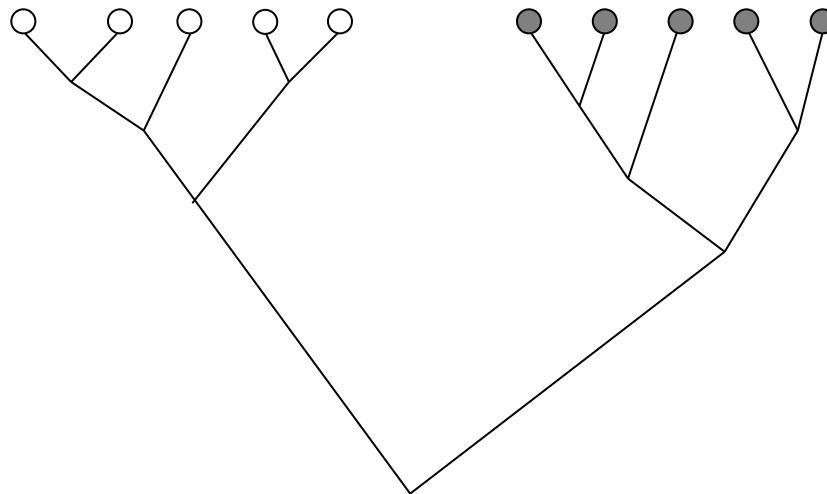
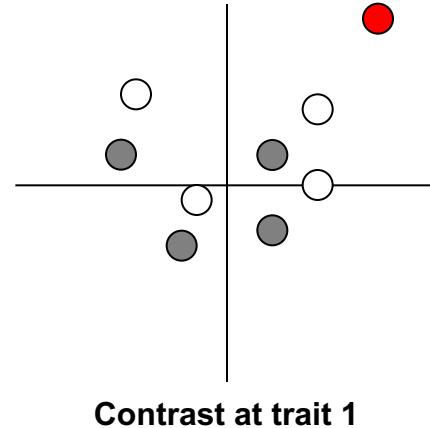


Phylogenies and statistics

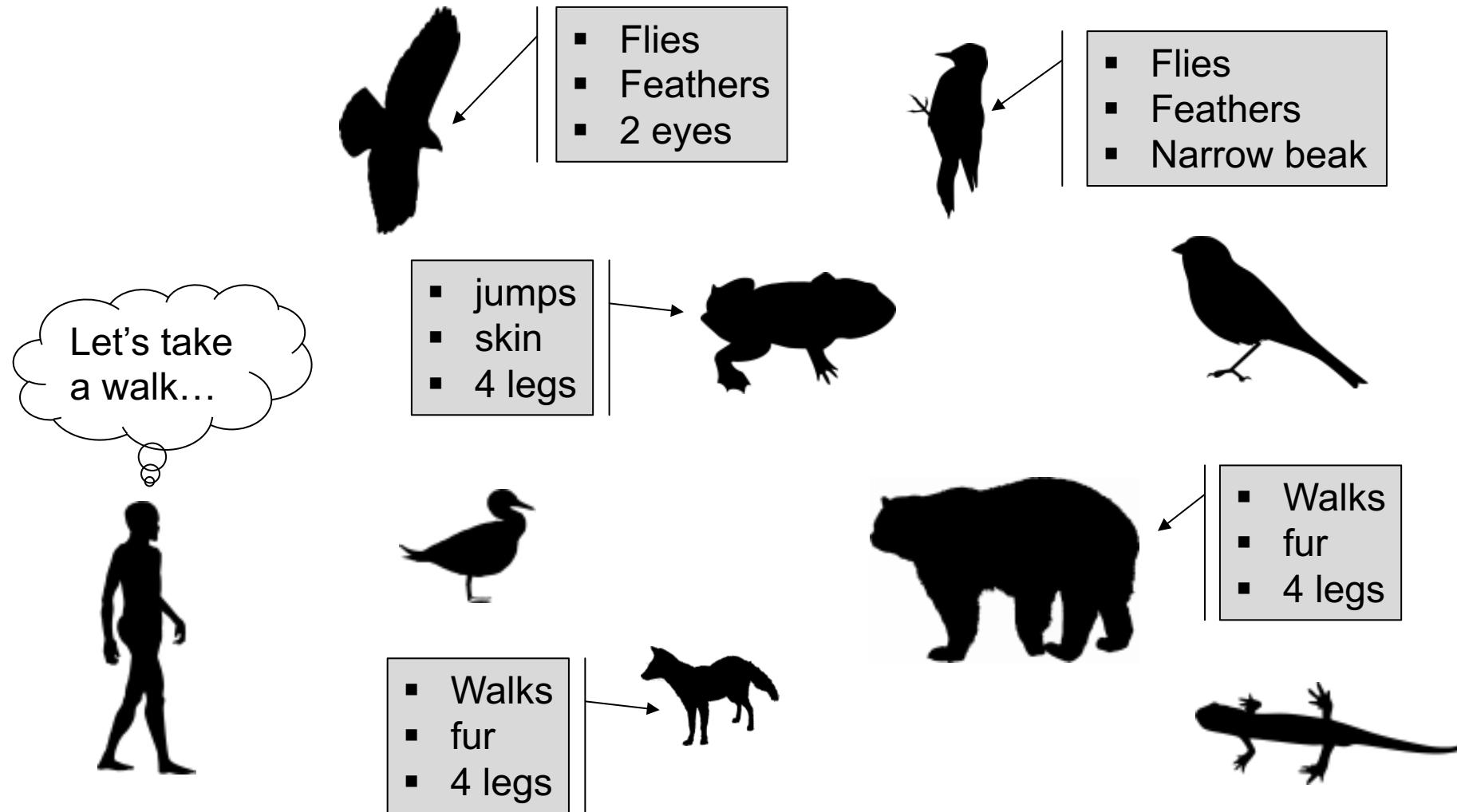


Contrast at trait 2



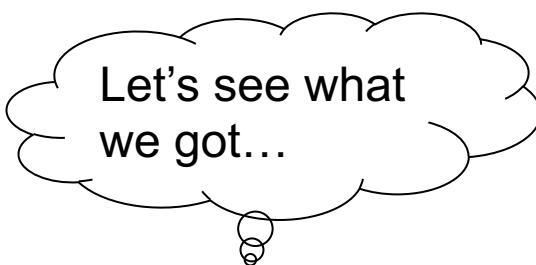
An introduction

An introduction



An introduction

	feathers	other
Animal flies	9	0
Animal doesn't fly	0	7

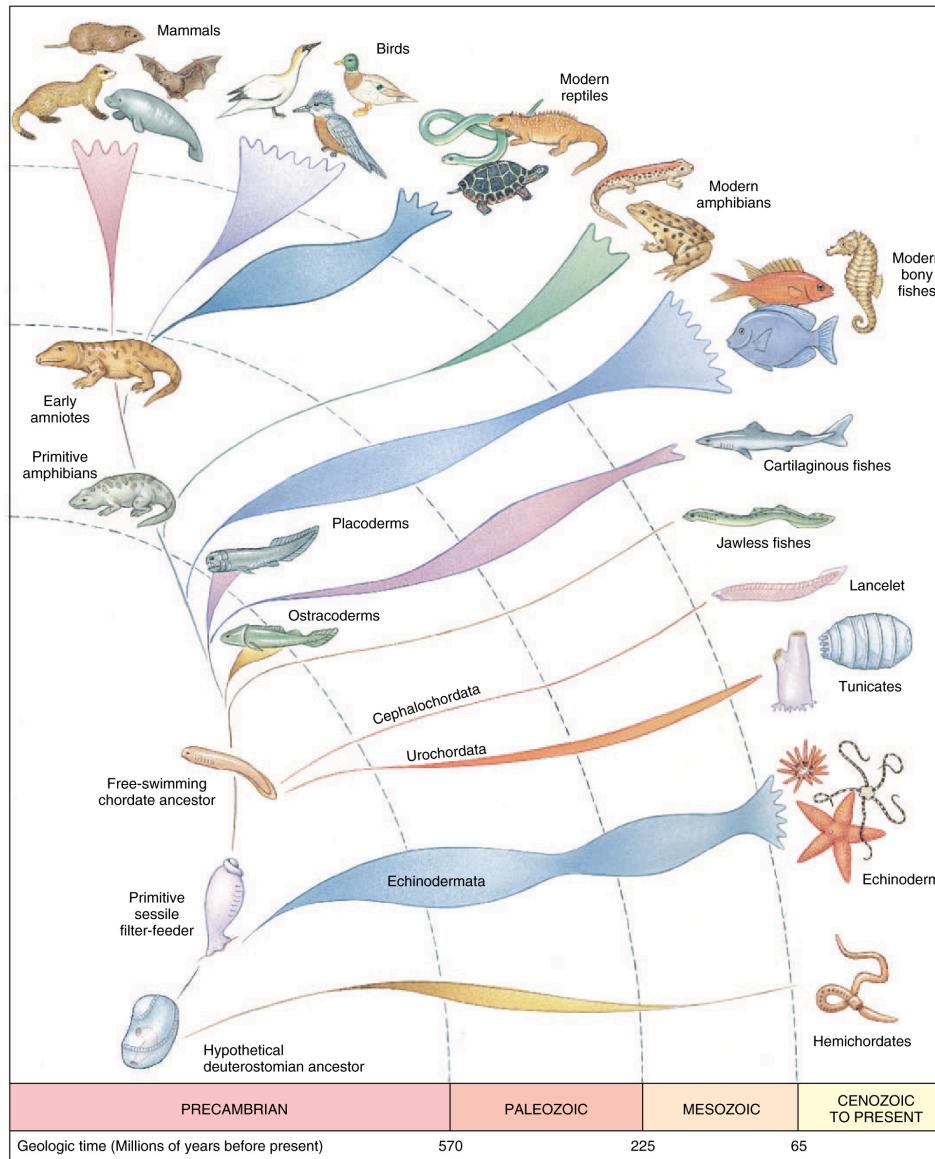


```
> fisher.test(matrix(c(9,0,0,7),2))
```

Fisher's Exact Test for Count Data

```
data: matrix(c(9, 0, 0, 7), 2)
p-value = 8.741e-05
```

Evolution of flight (and feathers)



Credit: University Of Kelaniya, Sri Lanka

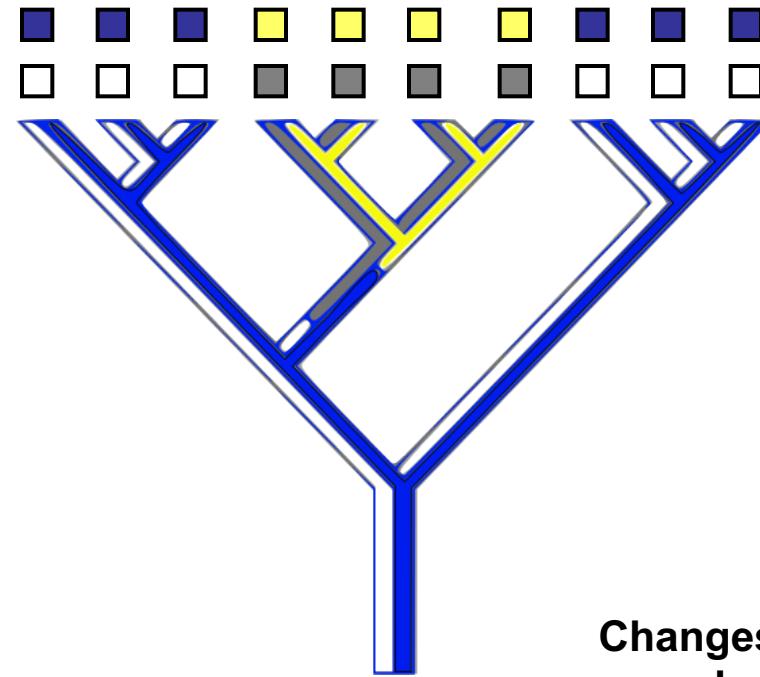
The comparative method

The comparative method

- Definition
 - It is the name given to a family of methods that aims at correcting for the phylogenetic non-independence of species when comparing them
- Why ?
 - Species cannot be considered without the context of evolution; the observations are not independent

A qualitative example

species	flower	stem
1	blue	spiny
2	blue	spiny
3	blue	spiny
4	blue	spiny
5	yellow	smooth
6	yellow	smooth
7	yellow	smooth
8	yellow	smooth
9	blue	spiny
10	blue	spiny



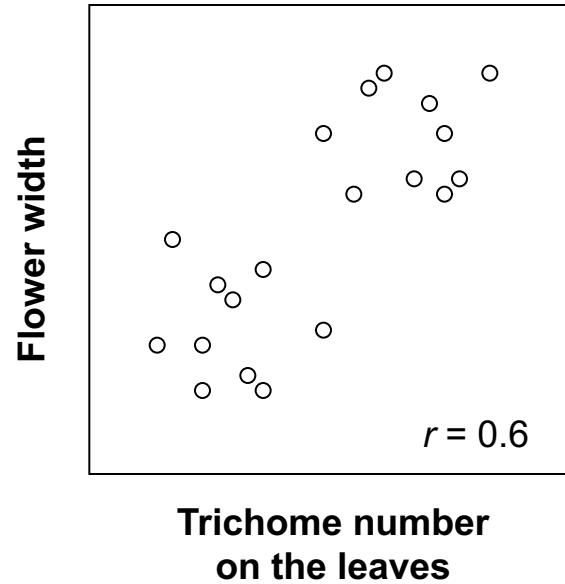
	blue	yellow
□ spiny	6	0
■ smooth	0	4

Fisher exact test
 $p = 0.00476$

Fisher exact test
 $p = 0.056$

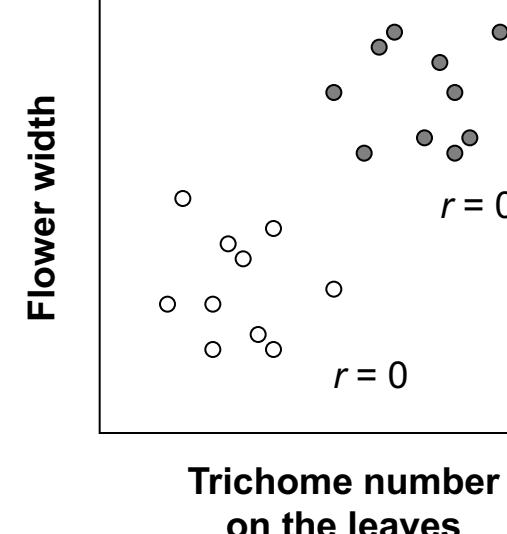
stem	flower	
	yes	no
yes	1	0
no	0	17

A quantitative example



Trichome number
on the leaves

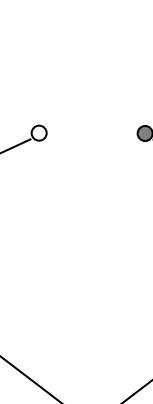
$r = 0.6$



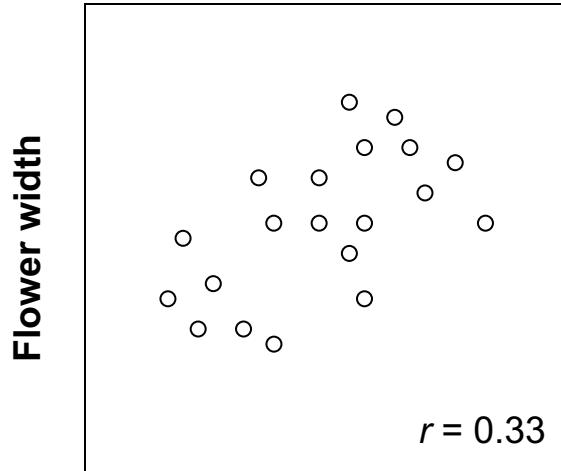
Trichome number
on the leaves

$r = 0$

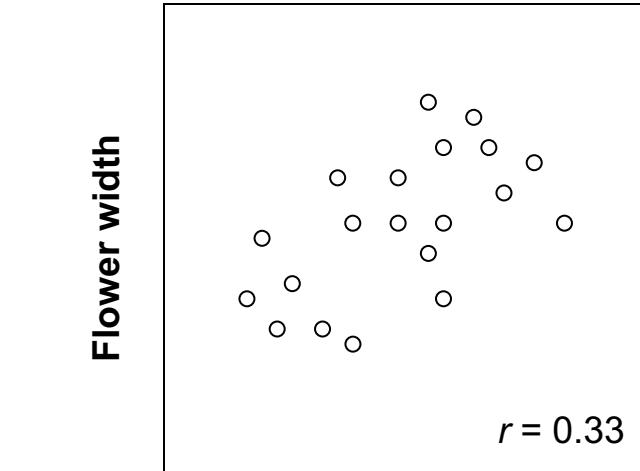
$r = 0$



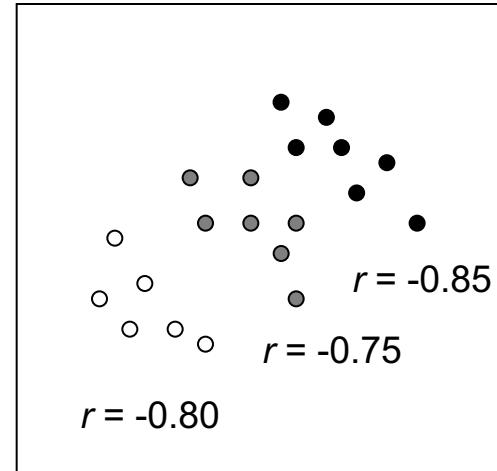
Another quantitative example



Trichome number
on the leaves



Trichome number
on the leaves

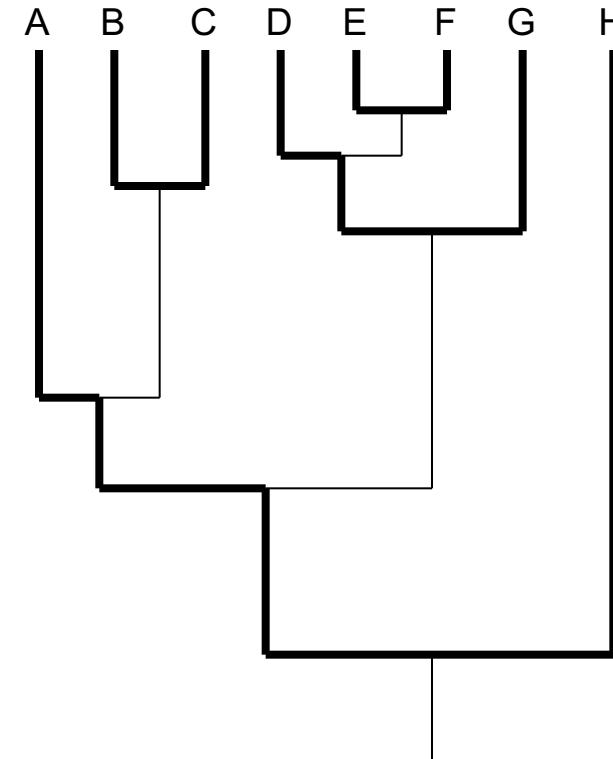
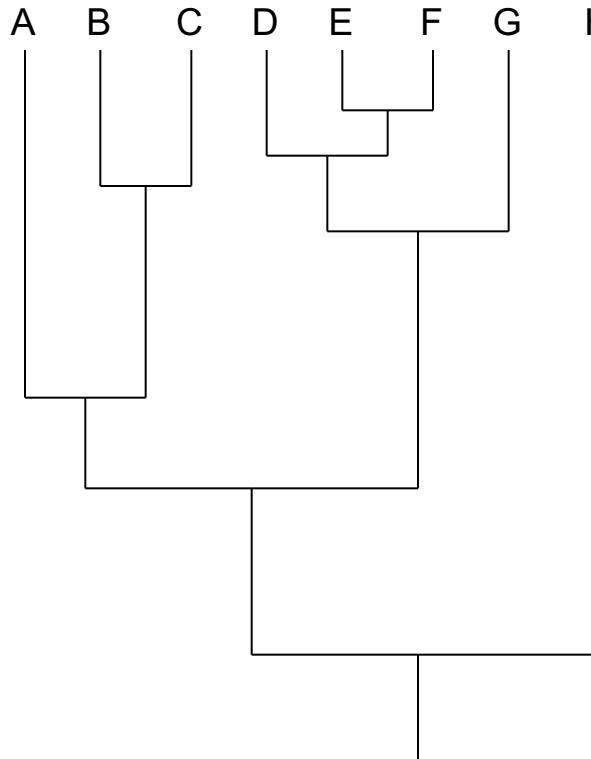


Comparative methods

Different approaches

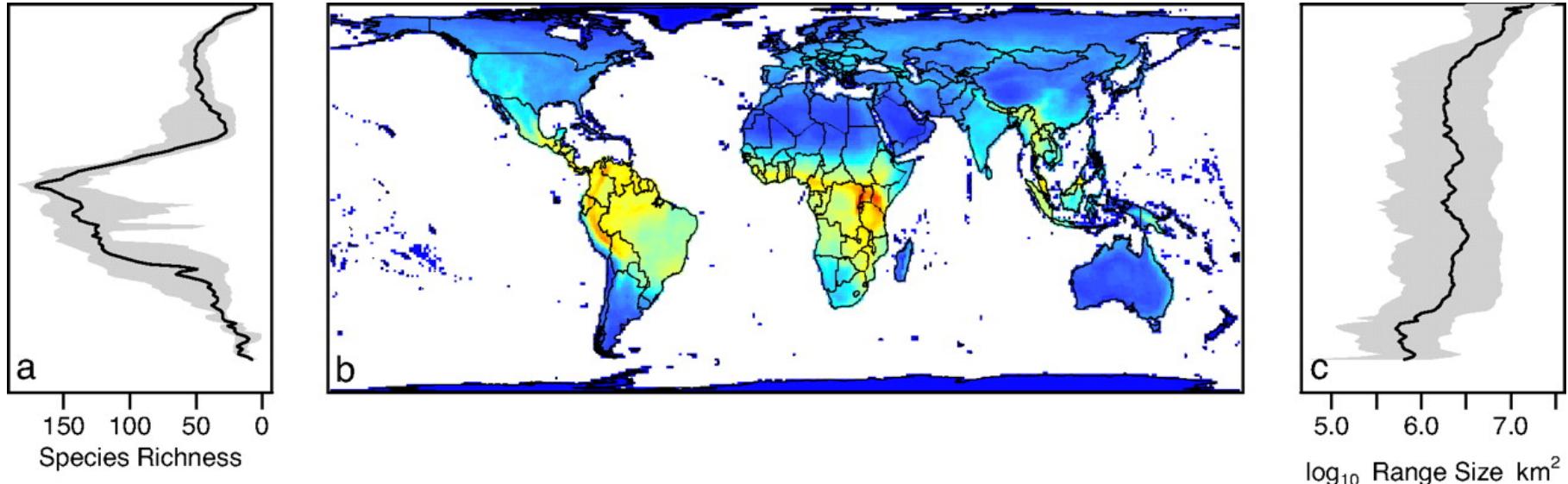
- Studying pairs of species
- Independent contrasts
- Phylogenetic generalized least squares (PGLS)
- Phylogenetic mixed models (PMM)

Pairs of species (sometimes sister clades)

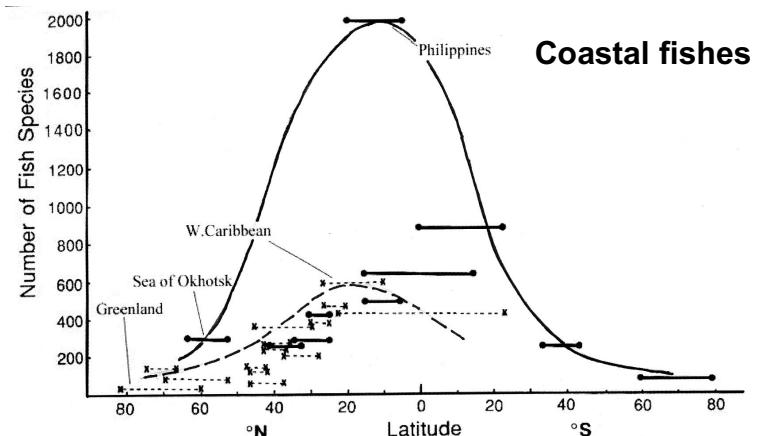


We can thus treat each comparison as independent from each other

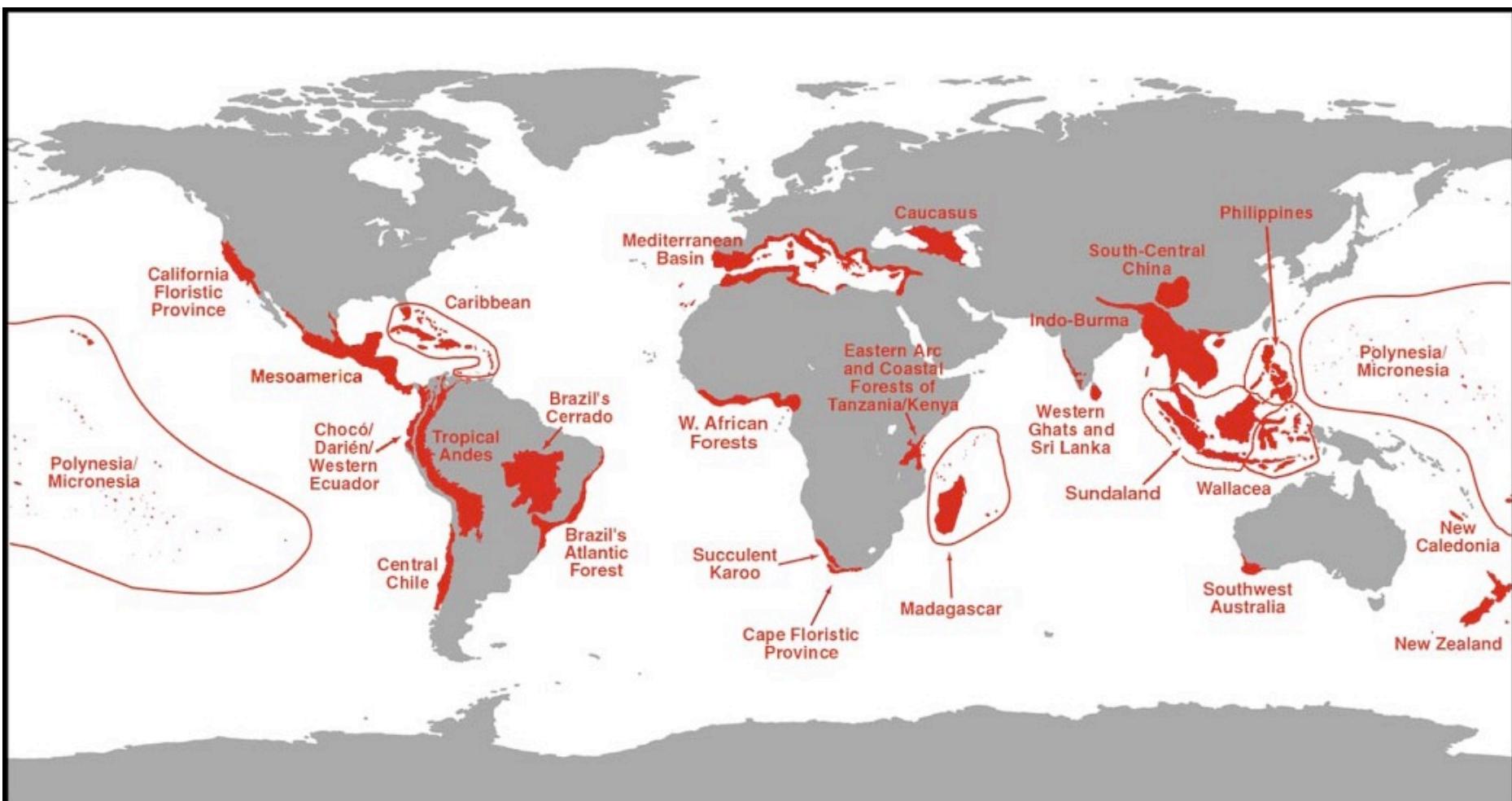
Biodiversity latitudinal gradient



Mammals - Davies T J et al. PNAS 2008;105:11556-11563

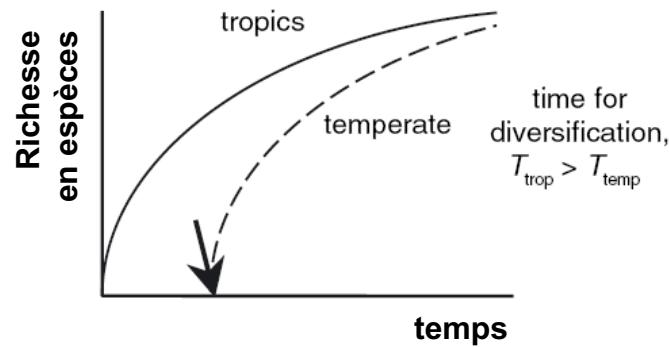


25 biodiversity hotspots

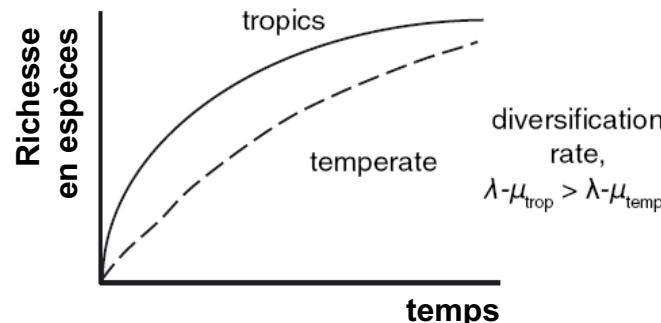


Some evolutionary hypotheses

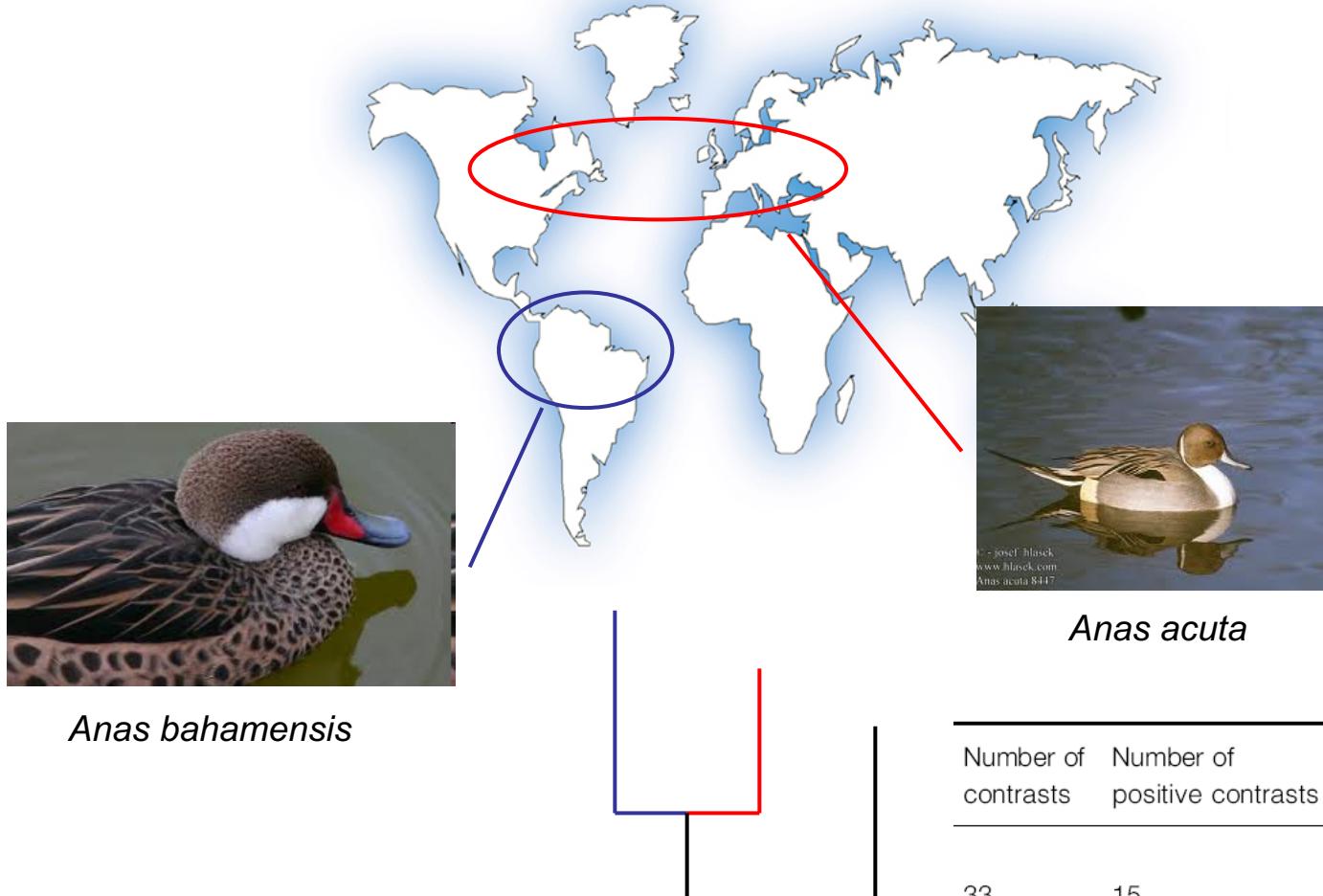
- More time for speciation in the tropics (older environments)



- Higher diversification rates in the tropics, due to:
 - Higher speciation rates in the tropics (Cradle theory)
 - Lower extinction rates in the tropics (Museum theory)



Test for higher diversification rate in the tropics

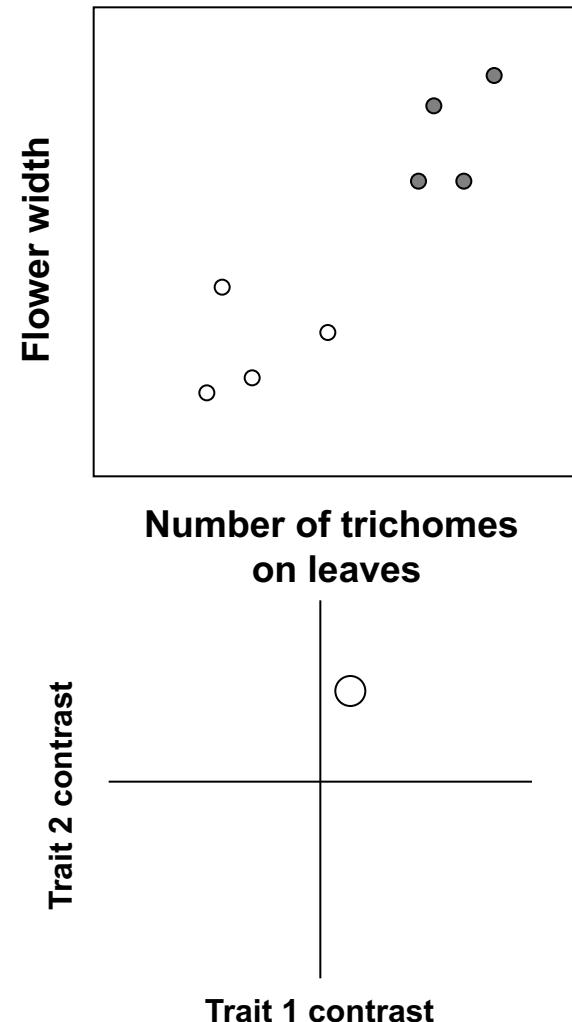
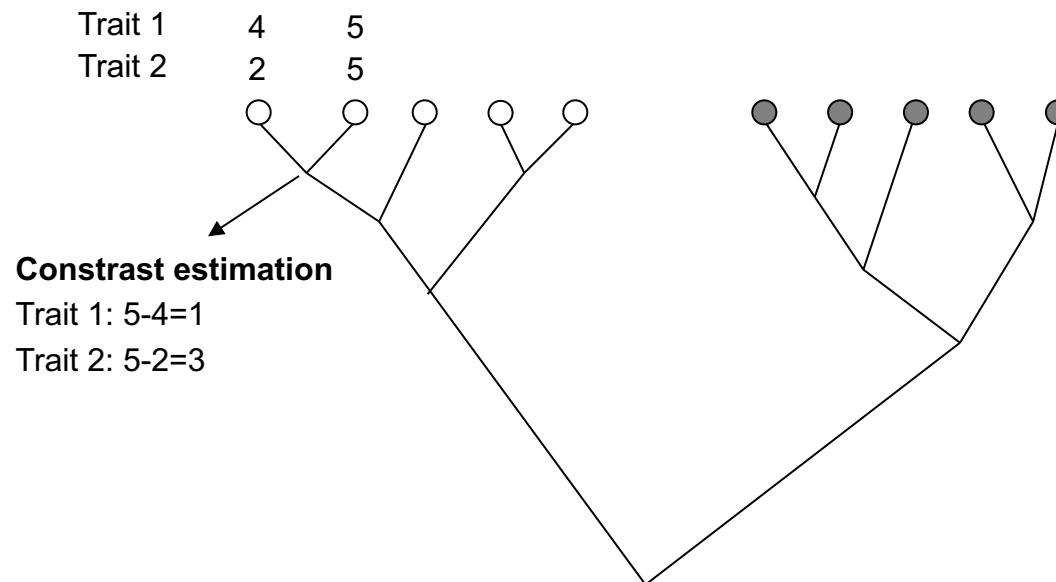


Bromham & Cardillo (2003)

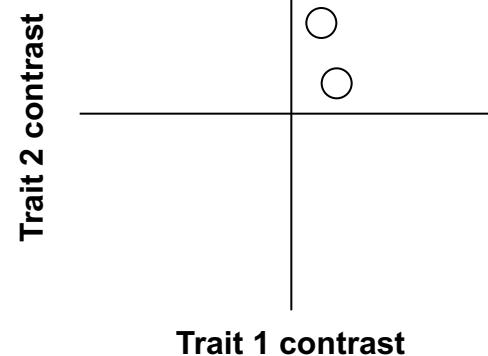
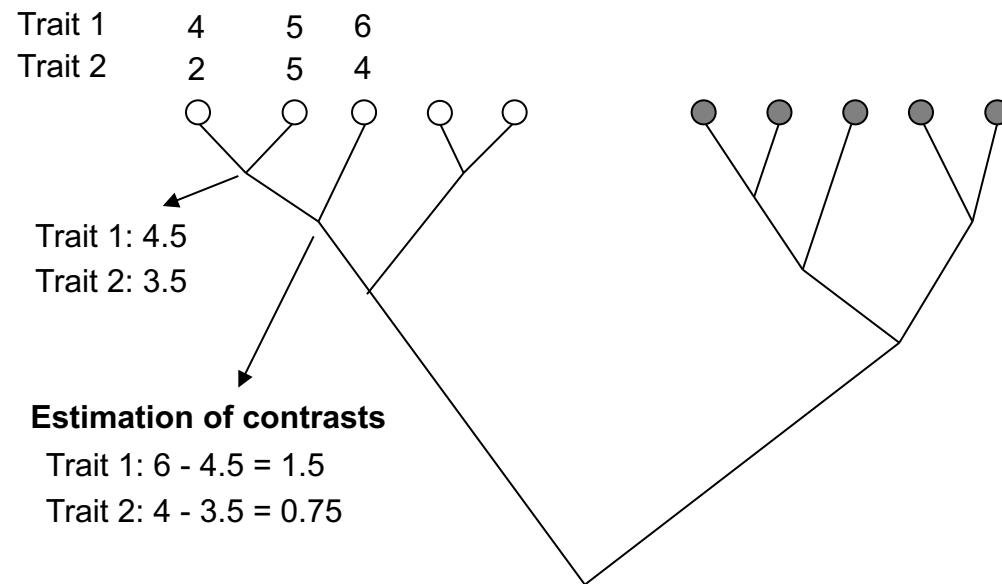
Not significant

Independent contrasts

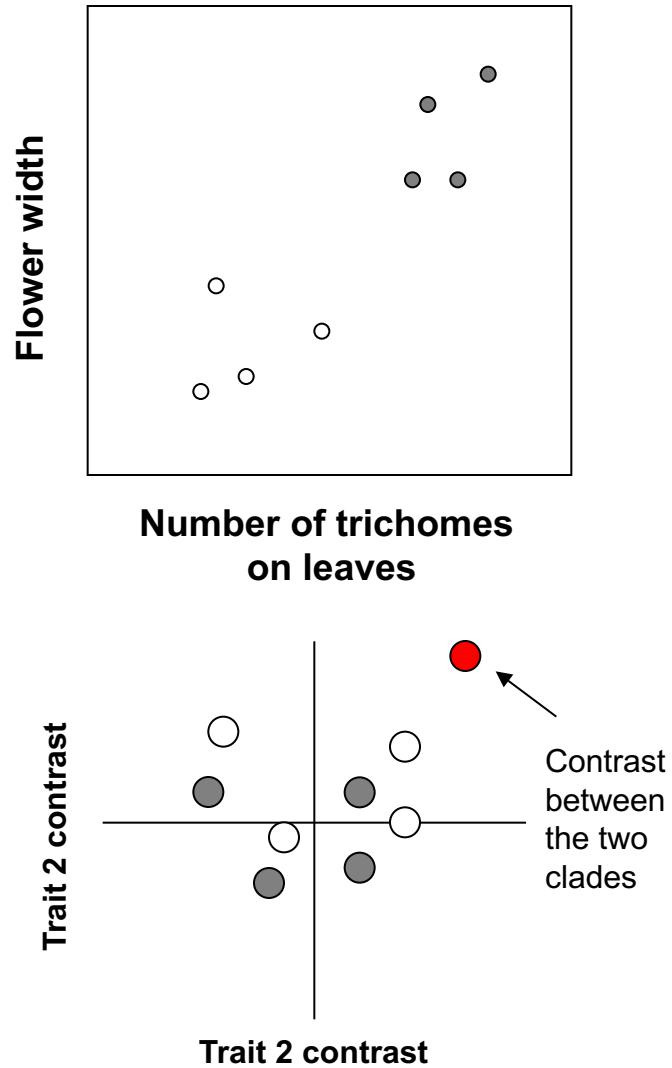
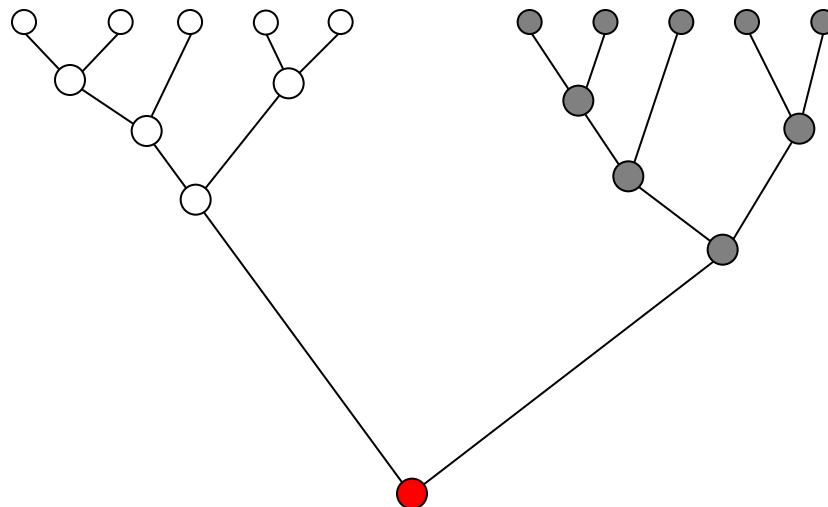
Objective: Test the correlation between characters while taking into account the evolutionary history of species



Independent contrasts

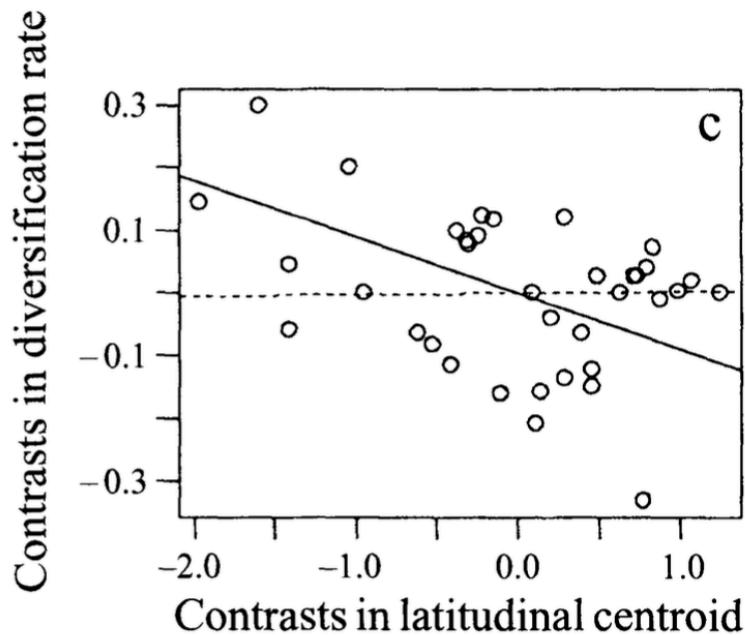


Independent contrasts



Test for higher diversification rate in the tropics

Test: Using a bird genera phylogeny, Cardillo et al. (2005) estimated for each genera their diversification rate and their mean latitude. They then estimated the PIC to test if there is a correlation between latitude and the diversification rate.



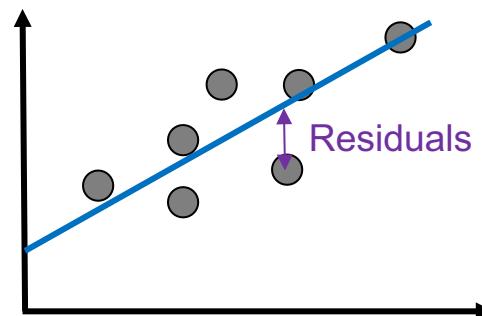
$P\text{-value} = 0.023$

Higher diversification rates
in the tropics

Phylogenetic Generalized Least Squares

Linear model (ordinary least squares – OLS)

$$\mathbf{y} = \alpha + \beta \mathbf{x} + \mathbf{e}$$



Linear model (ordinary least squares – OLS)

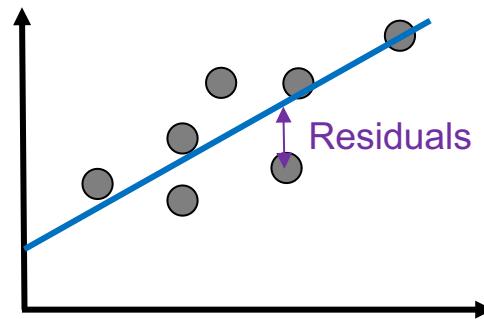
$$\mathbf{y} = \alpha + \beta \mathbf{x} + \mathbf{e}$$

Many assumptions

- Normality, homogeneity, fixed X , independence, and correct model specification
- Independence:
 - The value of Y_i at X_i should not be influenced by other values of X_i

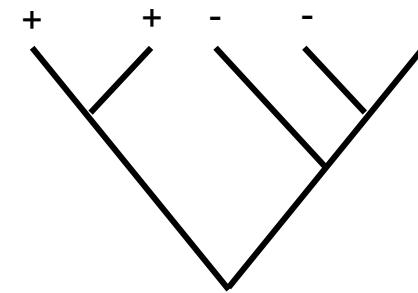
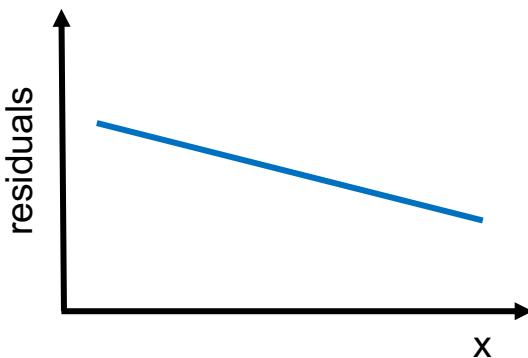
$$\mathbf{e} \sim \mathcal{N}(0, \sigma^2)$$

Examples of violations



Residuals correlated with the explanatory variable

Residuals correlated with the phylogenetic relationships



Practicals in R



www.github.com/simjoly/QCBS_workshop_2017

Phylogenetic generalized least squares

Phylogenetic generalized least squares (PGLS)

- A special case of generalized least squares (GLS)
 - Allow the residuals of the model to be correlated in a specific way
 - Used for spatial correlation, time series, phylogenetic relationships, etc.

Phylogenetic generalized least squares (PGLS)

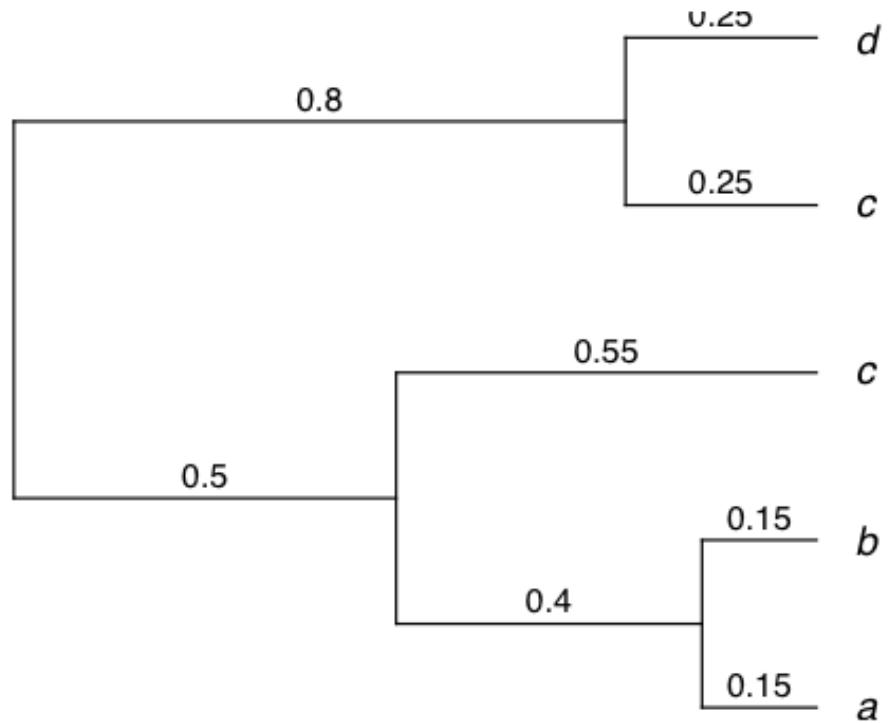
$$\mathbf{y} = \alpha + \beta \mathbf{x} + \mathbf{e}$$

$$\mathbf{e} \sim \mathcal{N}(0, \sigma^2 \mathbf{C})$$

$$\sigma^2 \mathbf{C} = \sigma^2 \begin{pmatrix} 1 & \rho_{12} & \rho_{13} & \dots & \rho_{1i} \\ \rho_{21} & 1 & \rho_{23} & \dots & \rho_{2i} \\ \rho_{31} & \rho_{32} & 1 & \dots & \rho_{3i} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \rho_{i1} & \rho_{i2} & \rho_{i3} & \dots & 1 \end{pmatrix}$$

correlation matrix

From a tree to a variance-covariance structure



	a	b	c	c	d
a	1.05	0.90	0.50	0.00	0.00
b	0.90	1.05	0.50	0.00	0.00
c	0.50	0.50	1.05	0.00	0.00
c	0.00	0.00	0.00	1.05	0.80
d	0.00	0.00	0.00	0.80	1.05

... to a correlation matrix

	a	b	c	c	d
a	1.05	0.90	0.50	0.00	0.00
b	0.90	1.05	0.50	0.00	0.00
c	0.50	0.50	1.05	0.00	0.00
c	0.00	0.00	0.00	1.05	0.80
d	0.00	0.00	0.00	0.80	1.05

VCV matrix



	a	b	c	c	d
a	1.000	0.857	0.476	0.000	0.000
b	0.857	1.000	0.476	0.000	0.000
c	0.476	0.476	1.000	0.000	0.000
c	0.000	0.000	0.000	1.000	0.762
d	0.000	0.000	0.000	0.762	1.000

correlation matrix

Back to PGLS

$$\mathbf{e} \sim \mathcal{N}(0, \sigma^2 \mathbf{C})$$

$$\sigma^2 \mathbf{C} = \sigma^2 \begin{pmatrix} 1 & \rho_{12} & \rho_{13} & \dots & \rho_{1i} \\ \rho_{21} & 1 & \rho_{23} & \dots & \rho_{2i} \\ \rho_{31} & \rho_{32} & 1 & \dots & \rho_{3i} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \rho_{i1} & \rho_{i2} & \rho_{i3} & \dots & 1 \end{pmatrix}$$

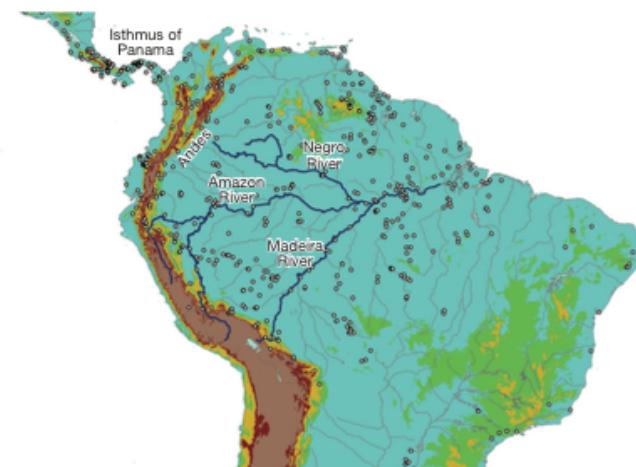
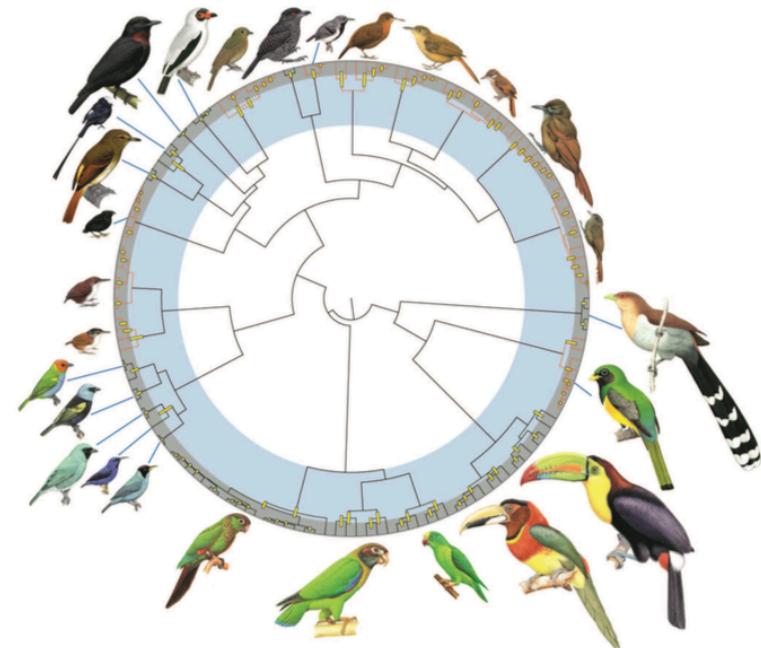
correlation matrix

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Example

- What drove bird diversification in the neotropics?
 - Lineage age
 - Foraging behaviour (stratum: understorey or canopy)
 - Ancestral area
 - Niche breadth
- Studied the diversity of 27 lineages of birds



Example

- What drove bird diversification in the neotropics?

Table 1 | Phylogenetic generalized least-squares regression showing the effects of historical and ecological variables on species diversity

Effect	Estimate	Standard error	t value	P	ΔAICc
Lineage age	0.1187	0.0283	4.1907	0.0004	6.9586
Foraging stratum	0.5188	0.2025	2.5623	0.0178	4.0122
Ancestral origin	-0.1921	0.2023	-0.9495	0.3527	-1.9546
Niche breadth	1.0097	1.0658	0.9473	0.3538	-1.9595

Relax the assumption that the residuals
need to be all phylogenetically correlated

The solution

- What happens if there are other sources of errors in the data than the phylogenetic correlations?

$$\mathbf{y} = \alpha + \beta \mathbf{x} + \mathbf{e}$$

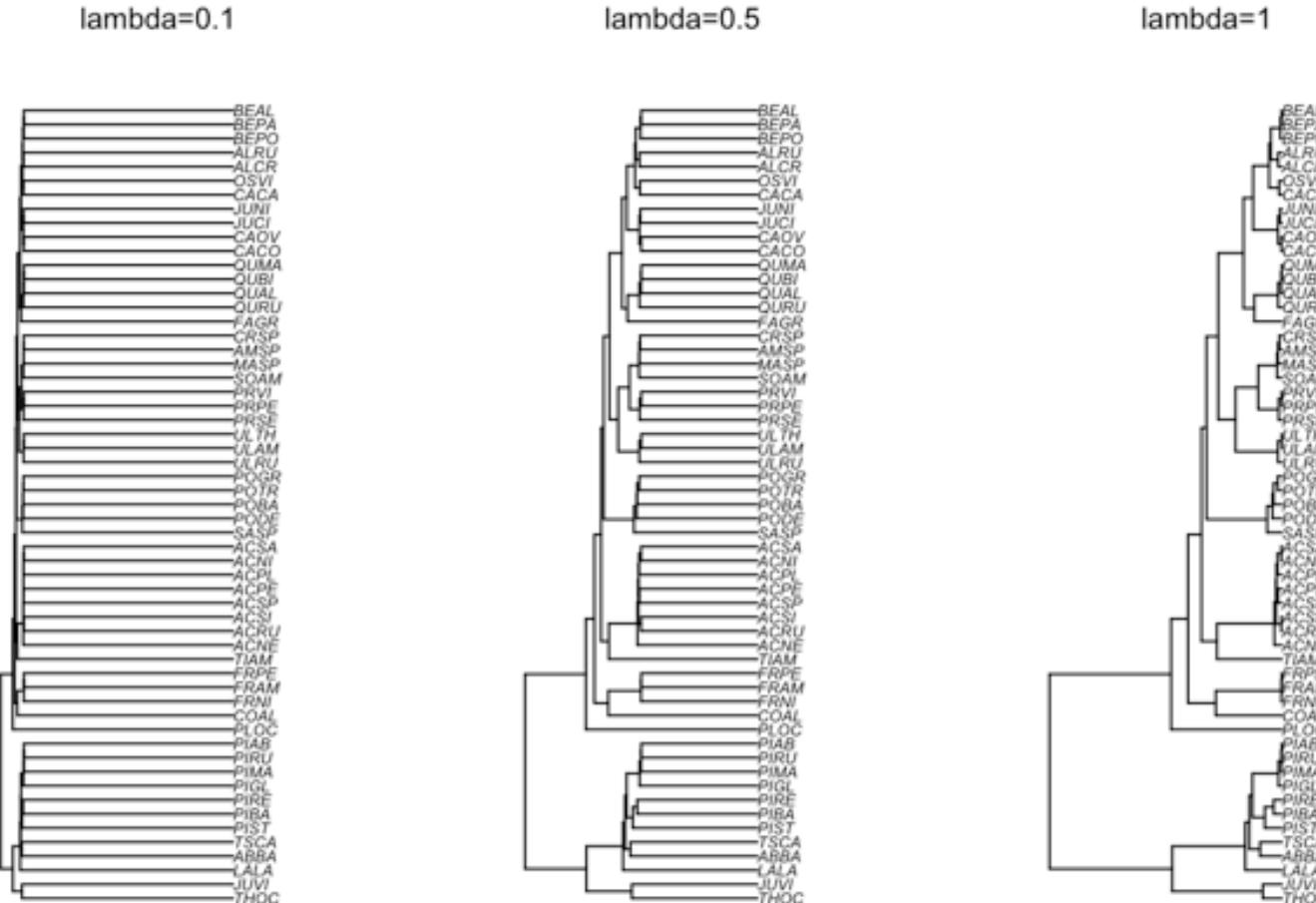
$$\mathbf{e} \sim \mathcal{N}(0, \sigma^2 \mathbf{C})$$

The solution: use the λ model

- Estimate a parameter λ in the GLS that determines the strength of the phylogenetic signal in the residuals.
 - $\lambda = 0$: no phylogenetic signal (equivalent to OLS)
 - $\lambda = 1$: perfect phylogenetic signal

$$\sigma^2 \mathbf{C} = \sigma^2 \begin{pmatrix} 1 & \lambda\rho_{12} & \lambda\rho_{13} & \dots & \lambda\rho_{1i} \\ \lambda\rho_{21} & 1 & \lambda\rho_{23} & \dots & \lambda\rho_{2i} \\ \lambda\rho_{31} & \lambda\rho_{32} & 1 & \dots & \lambda\rho_{3i} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \lambda\rho_{i1} & \lambda\rho_{i2} & \lambda\rho_{i3} & \dots & 1 \end{pmatrix}$$

Effect of parameter λ on the phylogeny



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Model Selection or Testing

Likelihood

$$L(D|M)$$

Concept of model choice

The choice of a model is generally based on the concept of parsimony, that stipulates that one should choose a more complex model only if it is necessary

A more complex model will always have a better fit (better likelihood), but its parameters will have greater variance (and thus greater uncertainty).

How then should we make the cutoff?

Likelihood Ratio Test

$$D = -2 \ln \frac{L(D|M_0)}{L(D|M_1)}$$

$$D = -2(\ln L(D|M_0) - \ln L(D|M_1))$$

The distribution of D can be approximated by a χ^2 distribution with x degree of freedom, where the degree of freedom correspond to the difference in parameters between the models.

Aikake Information Criterion (AIC)

$$AIC = -2\ln L(D|M) + 2k$$

where k is the number of parameters in the model.

The best model is the one with the smaller AIC.

Practicals in R



The Phylogenetic Mixed Model

Mixed Model

$$\mathbf{y} = \underbrace{\mu + \beta \mathbf{x}}_{\text{Fixed Effects}} + \underbrace{\mathbf{a}}_{\text{Random effect}} + \underbrace{\mathbf{e}}_{\text{Residuals}}$$

Fixed vs. random effects

- **Fixed effects**
 - The parameter you are interested in.
 - For instance, if you want to estimate the impact of temperature on generation times of frogs, then the temperature is a fixed effect.
- **Random effects**
 - Parameter that have been measured and that can affect your model. However, they are not of primary importance in your study.
 - e.g., Blocks in experimental settings, phylogenies!

The phylogenetic Mixed Model (PMM)

$$\mathbf{y} = \underbrace{\mu + \beta \mathbf{x}}_{\text{Fixed Effects}} + \mathbf{a} + \mathbf{e}$$

Phylogenetic effect

$$\mathbf{a} \sim \mathcal{N}(0, \sigma_a^2 \mathbf{A})$$

$$\mathbf{e} \sim \mathcal{N}(0, \sigma_e^2 \mathbf{I})$$

Heredity (or phylogenetic signal)

Variance structure

$$\mathbf{y} = \mu + \beta \mathbf{x} + \overbrace{\mathbf{a} + \mathbf{e}}$$

$$h^2 = \frac{\sigma_a^2}{(\sigma_a^2 + \sigma_e^2)}$$

Flexibility of the PMM

$$\mathbf{y} = \mu + \beta \mathbf{x} + \mathbf{a} + \mathbf{b} + \mathbf{e}$$

Fixed Effects Phylogenetic effect

Measurement error

The diagram illustrates a regression model with the following components:

- Fixed Effects:** Represented by the term $\mu + \beta \mathbf{x}$, which is grouped under a brace.
- Phylogenetic effect:** Represented by the term \mathbf{a} , indicated by an arrow pointing to it.
- Measurement error:** Represented by the term \mathbf{e} , indicated by an arrow pointing to it.

You can easily add more random effects. This is not possible with PGLS

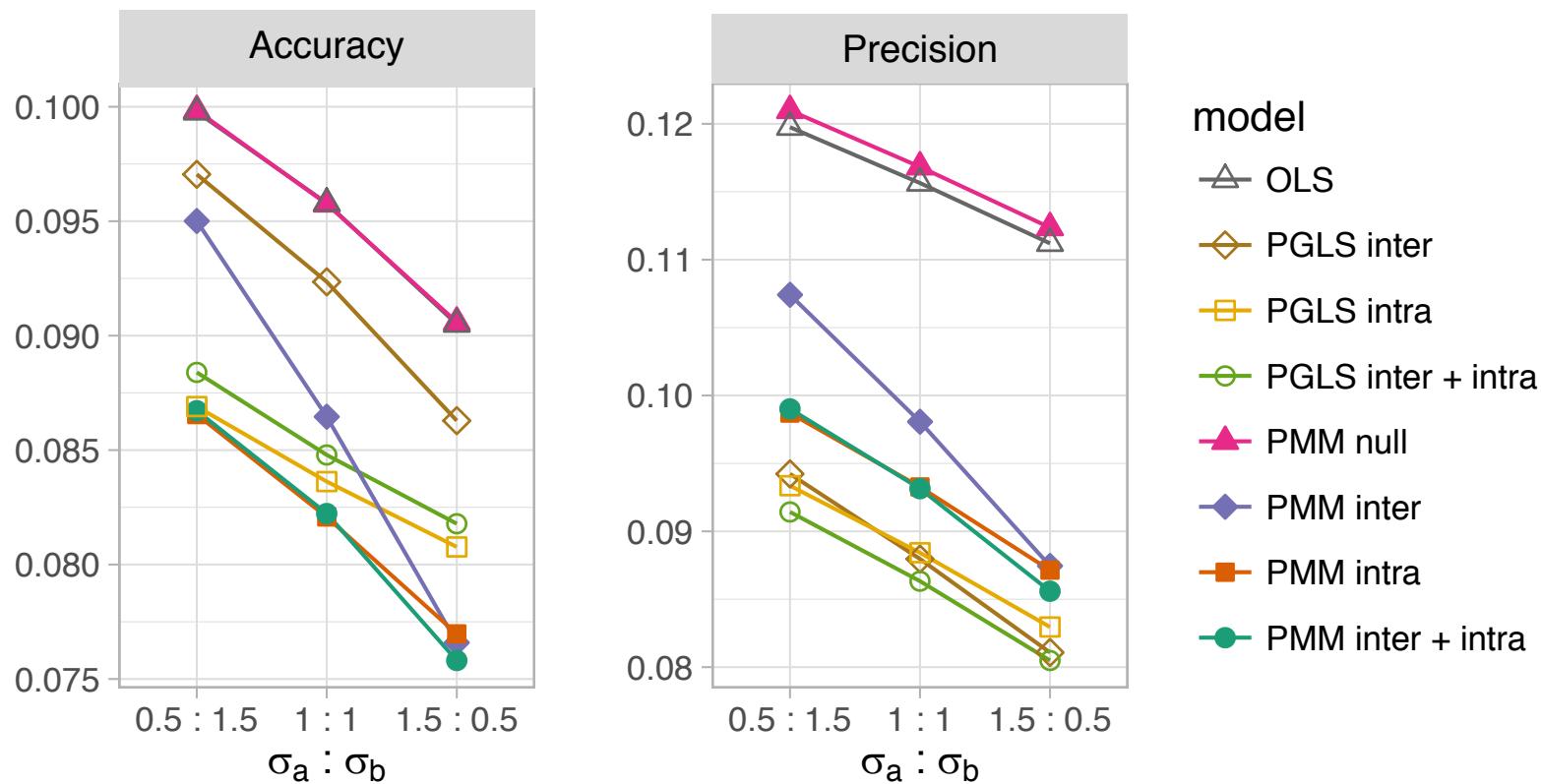
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Why use comparative methods?

Why use comparative methods?

- Better accuracy and precision for fixed effects



Why use comparative methods?

- Lower type I error and higher power

