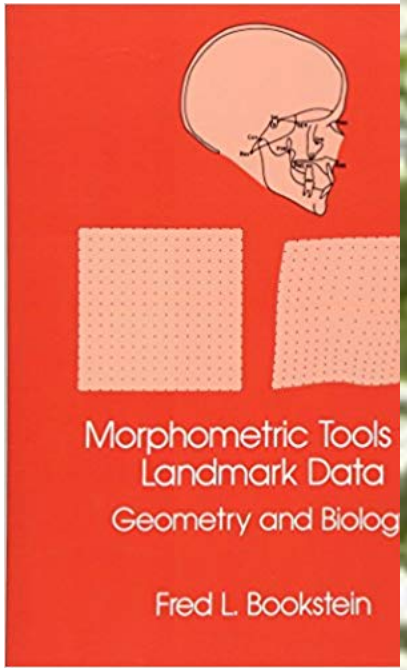


Edited by

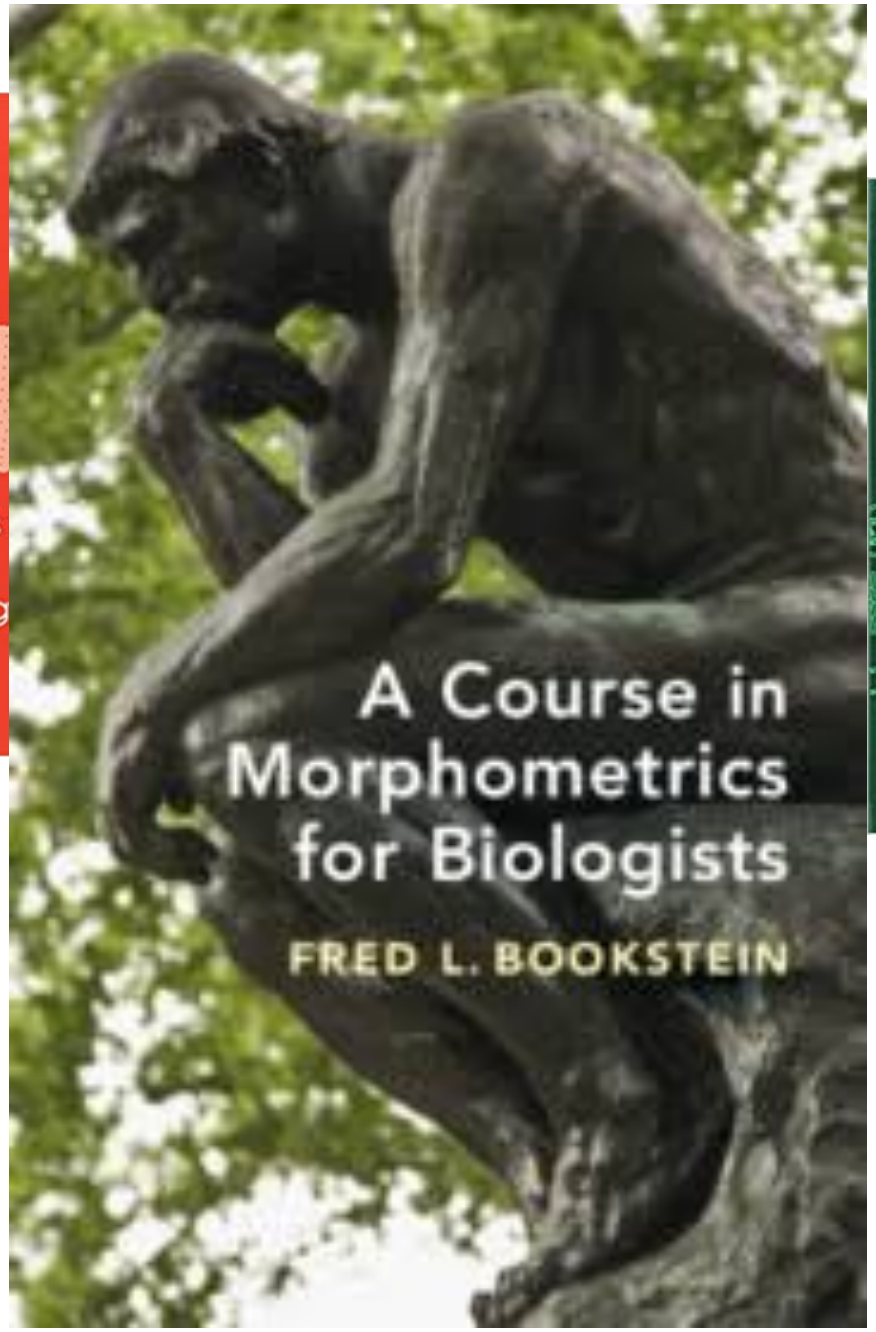
F. James Rohlf
Fred L. Bookstein

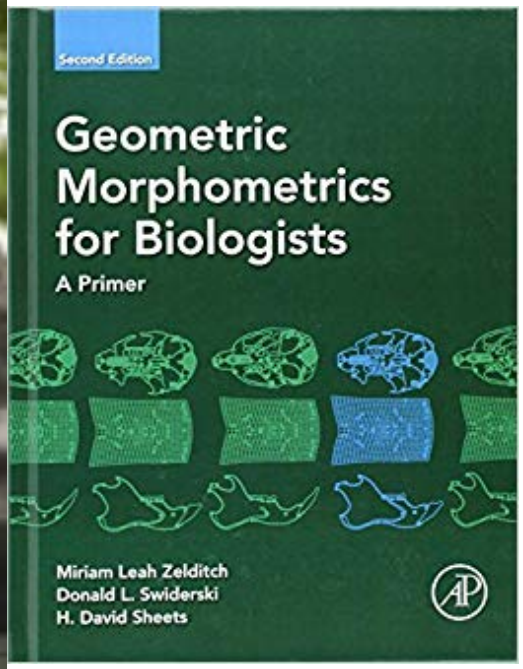
Special Publication Number 2
The University of Michigan Museum of Zoology

1990



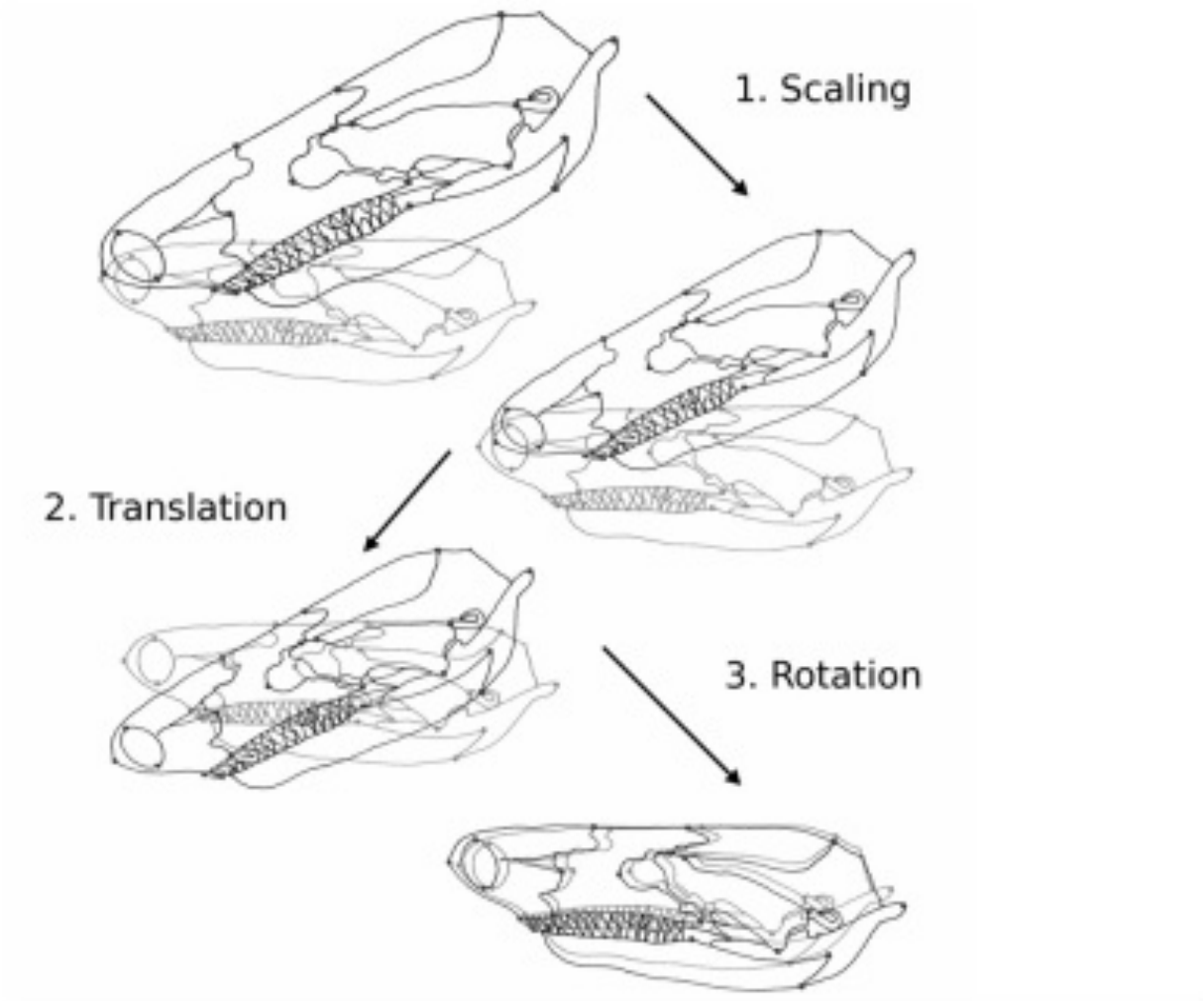
1992



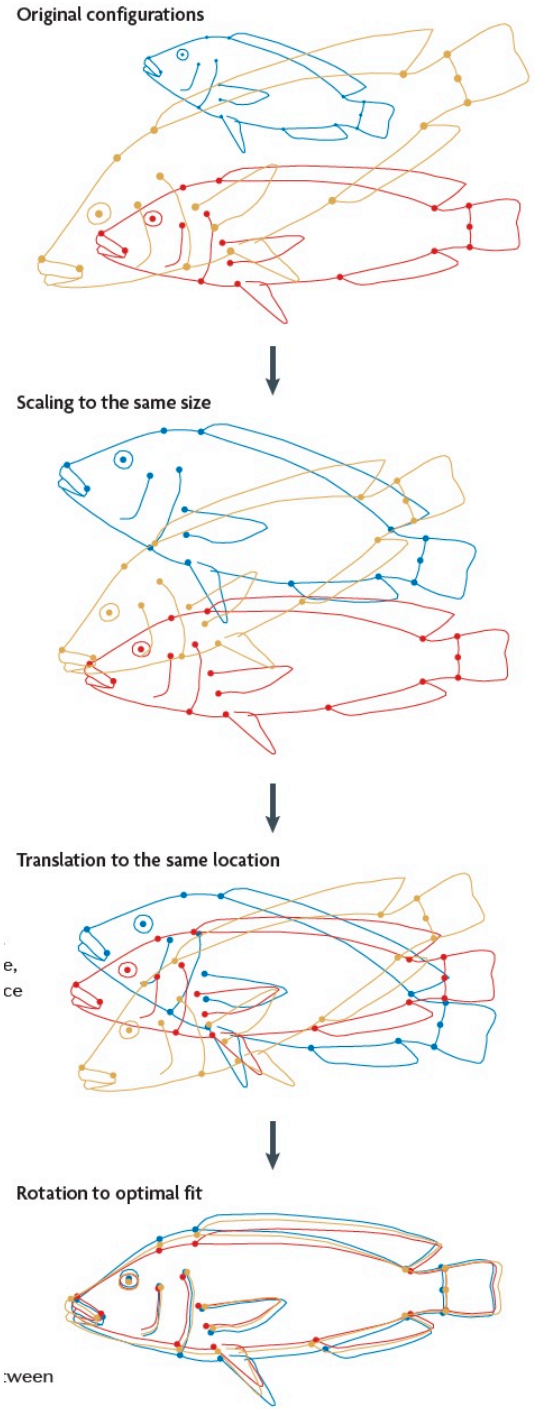


2004 e
2012

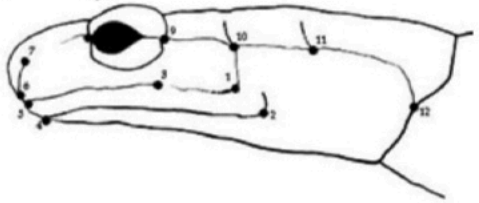
Operações que não mudam o formato do objeto



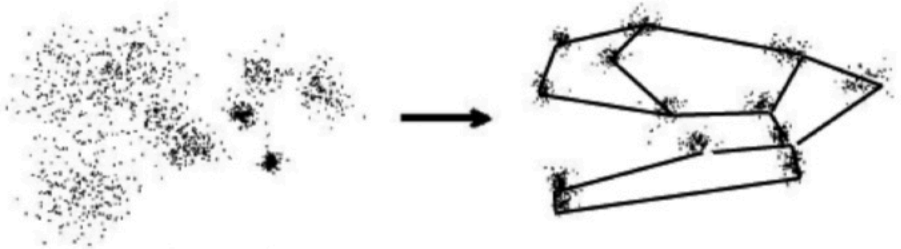
http://www.emmasherratt.com/morphometrics


Original configurations
Scaling to the same size
Translation to the same location
Rotation to optimal fit

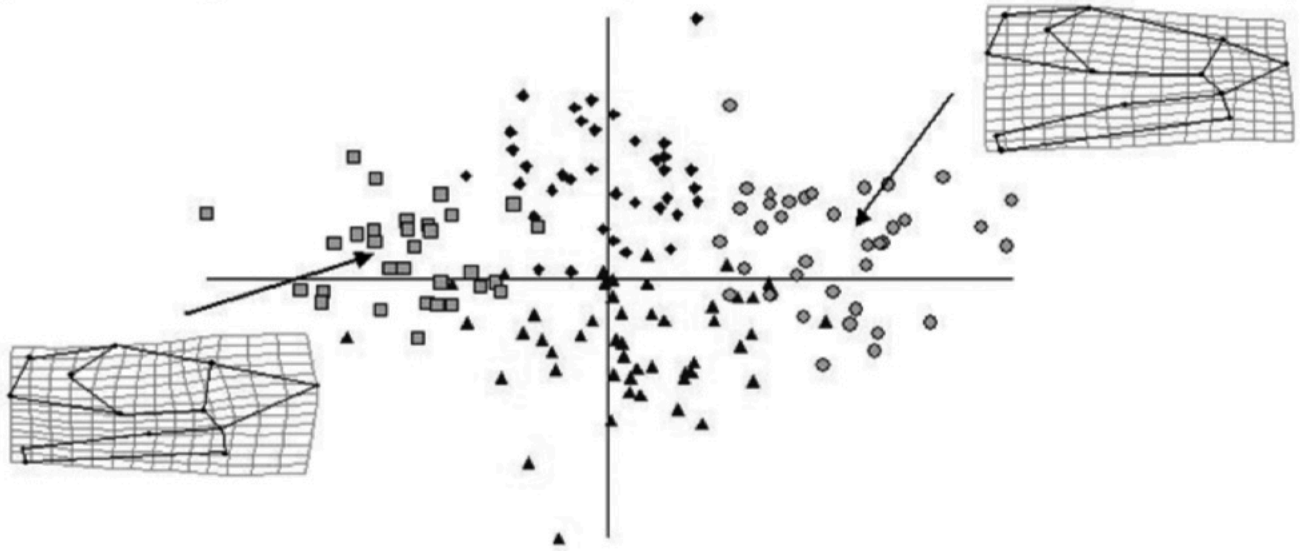
1) Digitize landmarks



2) GPA (remove non-shape variation)



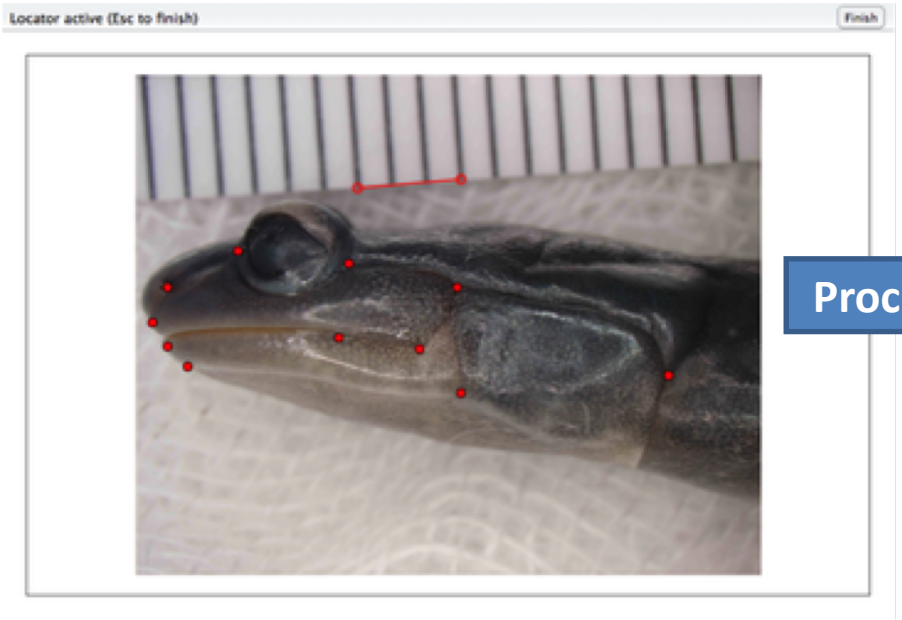
3) Statistical analysis (e.g., MANOVA)
4) graphical depiction of results (statistical and morphometric)



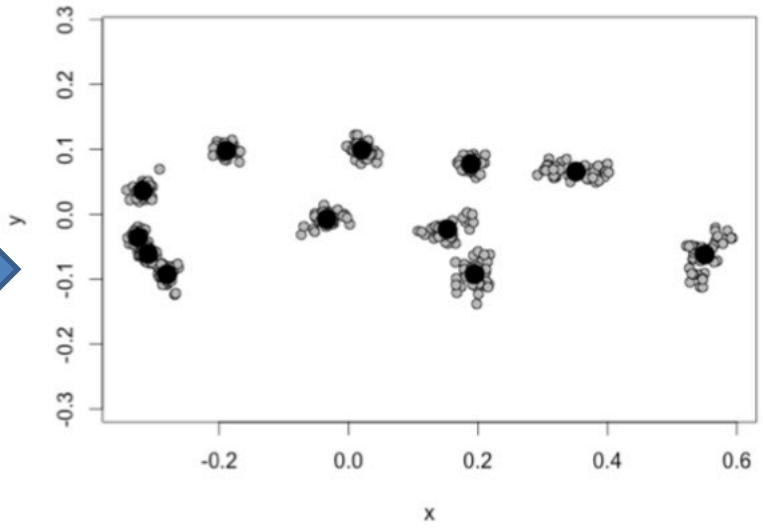
Adams et al. 2013

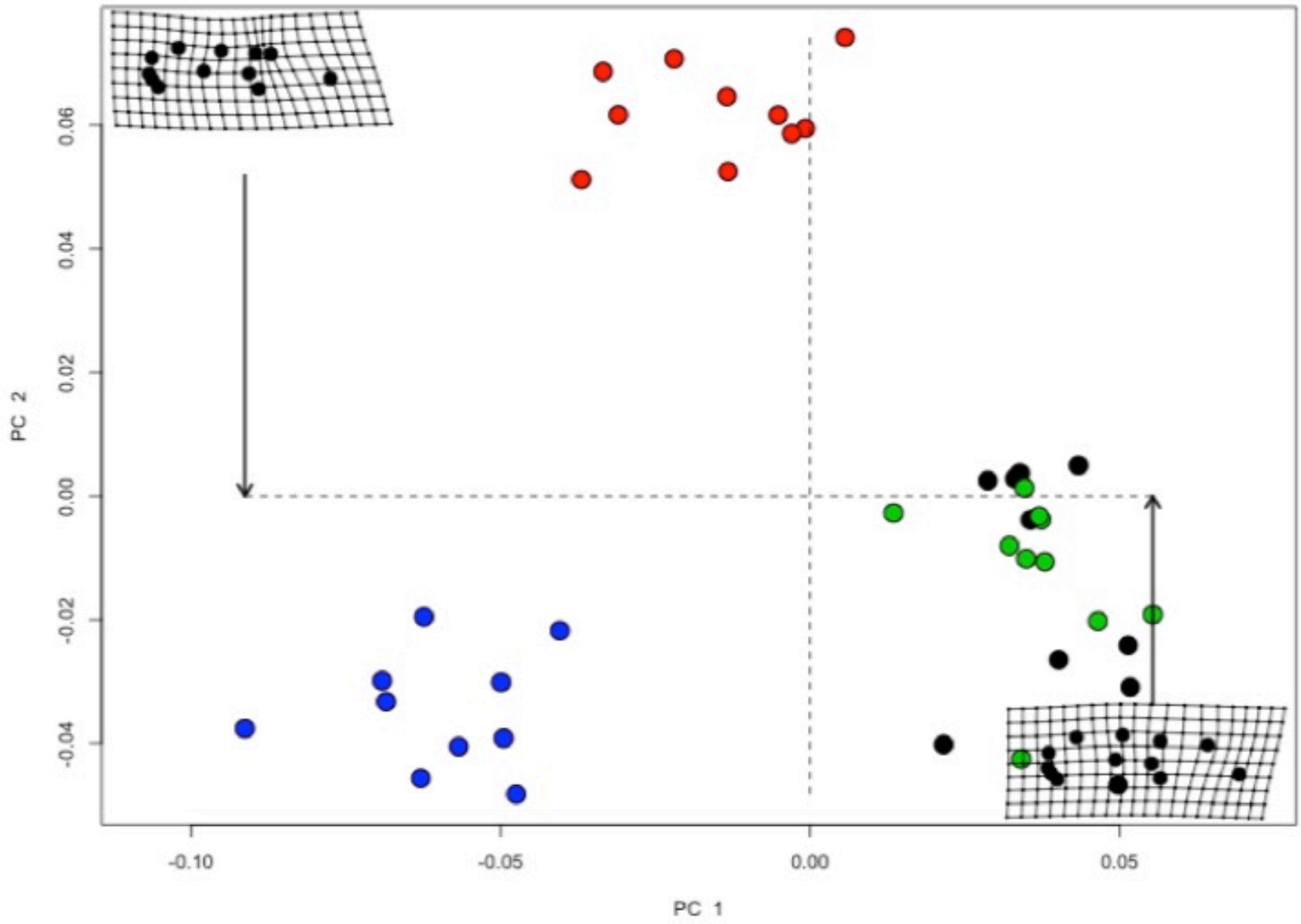
- Landmarks: coordenadas cartesiana (X,Y) que são homólogas entre exemplares (ou espécies)

- Semi-landmarks: não homólogos, usados para descrever contornos
  - Antigamente eram usados outline techniques


Locator active (Esc to finish)
Finish

Procrustes

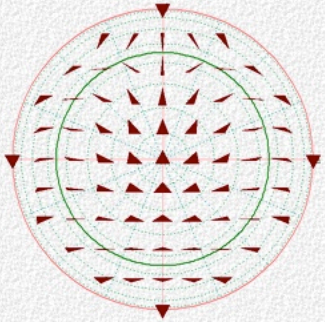

y
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
-0.2
0.0
0.2
0.4
0.6
x

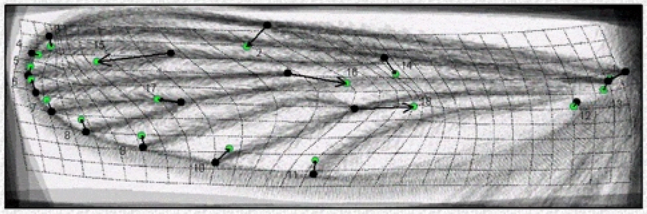

0.06
0.04
0.02
0.00
-0.02
-0.04
PC 2
-0.10
-0.05
0.00
0.05
PC 1

Morphometrics

at SUNY Stony Brook

Contents:





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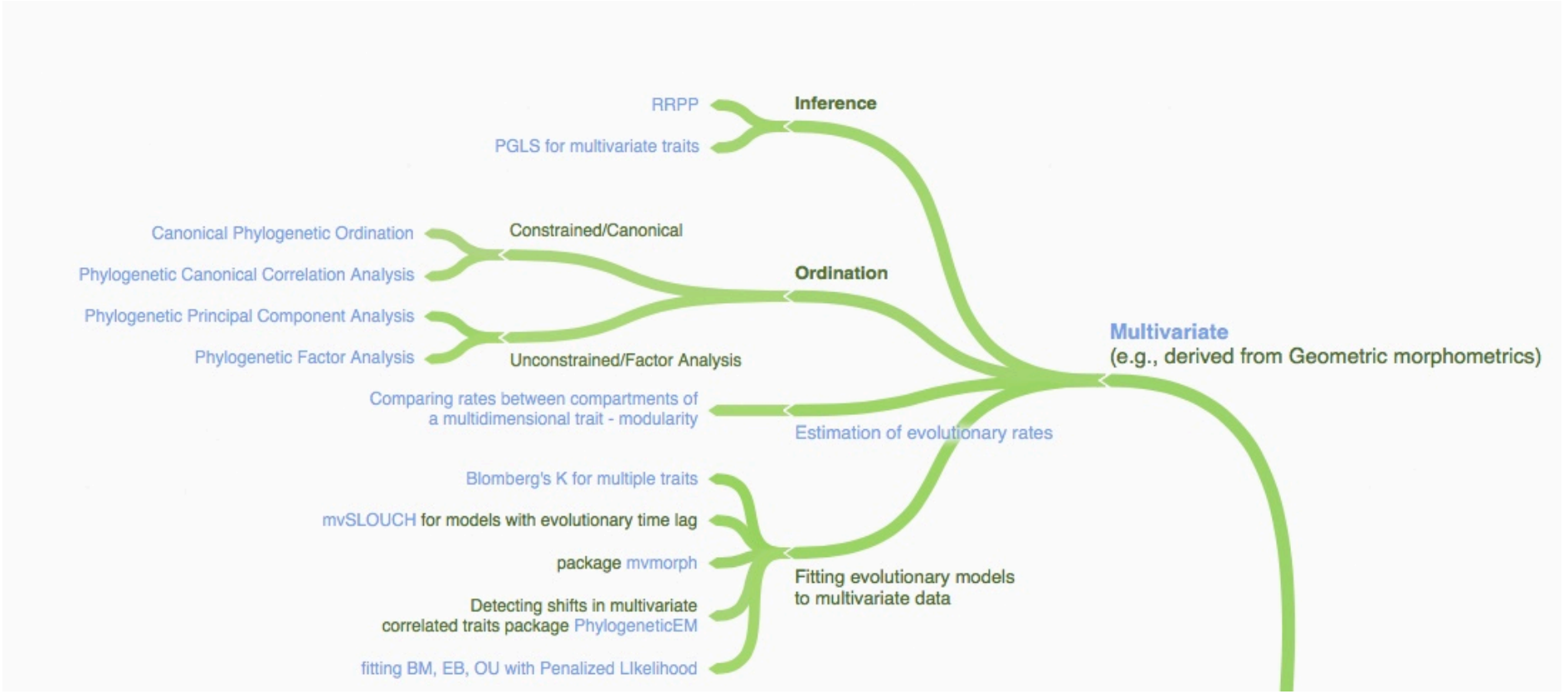
According to our counter, this site has now been accessed by people in more than 8050 cities around the world. The field is expanding! See the new map below for visits since April 2016.

Métodos comparativos

O que vimos até aqui?

- Formas de descrever um fenótipo
  - Contagem
  - Categorização (e.g., branco, preto)
  - Medidas lineares (e.g., tamanho corporal, altura)
- Mas e fenótipos multivariados?
  - *Formato* do corpo, formato da pata etc
  - Processos de seleção não necessariamente podem modificar o tamanho e sim a forma
  - Evolução correlacionada: um atributo pode ser modificado não por seleção sobre ele, mas sim por ação de seleção num atributo correlacionado


Multivariate
(e.g., derived from Geometric morphometrics)
Inference
RRPP
PGLS for multivariate traits
Ordination
Constrained/Canonical
Canonical Phylogenetic Ordination
Phylogenetic Canonical Correlation Analysis
Unconstrained/Factor Analysis
Phylogenetic Principal Component Analysis
Phylogenetic Factor Analysis
Estimation of evolutionary rates
Comparing rates between compartments of a multidimensional trait - modularity
Fitting evolutionary models to multivariate data
Blomberg's K for multiple traits
mvSLOUCH for models with evolutionary time lag
package mvmorph
Detecting shifts in multivariate correlated traits package PhylogeneticEM
fitting BM, EB, OU with Penalized LIkelihood

Syst. Biol. 63(2):166–177, 2014

DOI:10.1093/sysbio/syt105
Advance Access publication December 10, 2013

Quantifying and Comparing Phylogenetic Evolutionary Rates for Shape and Other High-Dimensional Phenotypic Data

DEAN C. ADAMS[1,2]

[1]*Department of Ecology, Evolution, and Organismal Biology; and* [2]*Department of Statistics, Iowa State University, Ames, IA 50011, USA*

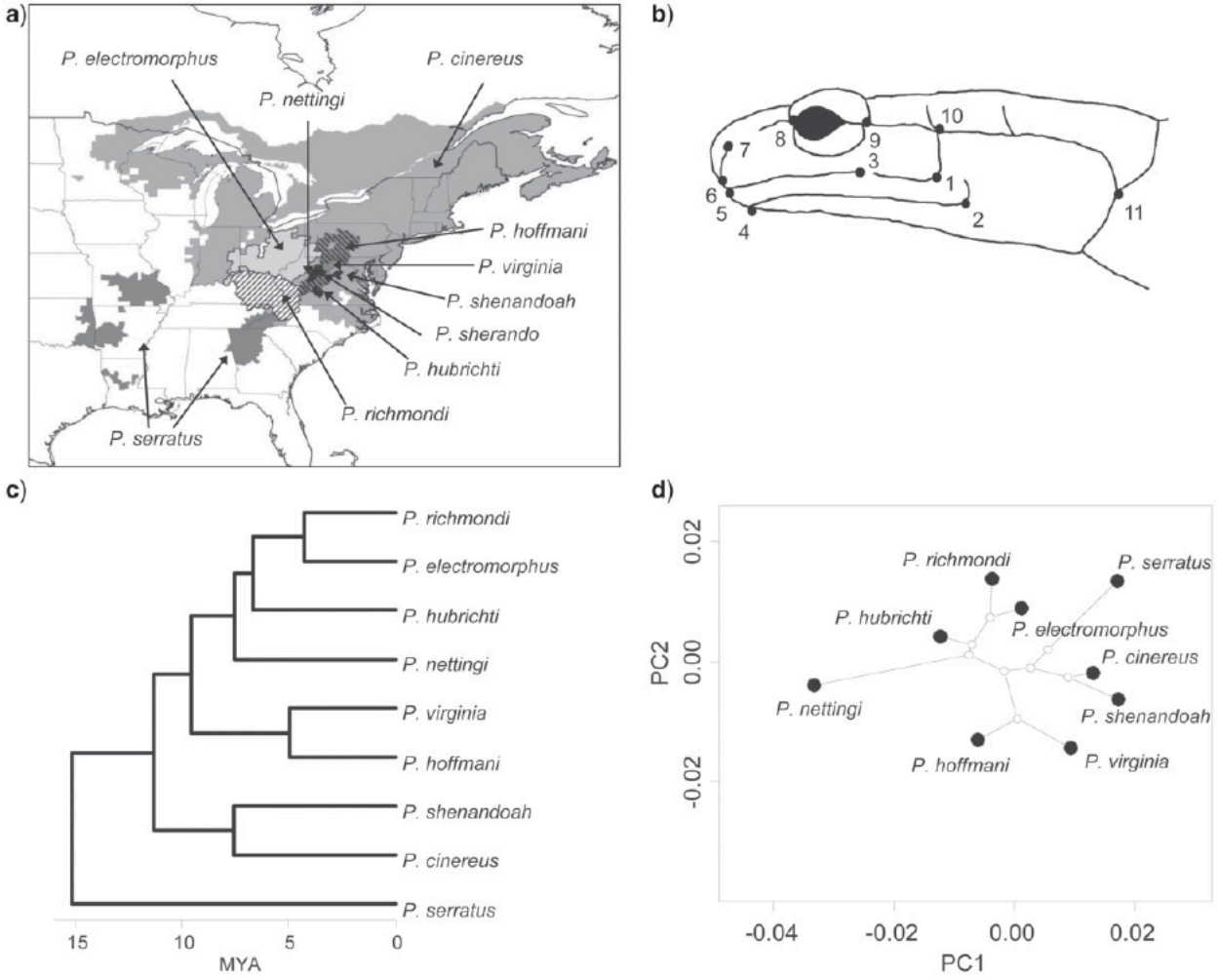
$$\sigma^2_{\text{mult}} = \frac{\mathbf{PD}^t_{\mathbf{U},0}\mathbf{PD}_{\mathbf{U},0}}{N}.$$

Syst. Biol. 63(5):685–697, 2014

DOI:10.1093/sysbio/syu030
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*



Salamandras do gênero Plethodon do leste dos EUA. Várias espécies do grupo P. cinereus tem distribuição restrira. Trabalhos com outros grupos demonstraram que espécies com distribuição restrira podem exibir elevadas taxas de evolução morfológica

PGLS para traits multivariados

doi:10.1111/evo.12463

A METHOD FOR ASSESSING PHYLOGENETIC LEAST SQUARES MODELS FOR SHAPE AND OTHER HIGH-DIMENSIONAL MULTIVARIATE DATA

Dean C. Adams[1,2,3]

Seleção de modelos para traits multivariados

Syst. Biol. 67(1):14–31, 2018

DOI:10.1093/sysbio/syx055
Advance Access publication July 13, 2017

Multivariate Phylogenetic Comparative Methods: Evaluations, Comparisons, and Recommendations

DEAN C. ADAMS[1,2,*] AND MICHAEL L. COLLYER[3]

Syst. Biol. 0(0):1–25, 2018

DOI:10.1093/sysbio/syy045

A Penalized Likelihood Framework for High-Dimensional Phylogenetic Comparative Methods and an Application to New-World Monkeys Brain Evolution

JULIEN CLAVEL, LEANDRO ARISTIDE, AND HÉLÈNE MORLON

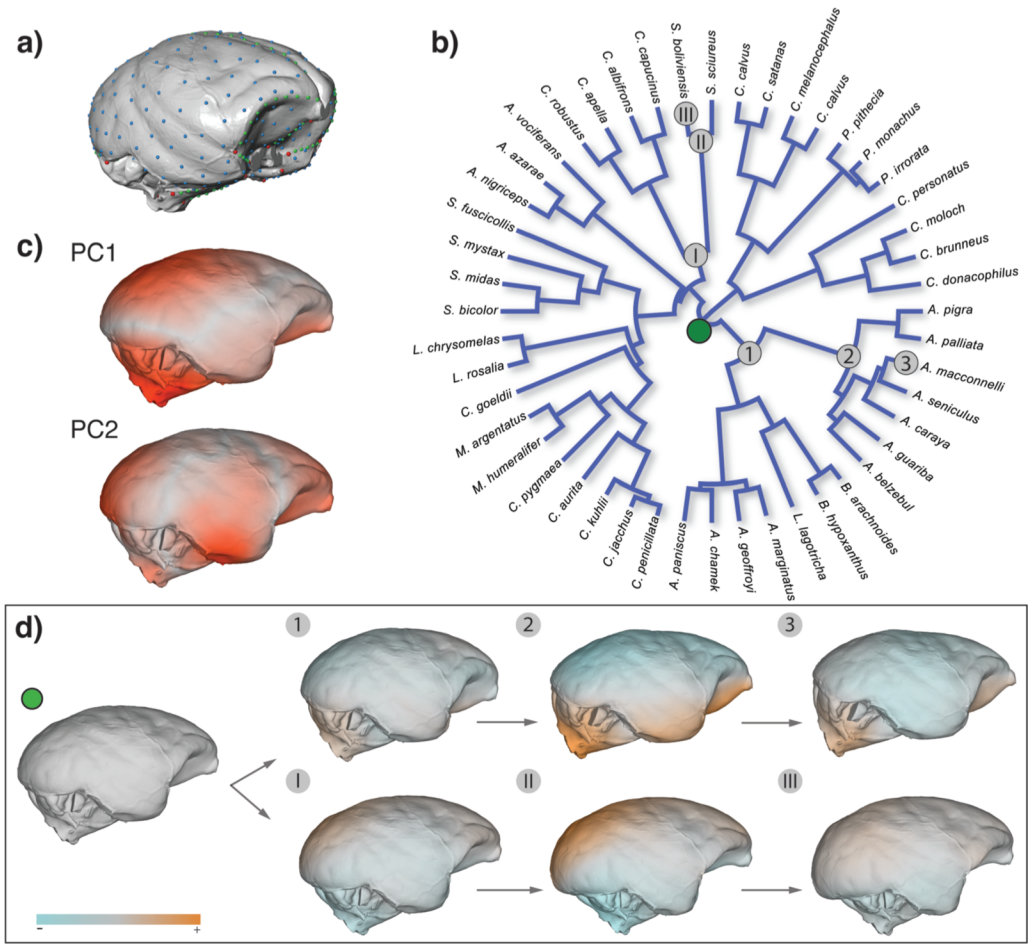
Methods in Ecology and Evolution

Methods in Ecology and Evolution 2015, **6**, 1311–1319 doi: 10.1111/2041-210X.12420

APPLICATION

mvMORPH: an R package for fitting multivariate evolutionary models to morphometric data

Julien Clavel[1,2*], Gilles Escarguel[2] and Gildas Merceron[3]



From: A Penalized Likelihood Framework for High-Dimensional Phylogenetic Comparative Methods and an Application to New-World Monkeys Brain Evolution
Syst Biol. Published online June 19, 2018. doi:10.1093/sysbio/syy045

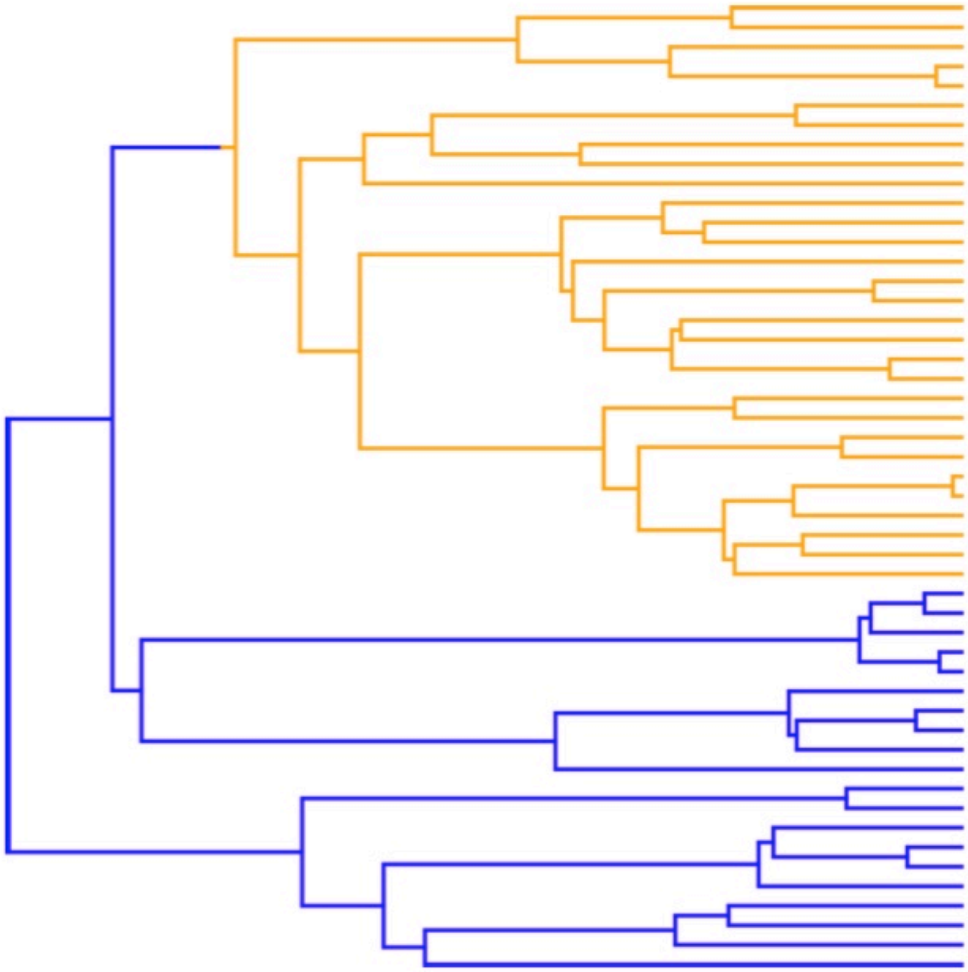
TABLE 2.

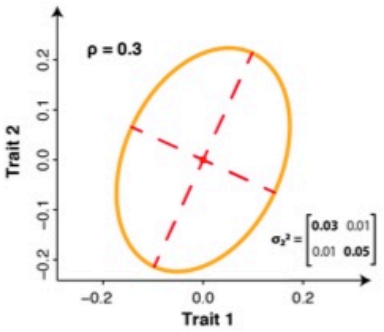
Support for BM, OU, and EB models for the evolution of New World monkeys' brain shape over 100 trees from the Bayesian posterior distribution

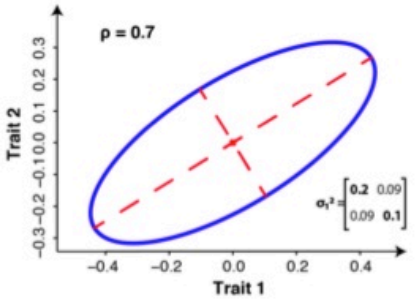
Model	GIC (mean ± 2 SD)	ΔGIC (2.5–97.5% range)	% trees preferred	Parameters[a] (mean ± 2 Sd)
BM	$-726\,505 \pm 410$	4.95–258	0	–
OU	$-726\,504 \pm 409$	1.03–260.4	3	$\alpha = 9.34\,e^{-5} \pm 4.8\,e^{-4}$
EB	$-726\,618 \pm 379$	0–0.30	97	$r = -0.91 \pm 0.69$

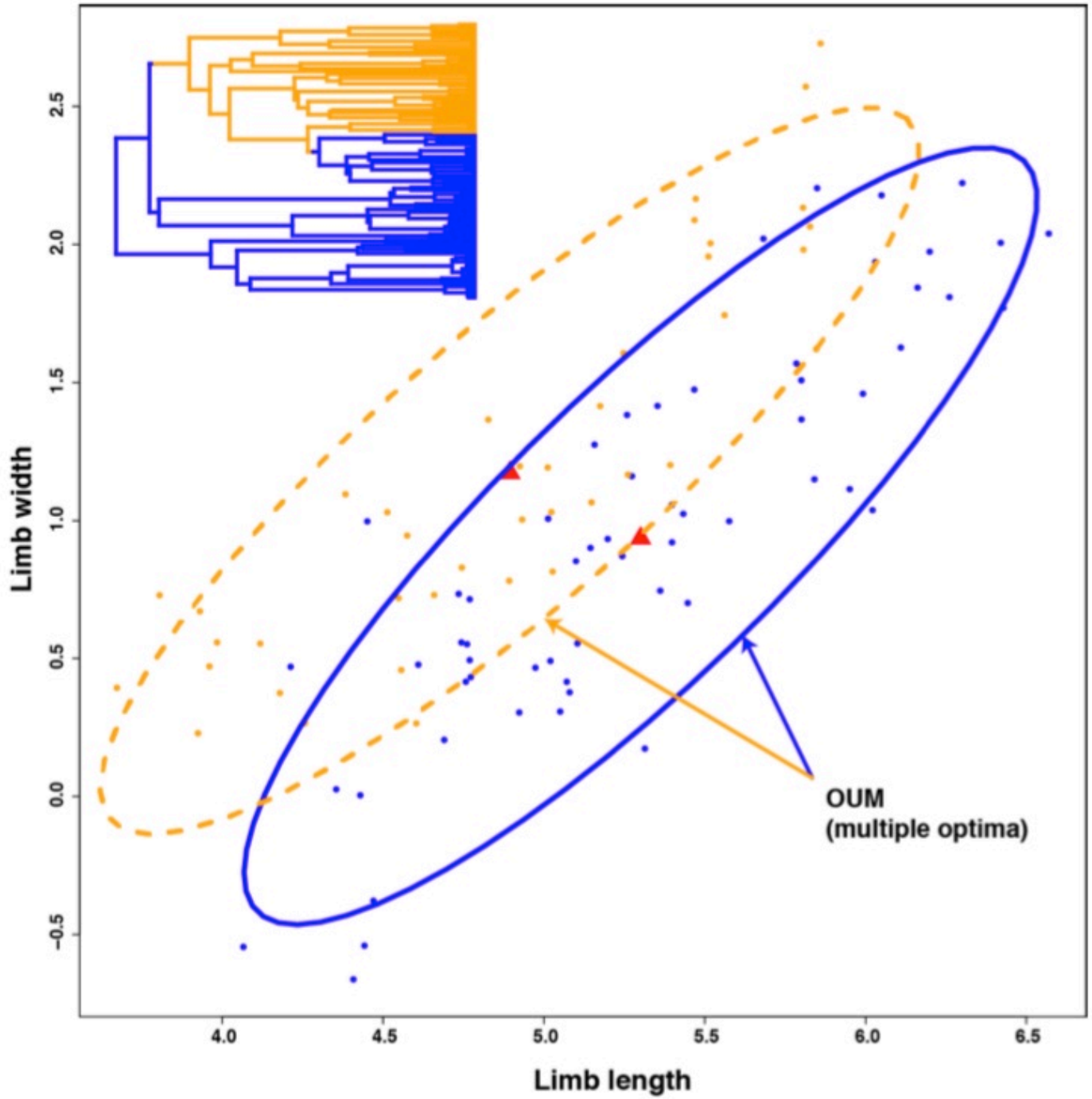
The EB model is preferred (lowest GIC value) in 97% of the trees.

[a] The Brownian parameters are given in the multidimensional $\boldsymbol{R}$ matrix (see also Fig. 4).




ρ = 0.3
Trait 2
Trait 1
0.2
0.1
0.0
−0.1
−0.2
−0.2
0.0
0.2
$\sigma_2^2 = \begin{bmatrix} \mathbf{0.03} & 0.01 \\ 0.01 & \mathbf{0.05} \end{bmatrix}$


ρ = 0.7
Trait 2
Trait 1
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
−0.4
−0.2
0.0
0.2
0.4
$\sigma_1^2 = \begin{bmatrix} \mathbf{0.2} & 0.09 \\ 0.09 & \mathbf{0.1} \end{bmatrix}$


Limb width
Limb length
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
4.0
4.5
5.0
5.5
6.0
6.5
OUM
(multiple optima)

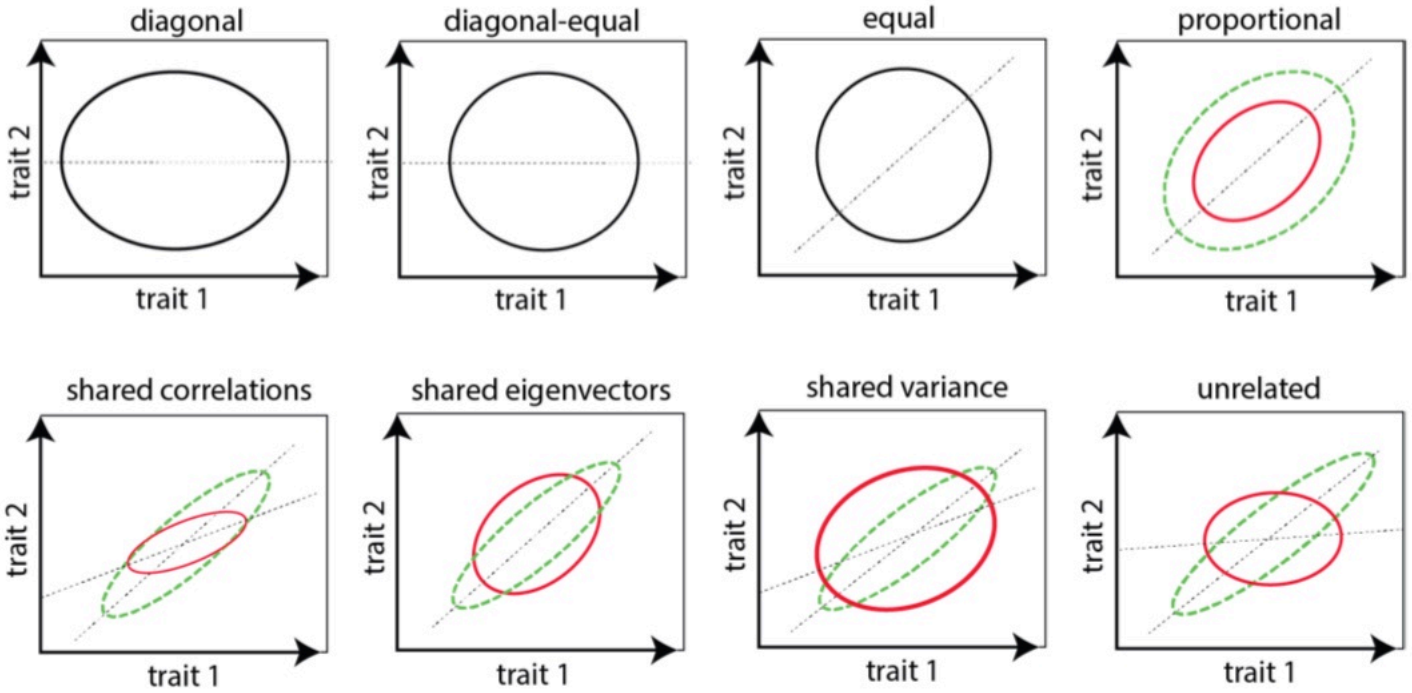


Fig. 2. *Bivariate representation of the covariance constraints used in mvMORPH.*

```r
# Fitting the models

# BM1 - (Equal rate matrix)
model_1<-mvBM(tree, data, model="BM1", diagnostic=FALSE, echo=FALSE)

# BMM - (Proportional rate matrices)
model_2<-mvBM(tree, data, param=list(constraint="proportional")
              , diagnostic=FALSE, echo=FALSE)

# BMM - (Shared eigenvectors between rate matrices)
model_3<-mvBM(tree, data, param=list(constraint="shared")
              , diagnostic=FALSE, echo=FALSE)

# BMM - (Similar correlations between rate matrices)
model_4<-mvBM(tree, data, param=list(constraint="correlation")
              , diagnostic=FALSE, echo=FALSE)

# BMM - (Similar variances between rate matrices)
model_5<-mvBM(tree, data, param=list(constraint="variance")
              , diagnostic=FALSE, echo=FALSE)

# BMM - (Independent rate matrices)
model_6<-mvBM(tree, data, model="BMM", diagnostic=FALSE, echo=FALSE)

# Compare the models with AIC
AIC(model_1)
```

```
> [1] 37.4709
```

```r
AIC(model_2)
```

```
> [1] 31.20892
```

```r
AIC(model_3)
```

```
> [1] 24.68785
```

```r
AIC(model_4)
```

```
> [1] 29.59168
```

```r
AIC(model_5)
```

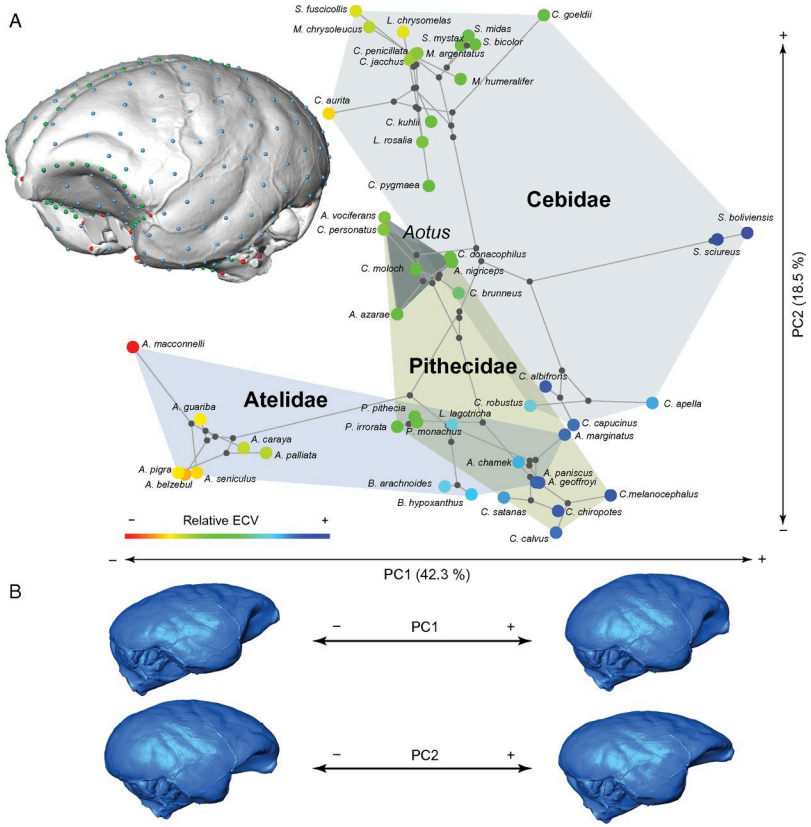
```
> [1] 38.76954
```

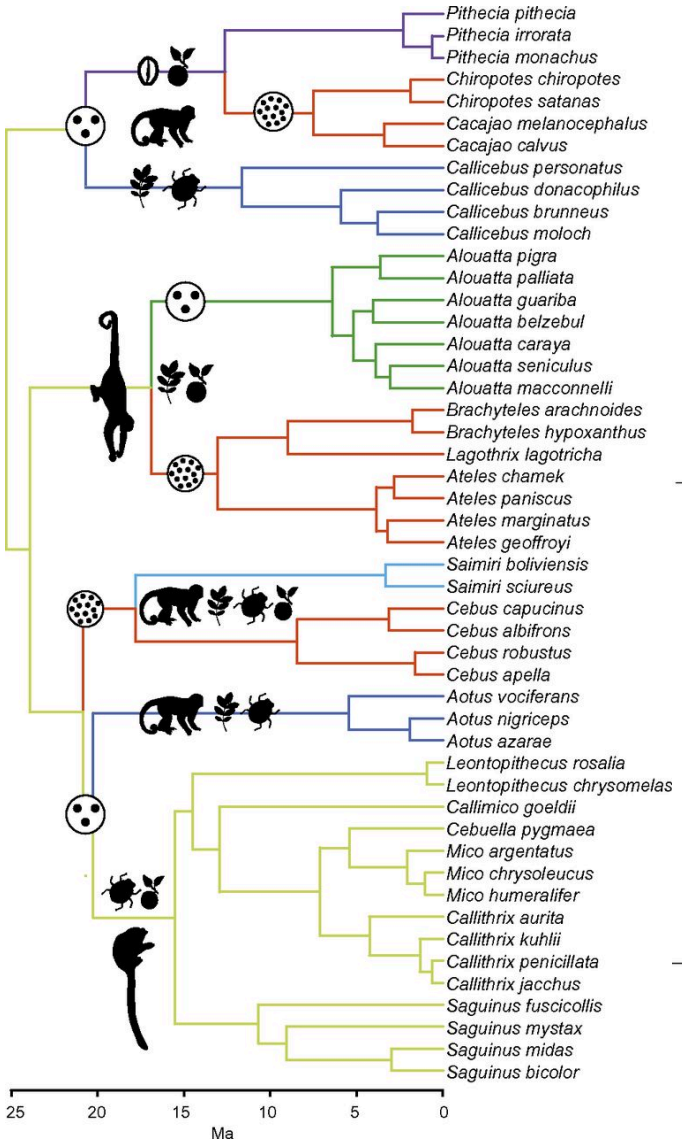
```r
AIC(model_6)
```

```
> [1] 25.99354
```

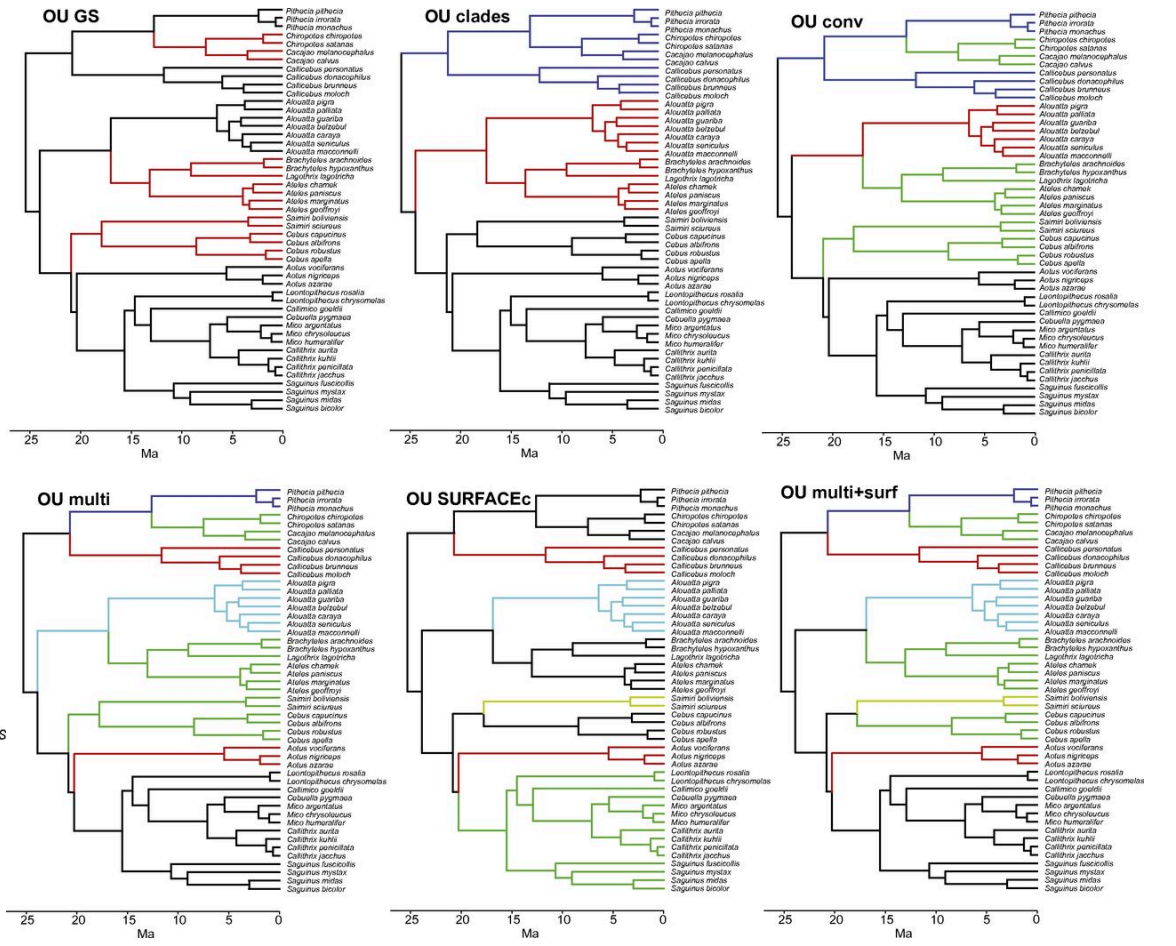
Brain shape convergence in the adaptive radiation of New World monkeys

Leandro Aristide[a], Sergio Furtado dos Reis[b], Alessandra C. Machado[c], Inaya Lima[c], Ricardo T. Lopes[c], and S. Ivan Perez[a,1]





Resultado do SURFACE



Modelos incluídos no mvMORPH

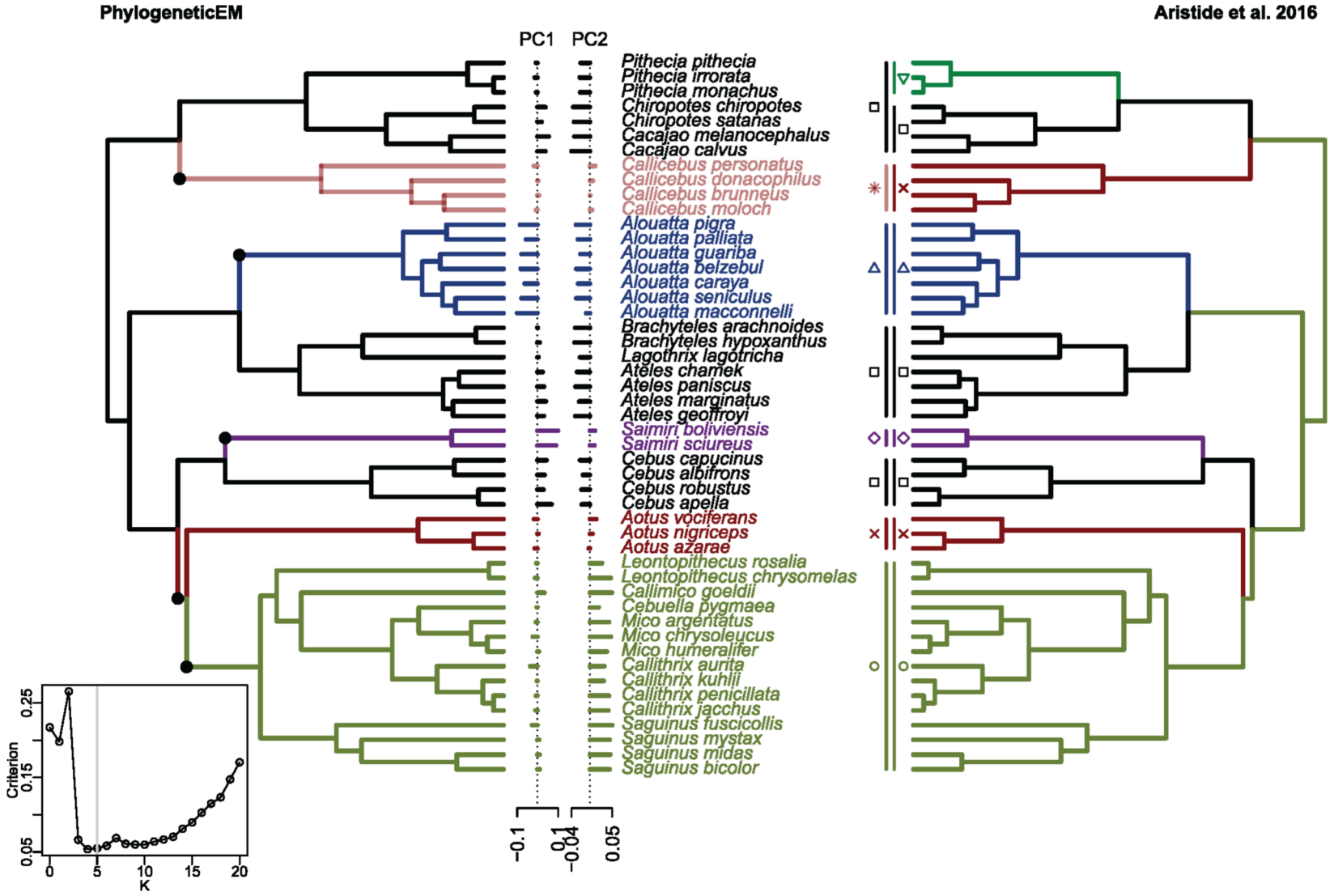
Mudanças de pico adaptativo levando em conta a correlação entre traits

Syst. Biol. 67(4):662–680, 2018

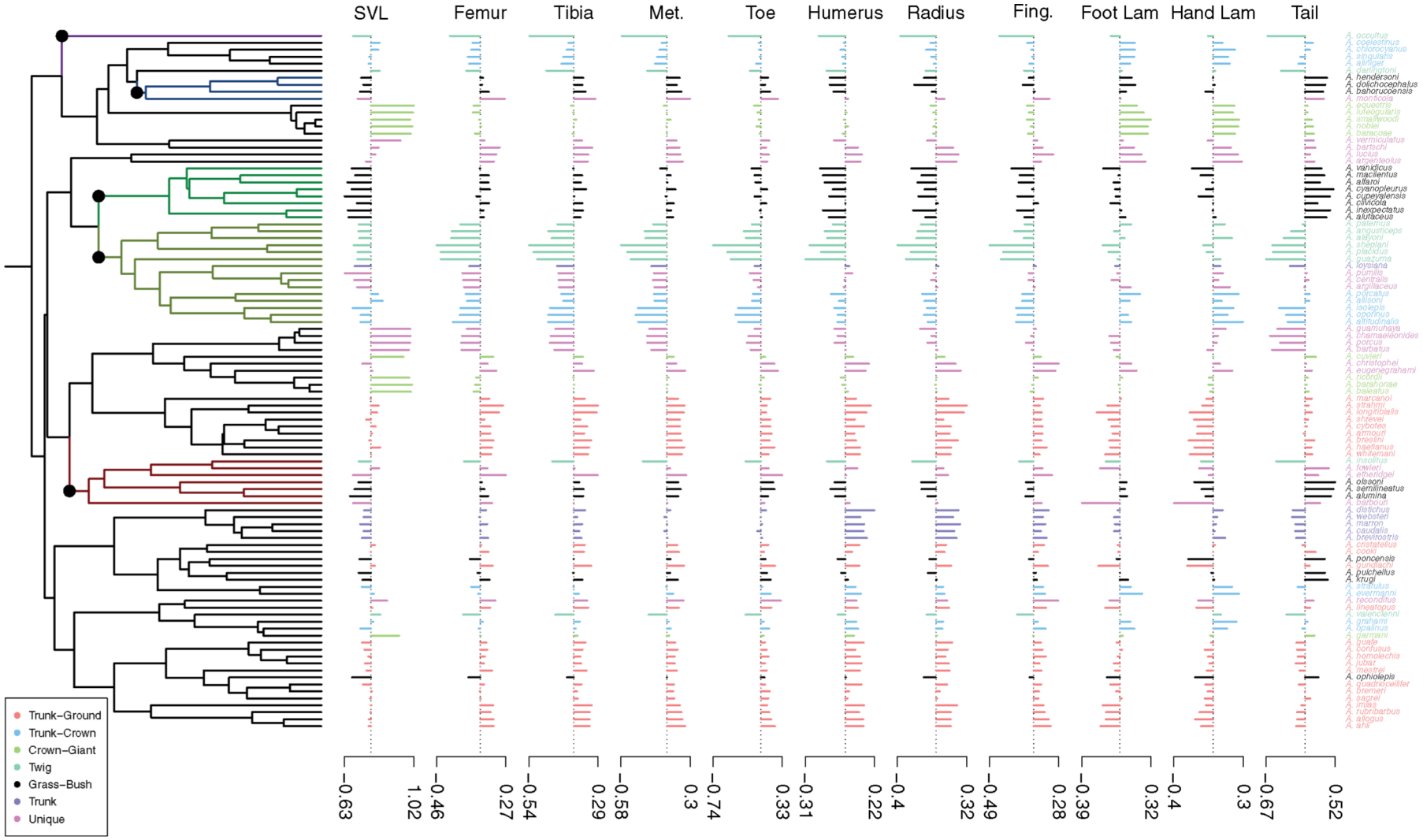
DOI:10.1093/sysbio/syy005
Advance Access publication January 27, 2018

Inference of Adaptive Shifts for Multivariate Correlated Traits

PAUL BASTIDE[1,2,*], CÉCILE ANÉ[3,4], STÉPHANE ROBIN[1], AND MAHENDRA MARIADASSOU[2]



From: Inference of Adaptive Shifts for Multivariate Correlated Traits
Syst Biol. 2018;67(4):662-680. doi:10.1093/sysbio/syy005



From: Inference of Adaptive Shifts for Multivariate Correlated Traits
Syst Biol. 2018;67(4):662-680. doi:10.1093/sysbio/syy005

Modularidade e integração de fenótipos complexos

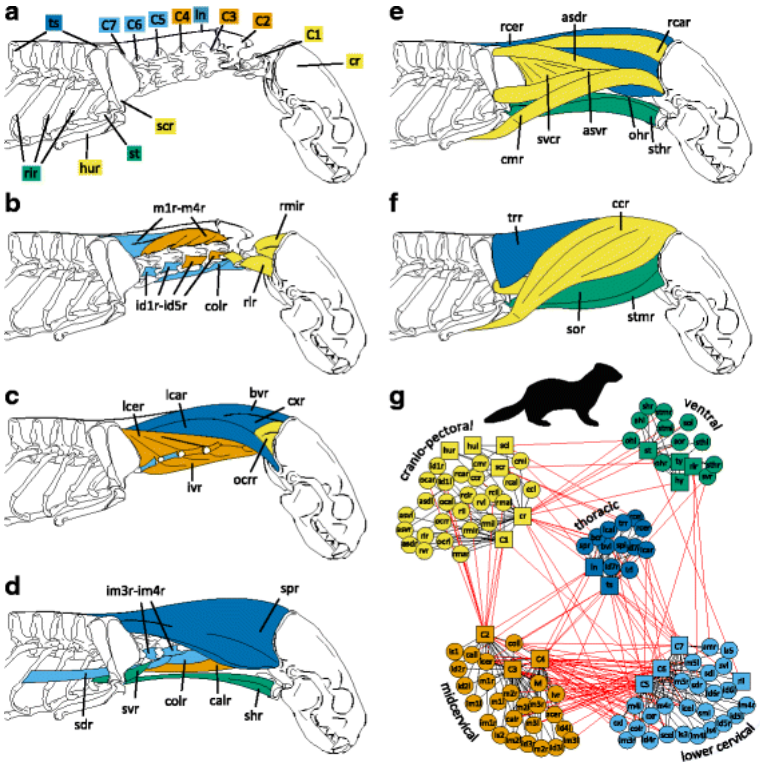
Arnold *et al. BMC Evolutionary Biology* (2017) 17:251
DOI 10.1186/s12862-017-1101-1

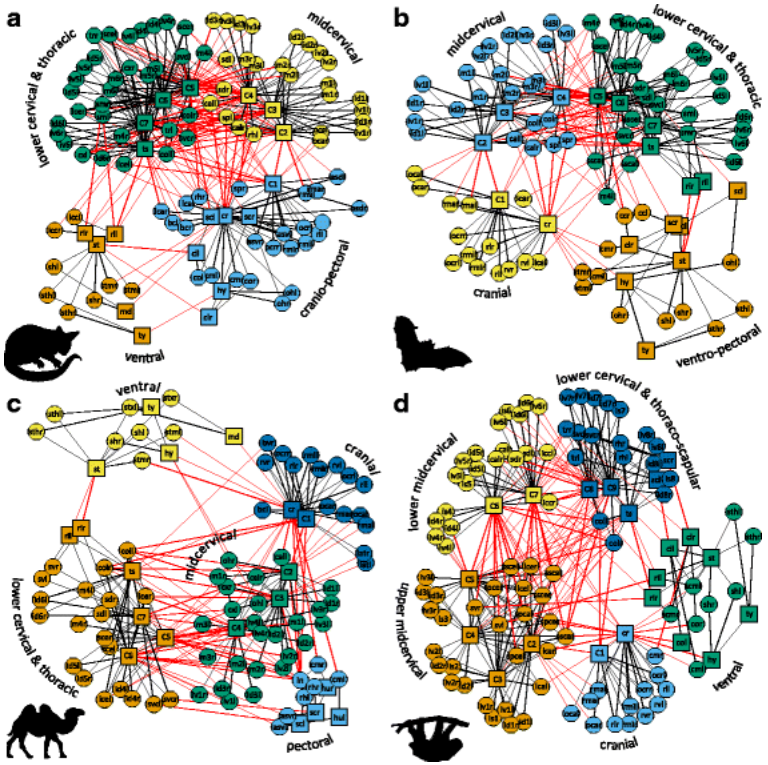
BMC Evolutionary Biology

RESEARCH ARTICLE Open Access

Musculoskeletal networks reveal topological disparity in mammalian neck evolution

Patrick Arnold[1,2*], Borja Esteve-Altava[3] and Martin S. Fischer[1]





Estimar taxas de evolução para diferentes módulos

Testar hipóteses de conjuntos modulares

Methods in Ecology and Evolution

Methods in Ecology and Evolution 2016, **7**, 565–572 doi: 10.1111/2041-210X.12511

Evaluating modularity in morphometric data: challenges with the RV coefficient and a new test measure

Dean C. Adams[1,2*]

ORIGINAL ARTICLE

doi:10.1111/evo.12743

A new phylogenetic test for comparing multiple high-dimensional evolutionary rates suggests interplay of evolutionary rates and modularity in lanternfishes (Myctophiformes; Myctophidae)

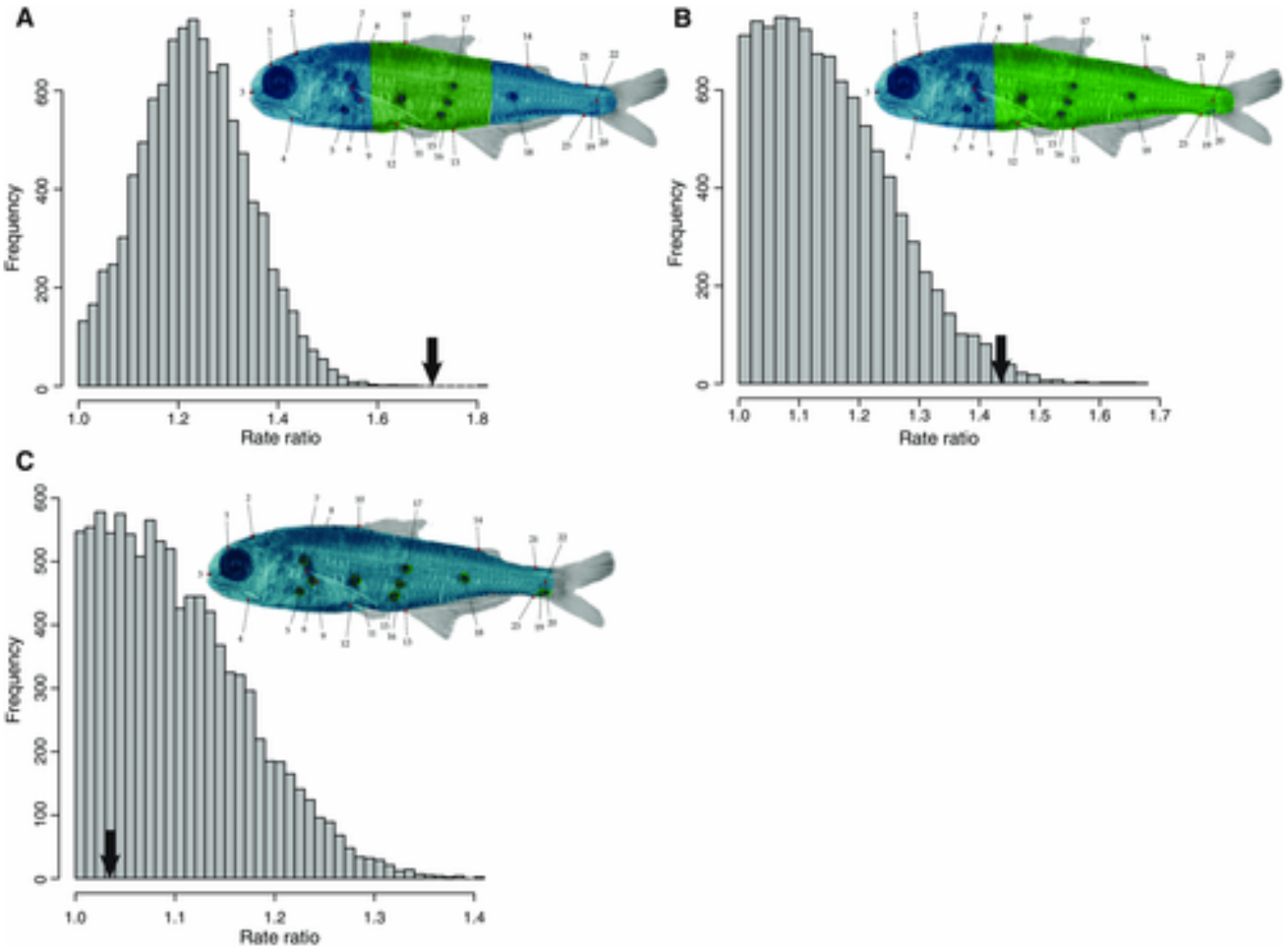
John S. S. Denton[1,2,3] and Dean C. Adams[4]

Testar taxas de evolução diferenciais para atributos envolvidos em módulos diferentes

Table 1. Hypotheses of modularity examined in this study, with landmark designations for each hypothesis and the predictions of each hypothesis with respect to relative rates, covariation, and modularity.

		Predictions		
Hypothesis	Landmarks in set	Rates	Covariation	Modularity
Growth gradients (H1)	**M1**: 1–9, 14, 18–23	$\sigma^2_{M1} > \sigma^2_{M2}$	–	H1
	M2: 10–13, 15–17			
Maneuverability/acceleration (H2)	**M1**: 1–9	$\sigma^2_{M1} \neq \sigma^2_{M2}$	–	H2
	M2: 10–23			
Information 1 (H3a)	**M1**: 1–4, 8–10, 12–14, 21–23	$\sigma^2_{M1} < \sigma^2_{M2}$	Strong	H3
	M2: 5–7, 11, 15–20			
Information 2 (H3b)		$\sigma^2_{M1} = \sigma^2_{M2}$	Weak or none	No prediction
Information 3 (H3c)		$\sigma^2_{M1} = \sigma^2_{M2}$	Strong	H1 or H2

A new phylogenetic test for comparing multiple high-dimensional evolutionary rates suggests interplay of evolutionary rates and modularity in lanternfishes (Myctophiformes; Myctophidae)



A new phylogenetic test for comparing multiple high-dimensional evolutionary rates suggests interplay of evolutionary rates and modularity in lanternfishes (Myctophiformes; Myctophidae), Volume: 69, Issue: 9, Pages: 2425-2440, First published: 17 August 2015, DOI: (10.1111/evo.12743)

Vidal-García and Scott Keogh *BMC Evolutionary Biology* (2017) 17:165
DOI 10.1186/s12862-017-0993-0

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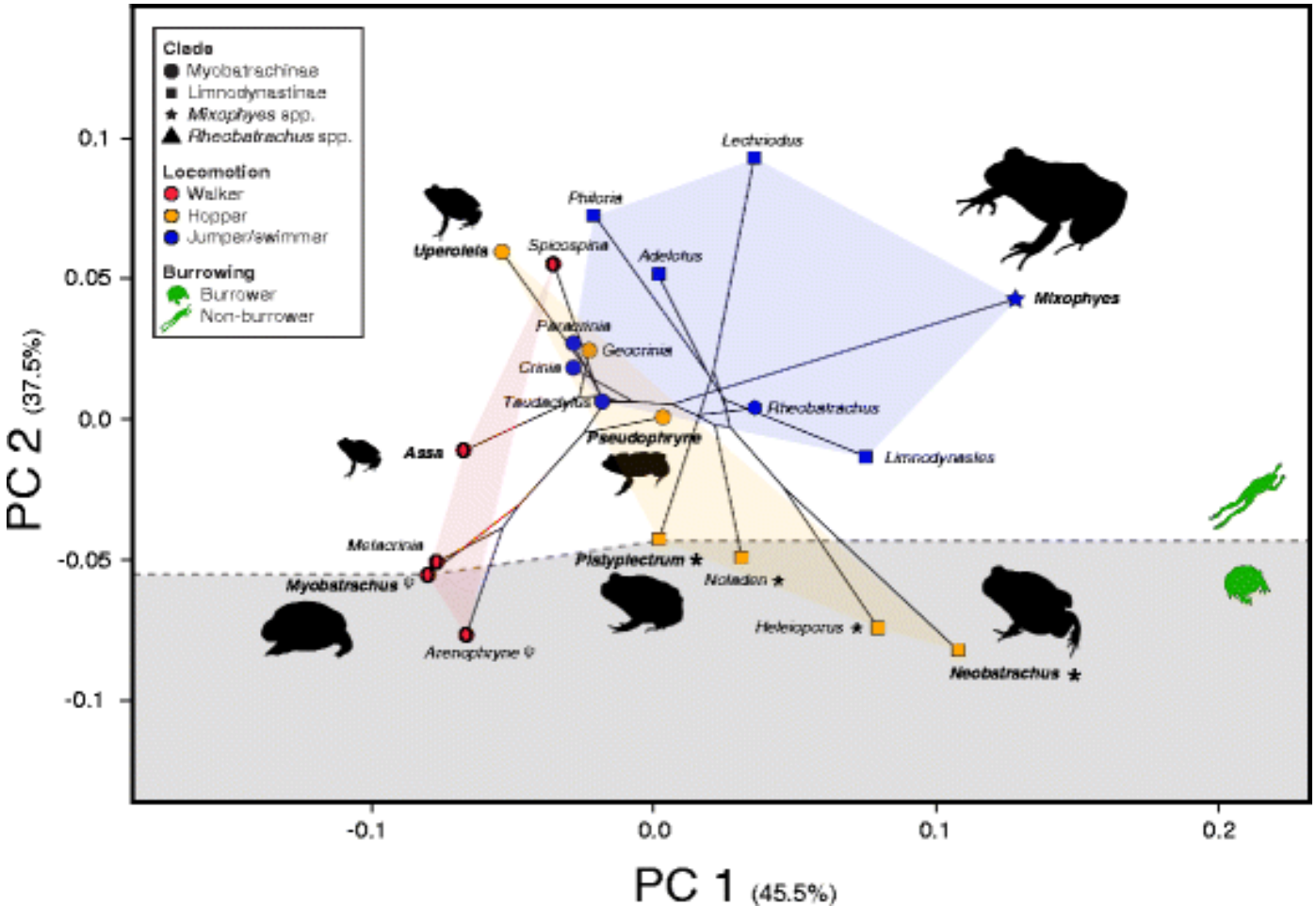
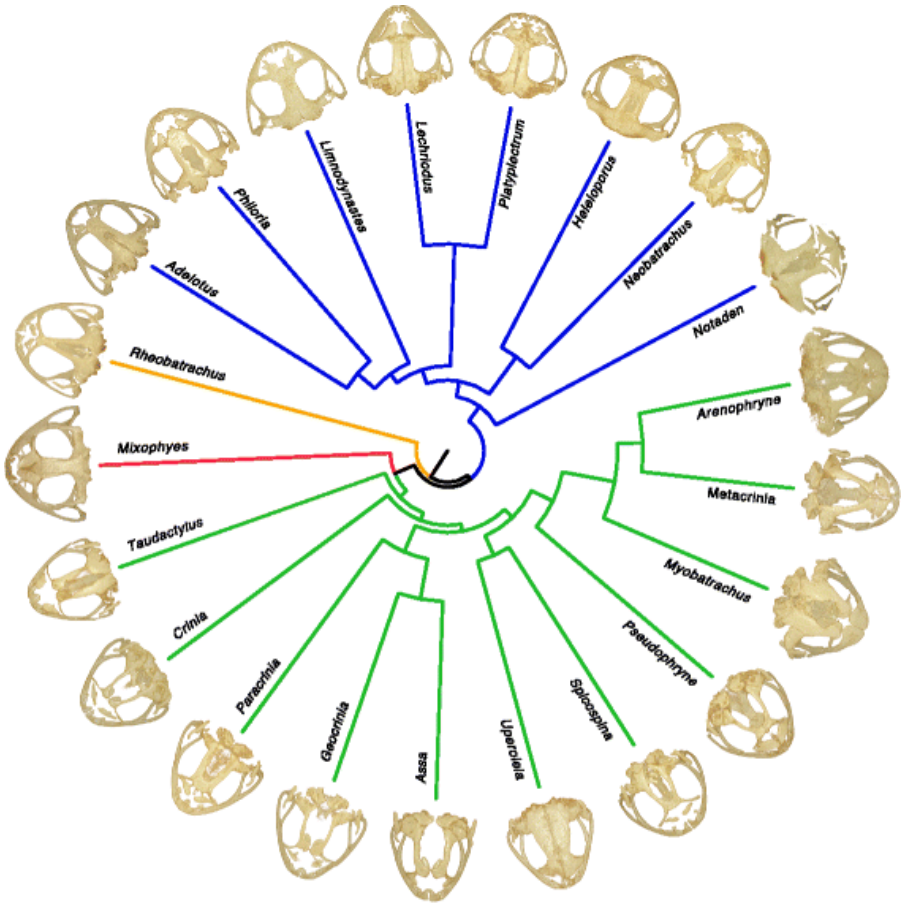
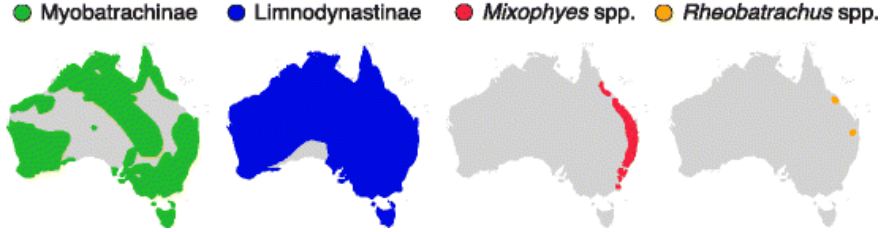
RESEARCH ARTICLE Open Access

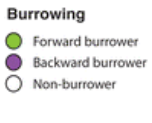
Phylogenetic conservatism in skulls and evolutionary lability in limbs – morphological evolution across an ancient frog radiation is shaped by diet, locomotion and burrowing

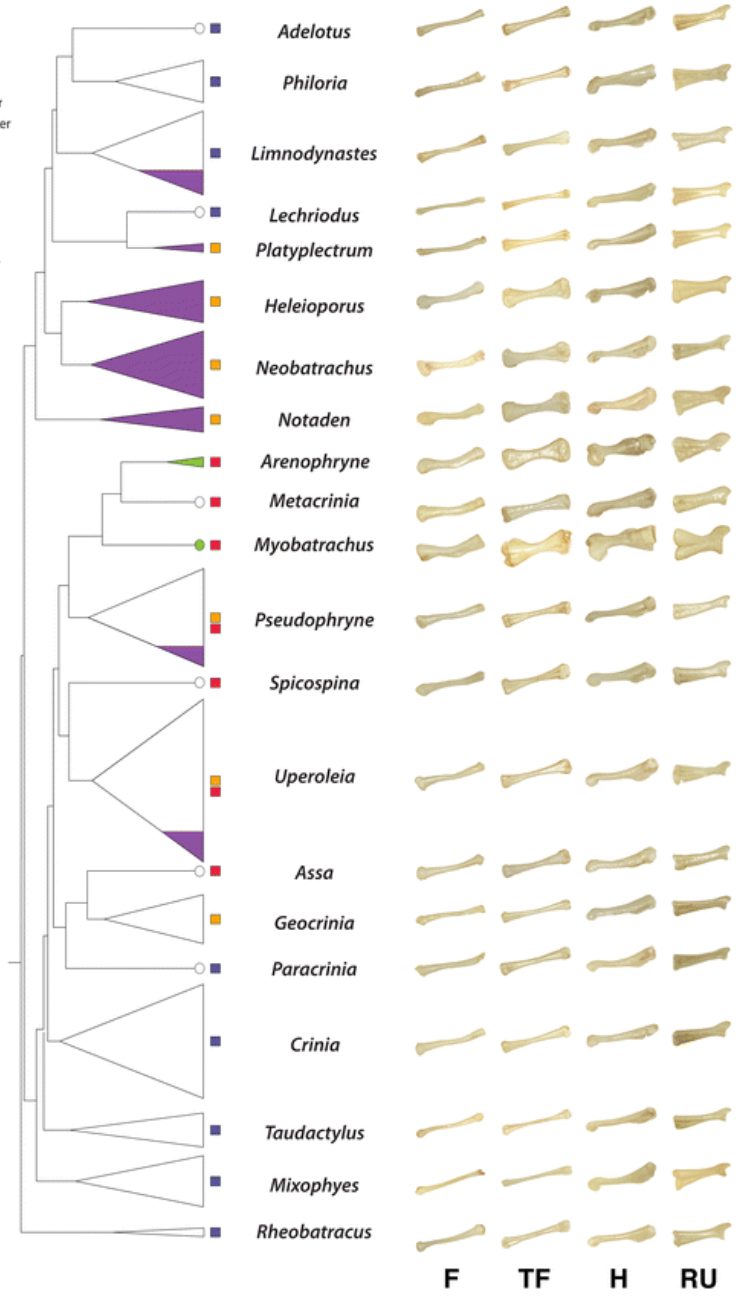
Marta Vidal-García* and J. Scott Keogh




Adelotus
Philoria
Limnodynastes
Lechriodus
Platyplectrum
Heleioporus
Neobatrachus
Notaden
Arenophryne
Metacrinia
Myobatrachus
Pseudophryne
Spicospina
Uperoleia
Assa
Geocrinia
Paracrinia
Crinia
Taudactylus
Mixophyes
Rheobatrachus


Myobatrachinae
Limnodynastinae
Mixophyes spp.
Rheobatrachus spp.


Burrowing
Forward burrower
Backward burrower
Non-burrower
Locomotor mode
Walker
Hopper
Jumper/swimmer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Spicospina
Uperoleia
Assa
Geocrinia
Paracrinia
Crinia
Taudactylus
Mixophyes
Rheobatracus
F
TF
H
RU