

Revisiting the bivalve and brachiopod saga using new tools and data: They really did not pass each other in the night

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Liow, Reitan & Harnik 2015. Ecological interactions on macroevolutionary time scales: clams and brachiopods are more than ships that pass in the night. *Ecology Letters*



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Paul Harnik Franklin & Marshall College Lancaster, PA





- Brachiopods common and diverse before 200 Million years ago
- Bivalves now common and diverse





Gould & Calloway 1980 Clams and brachiopods - ships that pass in the night. *Paleobiology*



 Miller & Sepkoski 1988. Modeling bivalve diversification: the effect of interaction on a macroevolutionary system. *Paleobiology*

• Aberhan, Kiessling & Fursich 2006. Testing the role of biological interactions in the evolution of mid-Mesozoic marine benthic ecosystems. *Paleobiology*

• Payne, Heim, Knope & McClain 2014. Metabolic dominance of bivalves predates brachiopod diversity decline by more than 150 million years. *Proc Royal Soc B*

- Miller & Sepkoski 1988. Modeling bivalve diversification: the effect of interaction on a macroevolutionary system. *Paleobiology -bivalve interspecific competition and mass extinction important*
- Aberhan, Kiessling & Fursich 2006. Testing the role of biological interactions in the evolution of mid-Mesozoic marine benthic ecosystems. *Paleobiology - predation important for brachiopod decline*
- Payne, Heim, Knope & McClain 2014. Metabolic dominance of bivalves predates brachiopod diversity decline by more than 150 million years. *Proc Royal Soc B – brachiopods were just never good enough*

Do clade-clade interactions influence macroevolutionary processes?





Problem 2 – external drivers

Climate, tectonics, volcanism, sea level.....

Fig from Hannisdal and Peters Science 2011

Problem 3 - causality



Do clade-clade interactions influence macroevolutionary processes?

What, if any, are the relationships between brachiopod and bivalve diversification?



Problem 1 – sampling bias; Solution 1A – Paleobiology Database

Paleobiology	
Database	
A	
\bigcirc	

Time intervals	I	П	III	IV
Species 1	1	0	0	0
Species 2	0	0	1	0
Species 3	0	1	0	0
Species 4	1	0	0	1
Species 5	1	1	1	1
Species 6	0	1	0	1
Species 7	1	0	1	1
Species 8	0	0	1	0
Species 9	1	0	0	0
Species 10	0	0	0	1

1 = observed 0 = not observed

Problem 1 – sampling bias; Solution 1B – Mark Recapture

Nichols & Pollock 1983. Estimating taxonomic diversity,

extinction rates, and speciation rates from fossil data using capture-recapture models. Paleobiology

Liow & Nichols 2010. Estimating rates and probabilities of origination and extinction using taxonomic occurrence data: Capture-recapture approaches. In: Short Courses in Paleontology: Quantitative Paleobiology (eds. Hunt & Alroy)

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1 = observed 0 = not observed **Problem 1 – sampling bias; Solution 1B – Mark Recapture**

Survival probabilities		ϕ_{I} (þ _{II} d	Þ _{III}
Time intervals	1	П	Ш	IV
Species 4	1	0	0	1
Sampling probabilities		\mathbf{p}_{II}	$\mathbf{p}_{\mathrm{III}}$	\mathbf{p}_{IV}

P("1001" | first observation) = $\phi_{I}(1-p_{II}) \phi_{II}(1-p_{III}) \phi_{III} p_{IV}$

Nichols & Pollock 1983. Estimating taxonomic diversity, extinction rates, and speciation rates from fossil data using capture-recapture models. *Paleobiology*

Liow & Nichols 2010. Estimating rates and probabilities of origination and extinction using taxonomic occurrence data: Capture-recapture approaches. In: *Short Courses in Paleontology: Quantitative Paleobiology* (eds. Hunt & Alroy)

Problem 1 – sampling bias; Solution 1B – Mark Recapture





Problem 2 – external drivers

Climate, tectonics, volcanism, sea level.....

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Problem 3 - causality



Basic linear SDE, an Ornstein-Uhlenbeck (OU) process

$$dX_1(t) = -\alpha_1(X_1(t) - \mu_1)dt + \sigma_1 dB_1(t)$$

Deterministic part

Stochastic part

Basic linear SDE, an Ornstein-Uhlenbeck (OU) process

 $dX_1(t) = \alpha_1(X_1(t) - \mu_1)dt + \sigma_1 dB_1$

Deterministic part Stochastic part $dX_1(t) = -\alpha_1(X_1(t) - \mu_1)dt + \sigma_1 dB_1(t)$

Correlation between X_1 and X_2

 $dX_2(t) = -\alpha_2(X_2(t) - \mu_2)dt + \sigma_2(1 - \rho^2)^{0.5}dB_2(t) + \rho\sigma_2dB_1(t)$

 $dX_{1}(t) = -\alpha_{1}(X_{1}(t) - \mu_{1})dt + \sigma_{1}dB_{1}(t)$ Correlation between X₁ and X₂ $dX_{2}(t) = -\alpha_{2}(X_{2}(t) - \mu_{2})dt + \sigma_{2}(1 - \rho^{2})^{0.5}dB_{2}(t) + \rho\sigma_{2}dB_{1}(t)$

Deterministic part

Stochastic part

 $dX_1(t) = -\alpha_1(X_1(t) - \mu_1)dt + \sigma_1 dB_1(t)$

 $dX_{2}(t) = -\alpha_{2}(X_{2}(t) - \mu_{2})dt + \sigma_{2}(1 - \frac{\rho^{2}}{\rho^{2}})^{0.5}dB_{2}(t) + \frac{\rho}{\rho}\sigma_{2}dB_{1}(t)$

 X_2 is driven by X_1

 $dX_2(t) = -\alpha_2(X_2(t) - \mu_2 - \beta[X_1(t) - \mu_1])dt) + \sigma_2 dB_2(t)dt$

Deterministic part

Stochastic part

 $dX_1(t) = -\alpha_1(X_1(t) - \mu_1)dt + \sigma_1 dB_1(t)$

 $dX_{2}(t) = -\alpha_{2}(X_{2}(t) - \mu_{2})dt + \sigma_{2}(1 - \frac{\rho^{2}}{\rho^{2}})^{0.5}dB_{2}(t) + \frac{\rho}{\rho}\sigma_{2}dB_{1}(t)$

 X_{2} is driven by X_{1} $dX_{2}(t) = -\alpha_{2}(X_{2}(t) - \mu_{2} - \beta [X_{1}(t) - \mu_{1}])dt) + \sigma_{2}dB_{2}(t)dt$



- Origination
- Extinction
- Sampling



Check for relationships among abiotic and bivalve and brachiopod time series

- Origination
- Extinction
- Sampling



Fig from Hannisdal and Peters Science 2011

- Null model no relationship
- Correlative
- Causal X₂ to X₁
- Causal X_1 to X_2

Check for relationships among abiotic and bivalve and brachiopod time series



Five potential external drivers have no detectable relationships to bivalve or brachiopod diversification (or sampling) across the Phanerozoic

Fig from Hannisdal and Peters Science 2011











Paleobiology Database Liow, Reitan & Harnik 2015 Ecology Letters

Mark recapture approaches

Linear Stochastic Differential Equations



Bivalves influenced brachiopod evolutionary dynamics on macroevolutionary time scales

- Bivalves have been "suppressing" brachiopod diversification
- Climate and sea-level changes have no measurable effects on diversification dynamics of bivalves or brachiopods on Phanerozoic time scales

Table 2A	Brachiopod extinction rate (logged)	Brachiopod origination rate (logged)	Bivalve extinction rate (logged)	Table 2B	Brachiopod extinction rate (logged)	Brachiopod origination rate (logged)	Bivalve extinction rate (logged)	Bivalve origination rate (logged)	Brachiopod sampling rate (logged)
Brachiopod origination rate (logged)	1.5% * ↑ β = +1.1 (0.49, 2.3)			Brachiopod sampling rate (logged)	61%	76%	11.3% * corr ρ = +0.56 (0.17, 0.81)	8.1% *	
Bivalve extinction rate (logged)	3.0E-7%*** corr ρ = +0.89 (0.73–0.98)	0.13%**		Bivalve sampling rate (logged)	0.06% *** corr ρ = +0.73 (0.47, 0.92)	72%	0.46% ** corr ρ = +0.70 (0.37, 0.90)	45%	5E-11%*** corr ρ = +0.90 (0.78, 0.96)
Bivalve origination rate (logged)	45%	0.05%*** corr ρ = +0.83 (0.53, 0.99)	1.2%** corr ρ = +0.74 (0.37, 0.97)						

The first line in each cell is the Bayesian posterior probability for the null hypothesis (no relationship). *means the posterior probability is lower than the multiple testing limit of 12.9%; **<1.29% and ***<0.13%. The second line in a cell denotes the most probable link model if the null hypothesis was rejected. The link model can be correlative ('corr'), or causative (arrows point towards the causal driver). Black link models are where the probability of the best link model is more than twice that of the next best link model and uncertain links are in grey. ρ characterises the correlation (eqn 3) while β characterises the strength of the causal relationship (eqn 4). The last line gives the 95% credibility interval for the ρ or β . See Table 1 for models used for each time series.



