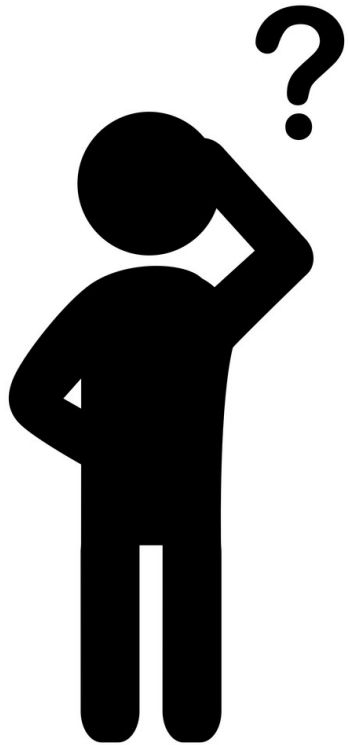# Detectando Modularidade

‘Modularidade: Conectando padrões e processos em evolução multivariada’

Monique N. Simon
IB – USP
monique.simon@usp.br

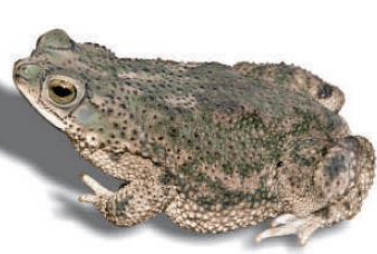# Why study variation in biology?

Where does variation comes from?

How is variation organized in populations?

What are the evolutionary consequences of a particular organization of variation?

Rhinella granulosa species complex

R. major *R. azarai* *R. bergi* *R. bernardoi*

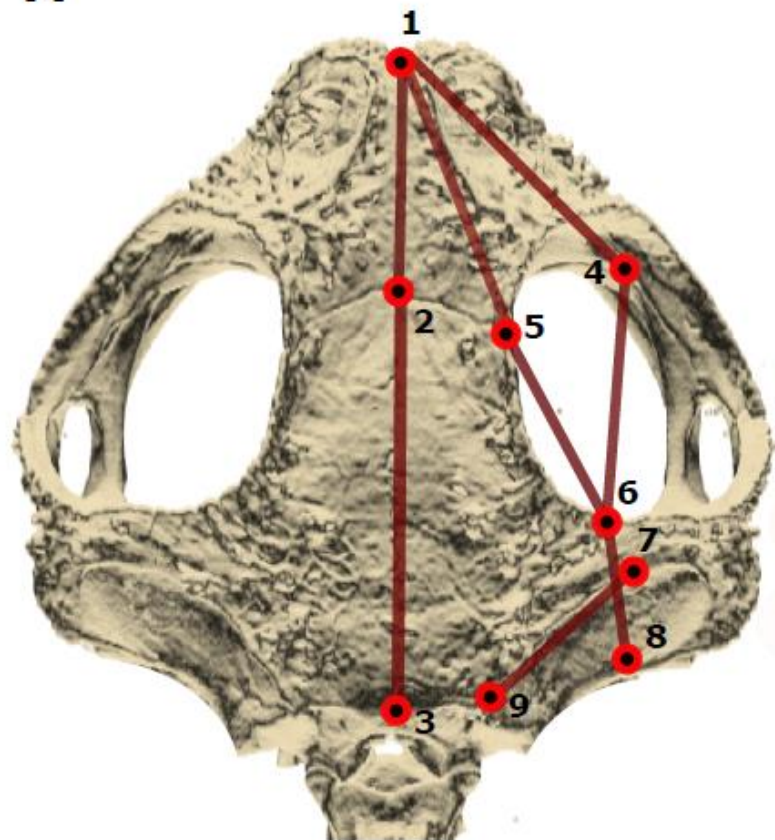*R. dorbignyi* *R. fernandezae* *R. pygmaea* *R.centralis*
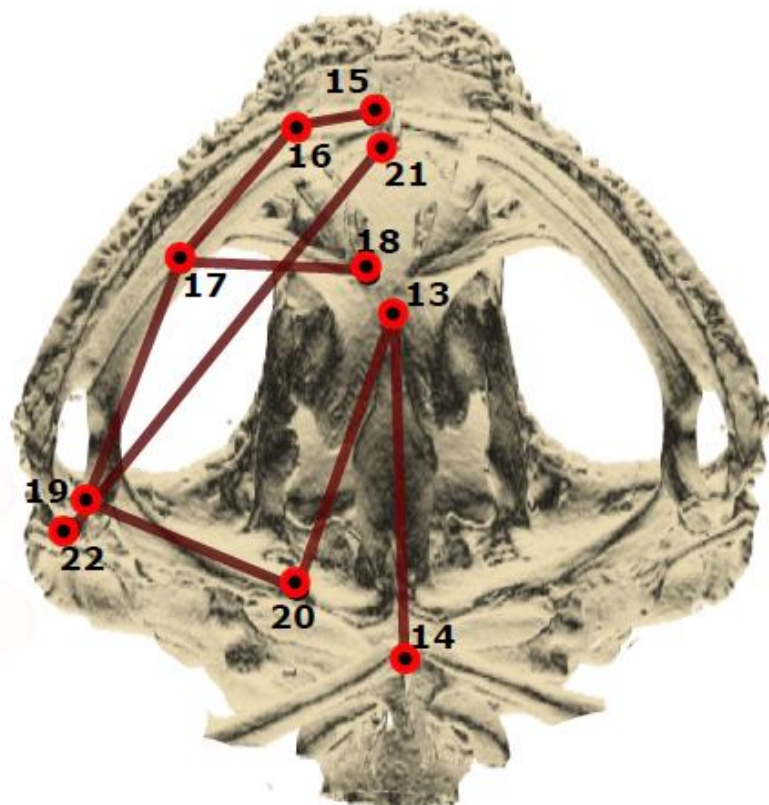
R.humboldti *R.merianae* *R.granulosa* *R.mirandaribeiroi*
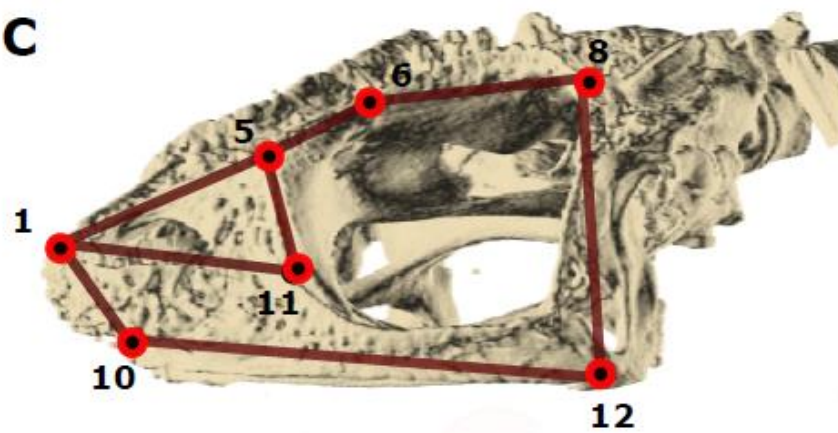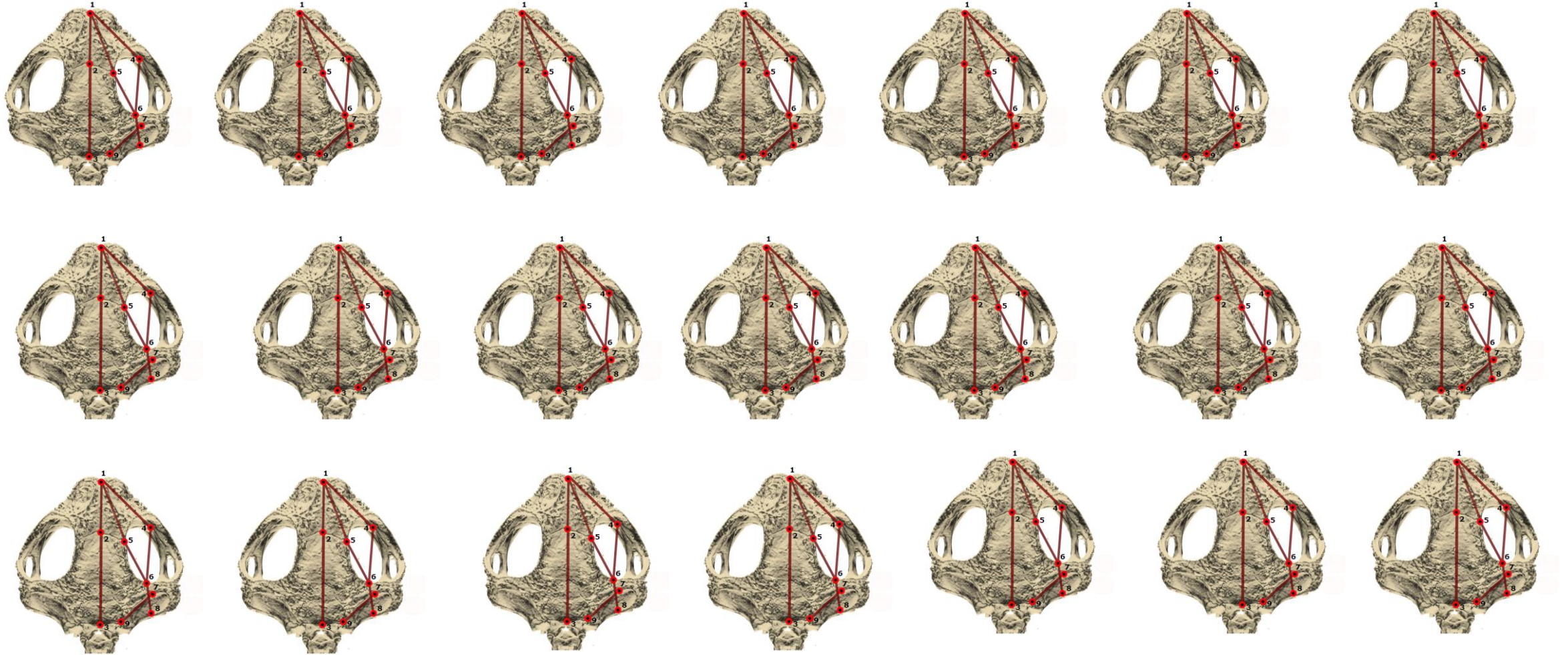
Measuring traits in populations: Variational modularity

Estimating covariance P-matrix
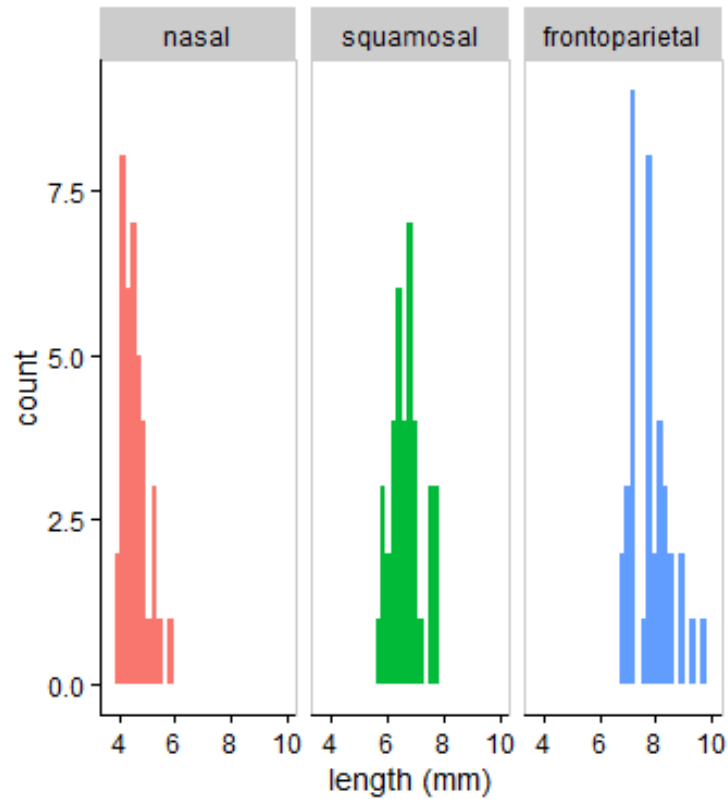
$$\text{Cov}(X, Y) = \frac{\sum(X_i - \overline{X})(Y_j - \overline{Y})}{n}$$

Estimating correlational P-matrix

High integration

Low integration
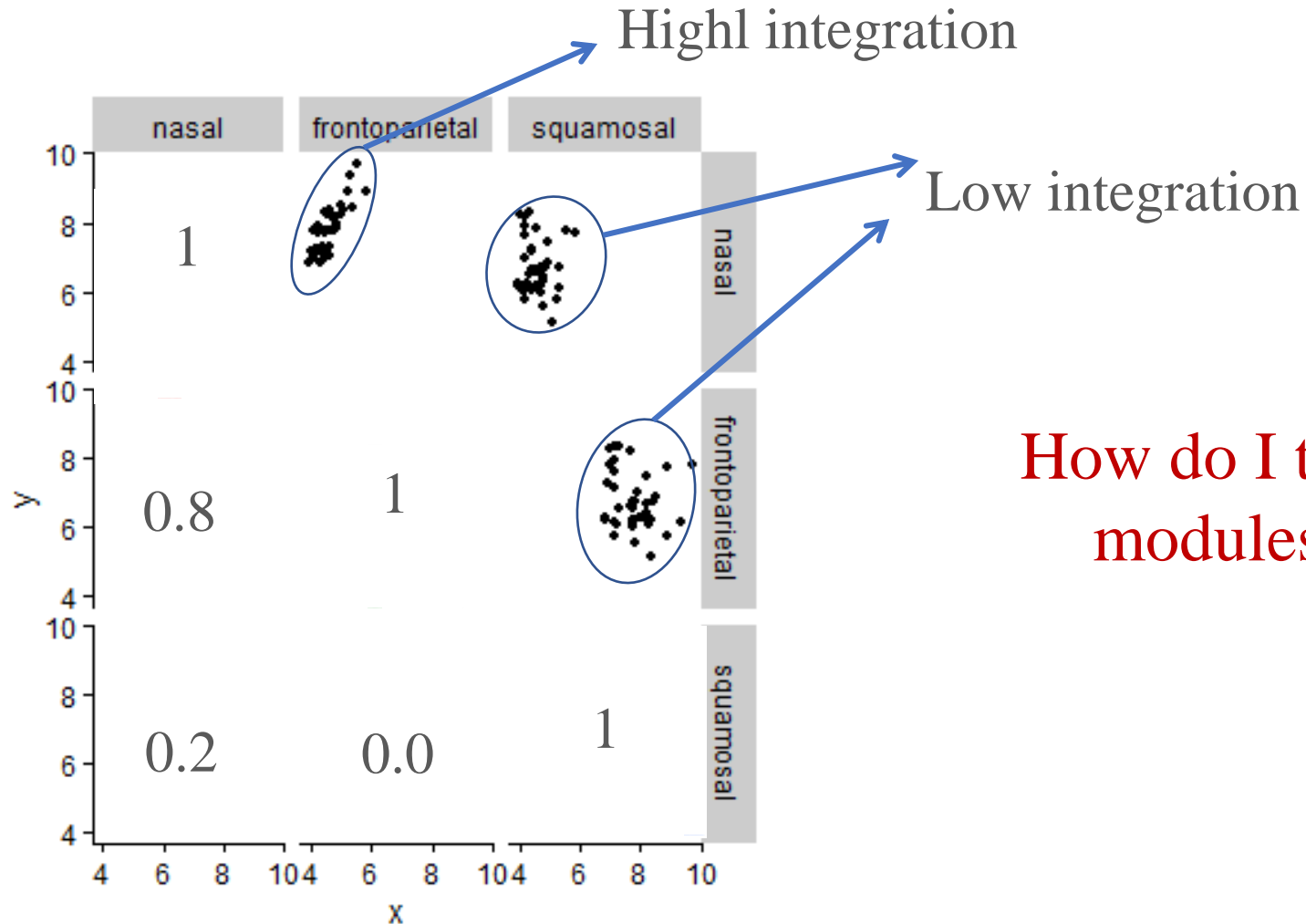
$$r = r_{xy} = \frac{\text{Cov}(x, y)}{S_x \times S_y}$$

How do I test for the existence of modules using correlations?

Estimating correlational P-matrix

$$r = r_{xy} = \frac{\text{Cov}(x, y)}{S_x \times S_y}$$

How do I test for the existence of modules using correlations?

Expectation: correlations within a module are higher than correlations between-modules.

Modularity hypothesis

Development

Constructing a theoretical modularity matrix

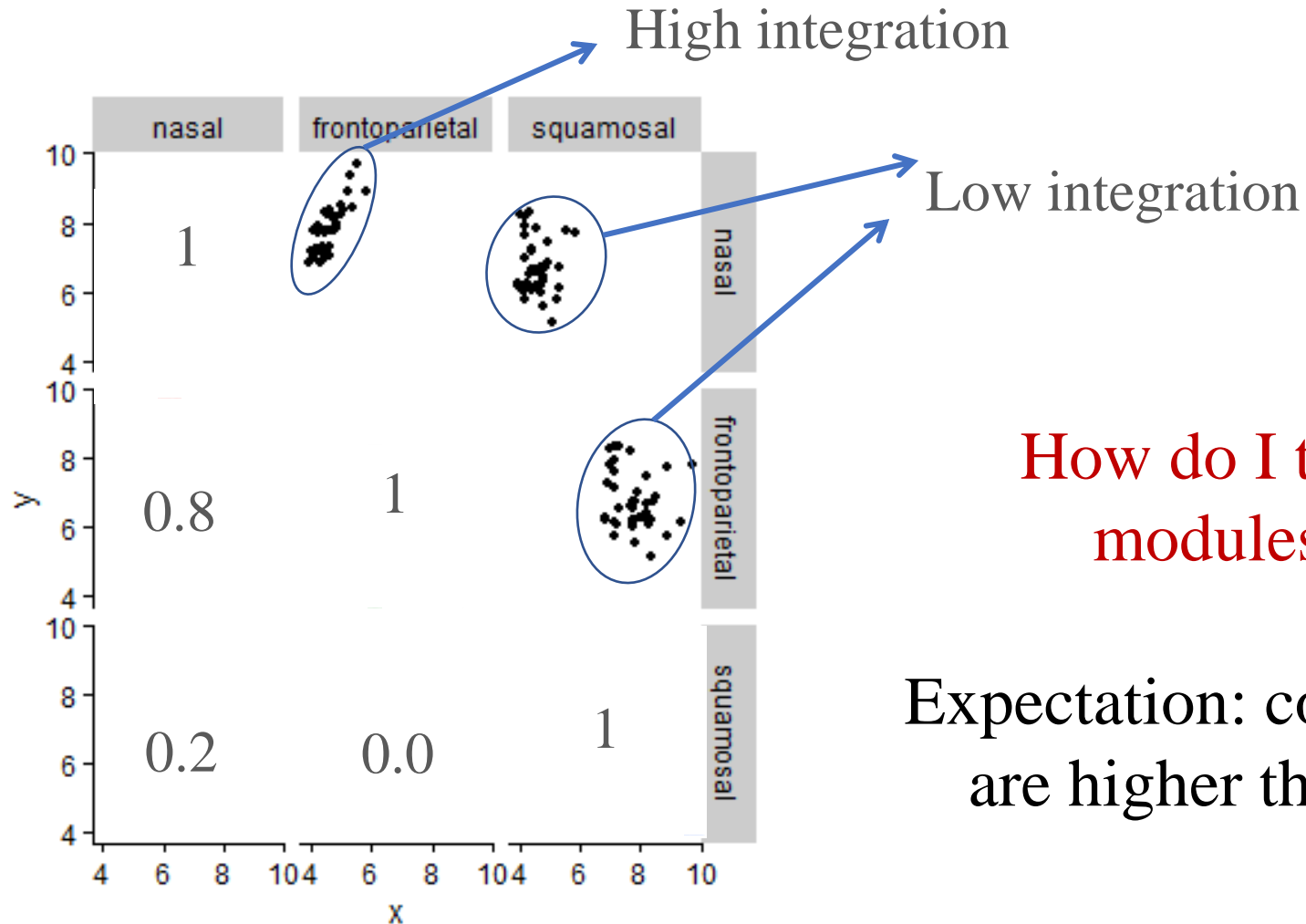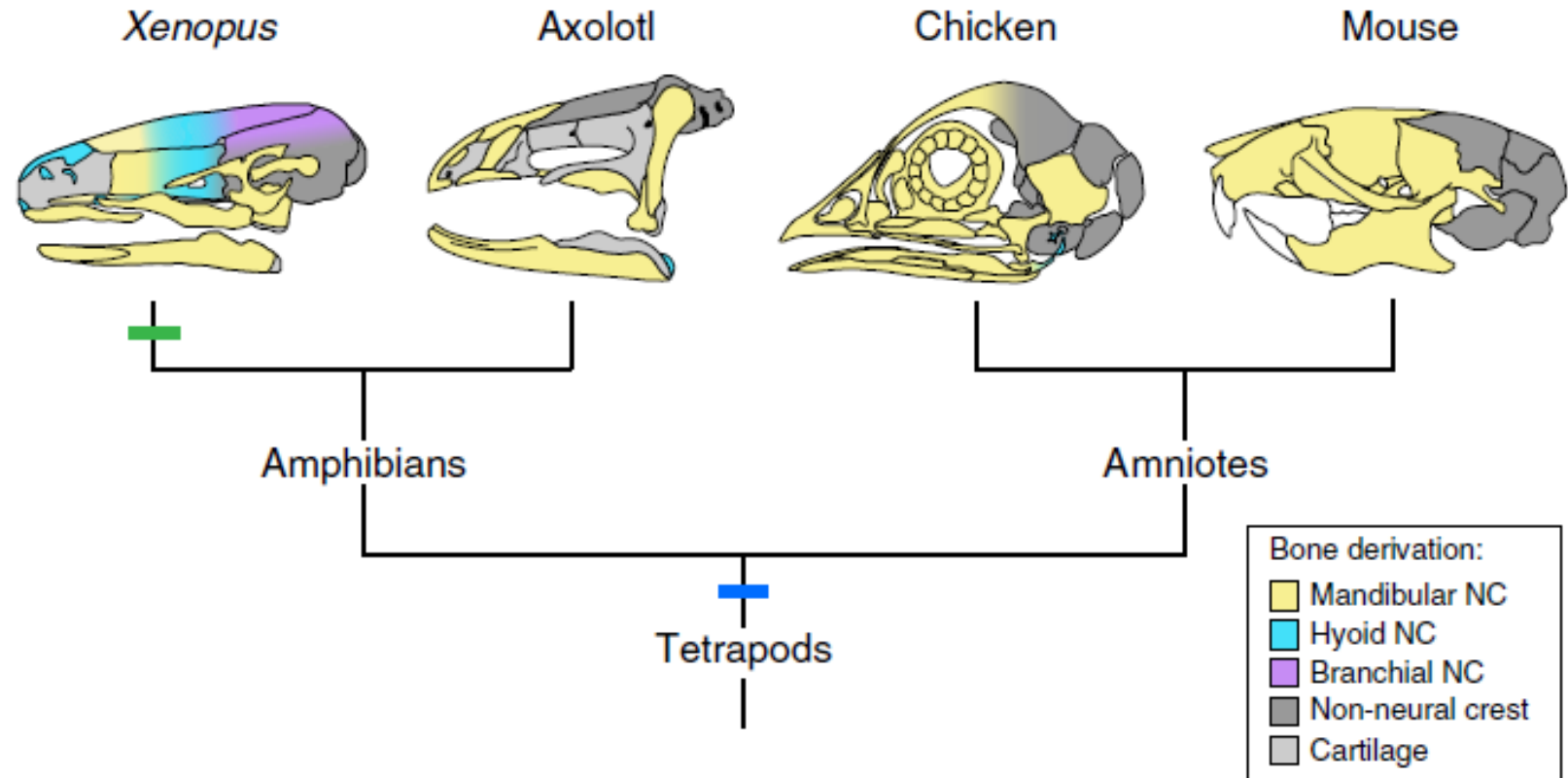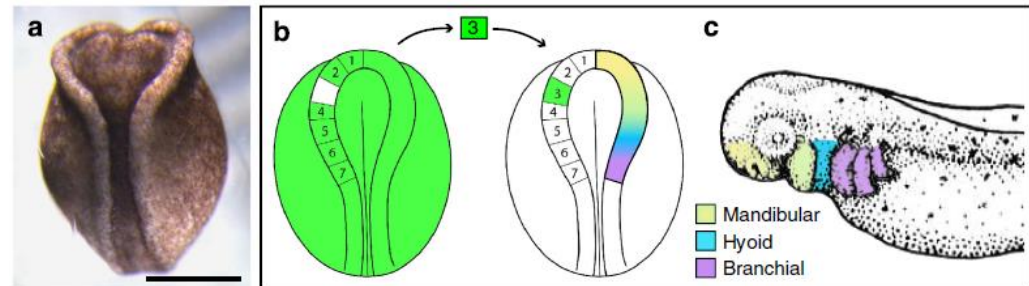| Bones	Mandibular	Hyoid	Branchial
nasal	0	1	0
frontoparietal	1	1	1
nasal	0	1	0
nasal	0	1	0
frontoparietal	1	1	1
orbit	-	-	-
squamosal	1	0	0
occipital	0	0	1
prenasal	-	-	-
nasal	0	1	0
nasal	0	1	0
maxilla	1	0	0
squamosal	1	0	0
parasphenoid	1	1	0
parasphenoid	1	1	0
premaxilla	1	1	0
maxilla	1	0	0
neopalatine	-	-	-
pterygoid	1	0	0
pterygoid	1	0	0
mandible	-	-	-

	nasal	frontoparietal	nasal	nasal	frontoparietal
nasal	0	0	0	0	0
frontoparietal	0	1	0	0	1
nasal	0	0	0	0	0
nasal	0	0	0	0	0
frontoparietal	0	1	0	0	1

	nasal	frontoparietal	nasal	nasal	frontoparietal
nasal	1	1	1	1	1
frontoparietal	1	1	1	1	1
nasal	1	1	1	1	1
nasal	1	1	1	1	1
frontoparietal	1	1	1	1	1

	nasal	maxilla	squamosal	parasphenoid	parasphenoid
nasal	0	0	0	0	0
maxilla	0	0	0	0	0
squamosal	0	0	0	0	0
parasphenoid	0	0	0	0	0
parasphenoid	0	0	0	0	0

Average correlations within (AVG+) and between (AVG-) hypothetical modules
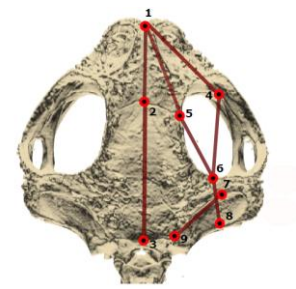
Theoretical matrix

	nasal	frontoparietal	nasal	nasal
nasal				
frontoparietal	0			
nasal	0	0		
nasal	0	0	0	
frontoparietal	0	1	0	0

Part of AVG+ set

Part of AVG- set

Empirical matrix

	nasal	frontoparietal	nasal	nasal
nasal				
frontoparietal	0.717			
nasal	0.842	0.831		
nasal	0.936	0.800	0.852	
frontoparietal	0.698	0.775	0.760	0.623

AVG+ = 0.775

AVG- = 0.784

Is AVG+ higher than AVG-?

Mantel test: matrix permutations
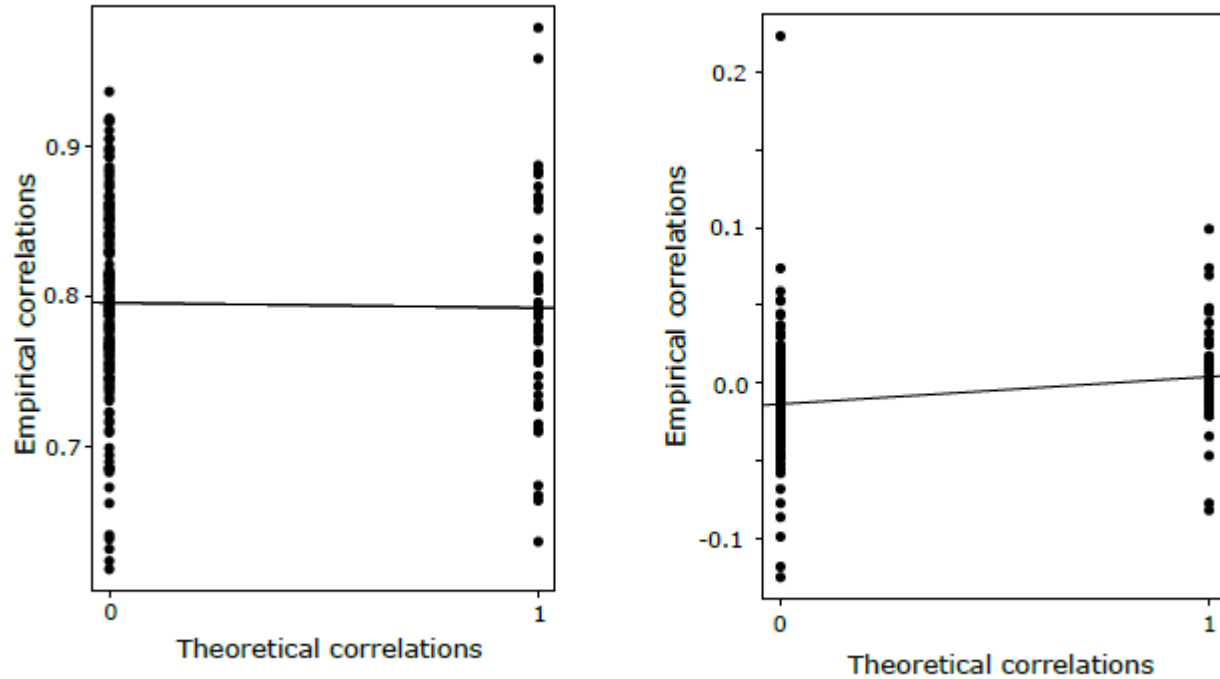
Matrix correlation of
correlation matrices!

Distribution of random
matrix correlations

A

Branchial — 10 ssp

Hyoid — 2 ssp

Mandibular — 4 ssp

Total Development — 2 ssp

Average residual correlation

R. centralis, R. humboldti, R. merianae, R. granulosa, R. mirandaribeiroi, R. major, R. bergi, R. pygmaea, R. dorbignyi, R. fernandezae, R. margaritifera

Mandibular
Hyoid
Branchial
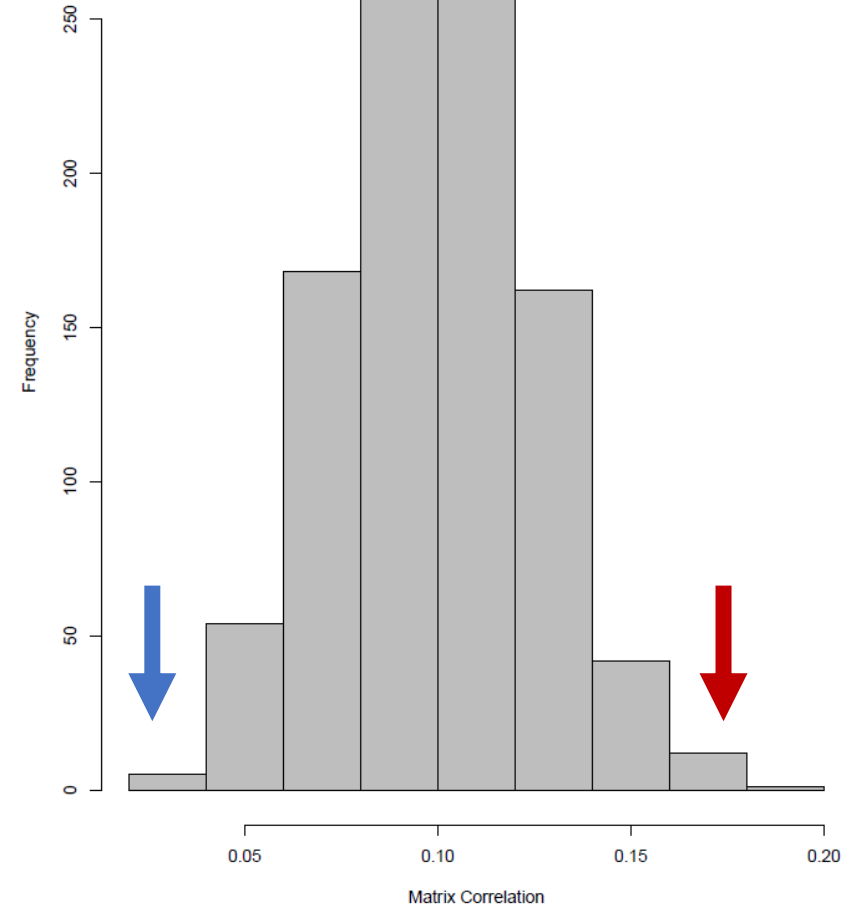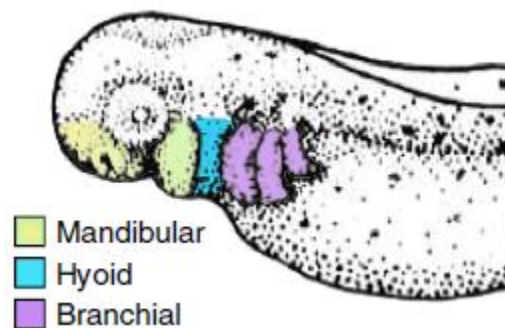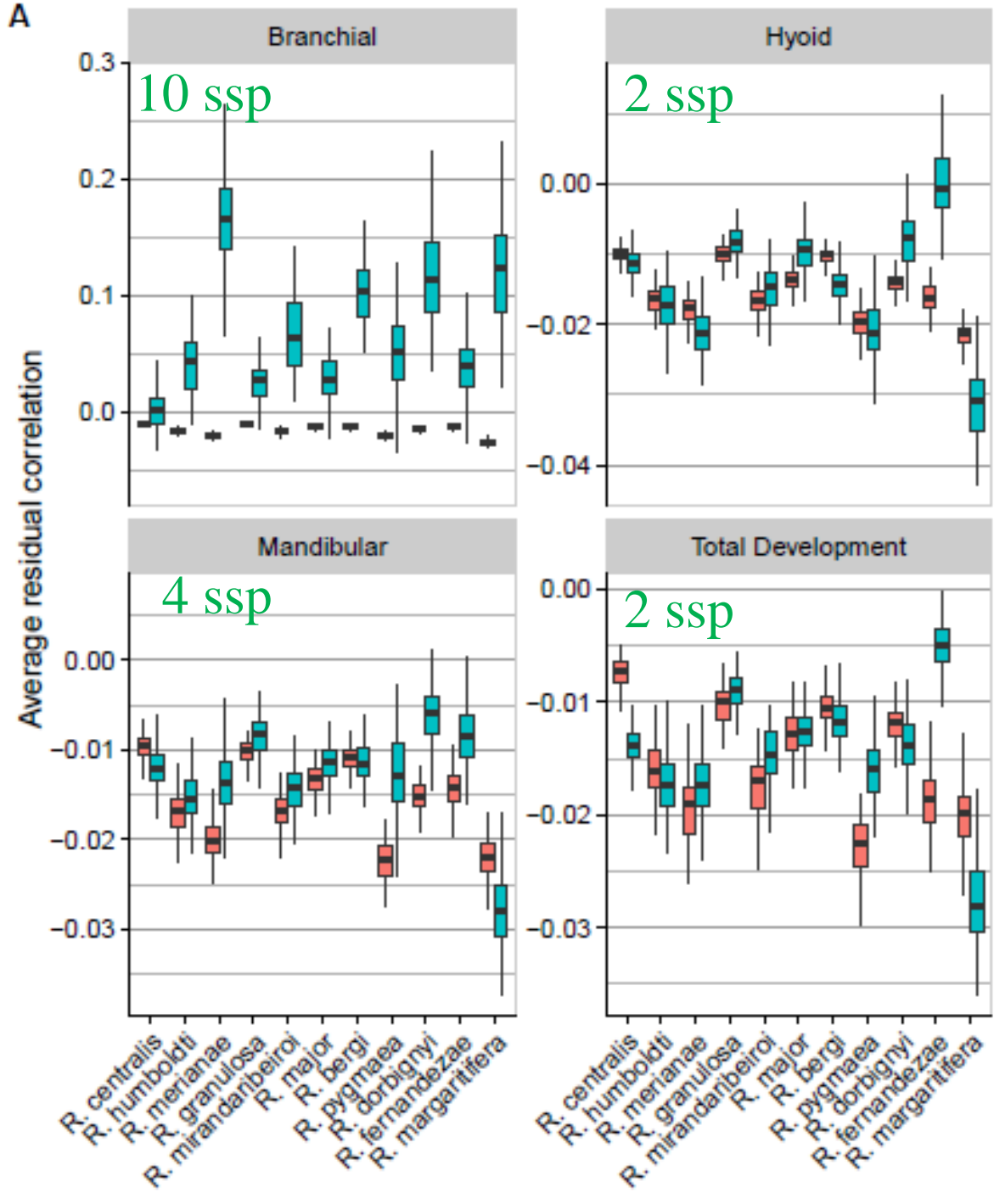
What about using geometric morphometrics to test for modularity?

Morphometric integration and modularity in configurations of landmarks: tools for evaluating a priori hypotheses

Christian Peter Klingenberg

Alveolar region

Ascending ramus

Hypothesis about boundaries of modules
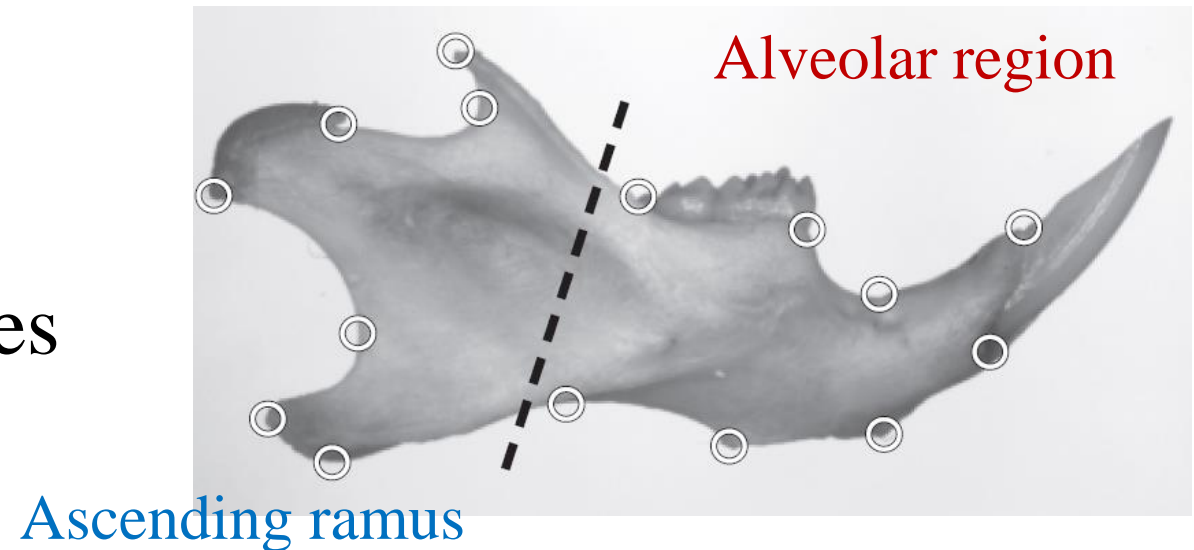
Different partitions of sets of landmarks
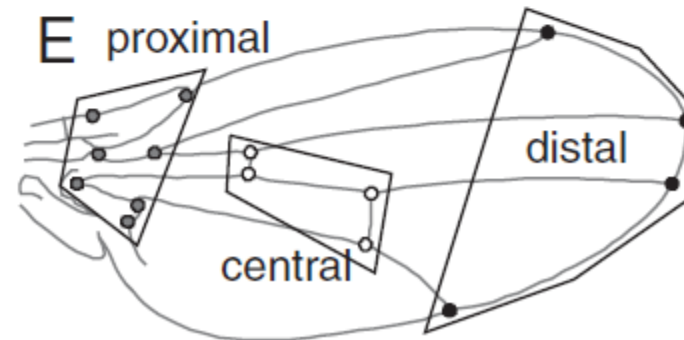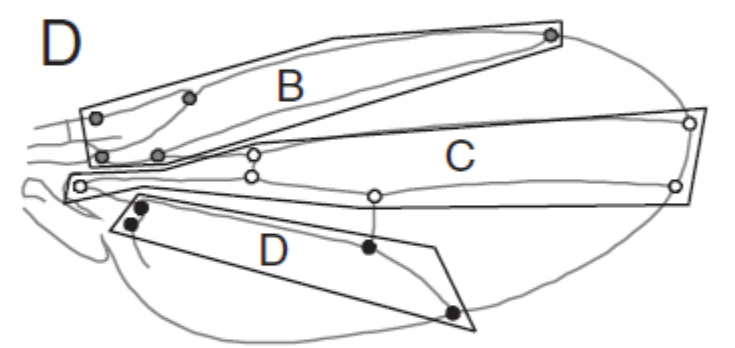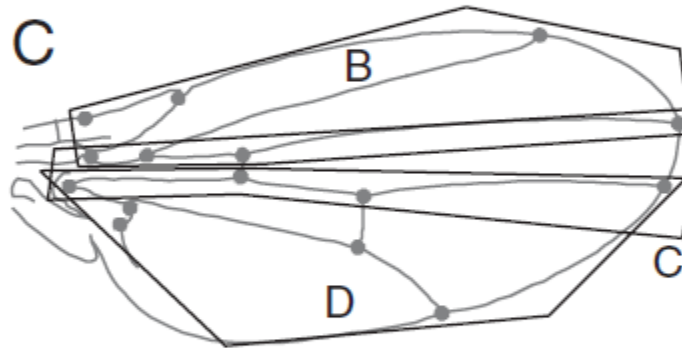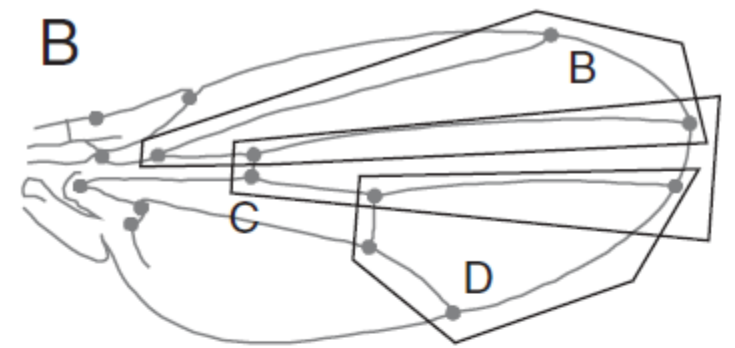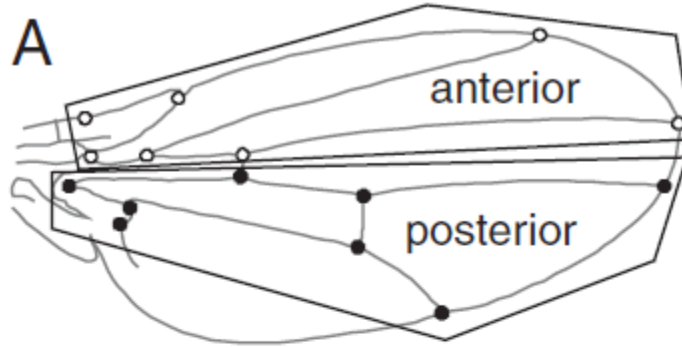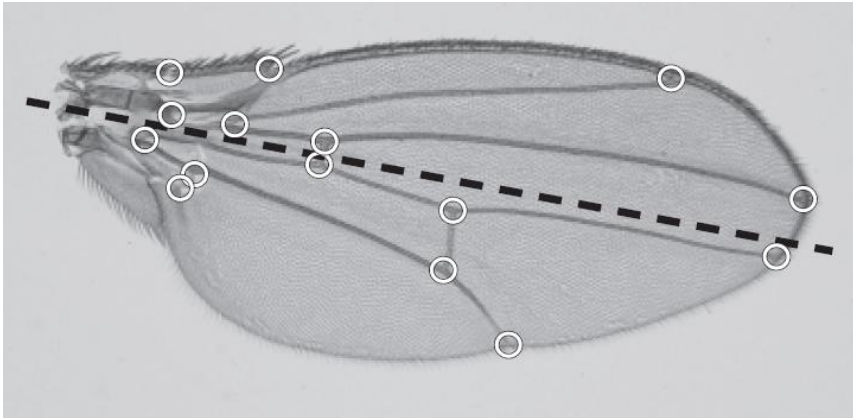
RV coefficient

Expectation: covariation between partitions corresponding to true modules should be lower than arbitrary partitions.

Sum of squared covariances between-partitions

Covariance matrices within each partition

$$\mathbf{S} = \begin{bmatrix} \mathbf{S}_1 & \mathbf{S}_{12} \\ \mathbf{S}_{21} & \mathbf{S}_2 \end{bmatrix}$$

Covariance matrices between-partition

$$RV = \frac{\mathrm{trace}(\mathbf{S}_{12}\mathbf{S}_{21})}{\sqrt{\mathrm{trace}(\mathbf{S}_1\mathbf{S}_1)\mathrm{trace}(\mathbf{S}_2\mathbf{S}_2)}}$$

Sum of squared covariances within-partitions

RV: measures the strength of association between the coordinates of two sets of landmarks.

Permutations of landmarks across partitions

Null distribution of RV coefficients: complete independence between subsets
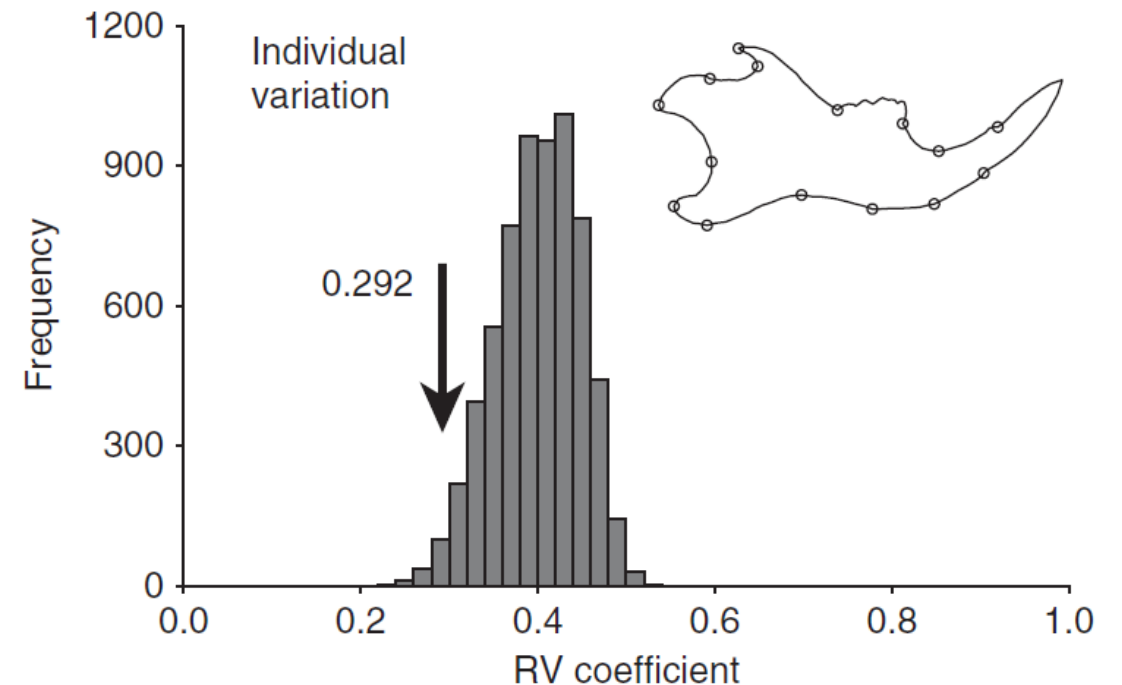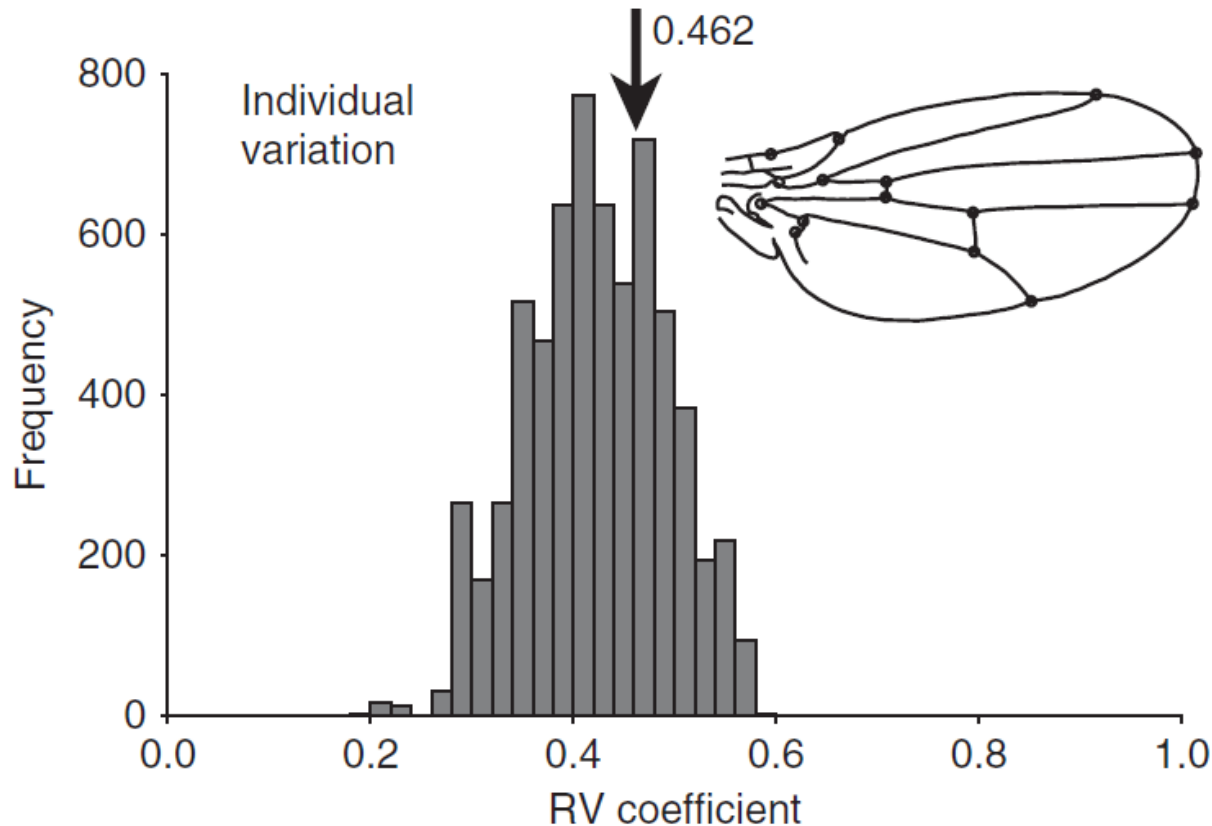
More than two partitions

E proximal

distal

central
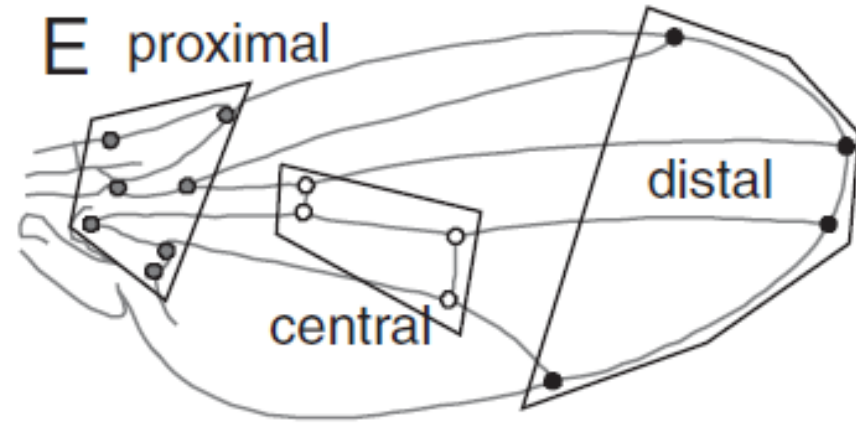
Multi-set RV coefficient = average of all pair-wise RV coefficients between sets

$$RV_{\mathrm{M}} = \frac{2}{k(k-1)} \sum_{i=1}^{k-1} \sum_{j=i+1}^{k} RV(i,j).$$

| Comparison | Variation among individuals | | | |
| | Joint Procrustes fit | | Separate Procrustes fits | |
	RV_{M}	P	RV_{M}	P
(D) Mutually exclusive wing sectors				
All three subsets	0.312	<0.0001	0.124	<0.0001
(E) Proximal, central and distal regions				
All three subsets	0.271	<0.0001	0.087	<0.0001

Competing modularity models
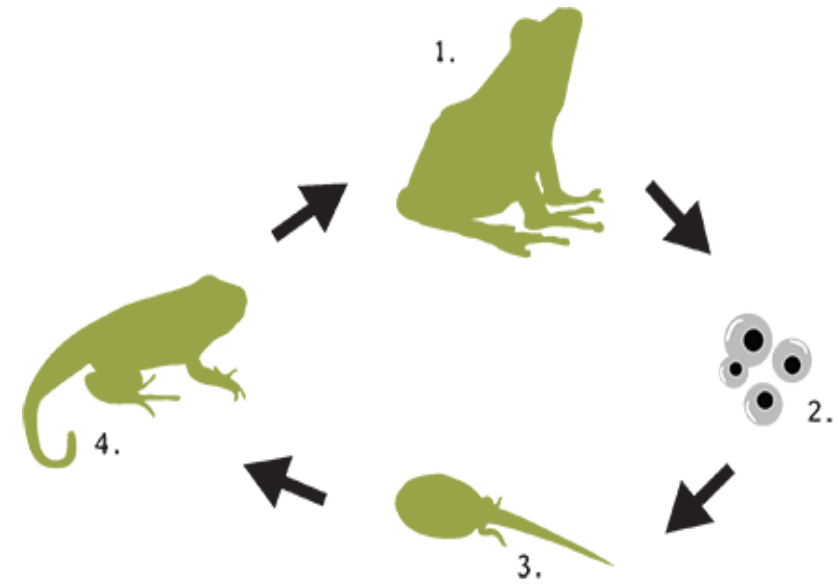
ORIGINAL RESEARCH

Evolution of a complex phenotype with biphasic ontogeny: Contribution of development versus function and climatic variation to skull modularity in toads

Monique Nouailhetas Simon | Gabriel Marroig

1. Neural Crest Migration

2. Neural Crest Patterning and Proliferation

3. Facial Process Fusion

4. Condensation and Differentiation

5. Cartilage Growth

6. Brain Growth

7. Muscle Bone Interactions

8. Somatic Growth

IGF Dependent   Growth Hormone Dependent

Prenatal   Postnatal

Conception   Ontogeny   Adult
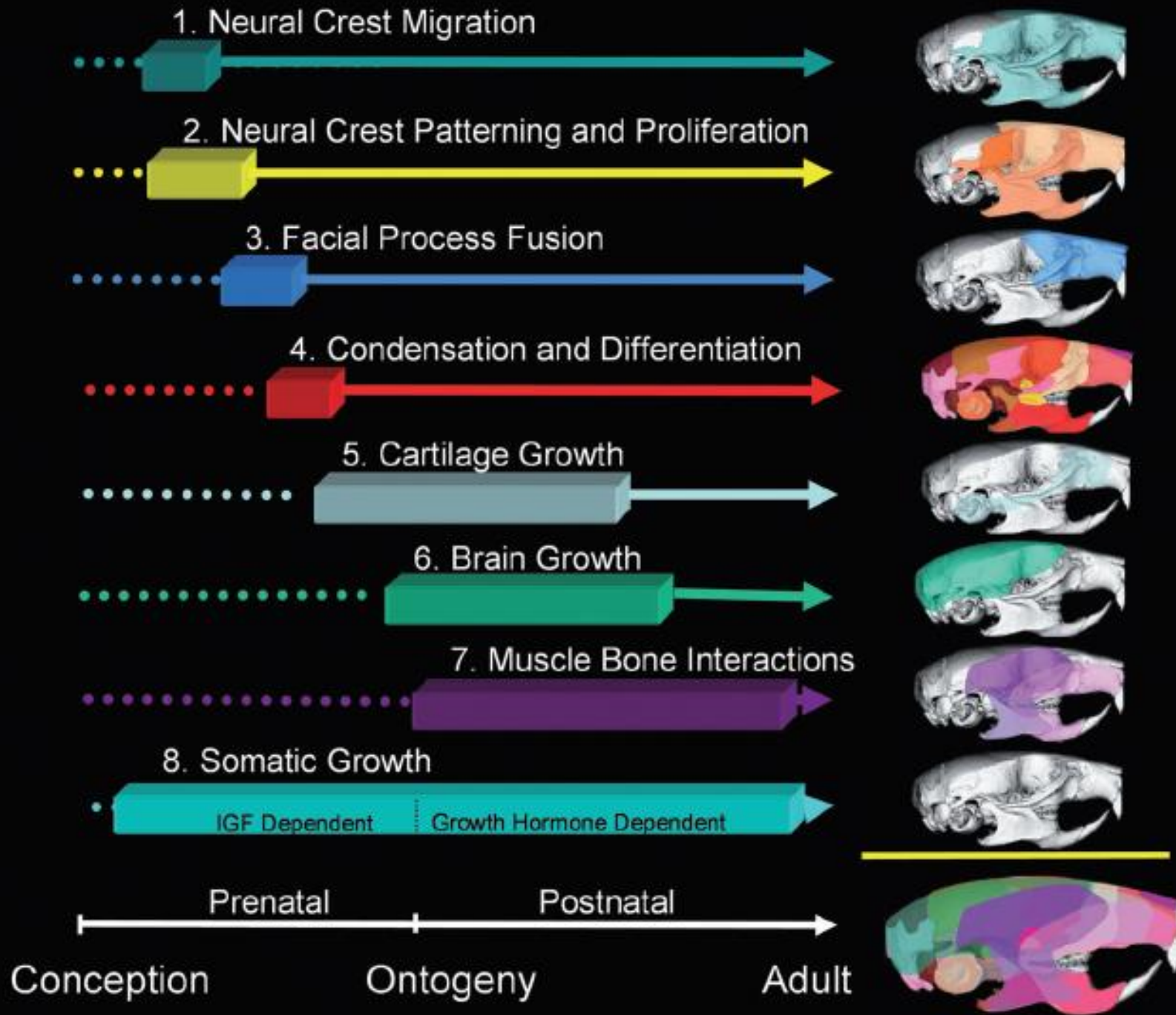
Biphasic Ontogeny

Terrestrial phase
Muscle-bone interactions
TH-driven differentiation
Somatic growth

Rupture in the timing of development

Aquatic phase
CNC migration

Metamorphosis
Extreme remodeling of the skull
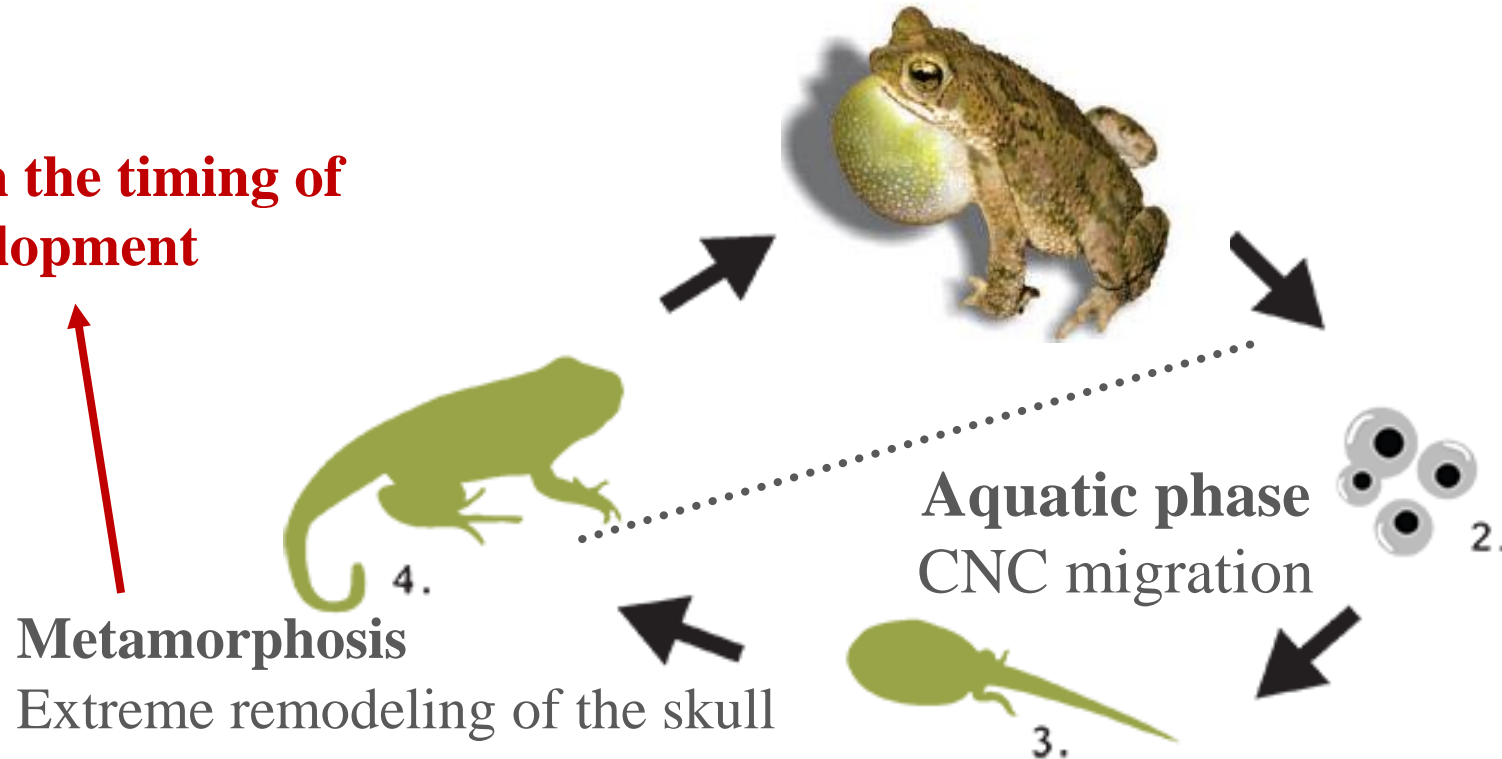
Hypothesis

Functional demands of the newly formed adult skull imposes a correlation pattern among skull traits that overrides the modularity signal due to earlier developmental porcesses.

Expecation: Stronger signal of functional than of developmental modularity in the adult skull of toads.
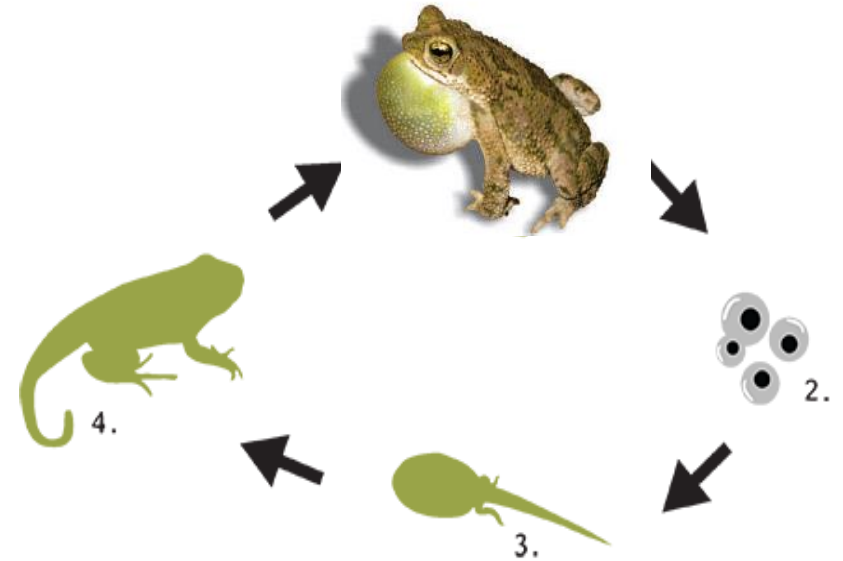
Modularity Models

DEVELOPMENT

Branchial

Hyoid

Mandibular

Mandibular
Hyoid
Branchial
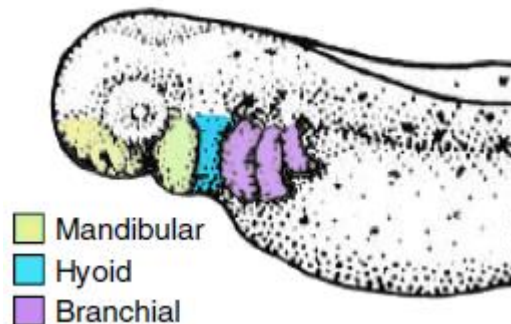
HORMONAL

T3 +

T3 ++

T3 +++
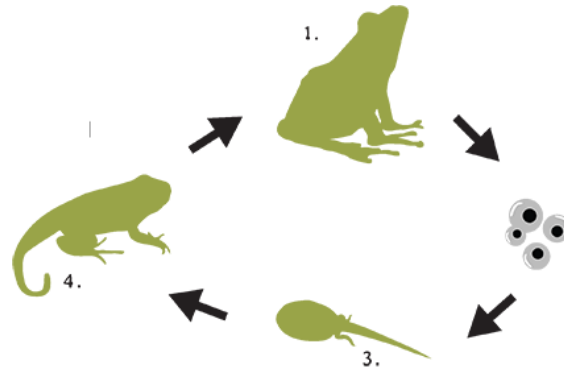
FUNCTIONAL

Neurocranium

Roof

Snout

Suspensorium

Orbit

Vomerine teeth — Maxillary teeth — Internal nostrils — Eustachian tube — Glottis — Esophagus — Tongue
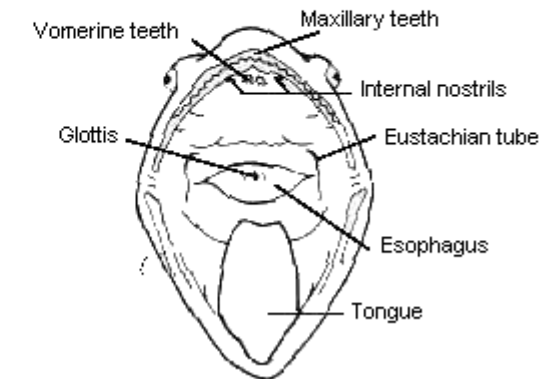
EMMLi: A maximum likelihood approach to the analysis of modularity

Anjali Goswami[1,2,3] and John A. Finarelli[4,5,6]

Modularity tests with a null hypothesis do not allow direct comparisons of distinct modularity models.

EMMLi = Evaluating Modularity with Maximum Likelihood

ML finds the value of θ that maximizes the $£(\theta, x)$: parameter that makes the data most probable

Modularity models with different complexities

squared diff between observed correlation values and mean populational correlation

$$LogL \propto -\frac{1}{2} Ln\left(\sigma_\rho{}^2\right) - \frac{(z_r - \mu_\rho)^2}{2\sigma_\rho{}^2}$$

variance in true correlation coefficient
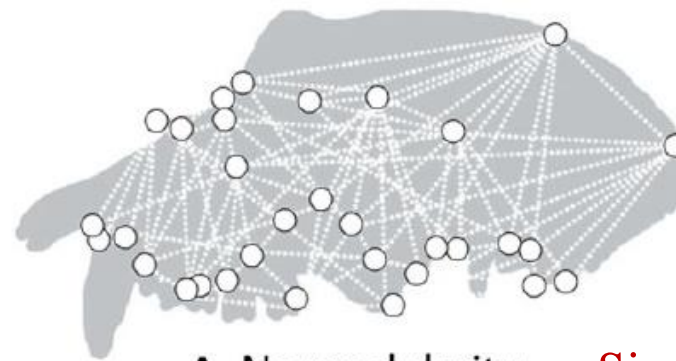
A No modularity

Single value for correlations among all traits
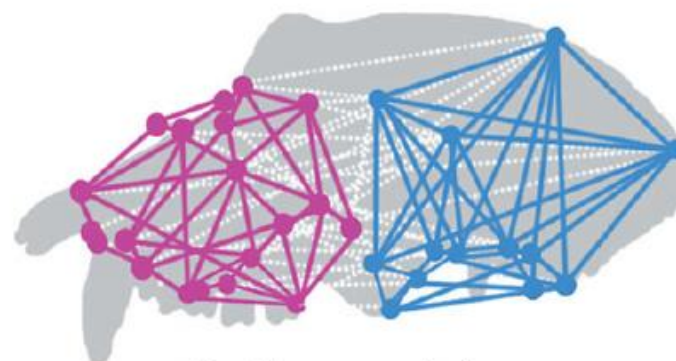
B Two modules

Different values for correlations within and between hypothetical modules
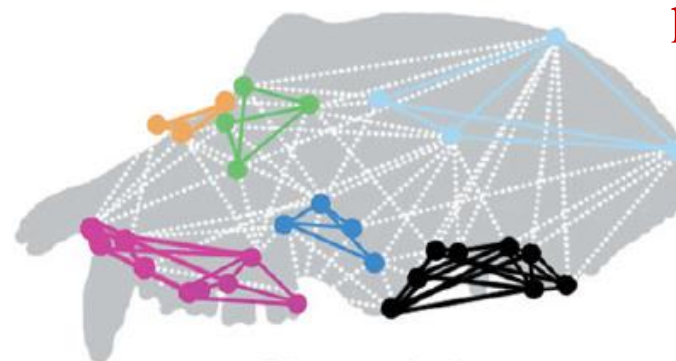
C Six modules

Comparing models with different complexities

Model LogL = sum of LogL for the set of observed correlations
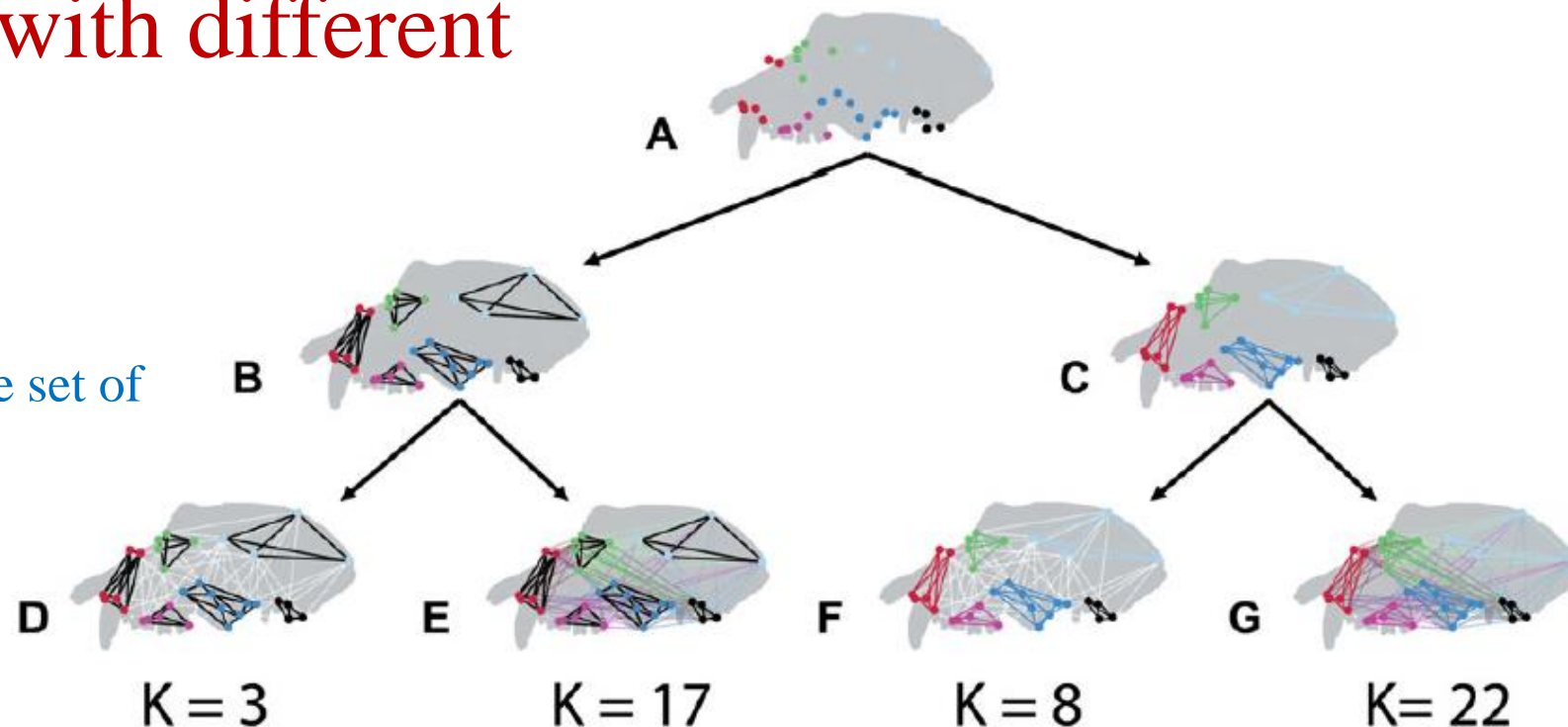
K = 3   K = 17   K = 8   K= 22

$$AIC_c = -2LogL + 2K + \frac{2K\ (K+1)}{N-K-1}$$

number of distinct optimal correlations

number of between-trait correlations

$$Model\ LogL \propto -\frac{1}{2}\Delta AIC_c$$

Comparing models with different complexities
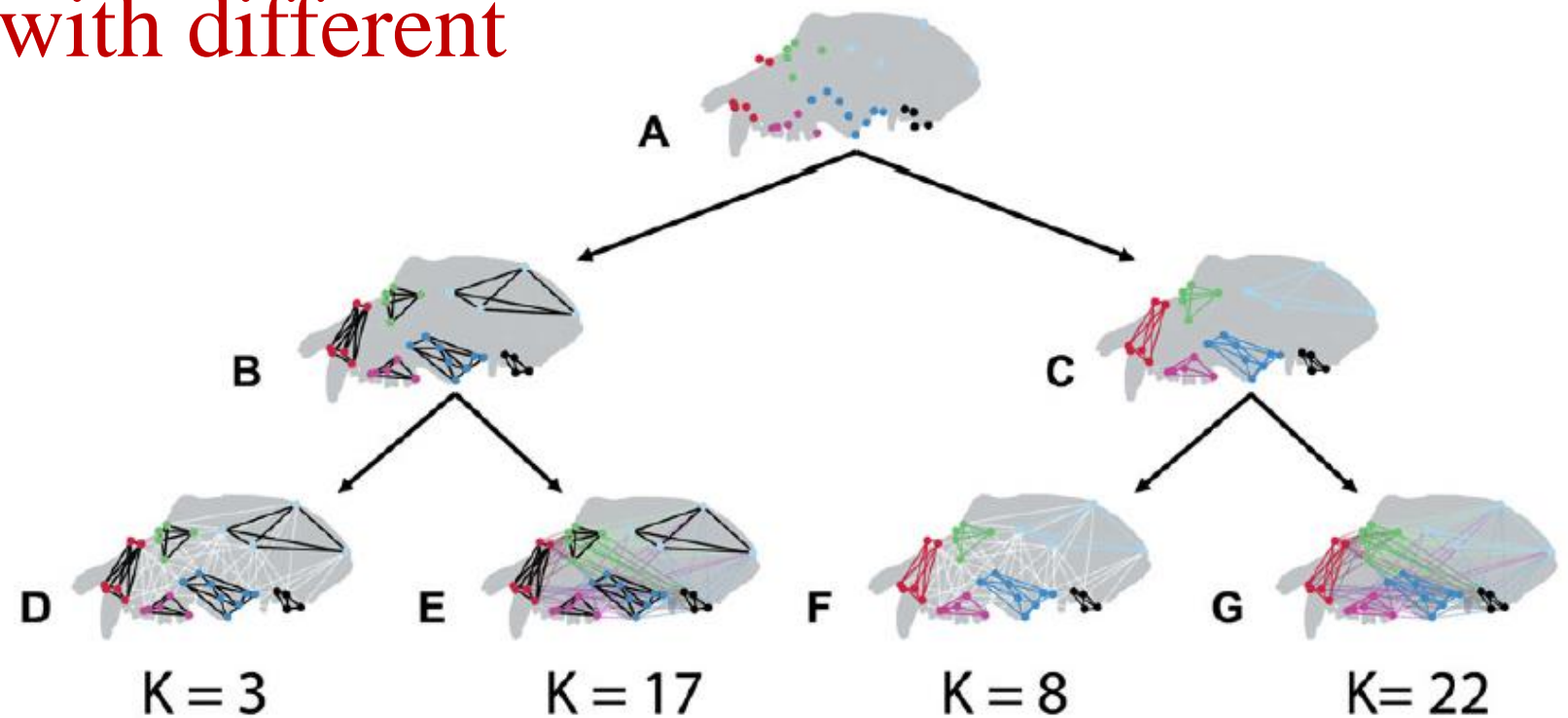
$$AIC_c = -2 Log L + 2K + \frac{2K \ (K+1)}{N - K - 1}$$

number of distinct optimal correlations

number of between-trait correlations

*Method does not really test for modularity because between-module correlations can be higher than within-module correlations!

Table 1. Model descriptions and parameterizations for the 31 model structures explored in this study.

Model ID	Base model structure	# Modules	Model description	# Parameters
1	No modules	0	One ρ for all correlations	2
2	Neurocranial/Facial model	2	One within module ρ for both modules, one between-module ρ	3
3	Neurocranial/Facial model	2	Two within-module ρs and one between-module ρ	4
4	Cheverud model	6	One within-module ρ and one between-module ρ	3
5	Cheverud model	6	Separate within-module ρs and one between-module ρ	8
6	Cheverud model	6	One within-module ρ and separate between-module ρs	17
7	Cheverud model	6	Separate within-module ρs and separate between-module ρs	22
8	Goswami model	6	One within-module ρ and one between-module ρ	3
9	Goswami model	6	Separate within-module ρs and one between-module ρ	8
10	Goswami model	6	One within-module ρ and separate between-module ρs	17
11	Goswami model	6	Separate within-module ρs and separate between-module ρs	22
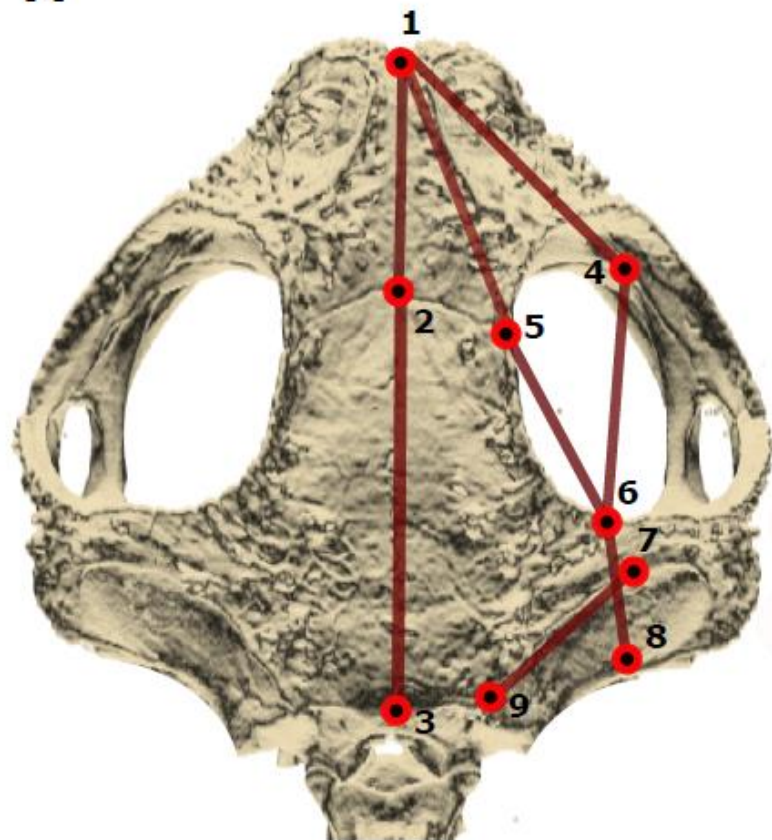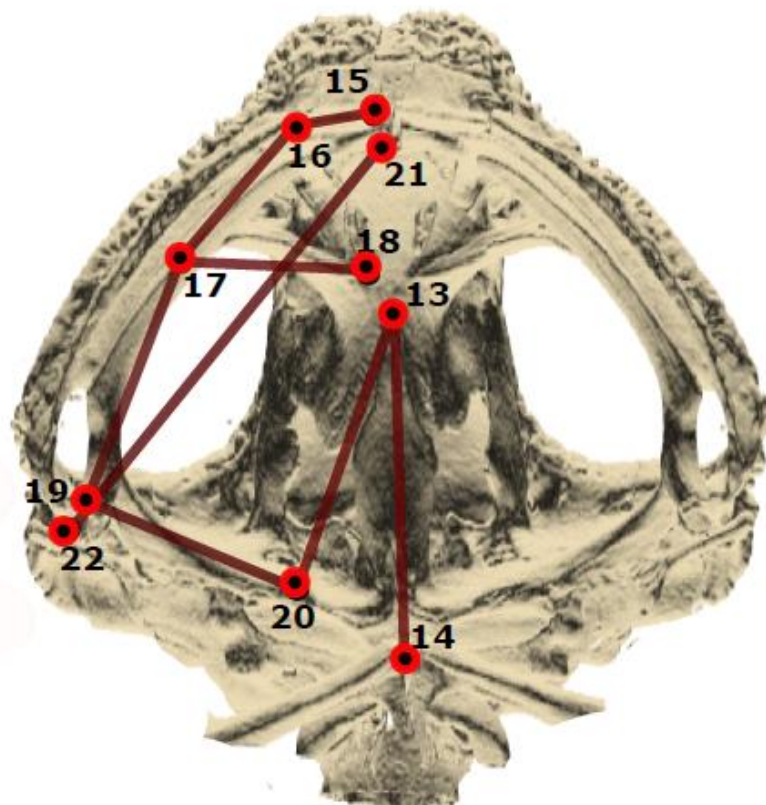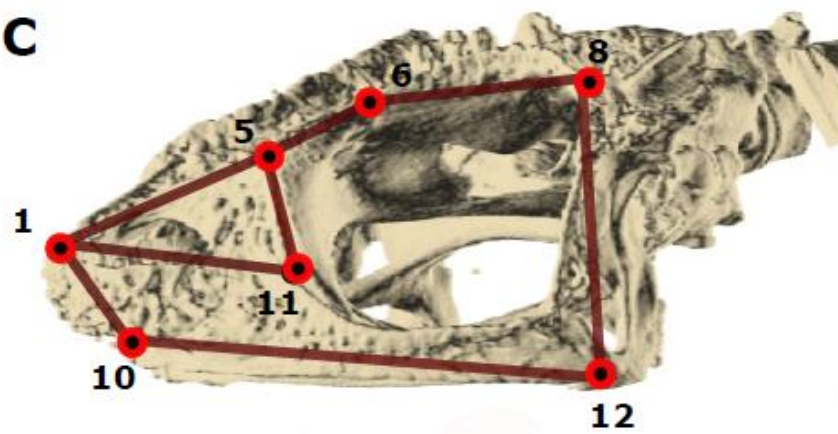
Removing size variation
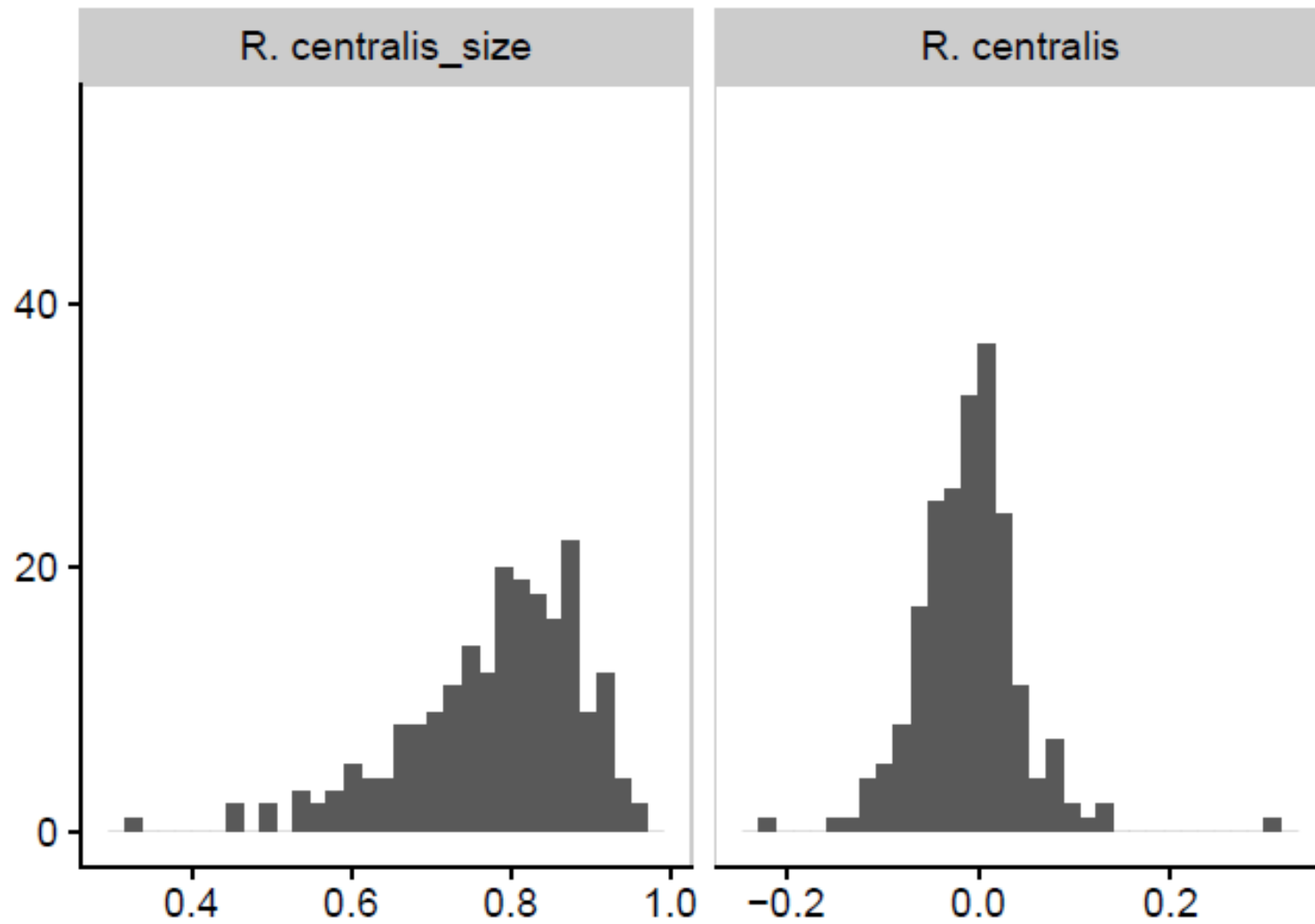
PC1 = size: 50% a 80% of total variation

(c)
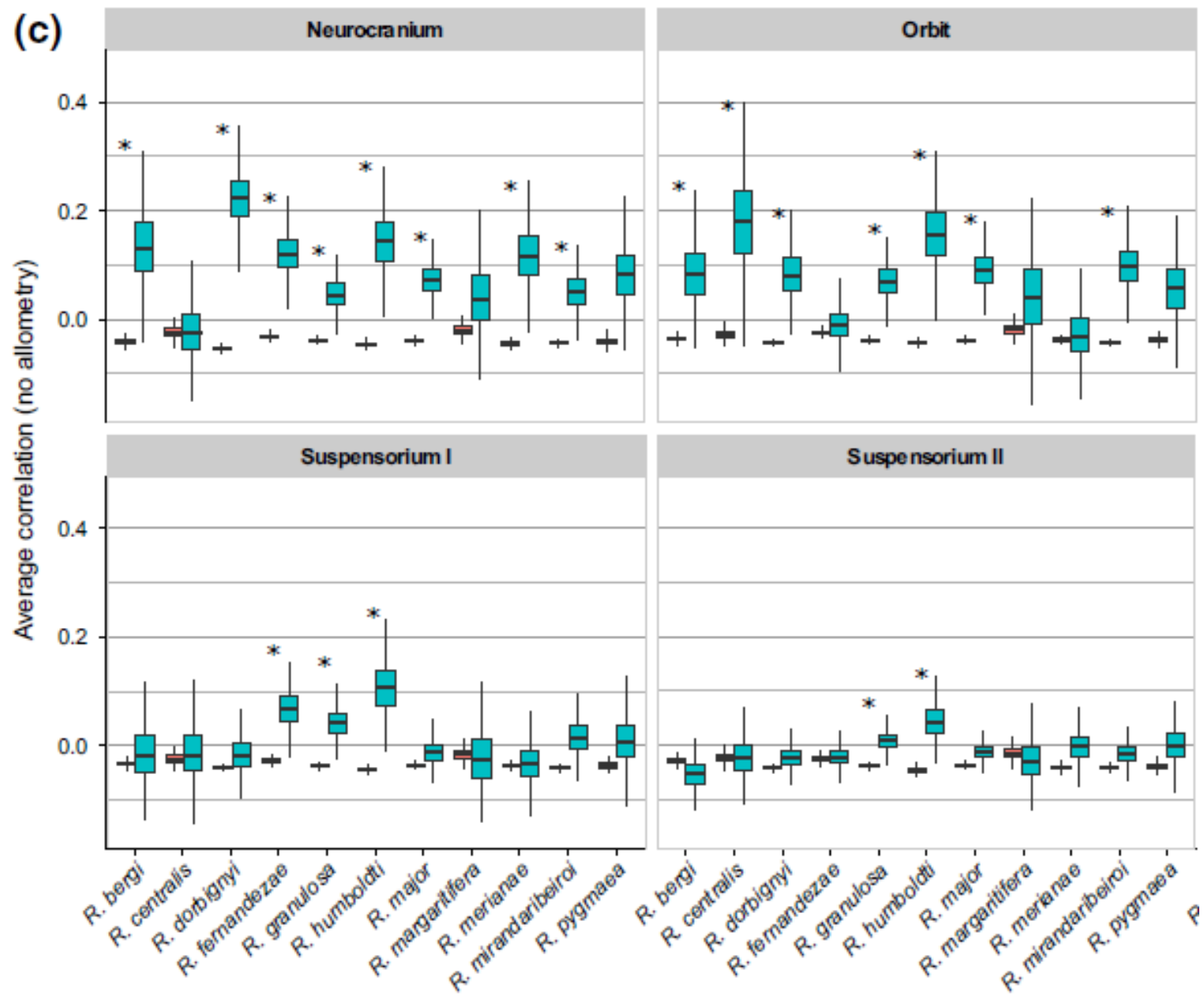
Bones	Developmental	Hormonal	Functional
Nasal	Hyoid (I, II, III)	T3++	Roof/snout
Frontoparietal	Hyoid (I, III)/mandibular (I, III)/branchial	T3+++	Roof/neurocranium/suspensorium II
Nasal	Hyoid (I, II, III)	T3++	Roof/snout
Nasal	Hyoid (I, II, III)	T3++	Roof/snout
Frontoparietal	Hyoid (I, III)/mandibular (I, III)/branchial	T3+++	Roof/neurocranium/suspensorium II/orbit
Orbit	–	–	Orbit
Squamosal	Mandibular (I, II, III)	T3++	Suspensorium (I, II)
Occipital	Branchial	T3+++	Roof
Prenasal	Hyoid (I, II, III)	T3++	Snout
Nasal	Hyoid (I, II, III)	T3++	Roof/snout
Nasal	Hyoid (I, II, III)	T3++	Roof/snout/orbit
Maxilla	Mandibular (I, II, III)	T3++	Snout
Squamosal	Mandibular (I, II, III)	T3++	Suspensorium (I, II)
Parasphenoid	Hyoid (I, II)/mandibular (I, II)	T3+++	Neurocranium
Parasphenoid	Hyoid (I, II)/mandibular (I, II)	T3+++	Neurocranium
Premaxilla	Hyoid (I, II)/mandibular (I, II)	T3++	Snout
Maxilla	Mandibular (I, II, III)	T3++	Snout
Neopalatine	–	T3+	Snout
Pterygoid	Mandibular (I, II, III)	T3+	Suspensorium (I, II)/orbit
Pterygoid	Mandibular (I, II, III)	T3+	Suspensorium (I, II)
Mandible	Mandibular (I, II, III)	T3+	Suspensorium (I, II)

Constructing modularity models for EMMLi

Distances	Developmental II	Hormonal II	Functional II	Functional IIIa
nasal	2	1	2	1
frontoparietal	1	2	1	1
nasal	2	1	2	1
nasal	2	1	2	1
frontoparietal	1	2	3	3
orbit	NA	NA	3	3
squamosal	NA	1	4	4
occipital	1	2	1	1
prenasal	2	1	2	2
nasal	2	1	2	2
nasal	2	1	3	3
maxilla	NA	1	2	2
squamosal	NA	1	4	4
parasphenoid	2	2	1	NA
parasphenoid	2	2	1	NA
premaxilla	2	1	2	2
maxilla	NA	1	2	2
neopalatine	NA	NA	2	2
pterygoid	NA	NA	3	3
pterygoid	NA	NA	4	4
mandible	NA	NA	4	4

Models	With size variation
Developmental Ia	Hyoid II*, mandibular II
Developmental Ib	Hyoid II, mandibular II*
Hormonal I	T3+, T3++
Functional I	Snout, suspensorium I
	No allometric Variation
Developmental II	Branchial, hyoid II
Hormonal II	T3++, T3+++
Functional II	Neurocranium*, snout, orbit, suspensorium I
Functional IIIa	Roof, snout*, orbit, suspensorium I
Functional IIIb	Roof*, snout, orbit, suspensorium I
Functional IV	Neurocranium*, snout, orbit
Functional Va	Roof, snout*, orbit
Functional Vb	Roof*, snout, orbit
Functional VI	Snout, orbit, suspensorium I

TABLE 3 Preferred modularity models for the toad species skull correlation pattern

Species	Model (with size)	MaxL	K	AICc	Post_Prob
R. centralis	Functional I	137.9	5	−265.4	0.40
R. humboldti	Functional I	113.5	4	−218.9	0.55
R. merianae	Functional I	87.3	4	−166.4	0.32
R. granulosa	Functional I	−194.2	5	398.6	0.37
R. mirandaribeiroi	Hormonal I	35.6	5	−61.0	0.36
R. major	Hormonal I	−374.2	5	758.6	0.50
R. bergi	Hormonal I	92.0	5	−173.8	0.44
R. pygmaea	Developmental Ib | Hormonal I	78.6 | 77.6	5 | 5	−146.9 | −144.9	0.4 | 0.12
R. dorbignyi	Developmental Ib	−410.5	5	831.2	0.50
R. fernandezae	Developmental Ib	−503.1	5	1016.6	0.50
R. margaritifera	Hormonal I	173.9	5	−337.6	0.50
	Model (no allometric size)				
R. centralis	Functional IIIb	76.10	7	−137.70	0.68
R. humboldti	Functional II	93.0	11	−162.6	0.89
R. merianae	Developmental II	24.30	5	−38.20	0.46
R. granulosa	Functional II	−276.60	11	576.50	0.94
R. mirandaribeiroi	Functional IV | II	−85.5 | −82.9	8 | 11	187.7 | 189.1	0.35 | 0.17
R. major	Functional II	−225	11	473.4	1.0
R. bergi	Developmental II	109.6	4	−211	0.39
R. pygmaea	Functional II | IIIb | IV	90.2 | 85.1 | 87.2	8 | 4 | 6	−163.8 | −162.0 | −162.0	0.25 | 0.10 | 0.10
R. dorbignyi	Functional II	45.1	11	−66.8	0.76
R. fernandezae	Functional II	−197	11	417.4	0.92
R. margaritifera	Functional II | IIIb	108.8 | 104.0	8 | 4	−201.0 | −199.9	0.24 | 0.14

Effect size: AVG diff

FUNCTIONAL MODEL		AVG diff = [AVG +] - [AVG -]							
no allometry		Neurocranium	Orbit	Roof	Snout	Suspensorium I	Suspensorium II	Total I	Total II
R. bergi	empirical	**0.176**	**0.123**	**0.101**	**0.081**	0.018	-0.022	**0.097**	**0.077**
	lower	0.042	0.011	0.027	0.019	-0.072	-0.073	0.031	0.018
	upper	0.312	0.242	0.187	0.152	0.120	0.034	0.159	0.136
R. centralis	empirical	0.004	**0.208**	0.042	**0.182**	0.010	0.001	**0.132**	**0.120**
	lower	-0.093	0.047	-0.017	0.085	-0.075	-0.060	0.058	0.048
	upper	0.116	0.373	0.112	0.283	0.122	0.078	0.202	0.190
R. dorbignyi	empirical	**0.278**	**0.126**	-0.003	**0.099**	0.024	0.020	**0.093**	**0.084**
	lower	0.178	0.044	-0.031	0.054	-0.034	-0.020	0.059	0.053
	upper	0.370	0.223	0.032	0.149	0.089	0.069	0.127	0.115
R. fernandezae	empirical	**0.154**	0.016	**0.134**	**0.157**	**0.099**	0.004	**0.159**	**0.140**
	lower	0.083	-0.047	0.083	0.109	0.029	-0.037	0.117	0.101
	upper	0.238	0.087	0.186	0.208	0.171	0.046	0.199	0.177
R. granulosa	empirical	**0.084**	**0.108**	**0.069**	**0.127**	**0.079**	**0.048**	**0.108**	**0.101**
	lower	0.028	0.052	0.037	0.093	0.027	0.012	0.075	0.070
	upper	0.142	0.170	0.101	0.164	0.133	0.086	0.139	0.132

Effect size: AVG diff

DEVELOPMENTAL MODEL		AVG diff = [AVG +] - [AVG -]							
no allometry		Branchial	Hyoid I	Hyoid II	Hyoid III	Mandibular I	Mandibular II	Mandibular III	Total II
R. bergi	empirical	**0.385**	**0.068**	**0.101**	**0.113**	-0.014	0.001	0.009	**0.063**
	lower	0.202	0.014	0.025	0.036	-0.047	-0.041	-0.041	0.004
	upper	0.568	0.134	0.189	0.197	0.025	0.056	0.064	0.130
R. centralis	empirical	0.050	-0.018	0.042	0.029	-0.069	-0.078	-0.009	-0.046
	lower	-0.145	-0.057	-0.021	-0.025	-0.099	-0.108	-0.055	-0.098
	upper	0.265	0.025	0.114	0.095	-0.040	-0.045	0.043	0.010
R. dorbignyi	empirical	**0.281**	0.005	0.022	0.008	-0.004	-0.029	0.011	-0.013
	lower	0.158	-0.019	-0.011	-0.024	-0.024	-0.046	-0.021	-0.037
	upper	0.414	0.029	0.058	0.047	0.023	-0.007	0.044	0.013
R. fernandezae	empirical	**0.183**	**0.152**	**0.176**	**0.180**	-0.033	-0.031	-0.008	**0.079**
	lower	0.075	0.104	0.119	0.121	-0.056	-0.056	-0.040	0.046
	upper	0.296	0.200	0.237	0.237	-0.007	-0.005	0.026	0.114
R. granulosa	empirical	**0.171**	**0.070**	**0.135**	**0.115**	-0.015	-0.020	**0.042**	**0.062**
	lower	0.084	0.042	0.094	0.077	-0.032	-0.036	0.014	0.033
	upper	0.262	0.101	0.178	0.152	0.001	-0.003	0.069	0.089

Conclusions

- Without size variation, most species have the functional model as the best supported;

- But, there is a strong signal of developmental modularity without size variation;

- We infer that the modularity signal due to embryonic origin of bones is blurred by the process of growth that occurs later in ontogeny.

Riedl's hypothesis: developmental system 'imitates' functional interactions relevant for fitness
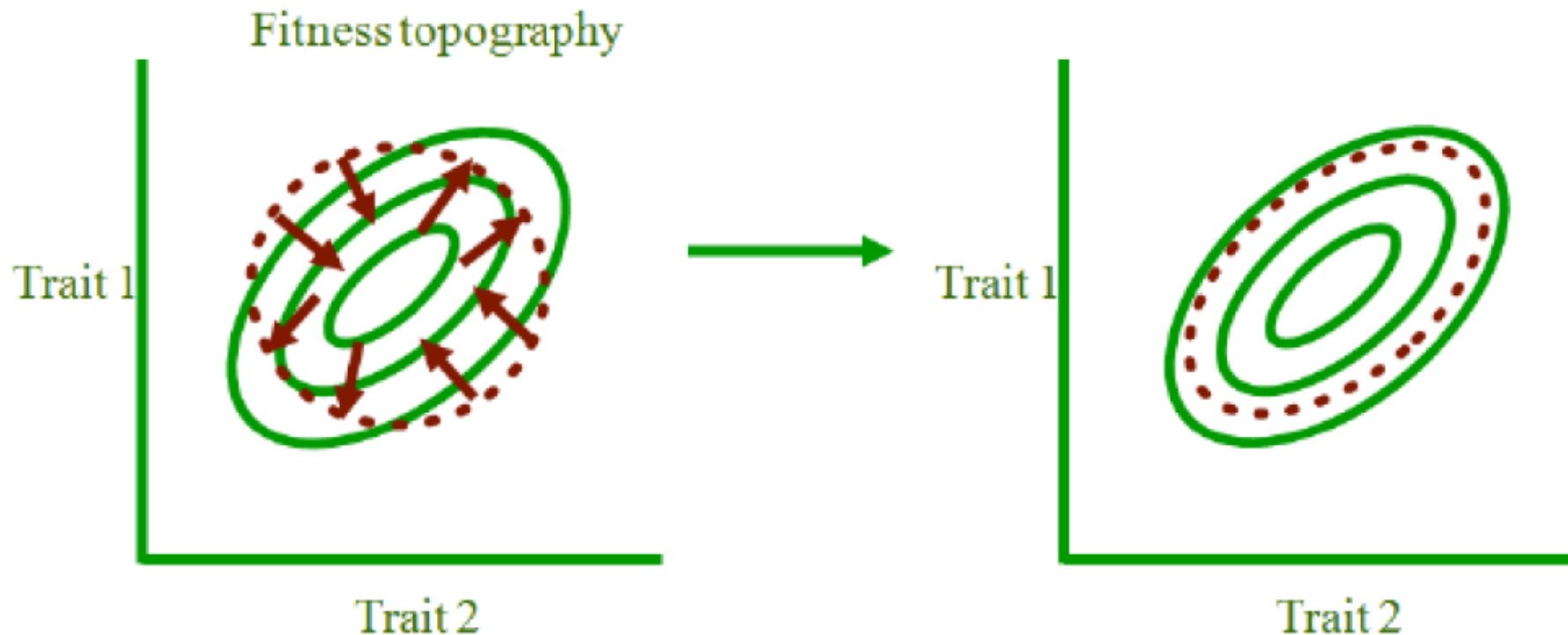
Riedl 1977; Lande 1980; Cheverud 1984

Quiz

How to construct a modularity model?