#### Micro to Macroevolution: What does Quantitative Genetics have to do with Comparative methods?

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# Methodological similarity

# Ingredients





#### **Estimating Additive Genetic Variance**

**Basic idea:** 

*Pedigree* provides *structured knowledge* and *expected similarity* betwen relatives, allowing partitioning of *phenotypic variance among individuals* and estimation of *heritable genetic variation* 

a	ID	Dam	ı Si	$\mathbf{re}$	b		(	
	$1(g_1)$	NA	N	A		2	L	(3)
	$2(g_1)$	NA	N.	A		V v	$\langle \rangle$	1
	$3(g_2)$	NA	N	A		(4)	(5	$\tilde{\mathbf{b}}$
	4	1	2			0	$\sim$ ]	,
	5	1	<b>3</b>				Ĕ	$\mathbf{\hat{s}}$
	6	5	4				G	$\langle  $
	7	6	3					(7)
	с	/ 1	0	0	0.5	0.5	0.5	0.25
		0	1	0	0.5	0	0.25	0.125
		0	0	1	0	0.5	0.25	0.625
	$\mathbf{A} =$	0.5	0.5	0	1	0.25	0.625	0.3125
		0.5	0	0.5	0.25	1	0.625	0.5625
		0.5	0.25	0.25	0.625	0.625	1.125	0.6875
		0.25	0.125	0.625	0.3125	0.5625	0.6875	1.125 /

# "The Comparative Method"







## Horned lizards are cool



# What caused these adaptations?





# Felsenstein 1985

# Why can't we do "regular" linear regression again?

# Non-in ppendence of spiries



**Y** ~ **X** 

# Why can't we do "regular" linear regression again?

# Non-independence of *residual error variation*





Pedigree/ Phylogeny & Model for random effects (e.g. Mendelian inheritance or BM)

> Response traits

Predictor traits/ Treatment/ Fixed effects







# **Brownian Motion**



Figure 3.5. Example of a phylogenetic tree (left) and its associated phylogenetic variance-covariance matrix  $\mathbf{C}$  (right).

<ol> <li>(1) (3)</li> </ol>		/ 1	0	0	0.5	0.5	0.5	0.25
JAA		0	1	0	0.5	0	0.25	0.125
(4) (5)		0	0	1	0	0.5	0.25	0.625
$\sim$	$\mathbf{A} =$	0.5	0.5	0	1	0.25	0.625	0.3125
<b>6</b>		0.5	0	0.5	0.25	1	0.625	0.5625
		0.5	0.25	0.25	0.625	0.625	1.125	0.6875
Ć		0.25	0.125	0.625	0.3125	0.5625	0.6875	1.125 /

#### Replace *individuals* with *species*

Basic idea:

*Phylogeny* provides *structured knowledge* and *expected similarity* betwen relatives, allowing partitioning of *phenotypic variance among species* and estimation of *"phylogenetic heritability" AKA phylogenetic signal* 



Figure 1: Illustration of the phylogenetic mixed model (PMM) drawn as a phylogeny in units of expected variance of character change. The PMM envisions extant taxon phenotypes to be the result of a linear combination of gradually accumulated evolutionary changes occurring along a true species phylogeny and short-lived evolutionary changes (possibly selective responses to rapid environmental shifts) occurring in each taxon independently and not passed on between ancestor and descendant taxa.

#### The "Animal Model"

- $y = X\beta + Za + e$  y = (nx1) vector of photoecies Means  $\beta = (px1)$  vector of Species Means  $\beta = (px1)$  vector of S
  - $\beta$  = (px1) vector of SP2a effect regression coefficients (FIXED)
  - $\mathbf{X} = (nxp)$  design matrix relating  $\mathbf{y}$  to  $\boldsymbol{\beta}$  (FIXED)
  - a = (qx1) vector of additive effects (q = number of individuals in the pedigree) (RANDOM)
  - Z = (nxq) design matrix relating y to a (RANDOM)
  - e = (nx1) vector of errors
- Solve for β and a
- Assume

Var(e) =  $I\sigma_e^2$  (errors are independent) Var(a) =  $A\sigma_a^2$  (var of a depends on rel- logen nip matrix A) cov(a,e) = 0  $\alpha = \sigma_e^2 / \sigma_a^2$  is known (!!!!) (need a starting point)

# What's different?

#### Entries of *A* in pedigrees vs. phylogenies Mendelian laws: Coefficient of relatedness = 0.5 for parents & offspring

Assumption of constant rate Brownian Motion: Covariance proportional to branch lengths. Equally well justified?

# What's different?

Interpretation of  $\sigma_a^2 \& \sigma_e^2$ 

Additive genetic variance & Environmental variance. Multivariate  $\sigma_a^2 = G$ -matrix

Brownian Motion rate & nonphylogenetic variance Multivariate  $\sigma_a^2 = R$ -matrix

 $\boldsymbol{\sigma}_{11}$ 12 Π

Variance & covariance in Breeding Values per unit of genetic relatedness

Variance & covariance in Trait divergence per unit of branch length (e.g. millions of years)  $R = \begin{matrix} \sigma_{11}^2 & \sigma_{12}^2 \\ \sigma_{12}^2 & \sigma_{22}^2 \\ \sigma_{12}^2 & \sigma_{22}^2 \end{matrix}$ 

# What would we predict about macroevolution from microevolution?

**Microevolutionary patterns** We now know that we can study evolution in real time

17.13 g 16.06 g (1978) (1976) **Response to selection** 6.7% Δ body size in **1** generation (2 years) Let's assume only 1% is evolutionary



(Grant and Grant, 2002)



### **Let's do the calculations:** If a population increased by 1% every generation starting from ~16 g:

In 200 years → 43 g In 500 years ▶ 193 g In 1,000 years ▶ 2.3 kg In 2,000 years 335 kg ► 6.47 x 10<sup>19</sup> kg In 10,000 years

## Aside: Why multiplicative increase?

#### Log transform size data! Read this paper:

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#### THE QUARTERLY REVIEW of BIOLOGY



MEASUREMENT AND MEANING IN BIOLOGY

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In 200 years → 43 g In 500 years → 193 g In 1,000 years → 2.3 kg In 2,000 years → 335 kg In 10,000 years → 6.47 x 10<sup>19</sup> kg

# But evolution often reverses itself!

# Let's instead simulate going up or down randomly

(Brownian motion)



(Grant and Grant, 2002)














Years

### What does the fossil record say?



# The pattern is stasis



Stephen Jay Gould

The Paradox of Stasis (Hansen & Houle 2004): Organisms seem to be able to evolve far more than they ever do

Empirical studies often find: Strong (and often persistent) directional selection (Hereford et al. 2004, Morrissey & Hadfield 2012) High levels of additive genetic variance (Mousseau & Roff 1987, Houle 1992) Rapid evolutionary rates

(Hendry & Kinnison 1999, Kinnison & Hendry 2002)

...yet stasis in the fossil record

(Gingerich 1983, 2002)

## Does microevolution even matter for long-term change?

### PUNCTUATED EQUILIBRIA: AN ALTERNATIVE TO PHYLETIC GRADUALISM

"... to it enli

Niles Eldredge · Stephen Jay Gould

"...paleontology deals with a phenomenon that belongs to it alone among the evolutionary sciences and that enlightens all its conclusions -- time."

- Eldredge & Gould, 1972



# How can we see the pattern across scales of time?

# All studies of phenotypic evolution measure comparable quantities



We measure two quantities:
(1) "time for evolution"
(2) Δ mean body size

















### "The Evolutionary Blunderbuss"



Uyeda et al., *PNAS,* 2011





### Simpson's Adaptive Zones



### Note that this implies *rate scaling*

#### **Rate = Change/Time**

If the numerator doesn't change, then rates will be fastest over short timescales!

Why this matters?

Everything will look like it's speeding up toward the present. Do we believe the past was like the present? Annual Review of Ecology, Evolution, and Systematics

Causes and Consequences of Apparent Timescaling Across All Estimated Evolutionary Rates

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#### Navigating "tip fog": embracing uncertainty in tip measurements

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Corresponding author: Department of Biological Sciences, University of Arkansas, 601 Science Engineering Hall, 850 W Dickson St, Fayetteville, AR 72701, United States. Email: jmbeauli@uark.edu J.M.B. and B.C.O. contributed equally.

#### Abstract

Nature is full of messy variation, which serves as the raw material for evolution. Overlooking this variation not only weakens our analyses but also risks selecting inaccurate models, generating false precision in parameter estimates, and creating artificial patterns. Furthermore, the complexity of uncertainty extends beyond traditional "measurement error," encompassing various sources of variance. To address this, we propose the term "tip fog" to describe the variance between the value from the overall modeled evolutionary process and what is recorded, without implying a specific mechanism. We show why accounting for tip fog remains critical by showing its impact on continuous comparative models and discrete comparative and diversification models. We rederive methods to estimate this variance and use simulations to assess its feasibility and importance in a comparative context. Our findings reveal that ignoring tip fog substantially affects the accuracy of rate estimates, with higher tip fog levels showing greater biases from the true rates, as well as affecting which models are chosen. The findings underscore the importance of model selection and the potential consequences of neglecting tip fog, providing insights for improving the accuracy of comparative methods in evolutionary biology.

Keywords: evolutionary rates, measurement error, intraspecific variation, tip fog, macroevolution, hidden Markov model

#### Discussion

While the importance of tip fog in continuous traits has long been acknowledged, we were surprised by how accurately it can be estimated from both continuous and discrete data directly. This is significant because tip fog is not just simply adding another parameter—it represents the extent to which tip data distorts or misrepresents the underlying reality. Given





Some proposals

### **Populations vs. lineages**

Eldredge, et al. 2005. *The dynamicsof evolutionary stasis. Paleobiology.* 

Bartoszek et al. 2017. Using the Ornstein-Uhlenbeck process to model the evolution of interacting populations, J. of Theoretical Biology





Species means = How we measure macroevolution

### Intraspecific competition

Haller & Hendry. 2014. *Solving the paradox of stasis: Squashed stabilizing selection and the limits of detection, Evolution* 



### **Temperature tracking**

Hunt et al. 2015. *Simple vs complex models of trait evolution and stasis as a response to environmental change, PNAS* 





Figure S6. Results of simulations from the temperature-tracking model, calibrated by *Poseidonamics major* (left) and *Neotoma cinerea* (right). Vertical axis is magnitude of evolutionary variation measured as the standard deviation of samples in a sequence, with the contribution from measurement error removed (see Methods). Horizontal axis is sequence duration, in years and on a  $\log_{10}$  scale (a value of 6 is 1 Myr). Points are semi-transparent and lines represent locally weighted (lowess) regressions with a smoother span = 0.5.

### **Randomly fluctuating selection**





Holstad et al. 2024 Evolvability predicts macroevolution under fluctuating selection. Science.

### **Multivariate genetic constraints?**

### (See paradox of predicatibility lecture by Fabio)








### Three modes of evolution? Remarks on rates of evolution and time scaling

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### Abstract

Rates of evolution get smaller when they are measured over longer time intervals. As first shown by Gingerich, rates of morphological change measured from fossil time series show a robust minus-one scaling with time span, implying that evolutionary changes are just as large when measured over a hundred years as when measured over a hundred-thousand years. On even longer time scales, however, the scaling shifts toward a minus-half exponent consistent with evolution behaving as Brownian motion, as commonly observed in phylogenetic comparative studies. Here, I discuss how such scaling patterns arise, and I derive the patterns expected from standard stochastic models of evolution. I argue that observed shifts cannot be easily explained by simple univariate models, but require shifts in mode of evolution as time scale is changing. To illustrate this idea, I present a hypothesis about three distinct, but connected, modes of evolution. I analyze the scaling patterns predicted from this, and use the results to discuss how rates of evolution should be measured and interpreted. I argue that distinct modes of evolution at different time scales act to decouple micro- and macroevolution, and criticize various attempts at extrapolating from one to the other.

Keywords: evolution rate, microevolution, macroevolution, Ornstein–Uhlenbeck process, maladaptation

## **The Elephant in the Dark**

*Each of us touches one place And understands the whole in that way.* 

*If each of us held a candle there, And if we went in together, We could see it.* 

# **Discussion:**

- What is the most compelling explanation for "million-year wait" and stasis?
- How should we conceive of adaptive radiations and key innovations?
- Does speciation matter? Does extinction?

• What can we measure that predicts constraints across timescales?

# More generally...

What happens to all the "stuff" we study at one level, when scale up to the next?

Molecular genetics: Rampant epistasis/ molecular interactions/GxE Scale up --> Additive model of QG(?)

EQG: G-matrices/constraints/ competition/coevolution Scale up --> Brownian Motion(?)