


Article

Fitting and evaluating univariate and multivariate models of within-lineage evolution

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Abstract.—The nature of phenotypic evolution within lineages is central to many unresolved questions in paleontology and evolutionary biology. Analyses of evolutionary time series of ancestor–descendant populations in the fossil record are likely to make important contributions to many of these debates. However, the limited number of models that have been applied to these types of data may restrict our ability to interpret phenotypic evolution in the fossil record. Using uni- and multivariate models of trait evolution that make different assumptions regarding the dynamics of the adaptive landscape, I evaluate contrasting hypotheses to explain evolution of size in the radiolarian *Eucyrtidium calvertense* and armor in the stickleback *Gasterosteus doryssus*. Body-size evolution in *E. calvertense* is best explained by a model in which the lineage evolves as a consequence of a shift in the adaptive landscape that coincides with the initiation of neosympatry with its sister lineage. Multivariate evolution of armor traits in a stickleback lineage (*G. doryssus*) shows evidence of adaptation toward independent optima on the adaptive landscape at the same time as traits change in a correlated fashion. The fitted models are available in the R package evoTS, which builds on the paleoTS framework.

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Introduction

Evolutionary time series of populations in the fossil record provide information on phenotypic change on time intervals in between generational and macroevolutionary timescales. Analyses of these types of data are thus poised to make important contributions to our current understanding of evolution across the timescale continuum. For more than 15 years, Hunt's paleoTS framework (Hunt 2006, 2008a, b; Hunt et al. 2008, 2015; Hunt and Carrano 2010) has been instrumental in generating new knowledge of evolutionary trait dynamics at the intersection between paleontology and evolutionary biology analyzing such time series. For example, trait evolution within lineages in the fossil record has been shown to be much more diverse than stasis alone (Hunt 2007; Hopkins and Lidgard 2012; Hunt et al. 2015); microevolutionary parameters have been successfully estimated from fossil data (Hunt et al. 2008); and rates of

evolution can be estimated using similar models, as in phylogenetic comparative methods (Hunt 2012). The new insights into phenotypic evolution provided by the paleoTS framework have thus contributed to a closer integration of paleontology and evolutionary biology.

Despite its success and impact, an extension of the paleoTS framework may be useful. First, a common use of the paleoTS R package is to investigate the relative fit of the three canonical models—stasis, unbiased random walk, and trend (modeled as an biased random walk)—to fossil time series. These models have a long history within paleontology (e.g., Raup 1977; Roopnarine 2001; Sheets and Mitchell 2001) but are not always able to adequately capture trait dynamics within lineages in the fossil record (Voje 2018; Voje et al. 2018). Fitting and comparing a larger range of evolutionary models may enable a richer interpretation of evolutionary change within lineages (Fig. 1).

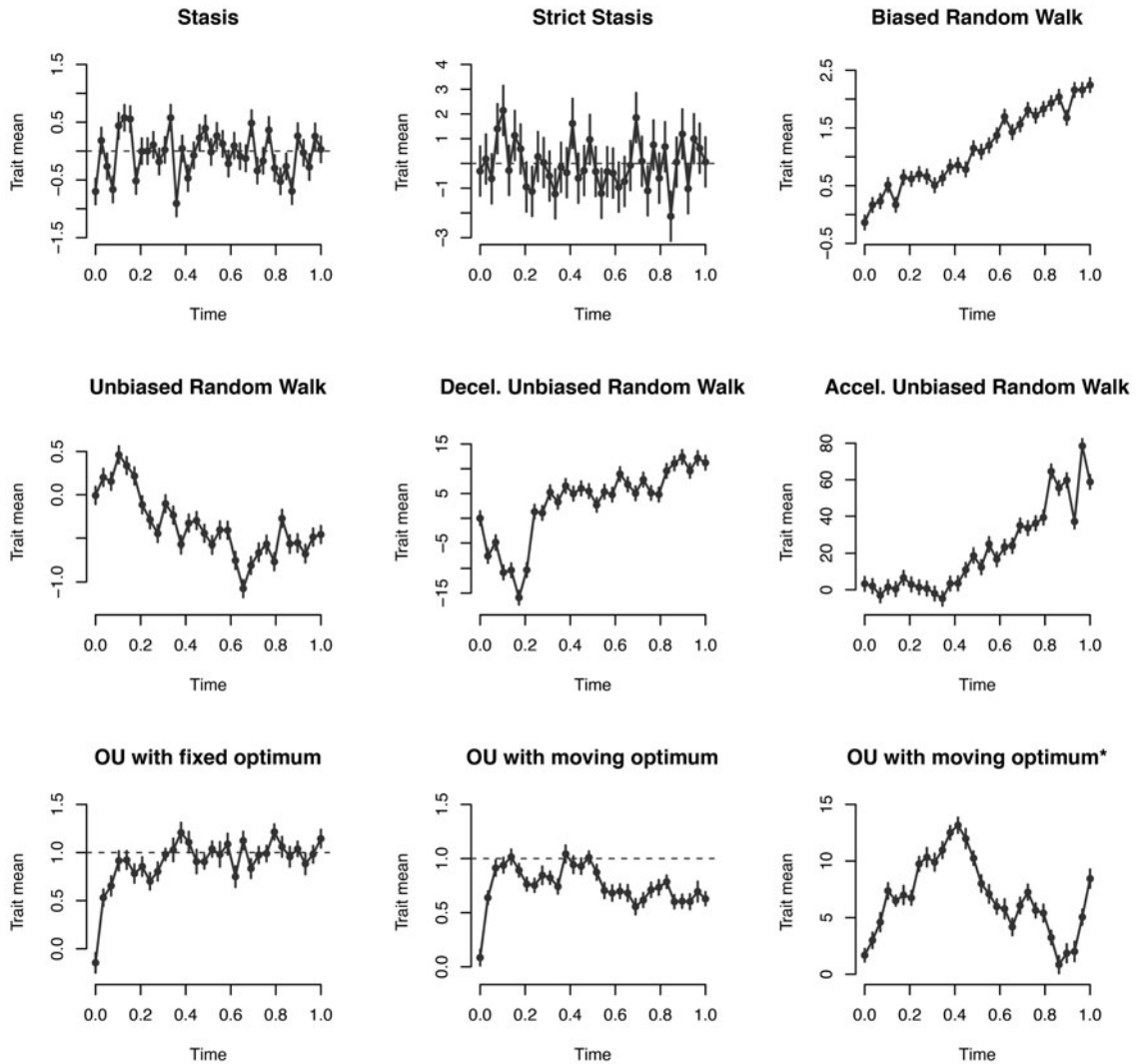


FIGURE 1. Univariate evolution models that can be fit and compared in evoTS. The models stasis, strict stasis, biased and unbiased random walk, and Ornstein-Uhlenbeck (OU) with fixed optimum are implemented in paleoTS (Hunt 2006; Hunt et al. 2008, 2015). The other models are implemented in evoTS. All models can be fit and compared in evoTS. In the OU model with a moving optimum, the population is either displaced from the optimum at the start of the sequence or is residing on or very close to the optimum (latter model indicated by *). The dotted horizontal line shows the position of the optimum in the OU model with a fixed optimum and the starting value of the optimum for the model where the optimum is allowed to change.

Second, the adaptive landscape has been suggested as a conceptual bridge between our understanding of microevolutionary processes and evolution observed across longer timescales (Simpson 1944; Arnold et al. 2001; Hansen 2012). However, knowledge of the dynamics of the adaptive landscape across time is poor. Macroevolution is likely associated with movements

of peaks on the adaptive landscape, but a fixed adaptive landscape is commonly assumed in microevolutionary studies, which is also the case for the models implemented in paleoTS. Inferring the dynamics of the adaptive landscape from evolutionary time series may contribute to a better understanding of the dynamic nature of peak movements at different time intervals.

Third, evolution is inherently a multivariate phenomenon. Pleiotropy is omnipresent (e.g., Walsh and Blows 2009) and selection on one trait may cause genetically linked traits to evolve (Lande 1979; Lande and Arnold 1983). Traits may also commonly experience correlated selection. Multivariate models are useful for investigating whether traits change in a correlated or uncorrelated manner, whether one trait/variable affects the optimum of a second trait, or whether adaptation in traits happens independently. The univariate models in paleoTS are of limited use for assessing the consequences of the multivariate nature of selection and evolution within lineages.

Here, I explore these three avenues of research by fitting uni- and multivariate models to examine evolution of size in a radiolarian lineage and multivariate evolution of armor traits in a stickleback lineage. Analyses employ the new R package, *evoTS*. As the univariate models in *evoTS* are natural extensions and modifications of the models in *paleoTS*, I start by introducing the univariate models available in *paleoTS* before I explain the expanded univariate models implemented in *evoTS*. I then apply these models to a well-known and previously published dataset, the evolution of size in the radiolarian lineage *Eucyrtidium calvertense* during allopatry and in a subsequent phase of neosympatry with its sister lineage *Eucyrtidium matuyamai* (Kellogg 1975). I continue by introducing the multivariate models implemented in *evoTS* before I apply them in a reanalysis of a published dataset of two armor traits in a stickleback lineage (Bell et al. 2006; Hunt et al. 2008).

evoTS Is Compatible with paleoTS

I have developed *evoTS* to mirror the user experience from *paleoTS* as much as possible. The two frameworks use the same data format and the model-fitting procedures are built on the same assumptions. For example, all models assume the population (sample) means in the sequence of ancestor–descendants have a joint distribution that is multivariate normal with an expected mean vector and covariance matrix that are functions of the parameters of each model, the time intervals separating the populations (samples) in the sequence, and the

sampling variances of the trait means calculated for each population (sample). The expected distribution of sample means is thus defined by their means, variances, and covariances given the assumption of multivariate normality. All models in *evoTS* have been implemented using the joint parameterization routine from *paleoTS* (Hunt 2008a), with the autocorrelation among samples being accounted for in the log-likelihood function. As in the *paleoTS* package, *evoTS* uses a quasi-Newton optimization routine for estimating maximum likelihood parameter estimates for univariate models, while the Nelder-Mead hill climbing algorithm is the default option for some of the multivariate models. Relative model fit is evaluated based on the small sample-corrected version of the Akaike information criterion (AICc) (Akaike 1974; Burnham and Anderson 2002).

Univariate Models in paleoTS

Unbiased random walk, biased random walk (trend model), and stasis were the first models implemented in the *paleoTS* framework (Hunt 2006). An unbiased random walk models evolution of a trait mean as independent draws from a normal distribution with mean zero ($\mu = 0$) and a variance (σ_{step}^2) commonly referred to as the step variance (Hunt 2006). Each draw represents a discrete evolutionary “step,” and the expected amount of evolution in the trait mean z per time step i is 0.

$$E[z_i] = z_0 \quad (1)$$

The trait mean is therefore not expected to be different from the ancestral state z_0 , but the variance around this expectation increases linearly with elapsed time,

$$\text{Var}[z_i] = \sigma_{\text{step}}^2 t_i + \varepsilon_i \quad (2)$$

where t_i is the elapsed time from the start of the time series to sample i (time at the start of the time series is always 0). The variance in each sample is influenced by the sampling error (ε_i) in estimating the trait mean, which is equal to the sample variance divided by the sample size (i.e., number of measured specimens) for

that sample. The covariance among sample means is given by:

$$\text{Cov}[z_i, z_j] = \sigma_{\text{step}}^2 t_{\min} \quad (3)$$

where t_{\min} represents the time interval between the start of the sequence and the earliest of the samples z_i and z_j .

The biased random walk (sometimes referred to as a trend model; e.g., see Hansen [1997]) is identical to an unbiased random walk except for a nonzero mean ($\mu \neq 0$) of the normal distribution from which evolutionary steps are drawn (Hunt 2006). A larger deviation from 0 of the mean translates into a stronger tendency to change unidirectionally in trait space. The expressions for the variance and covariance are identical for the biased and unbiased random walk (eqs. 2 and 3), while the expected mean trait value is given by:

$$E[z_i] = z_0 + \mu t_i \quad (4)$$

Various definitions of stasis have been employed in research that aims to quantify change in evolutionary time series (e.g., Bookstein 1987; Gingerich 1993; Roopnarine 2001; Sheets and Mitchell 2001). The stasis model in paleoTS is similar to a white noise process where trait evolution consists of uncorrelated fluctuations around a fixed trait value (θ) (Hunt 2006). The fluctuations around the fixed mean are described by a variance parameter (ω), which is assumed to stay constant over time. Time is accordingly not a relevant parameter in the stasis model. The strict stasis model (Hunt et al. 2015) is identical to the previously described stasis model, except that $\omega = 0$, which can be the case when the variance among trait means is smaller than the sampling error in the trait means, that is, the observed differences among trait means can be explained by sampling error alone (see also Hannisdal 2006).

Hunt et al. (2008) extended the paleoTS framework with the implementation of an Ornstein-Uhlenbeck (OU) model describing evolution of a trait toward a fixed peak in the adaptive landscape (Hansen 1997). The OU process is the simplest stochastic model that allows evolution toward a specific state and is

given by the following differential equation:

$$dy = \alpha(\theta - y)dt + \sigma_y dW_y \quad (5)$$

where dy is the change in the trait (y) over a time step dt , α describes the rate of evolution toward the optimum θ , dW_y represents independent and normally distributed changes with mean 0 and unit variance, with σ_y being the standard deviation of this white noise process. The first part of the OU process is deterministic and describes how the trait is pulled toward the optimum at a rate given by α . The second part is a stochastic process adding random noise scaled by the σ_y parameter to the trait dynamics. The expected change in a trait mean z per time step i and its variance and covariance are given by:

$$E[z_i] = e^{(-\alpha t_i)} z_0 + [1 - e^{(-\alpha t_i)}] \theta \quad (6)$$

$$\text{Var}[z_i] = (\sigma_{\text{step}}^2 / 2\alpha) [1 - e^{(-2\alpha t_i)}] + \varepsilon_i \quad (7)$$

$$\text{Cov}[z_i, z_j] = (\sigma_{\text{step}}^2 / 2\alpha) e^{(-\alpha t_{ij})} [1 - e^{(-2\alpha t_{\min})}] \quad (8)$$

where θ is the optimal trait value and t_{ij} is the time separating samples i and j (Hansen 1997; Hunt et al. 2008).

Univariate Models in evoTS

Simple models often sacrifice precision and nuance to distill general properties from data (Levins 1966). An evolutionary time series showing a relative better fit to an unbiased random walk compared with a stasis model does not mean trait evolution was random in each generation in the analyzed lineage. Rather, it suggests that the observed trait dynamics are more consistent with a pattern of “meandering” evolution, in which random changes in the trait mean accumulate over time, rather than with random fluctuations around a constant mean (akin to a white noise process). Adding or changing a few parameters in the models implemented in paleoTS can aid in extracting additional information not captured by the original models.

In the following sections, I describe the univariate models implemented in evoTS and

briefly discuss how they can be interpreted when fit to evolutionary sequences. evoTS is available for download from the Comprehensive R Archive Network (CRAN) (<http://cran.r-project.org>). The online vignette contains a detailed walk-through that explains from a user perspective how to fit all the different univariate models in evoTS (and paleoTS) and how to evaluate their relative fit to data (klvoje.github.io/evoTS/index.html).

Time-Varying Unbiased Random Walks

The rate of evolution is constant in an unbiased random walk, which means the trait variance is expected to increase linearly with time. A natural extension of this model is to allow the rate of evolution to change with time. The decelerated model of evolution implemented in evoTS is an unbiased random walk where the net rate of change declines exponentially through time. This model is basically identical to the early burst model developed for phylogenetic comparative data to test for a decelerated rate of evolution at the clade level (e.g., Cooper and Purvis 2010; Harmon et al. 2010). The expected evolutionary divergence between ancestor and descendant populations is zero in the decelerated evolution model (eq. 1) and its variance and covariance are given by:

$$\text{Var}[z_i] = \sigma_{\text{step},0}^2 \frac{(e^{rt_i} - 1)}{r} + \varepsilon_i \tag{9}$$

$$\text{Cov}[z_i, z_j] = \sigma_{\text{step},0}^2 \frac{(e^{rt_{\min}} - 1)}{r} \tag{10}$$

where $\sigma_{\text{step},0}^2$ is the initial value for the step distribution, and r describes the exponential decay in the rate change through time and is thus constrained to be < 0 (Harmon et al. 2010). An accelerating model of evolution is identical to the decelerated model, except that the r parameter is constrained to be > 0 . The time it takes to halve (for the decelerated evolution model) or double (for the accelerated evolution model) the rate of evolution is given by $\ln(2)/|r|$. The estimating algorithm in evoTS generally produces precise estimates of the r parameter in the decelerated and accelerated models (more details are given in Supplementary Fig. 1).

Model Interpretation.—A linearly increasing trait divergence with time will rapidly produce magnitudes of evolutionary change rarely observed in nature (e.g., Lynch 1990; Gingerich 2001; Estes and Arnold 2007; Uyeda et al. 2011). A decelerating rate of evolution mitigates this problem. Although many evolutionary scenarios and processes can be compatible with unbiased random walk models, a decrease in the rate of evolution over time might occur, for example, when a lineage experiences less selection after a period of higher initial rates of evolution due to changes in the environmental conditions (e.g., Voje 2020). A reduced rate may also occur if the effect of drift is reduced over time (i.e., due to increasing population size). An accelerated rate of evolution is not sustainable across long timescales but might fit lineages that experience an increased effect of drift or increasing environmental perturbations. Note that interpreting the trait dynamics as the results of neutral drift only may not be a plausible interpretation for ecologically relevant traits across long timescales (e.g., Hansen 2012). An alternative—and perhaps more likely—interpretation of unbiased random walk models is that they provide information on peak movements of the adaptive landscape. This is indeed a common interpretation of the related Brownian motion model in phylogenetic comparative approaches (Felsenstein 1988). As long as populations are sufficiently evolvable to immediately track changes in the locations of peaks in the adaptive landscape, the step variance (σ_{step}^2) provides insight on the rate of change of the adaptive peak itself according to this interpretation of the model. The decelerated and accelerated models may therefore represent scenarios where the rate of peak movements changes with time.

OU Models with Moving Optimum

A natural extension of the fixed-peak OU model implemented in paleoTS is to allow the peak to change. A model where the optimum is changing according to Brownian motion was proposed by Hansen et al. (2008) for analysis of phylogenetic comparative data. Adjusted to describe evolution of a single lineage, the expected trait mean is given by equation (6), while the variance and covariance are

given by the following expressions:

$$\begin{aligned} \text{Var}[z_i] = & \left[\frac{\sigma_{\text{step}}^2 + \sigma_{\theta}^2}{2\alpha} \right] [1 - e^{(-2\alpha t_i)}] \\ & + \sigma_{\theta}^2 t_i [1 - 2(1 - e^{-\alpha t_i})/\alpha t_i] \\ & + \varepsilon_{\text{min}} \end{aligned} \quad (11)$$

$$\begin{aligned} \text{Cov}[z_i, z_j] = & \left[\frac{\sigma_{\text{step}}^2 + \sigma_{\theta}^2}{2\alpha} \right] [1 - e^{(-2\alpha t_{\text{min}})}] e^{-\alpha t_{ij}} \\ & + \sigma_{\theta}^2 t_{\text{min}} [1 - (1 + e^{-\alpha t_{ij}})(1 - e^{-\alpha t_{\text{min}}})/\alpha t_{\text{min}}] \end{aligned} \quad (12)$$

where θ_0 is the initial (ancestral) optimum, σ_{θ}^2 is the (step) variance of the stochastic perturbations of the optimum. The half-life, $\ln(2)/\alpha$, is a reparameterization of the speed of adaptation in this process that is easy to interpret, as it is the time it takes for the trait to move halfway from the ancestral state to the optimum. The estimation algorithm is able to identify model parameters well, but outliers occur. Precision increases with longer time series (see Supplementary Fig. 2 for more details).

Model Interpretations.—The stability of the adaptive landscape is debated and is likely affected by many factors (e.g., Slater and Friscia 2019). A lineage in a hyper-stable niche may reside on a fixed peak, while a lineage inhabiting a more unstable environment may experience a more dynamic adaptive landscape. For example, traits with specialized ecological roles insensitive to changes in overall size (i.e., allometry) may reside on stable peaks, while the peak of a size-associated trait easily affected by changing ecological conditions may be in constant flux. Being able to explicitly test whether a fixed or a dynamic optimum model best fit a given evolutionary sequence may provide a valuable perspective on the dynamic nature of the adaptive landscape.

Mode-Shift Models

There is no a priori reason why a lineage should be described by a single evolutionary process (Hunt 2008b; Hunt et al. 2015). Mode-shift models allow two or more separate segments of a time series to evolve according to different models. evoTS includes a function that

enables the testing of all possible pairwise combinations of four models: unbiased random walk, biased random walk, stasis, and OU. This function also allows for the independent parameterization of the same model for two separate segments. In addition to assessing all possible switch points in mode of evolution, it is also possible to define where in the sequence a shift in mode occurs, a helpful feature if we have an a priori hypothesis for when a shift happened.

Applying the Univariate Models

Changes in the adaptive landscape may affect how lineages evolve. I reinvestigate an evolutionary sequence of a radiolarian lineage to assess the dynamics of the adaptive landscape across a few million years and whether it affects size change in the lineage.

Background

Kellogg (1975) investigated whether size evolution in the radiolarian lineage *Eucyrtidium calvertense* showed trait dynamics consistent with a scenario of character displacement (Fig. 2). *Eucyrtidium matuyamai* evolved from *E. calvertense* in subarctic waters, and the two lineages differentiated during a period of allopatry. The two species came into secondary contact when a population of *E. matuyamai* migrated to subtropical waters. During this neosympatric phase, the two lineages differentiated in size, with *E. matuyamai* evolving to become about 25% larger and *E. calvertense* to become about 10% smaller. Kellogg (1975) concluded that the evolutionary sequence of *E. calvertense* in subtropical waters showed little net change during the allopatric phase, but a trend toward smaller size in the neosympatric phase, a type of trait dynamics Kellogg (1975) interpreted to be consistent with the process of character displacement. The evolutionary sequence spans 3.67 Myr and consists of 49 samples with median and mean numbers of measured specimens per sample of 25 and 25.4, respectively (Fig. 2). The allopatric and neosympatric phases last for about 1.70 and 1.97 Myr, respectively.

Fitted Models

A mode-shift model consisting of two OU models (i.e., an OU–OU model) can assess

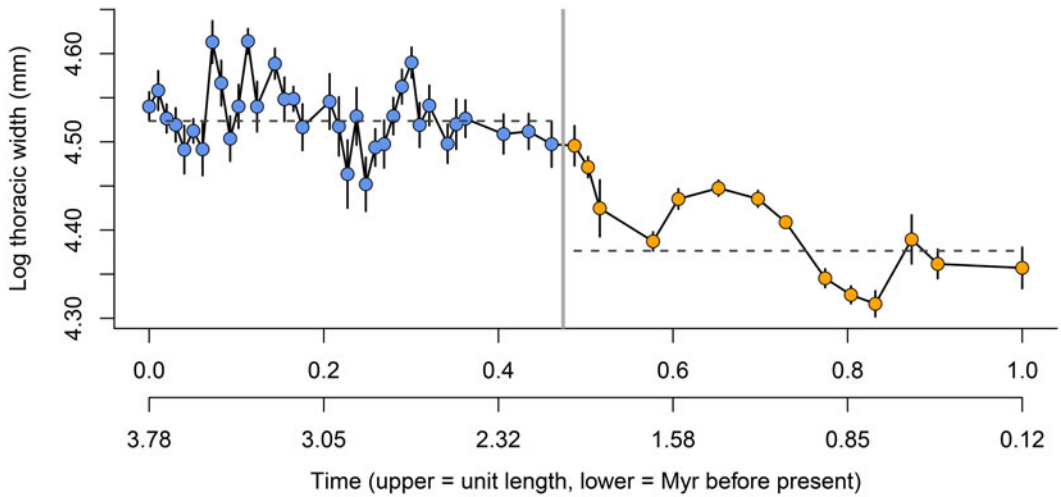


FIGURE 2. Size evolution in *Eucyrtidium calvertense* (Kellogg 1975). The vertical gray bar indicates the shift from allopatry to sympatry with *Eucyrtidium matuyamai*. Blue dots belong to the allopatric phase, and orange points belong to the sympatric phase. The best model is a mode-shift model consisting of two Ornstein-Uhlenbeck (OU) processes with fixed optima. The maximum likelihood parameter estimates (\pm SE) of this model are: $z_0 = 4.543 (\pm 0.019)$, $\theta_1 = 4.524 (\pm 0.009)$, $\theta_2 = 4.377 (\pm 0.021)$, $\sigma_{\text{step},1}^2 = 0.183 (\pm 0.130)$, $\sigma_{\text{step},2}^2 = 0.046 (\pm 0.027)$, $\alpha_1 = 94.282 (\pm 64.671)$, $\alpha_2 = 18.833 (\pm 10.231)$. The broken horizontal lines represent the fixed optimal trait values from the OU-OU model.

whether the initiation of the neosympatric phase led to a sudden change in the position of the adaptive peak for size in *E. calvertense*. I also fit OU processes with a constantly changing optimum to investigate how well models assuming continuous change of the adaptive landscape explained the data. To investigate whether models assuming a fixed adaptive landscape outcompeted the models assuming a dynamic landscape, I fit the stasis model, the trend model (i.e., a biased random walk), and unbiased random walk model with fixed, decelerating, and accelerating rates of evolution, and mode-shift models where the allopatric and neosympatric parts were either modeled as two unbiased random walks or where the second model was a biased random walk. Data and R scripts for replicating the analyses are available in the Supplementary Material.

Results

The OU-OU mode-shift model showed the best relative fit to the data (Table 1), with an optimal trait value during the sympatric phase (4.38 log micrometer) that was 13%

smaller compared with the optimum during the sympatric phase (4.52 log micrometer). The adaptive process is faster in the allopatric phase ($\ln(2)/\alpha = 0.007$, which translates into a half-life of about 27,000 years) compared with the sympatric phase ($\ln(2)/\alpha = 0.037$, i.e., a half-life of about 135,000 years; Table 2). The log-likelihood surfaces of the half-life values show some overlap in the two phases (Fig. 3), but while a half-life of 4.05% (about 150,000 years) of the sequence length is within 2 log-likelihood units in the allopatric phase, the equivalent value of the second phase is 31.51% (about 1,160,000 years). The stochastic part of the trait dynamics is also elevated during the allopatric phase ($\sigma_{\text{step},1}^2 = 0.183$) compared with the sympatric phase ($\sigma_{\text{step},2}^2 = 0.046$). To investigate whether the difference in temporal resolution between the two segments could explain the difference in trait dynamics, I subsampled the first segment 1000 times to match the length of the second segment (14 samples) and re-estimated the half-life and σ_{step}^2 parameters. The median estimates of the half-life and σ_{step}^2 from the subsampled data were 0.010 and 0.111, which

TABLE 1. Model fit to the *Eucyrtidium calvertense* sequence. The log-likelihood (log-lik.) and the relative model fit for the candidate models fit to the evolutionary sequence of *E. calvertense*. OU, Ornstein-Uhlenbeck; K, number of parameters in model; AICc, Akaike information criterion corrected for small sample size; *, the population at the start of the sequence is residing on or very close to the optimum.

Model type	Model	K	log-lik.	AICc	Δ AIC	AICc weight
No mode shift	Stasis	2	59.579	-114.896	55.562	0.000
	Biased random walk (trend)	3	87.422	-168.312	2.147	0.087
	Unbiased random walk	2	86.952	-169.644	0.815	0.169
	Decelerated evolution	3	88.032	-169.531	0.927	0.160
	Accelerated evolution	3	86.952	-167.371	3.087	0.054
	OU with fixed optimum	4	88.078	-167.247	3.211	0.051
	OU with moving optimum	4	89.478	-170.046	0.412	0.207
	OU with moving optimum*	5	88.078	-164.761	5.697	0.015
	Mode shift	Two unbiased random walks	4	84.942	-160.974	9.484
Unbiased and biased random walk		5	85.562	-159.729	10.729	0.001
Two OU models		8	95.029	-170.458	0.000	0.254

TABLE 2. Maximum likelihood parameter estimates for the candidate models fit to the *Eucyrtidium calvertense* sequence. See equations and main text for definitions of the different model parameters. The numbers in parentheses are standard errors calculated from the square root of the inverse of the diagonal of the Hessian matrix. OU, Ornstein-Uhlenbeck; *, the population at the start of the sequence is residing on or very close to the optimum.

Model	Parameter estimates (SE)
Stasis	$\theta = 4.49$ (0.01), $\omega = 0.01$ (0.00)
Biased random walk	$z_0 = 4.54$ (0.02), $\mu = -0.19$ (0.19), $\sigma_{\text{step}}^2 = 0.04$ (0.05)
Unbiased random walk	$z_0 = 4.54$ (0.02), $\sigma_{\text{step}}^2 = 0.04$ (0.00)
Decelerated evolution	$z_0 = 4.54$ (0.02), $\sigma_{\text{step}}^2 = 0.10$ (—), $r = -2.08$ (0.01)
Accelerated evolution	$z_0 = 4.54$ (0.23), $\sigma_{\text{step}}^2 = 0.04$ (—), $r = 0.00$ (0.61)
OU with fixed optimum	$z_0 = 4.55$ (0.02), $\sigma_{\text{step}}^2 = 0.04$ (0.02), $\theta = 4.40$ (0.09), $\alpha = 3.21$ (3.09)
OU with moving optimum	$z_0 = 4.54$ (0.02), $\sigma_{\text{step}}^2 = 0.22$ (0.29), $\sigma_{\text{step,opt}}^2 = 0.02$ (0.01), $\alpha = 205.57$ (325.00)
OU with moving optimum*	$z_0 = 4.55$ (0.02), $\theta_0 = 4.40$ (0.09), $\sigma_{\text{step}}^2 = 0.04$ (0.02), $\sigma_{\text{step,opt}}^2 = 0.00$ (—), $\alpha = 3.21$ (2.70)
Two unbiased random walks	$z_0 = 4.52$ (0.02), $\sigma_{\text{step,1}}^2 = 0.06$ (0.03), $\sigma_{\text{step,2}}^2 = 0.04$ (0.02)
Unbiased and biased random walk	$z_0 = 4.52$ (0.01), $\sigma_{\text{step,1}}^2 = 0.06$ (0.03), $\mu = -0.21$ (0.28), $\sigma_{\text{step,2}}^2 = 0.04$ (0.02)
Two OU models	$z_0 = 4.54$ (0.02), $\sigma_{\text{step,1}}^2 = 0.18$ (0.13), $\theta_1 = 4.52$ (0.01), $\alpha_1 = 94.28$ (64.67) $\sigma_{\text{step,2}}^2 = 0.05$ (0.03), $\theta_2 = 4.38$ (0.02), $\alpha_2 = 18.83$ (10.23)

suggests that differences in temporal resolution alone cannot explain the difference in the estimated trait dynamics between the two segments. The allopatric phase therefore appears to be characterized by faster evolution toward the fixed optimum and larger stochastic deviations from the optimum compared with the sympatric phase.

Models that differ in their relative model fit by a few AICc units may be worth considering as plausible or suitable alternative explanations of an empirical dataset (Burnham et al. 2011). The OU model with a constantly changing optimum has a very similar fit compared with the best model (Δ AICc = 0.412). The alpha parameter describing the rate of evolution toward the moving optimum is large (205.57), translating into a point estimate of the half-life of about 10,000 years. The point estimate of the rate of change in the optimum ($\sigma_{\text{step,opt}}^2 = 0.02$)

indicates a non-fixed optimum through time. The stochastic part of the trait dynamics is rather large ($\sigma_{\text{step}}^2 = 0.22$), suggesting size evolution in *E. calvertense* has contributions from both the deterministic and stochastic part of the OU model. A reasonable interpretation of the trait dynamics in *E. calvertense* according to the parameter values of this OU model is as a white noise process around a stochastically moving peak. Note that both the unbiased random walk and the decelerating unbiased random walk show a similar, albeit somewhat poorer, fit to the data compared with the OU process with a moving optimum. This is not surprising, as the optimum in the OU process changes according to an unbiased random walk. The better fit of the OU model is due to the size of the fluctuations around the optimum, which is sufficiently large not to be accounted for by measurement error in the

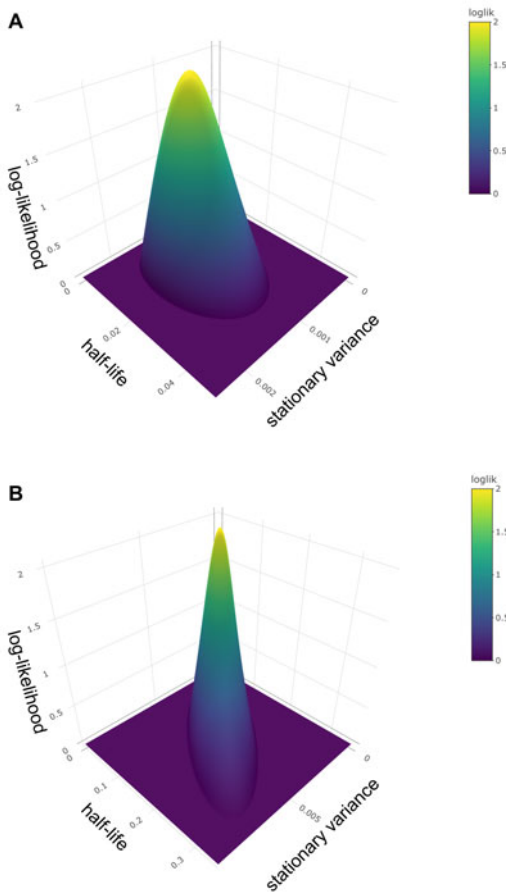


FIGURE 3. Log-likelihood surfaces for the Ornstein-Uhlenbeck (OU-OU) model. The panels show the support surface for the OU model describing the evolutionary sequence before and after the mode shift, respectively. The elevated area represents parameter estimates that are within two log-likelihood units of the best estimate. A, The first part of the sequence; the two-unit support surface includes immediate adaptation (i.e., half-life = 0) and extends up to 0.040. B, The second part of the sequence where a half-life of zero is not part of the support surface (0.019–0.315). The ranges of support for the two stationary variances are 0.000–0.002 and 0.001–0.008. Note that these results are conditional on the best estimate of the other parameters in the model (i.e., the ancestral state and the optimum).

samples. Not controlling for error in the samples would therefore unduly favor the unbiased random walk instead of the OU process.

In summary, the best model among the candidates suggests the position of the optimum changed toward a smaller optimal size when *E. calvertense* comes into secondary contact with *E. matuyamai*. Evolution toward a randomly

changing optimum in both the allopatric and sympatric phases of the evolutionary sequence, or “meandering” evolution described by unbiased random walk models, are also likely models of the trait dynamics in *E. calvertense*.

Multivariate Models in evoTS

Much can be learned from studies of single traits, but a trait-by-trait approach has some important shortcomings. The omnipresence of pleiotropy suggests only a very small number of truly genetically independent traits exist (Barton 1990; Johnson and Barton 2005; Walsh and Blows 2009). Evolutionary change in a trait is only rarely due to selection operating on that trait alone, as selection on genetically linked traits may also affect the focal trait (Lande 1979; Lande and Arnold 1983; Hansen and Houle 2008). Traits that are genetically independent may still be functionally dependent, which means they may experience coordinated selection and therefore have a tendency to evolve in concert. Trait evolution is thus inherently a multivariate process that requires multivariate models to be more fully understood.

The following sections provide a description of the multivariate models available in evoTS and how they can be interpreted. The online vignette details from a user perspective how to fit the different multivariate models implemented in evoTS, including walk-throughs and examples of how to test different hypotheses of evolution and adaptation ([klvoje.github.io/evoTS/index.html](https://github.io/evoTS/index.html)).

Multivariate Unbiased Random Walks

The multivariate unbiased random walk model can assess whether a set of traits evolve in a coordinated fashion or not. This is done by estimating an evolutionary rate matrix **R** (Felsenstein 2004; Revell and Harmon 2008; Revell and Collar 2009). The **R** matrix describes the rate of evolution in the investigated traits on the diagonal (i.e., the diagonal contains the step variances) and the covariance of the changes in the traits in the off-diagonal elements. The multivariate variance–covariance matrix for the unbiased random walk model (**V**) is computed using the Kronecker product

of the \mathbf{R} matrix and a “distance matrix” \mathbf{C} , describing how the different samples/populations are separated in time.

$$\mathbf{V} = \sum_{i=1}^m \mathbf{R}_i \otimes \mathbf{C}_i \quad (13)$$

where m represents the number of non-overlapping segments of a time series that have their own \mathbf{R} matrix. Sampling error of the trait mean (calculated as the sample variance divided by the sample size) is added to the diagonal of \mathbf{V} . To ensure symmetric positive definiteness of the \mathbf{V} matrix during log-likelihood optimization, \mathbf{R} is parameterized by its Cholesky decomposition as the cross-product of upper triangular matrices:

$$\mathbf{R} = \mathbf{L}\mathbf{L}^T \quad (14)$$

where \mathbf{L} is a square matrix with positive diagonal entries. \mathbf{L} is upper triangular if there are off-diagonal elements in \mathbf{R} . As for the univariate unbiased random walk, it is possible to test for a decrease or increase in the rate of change over time in the multivariate unbiased random walk model in evoTS. The r parameter adjusting the rate is assumed common for all the traits. Simulations show that the estimating procedure produces unbiased parameters even at sequence lengths of about 10 samples (see Supplementary Fig. 3 for more info).

Model Interpretation.—Potential causes of correlated trait evolution are many. Traits may, for example, independently follow optima governed by the same environmental drivers, show concerted evolution due to shared direct or indirect selection, or be affected similarly by genetic drift.

Note that the \mathbf{R} matrix is not the same as the genetic (\mathbf{G}) or phenotypic (\mathbf{P}) covariance matrices commonly estimated in quantitative genetics. However, the \mathbf{R} matrix is connected to these matrices under certain assumptions. For example, the \mathbf{R} matrix is expected to be proportional to the additive genetic variance–covariance matrix (\mathbf{G}) if the traits evolve due to genetic drift only (Lande 1979; Felsenstein 1988). Estimating \mathbf{R} can thus aid in assessing

to what extent evolution within lineages matches predictions from quantitative genetics.

Multivariate OU Models

Multivariate evolution is more than correlated change. Multivariate versions of the OU process allow for sophisticated investigations of a range of hypotheses regarding evolution and adaptation and are described by the following differential equation (Bartoszek et al. 2012; Reitan et al. 2012; Clavel et al. 2015):

$$d\mathbf{Z}(t) = \mathbf{A}[\boldsymbol{\theta}(t) - \mathbf{Z}(t)]dt + \mathbf{R}d\mathbf{W}(t) \quad (15)$$

where \mathbf{A} is a square matrix (with dimensions equal to the number of traits) describing the rate of evolution toward the optimal trait values, $\boldsymbol{\theta}$ is a vector containing the optimum for each trait, \mathbf{R} is a square matrix (with dimensions equal to the number of investigated traits) describing the stochastic changes in the traits, and \mathbf{W} is the diffusion parameter. Under the assumption that we only have one selective regime (optimum) per trait, the expected trait means of the OU process are the weighted sum of the optimum and the ancestral trait value (Hansen 1997):

$$E[\mathbf{Z}_i] = e^{(-\mathbf{A}t_i)}\mathbf{z}_0 + [1 - e^{(-\mathbf{A}t_i)}]\boldsymbol{\theta} \quad (16)$$

where \mathbf{Z}_i is a vector containing the expected trait values for sample i , \mathbf{z}_0 is a vector containing the ancestral trait means, and t_i is the time interval from the ancestral population mean (the start of the time series, which has a time of 0) to the i th population mean.

The variance and covariance of sample/population means are given by the following expression (Bartoszek et al. 2012; Reitan et al. 2012; Clavel et al. 2015):

$$\text{Cov}(z_i, z_j) = \left[\mathbf{Q} \left(\left\{ \frac{1}{\lambda_k + \lambda_l} [1 - e^{-(\lambda_k + \lambda_l)t_{\min}}] \right\}_{1 \leq k, l \leq m} \right) \odot \mathbf{Q}^{-1} \mathbf{L}\mathbf{L}^T (\mathbf{Q}^{-1})^T \right] \mathbf{Q}^T e^{-\mathbf{A}^T t_{ij}} \quad (17)$$

where \mathbf{Q} is the orthogonal matrix of eigenvectors of \mathbf{A} , $\mathbf{L}\mathbf{L}^T$ is the Cholesky decomposition

of the **R** matrix ($\mathbf{R} = \mathbf{L}\mathbf{L}^T$), λ_i is the i th eigenvalue of **A**, t_{\min} is the time interval between the start of the sequence and the earliest of the samples z_i and z_j , t_{ij} is the time separating two samples z_i and z_j , and \odot represents the Hadamard (element-wise) matrix product. Under the assumption that the **A** matrix has a number of linear independent eigenvectors equal to the number of traits investigated, **A** can be expressed by its eigendecomposition:

$$\mathbf{A} = \mathbf{Q}\mathbf{\Lambda}\mathbf{Q}^{-1} \tag{18}$$

where $\mathbf{\Lambda}$ is a matrix with the eigenvalues (λ) of **A** on the diagonal. The matrix exponential in equation (17) can then be solved using the eigendecomposition of **A** (Bartoszek et al. 2012; Reitan et al. 2012; Clavel et al. 2015):

$$e^{-\mathbf{A}t} = \mathbf{Q}\text{diag}(e^{-\lambda_1 t}, \dots, e^{-\lambda_m t})\mathbf{Q}^{-1} \tag{19}$$

Precise estimation of parameters is a challenge that tends to increase with model complexity. Parameter estimation under univariate and multivariate phylogenetic OU models can be difficult (Hansen et al. 2008; Bartoszek et al. 2012, 2023; Ho and Ané 2014; Cressler et al. 2015), but simulations show that multivariate OU model parameters in evoTS are overall identifiable. Precision is high for diagonal elements in **R** and **A** and the optima even for short time series. The median parameter estimate of the off-diagonal element in **A** is in the proximity of the true value for short sequence lengths and approaches the true value with increasing sequence lengths (see Supplementary Fig. 4 for more info).

Model Interpretation.—The **A** and **R** matrices are key to defining the trait dynamics in a multivariate OU model. The elements in **R** control the stochastic parts of the trait dynamics in the OU process and can be interpreted similarly as **R** in the multivariate unbiased random walk: the diagonal elements in **R** represent the step distributions (step variances) of the changes in each individual trait, while any nonzero off-diagonal elements represent the covariance of the stochastic changes in the traits. The elements in the **A** matrix affect the deterministic part of the OU process, that is, the adaptive

process of traits evolving toward optima. The diagonal elements in **A** are the individual alpha parameters for each trait, while a nonzero off-diagonal element reflects how changes in the trait affect the optimum of another trait. Four broad categories of hypotheses can be investigated based on how the **A** and **R** matrices are parameterized.

Independent Trait Evolution.—Both the deterministic and stochastic parts of the evolutionary trait dynamic are independent for each trait. This model is the equivalent of fitting univariate OU models to each trait separately and is parameterized in the multivariate version by allowing only diagonal elements in the **A** and **R** matrices to be nonzero.

Independent Adaptation.—Each trait adapts independently to its optimum, but the stochastic part of the trait dynamics is correlated. This model is obtained if the **A** matrix is diagonal while the **R** matrix has nonzero off-diagonal elements.

Non-independent Adaptation.—Changes in trait X affect the optimum of trait Y , but changes in Y do not affect the optimum of trait X . **A** can be a nonsymmetric matrix (contrary to the **R** matrix), which means one trait is allowed to affect the optimum of another trait, but not vice versa. A negative number in an off-diagonal element in **A** means the trait is evolving toward the optimum, while a positive number means the trait is evolving away from the optimum. The stochastic changes in the trait (controlled by the parameterization of the **R** matrix) can be either correlated or uncorrelated.

Reciprocal Adaptation.—Traits affect one another’s optima. This is the case if their respective off-diagonal elements in **A** are nonzero. One trait may assert a larger effect on the optimum of another trait. The stochastic changes in the trait can be either correlated or noncorrelated.

An **A** matrix with nonzero off-diagonal elements investigates Granger causality between the traits/variables (Granger 1969; Schweder 1970; Reitan et al. 2012; Hannisdal and Liow 2018; Reitan and Liow 2019). Granger causality is a statistical concept that is used to determine whether one time series is useful in predicting another. Simply speaking, we have

evidence for Granger causality if observations in one time series are useful for forecasting future observations in one or several other time series. The multivariate OU process therefore allows us to move beyond interpreting correlations among variables in time series. A correlation is symmetric (the correlation between X and Y is the same as the correlation between Y and X), but that is not needed for Granger causality. X can (Granger) cause Y , without Y Granger-causing X . Forecasting using Granger causality is only possible if there is some lag in the tracking of the optimum, that is, if a trait is unable to immediately respond to changes in the optimum. The rate of adaptation in the multivariate OU model is determined by the entries in the A matrix and can be conveniently calculated by the half-life. As in the univariate OU model, the half-life ($\ln(2)/\alpha_{ii}$) describes the time it takes for the trait to move halfway from the ancestral state to the new optimal state.

The multivariate OU model is reduced to an unbiased random walk if the diagonal elements in A are zero. Within the multivariate OU process, it is therefore possible to allow traits/variables that change according to an unbiased random walk to affect the optimum of traits evolving according to an OU process. Models with a mix of traits evolving as either OU or as an unbiased random walk have been termed “OUBM models” in the phylogenetic comparative literature (e.g., Bartoszek et al. 2012, 2023). An OUBM model may, for example, be a sensible choice if we want to investigate whether an environmental variable (e.g., a paleoclimatic proxy) that we assume changes as an unbiased random walk affects the optimum of a trait we assume evolves according to an OU process.

Applying the Multivariate Models

Analyzing several traits or variables jointly using multivariate models enables a more sophisticated assessment of alternative hypotheses of the observed trait dynamics in the data relative to analyzing each trait separately. I apply multivariate models on a dataset on armor trait evolution in a threespine stickleback lineage (*Gasterosteus doryssus*) that has

previously been analyzed using univariate models (Bell et al. 2006; Hunt et al. 2008). Strong genetic covariances among armor traits (Leinonen et al. 2011) and evidence that different armor traits are affected by the same loci (Cresko et al. 2004) in extant threespine sticklebacks (*Gasterosteus aculeatus*) suggest armor traits may not evolve independently. Armor traits are also likely to serve similar ecological functions and may therefore often experience similar selection pressures. A multivariate approach is therefore warranted when analyzing armor traits in threespine sticklebacks.

Background

Bell et al. (2006) analyzed morphological evolution in three skeletal traits in a fossil stickleback lineage (*G. doryssus*) across more than 7000 years from well-preserved lake sediments. The three traits are part of the armor of the fish: number of dorsal spines, number of touching pterygiophores, and a pelvic trait measured based on scores of the completeness of the pelvic condition. All three traits show a clear trend of reduction in number (and score) during the time series, likely as a consequence of a reduced predation pressure in the lake (Bell et al. 2006). However, Bell et al. (2006) did not find strong evidence for natural selection in these time series, as falsifying a null model of neutral evolution (drift) proved difficult. Hunt et al. (2008) reanalyzed the data using paleoTS and found that an OU model with a fixed optimum showed a much better relative fit to each of the three stickleback traits compared with an unbiased random walk (drift model), thus supporting adaptive evolution toward trait-specific optima. The multivariate analysis of the data in this paper assesses the extent to which evidence exists for correlated and/or adaptive coevolution of the armor traits.

Respecting the scale type of the investigated variables in quantitative analyses is important for producing meaningful results (Houle et al. 2011; Voje et al. 2020). The uni- and multivariate models in evoTS (and paleoTS) can only be meaningfully applied to data on scale types where calculations of variances and covariances are valid. The two count traits in the stickleback data from Bell et al. (2006) are on a

ratio scale (Stevens 1946), while the scale type of the pelvic score is more difficult to define. The description of how the score was applied (Bell et al. 2006: p. 567) suggests a nonlinear relationship between increments of the score, which disqualifies it as a measurement on a ratio or interval scale (Stevens 1946), thus making calculations of variances and covariances nonsensical. The pelvic score was accordingly not included in the analysis. The two remaining traits were log-transformed before the models were fit. I removed one and two samples from the number of spines and number of touching pterygiophores, respectively, to make samples overlap in time. The total length of the multivariate dataset is 54 samples (Fig. 4).

Fitted Models

I fit multivariate unbiased random walks assuming either uncorrelated (only diagonal elements in **R**) or correlated stochastic changes (completely parameterized **R**) in the two traits. I also fit different implementations of the multivariate OU model to investigate (1) if the two traits evolved independently (only diagonal elements in the **A** and **R** matrices), (2) if the traits showed evidence of independent adaptation but correlated stochastic evolution (only diagonal elements in **A**, but a fully

parameterized **R**), (3) if one trait affected the optimum of the other trait (upper and lower triangular **A**, respectively, with a diagonal **R**), and if (4) both traits affect the optimum of the other trait (fully parameterized **A** and only diagonal elements in **R**). The two last model types (3 and 4) investigate Granger causality between the two traits, that is, whether we find evidence of changes in the traits affecting the optimum of the other trait.

Complex multivariate models may have multi-peaked log-likelihood surfaces. The numerical optimization procedure was therefore initiated from 100 different starting points in parameter space for each model to reduce the risk of converging on a local peak.

Results

A multivariate OU model with independent adaptation and correlated stochastic changes showed the best relative model fit, but a model where the traits evolve independently has a similar fit according to AICc (Table 3). Models involving Granger causality (**A** matrices with nonzero off-diagonal elements) and the multivariate unbiased random walks are not supported. The point estimate of the half-life for the log number of spines is 1338 years according to the best model (769 generations

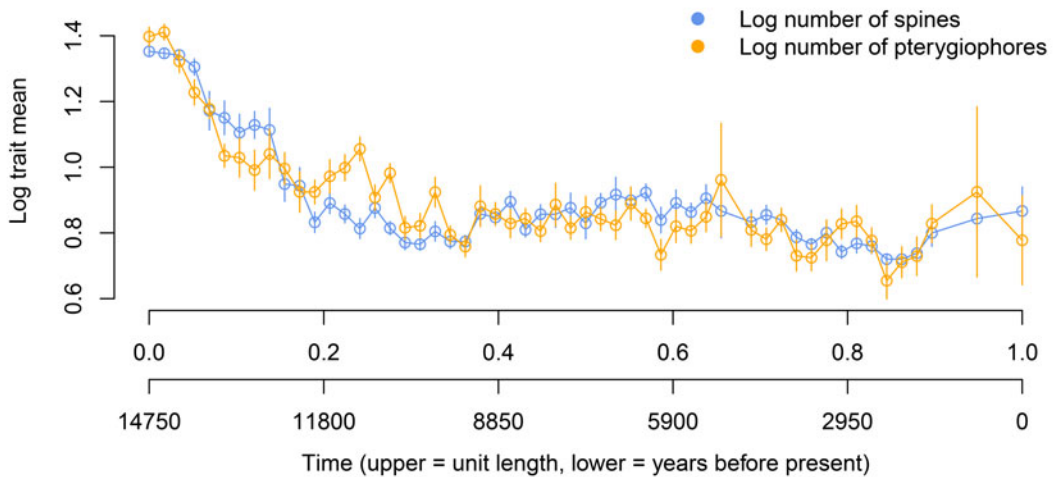


FIGURE 4. Multivariate evolution in a stickleback lineage. The vertical lines represent one standard error of the trait mean.

TABLE 3. Model fit to the multivariate stickleback sequence data. The log-likelihood (log-lik.) and the relative model fit for the candidate models fit to the evolutionary sequence of stickleback. OU, Ornstein-Uhlenbeck; URW, unbiased random walk; K, number of parameters in model; AICc, Akaike information criterion corrected for small sample size.

Model type	Multivariate model	K	Log-lik.	AICc	Δ AICc	AICc weight
URW	Independent URW	4	147.479	-286.142	27.317	0.000
	Correlated evolution	5	155.559	-299.868	13.590	0.001
OU	Independent evolution	8	165.731	-312.261	1.197	0.285
	Independent adaptation	9	167.780	-313.469	0.000	0.518
	Spines affecting touching pterygiophores	9	166.868	-311.646	3.999	0.070
	Touching pterygiophores affecting spines	9	166.944	-311.797	3.606	0.085
	Reciprocal effects in optima	10	167.106	-309.095	5.612	0.031

TABLE 4. Maximum likelihood parameter estimates for the candidate models fit to the multivariate evolutionary sequence of stickleback armor trait evolution. URW, unbiased random walk.

Multivariate model	Parameter estimates (SE)
Independent URW	$z_{0,1} = 1.35$ (0.02), $z_{0,2} = 1.39$ (0.03), $R_{1,1} = 0.09$ (0.04), $R_{2,2} = 0.14$ (0.06)
Correlated evolution	$z_{0,1} = 1.36$ (0.02), $z_{0,2} = 1.39$ (0.03), $R_{1,1} = 0.09$ (0.00), $R_{2,2} = 0.11$ (0.00), $R_{1,2} = 0.08$ (0.00)
Independent evolution	$z_{0,1} = 1.37$ (0.02), $z_{0,2} = 1.43$ (0.03), $R_{1,1} = 0.05$ (0.00), $R_{2,2} = 0.05$ (0.01), $A_{1,1} = 6.34$ (1.63), $A_{2,2} = 7.98$ (1.87), $\theta_1 = 0.80$ (0.04), $\theta_2 = 0.80$ (0.04)
Independent adaptation	$z_{0,1} = 1.37$ (0.02), $z_{0,2} = 1.42$ (0.02), $R_{1,1} = 0.04$ (0.00), $R_{2,2} = 0.08$ (0.00), $R_{1,2} = -0.03$ (0.00), $A_{1,1} = 6.72$ (1.70), $A_{2,2} = 8.13$ (2.23), $\theta_1 = 0.81$ (0.04), $\theta_2 = 0.81$ (0.04)
Spines affecting touching pterygiophores	$z_{0,1} = 1.36$ (0.02), $z_{0,2} = 1.43$ (0.03), $R_{1,1} = 0.05$ (—), $R_{2,2} = 0.05$ (—), $A_{1,1} = 17.70$ (7.65), $A_{2,2} = 8.84$ (2.18), $A_{1,2} = -12.72$ (8.42), $\theta_1 = 0.81$ (0.03), $\theta_2 = 0.82$ (0.04)
Touching pterygiophores affecting spines	$z_{0,1} = 1.37$ (0.02), $z_{0,2} = 1.43$ (0.03), $R_{1,1} = 0.05$ (0.00), $R_{2,2} = 0.07$ (0.01), $A_{1,1} = 5.44$ (1.54), $A_{2,2} = 16.61$ (7.67), $A_{2,1} = -9.78$ (8.07), $\theta_1 = 0.79$ (0.05), $\theta_2 = 0.79$ (0.04)
Reciprocal effects in optima	$z_{0,1} = 1.37$ (0.02), $z_{0,2} = 1.43$ (0.02), $R_{1,1} = 0.05$ (—), $R_{2,2} = 0.06$ (0.01), $A_{1,1} = 5.25$ (—), $A_{2,2} = 15.77$ (4.79), $A_{1,2} = 1.22$ (—), $A_{2,1} = -9.84$ (—), $\theta_1 = 0.81$ (0.04), $\theta_2 = 0.80$ (0.03)

given a generation time of 2 years, as assumed in Hunt et al. [2008]; Table 4), while the corresponding estimate for log number of touching pterygiophores is 1276 years (638 generations). These rates of adaptation are similar to the rates reported in Hunt et al. (2008). The strength of the correlation in the stochastic trait changes is 0.48, which suggests that there may be a common, but unknown, underlying driving force for certain parts of the stochastic trait dynamics. The source of this stochasticity is not known, but genetic drift may be a contributing factor, as suggested by the univariate analyses of Hunt et al. (2008). Moreover, the presence of correlated changes in the multivariate trait dynamics aligns with research on living sticklebacks, which has found evidence of a shared genetic basis for some armor traits (e.g., Cresko et al. 2004; Leinonen et al. 2011).

Discussion

Analysis of evolutionary time series in the rock record represents a unique contribution from paleontology to further the development

of evolutionary biology. For example, the adaptive landscape has for decades been suggested as a conceptual bridge to bring our understanding of microevolution and macroevolution closer to one another (e.g., Simpson 1944; Arnold et al. 2001; Hansen 2012). Shifts in the adaptive landscape along branches of a phylogeny using OU processes are commonly explored (e.g., Ingram and Mahler 2013; Uyeda and Harmon 2014; Khabbazian et al. 2016), but whether detected shifts in optima represent sudden and major changes of the adaptive landscape or whether they instead reflect cumulative changes in the position of adaptive peaks across time is poorly known (e.g., Uyeda and Harmon 2014). Inferring the dynamics of the adaptive landscape through analysis of evolutionary time series may shed light on this and other questions regarding the dynamic nature of the adaptive landscape at different temporal scales. This potential is exemplified by the reanalysis of size evolution in the radiolarian lineage *Eucyrtidium calvertense*. The best-fit model for the *E. calvertense* data suggests that size evolution in the lineage was affected by a

major and sudden change in the adaptive landscape, while a model where the adaptive landscape changed more gradually had a poorer, but still similar, fit.

Multivariate models allow tests of a range of different hypotheses that are difficult to assess by relying on univariate models only. Two traits that appear to evolve together (i.e., show correlated evolution) over time may, for example, be influenced by the same selective agent (e.g., temperature). Another possibility is that only one of the traits is directly affected by the selective agent and that changes in this trait lead to changes in the optimal value of the second trait, resulting in a somewhat lagged evolutionary response in the second trait relative to the first trait. Investigating competing explanations for multivariate trait dynamics requires a multivariate approach. The reanalysis of the stickleback data (Bell et al. 2006; Hunt et al. 2008) examined various hypotheses regarding evolution and adaptation in two armor traits. The results support independent evolution of each armor trait toward separate optima on the adaptive landscape, but a substantial portion of the stochastic changes in the two traits were correlated. The field of quantitative genetics has convincingly demonstrated how genetic correlations may affect phenotypic evolution (Lande 1979; Lande and Arnold 1983; Walsh and Blows 2009), and some armor traits in extant threespine stickleback have been found to covary genetically (e.g., Cresko et al. 2004; Leinonen et al. 2011), suggesting these traits are likely to have a reduced capacity to evolve completely independently of each other. One possible interpretation of the detected non-independence in part of the evolution of the two armor traits is therefore due to a shared genetic background. An alternative and not mutually exclusive explanation is that these two armor traits have experienced correlated selection.

It is important to note that the interpretation of the various univariate and multivariate trait models in *evoTS* (and *paleoTS*) may vary depending on the time interval covered by the data analyzed. For example, the OU process has been used to describe microevolutionary changes in a population close to a fixed peak in the adaptive landscape (Lande 1976; Hansen

and Martins 1996), but it is also commonly used to model evolution within and between adaptive zones on among-species comparative data (e.g., Mahler et al. 2013; Moen et al. 2016; Toljagić et al. 2018). Fitting OU models to evolutionary time series of modern lineages where the data have a generational resolution allows for the estimation of microevolutionary parameters and the development of a process-based interpretation of the trait dynamics based on the parameters in the OU model (for an example, see Lo Cascio Sætre et al. 2017). The fossil record may not always have the necessary resolution for interpreting the model directly in terms of microevolutionary processes, in which case a more phenomenological interpretation of the fitted models may be more appropriate. For example, interpreting the stochastic part of the trait dynamics in an OU model as primarily a result of genetic drift may be more suitable when fitting the model to modern data with high time resolution than when fitting it to data with lower time resolution (Hansen et al. 2008). However, there is no strict boundary between when a process-based and when a more phenomenological interpretation is most suitable. In their analysis of the same fossil stickleback lineage analyzed in this study, Hunt et al. (2008) demonstrated that microevolutionary parameters can be meaningfully estimated when fitting the OU model to data from the fossil record. Therefore, the best way to interpret the model parameters should be assessed on a case-by-case basis.

The number of models and software available for conducting phylogenetic comparative analyses have steadily increased for more than 30 years, giving ample opportunities for exploring a large range of hypotheses of trait dynamics on macroevolutionary timescales (e.g., see Pennell and Harmon 2013). Analysis of evolutionary time series has not experienced a similar momentum, likely due to the smaller number of available evolutionary time series relative to phylogenetic comparative data. The R package *paleoTS* has for a long time been the most popular software for fitting models to evolutionary time series. The implemented univariate and multivariate models in *evoTS* extend the model options available in *paleoTS*. However, *evoTS* is not the only software that

allows fitting models to evolutionary time series. *layeranalyzer* (Reitan and Liow 2019) is a tool that can be used to explore correlations and causal relationships among variables in time series and can fit most of the models implemented in *evoTS*. *mvmorph* (Clavel et al. 2015) is mainly targeted toward analysis of multivariate phylogenetic comparative data, but several of the implemented models can also be fit to time series. The main advantage of *evoTS* is that it works as an extension of the much-used *paleoTS* framework and is therefore specifically tailored toward analysis of evolutionary time series. The combined suite of univariate and multivariate models in *paleoTS* and *evoTS* is also not found in any alternative software.

Connecting known microevolutionary processes to macroevolutionary patterns remain a central challenge in biology (e.g., Jablonski 2000, 2017; Arnold et al. 2001; Hansen 2012). While data on generational changes and among-taxa differences are readily available for many organismal groups, information on how lineages evolve in between micro- and macroevolutionary timescales is rare in comparison. Furthermore, how to interpret evolutionary change recorded in the rock record has been debated for decades (e.g., Eldredge and Gould 1972; Charlesworth et al. 1982; Gingerich 1984, 2019; Stanley 1985; Bookstein 1987; Hunt 2007; Vojte 2016), and the nature of evolutionary change within lineages remains controversial (Lieberman and Eldredge 2014; Pennell et al. 2014a,b; Venditti and Pagel 2014). Investigating and comparing a larger range of models and hypotheses when analyzing phenotypic change within lineages may contribute to these ongoing discussions.

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Declaration of Competing Interests

The author declares no competing interests.

Data Availability Statement

The R package *evoTS* is available for download from the Comprehensive R Archive Network (CRAN). Data and R code are available from the Dryad Digital Repository: <https://doi.org/10.5061/dryad.c59zw3rcp>.

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