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Adaptive alignment of plasticity with genetic variation and selection

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Abstract

Theoretical research has outlined how selection may shape both genetic variation and the expression of phenotypic plasticity in multivariate trait space. Specifically, research regarding the evolution of patterns of additive genetic variances and covariances (summarized in matrix form as **G**) and complimentary research into how selection may shape adaptive plasticity lead to the general prediction that **G**, plasticity, and selection surfaces are all expected to align with each other. However, less well discussed is how this prediction might be assessed and how the modelled theoretical processes are expected to manifest in actual populations. Here, we discuss the theoretical foundations of the overarching prediction of alignment, what alignment mathematically means, how researchers might test for alignment, and important caveats to this testing. The most important caveat concerns the fact that, for plasticity, the prediction of alignment only applies to cases where plasticity is adaptive, whereas organisms express considerable plasticity that may be neutral or even maladaptive. We detail the ramifications of these alternative expressions of plasticity vis-à-vis predictions of alignment. Finally, we briefly highlight some important interpretations of deviations from the prediction of alignment and what alignment might mean for populations experiencing environmental and selective changes.

Keywords: Plasticity, **G** matrix, selection surfaces, vector correlations

Introduction

Understanding the distribution of phenotypes within a population requires understanding three major and interacting contributors: genetic variation, phenotypic plasticity, and how each is shaped by natural selection. Selection shapes the distribution of phenotypes in many ways but, most simply, it is predicted to drive a population's mean phenotype towards a fitness optimum and deplete genetic variation around that optimum (Fisher 1930, Figure 1A). In particular, under stabilizing selection, a population which has its mean at the fitness optimum is expected to lose variation around this mean, with the distribution of phenotypes narrowing around the optimum (Figure 1A). However, selection does not usually operate on single traits (Lande 1979, Lande and Arnold 1983), but instead affects multiple traits simultaneously. For example, particular combinations of traits might have a higher fitness compared to others combinations, i.e. correlational selection (Figure 1B; Endler 1986), and thus a population's distribution of phenotypes in multivariate trait space is expected to narrow around a multivariate optimum (Figure 1C) and can give rise to covariances among traits at the genetic level (Phillips and Arnold 1989, Armbruster and Schwaegerle 1996, Roff 1997).

This narrowing of variation around an optimum changes the distribution of phenotypes in a population by changing the amount of genetic variation for those traits under selection (direct or otherwise) and by changing the magnitude and direction of trait covariances. Put another way, selection can affect the multidimensional geometric structure of genetic variances and covariances, as captured by the "**G** matrix" (following conventional notation bold values denote matrices and vectors rather than single values or

effects). Phillips and Arnold (1989) provided the means by which the response of **G** to selection could be calculated (equation 2 therein) and simulation experiments have subsequently explored the long-term dynamics of how **G** is expected to track fitness optima (e.g. Jones et al. 2003, Jones et al. 2004, 2007). One general finding from both analytical theory and simulations is that, over time and under directional selection, **G** is expected to *align* with the direction of selection, as measured either by selection gradients, **β** (Lande 1980), or Gaussian selection surfaces **ω**, (Jones et al. 2007, Arnold et al. 2008). Alignment in this regard can be defined as the dominant eigenvector of the **G** matrix ($\mathbf{g}_{max}$,, Schluter 1996) being collinear with a selection gradient or the dominant eigenvector of a static selection surface (Arnold et al. 2008) and can more generally be defined as geometric collinearity. Note that this alignment occurs under directional selection, where the fitness optimum is outside the existing genetic variation. Under stabilizing selection genetic variation will be depleted, and $\mathbf{g}_{max}$ will be in the direction of weakest selection (Figure 1B and 1C).

Two related factors affect the alignment between **G** and the selection surface: i) the stability of **G** over evolutionary time, and ii) whether the fitness optimum is constant, fluctuating, or changing in a constant direction. The stability of **G** will be determined by the relative contribution of pleiotropy versus selection-induced linkage disequilibrium (Roff 1997, Conner 2002, Conner et al. 2011), the contribution of mutations to covariances (e.g. Jones et al. 2007, Arnold et al. 2008), and the orientation of **G** relative to selection. For a linearly moving optimum, Jones at al. (2004) showed that **G** was more stable if the movement of the optimum was in the same direction as the $\mathbf{g}_{max}$. In contrast, an optimum moving in a direction different from $\mathbf{g}_{max}$, will decrease the stability of **G** (Jones et al., 2004).

$\mathbf{g}_{max}$ will therefore be better aligned with the selection surface if the optimum is stable or moving in a constant direction.

While the above discussion provides general expectations as to the relationship between genetic covariation and selection, it ignores the fact that the distribution of phenotypes within a population is only partially due to genetic variation. In fact, the average heritability of traits is estimated to be around 0.3 – 0.4 for behavior, physiological, and life-history traits and 0.55 for morphological traits (Mousseau and Roff 1987, Stirling et al. 2002, Dochtermann et al. in review). The remaining ~70 – 45% of phenotypic variation stems from the influence of environmental factors on phenotypes, i.e. phenotypic plasticity—as well as developmental noise—raising the question of whether we can similarly predict how environmental contributions to phenotypic variation and covariation should be oriented relative to selection.

Differences among individuals in phenotype due to differences in the environment experienced by these individuals fall under a broad operational definition of phenotypic plasticity (Lynch and Walsh 1998). If we partition phenotypic variation solely into genetic variation (i.e. **G**) and environmental variation (i.e. **E**), **E** necessarily captures the effects of plasticity on phenotypic variation (Whitman and Agrawal 2009). **E** also captures the effects of correlated plasticity on the expression of phenotypic traits: the off-diagonal elements of **E** are trait covariances due to environmental effects. These off-diagonal elements represent "multivariate trait plasticity" (Whitman and Agrawal 2009) which may stem from common developmental pathways, trade-offs in allocation of energy, or optimal combinations of phenotypic expression. When there is among-genotype variation in plasticity within a

population—i.e. gene-by-environment interactions—plasticity can also respond to selection. Specifically, plasticity is expected to evolve such that the fitness of individuals increases when plasticity is expressed. Thus, if adaptive, plasticity should be aligned with selection surfaces (Gavrilets and Scheiner 1993, Draghi and Whitlock 2012). Put another way, adaptive plasticity is expected to alter an individual's phenotype to be closer to a fitness optima (Gotthard and Nylin 1995) and so the expression of variation due to environmental effects will be oriented in the direction of selection. The multivariate expression of plasticity, as summarized by the geometric properties of **E**, will thus be expected to align with directional selection surfaces.

Interestingly, plasticity itself might also contribute to alignment between genetic covariation and the selection surface (Draghi and Whitlock 2012). Draghi and Whitlock (2012) argued that because the mechanisms necessary for phenotypic plasticity are expected to be more strongly expressed along the main axis of a selection surface, this would also increase the genetic variance found in this dimension. Phenotypic plasticity therefore contributes to the accumulation of cryptic genetic variation (Gibson and Dworkin 2004). Because adaptive plasticity masks this genetic variation it is under weakened selection and genetic variation will therefore be greatest in the direction of plasticity, except when depleted under very strong selective pressure (Gavrilets and Scheiner 1993). If the new fitness optimum is stable over evolutionary time, this adaptive facilitation may ultimately contribute to evolution via genetic assimilation (Lande 2009), and $\mathbf{g}_{max}$ and the fitness surface will again be aligned.

89 The relevance of the above areas of research can be synthesized as: *i*) the
90 distribution of genetic variation should align with selection surfaces (Jones et al. 2003,
91 Jones et al. 2004, 2007, Arnold et al. 2008), *ii*) if plasticity is adaptive, it should be
92 expressed such that variation aligns with selection surfaces (Gotthard and Nylin 1995,
93 Draghi and Whitlock 2012), and *iii*) genetic variation and variation due to plasticity should
94 be aligned if both are aligned to selective surfaces and this may be reinforced by the
95 influence of plasticity on adaptation (Draghi and Whitlock 2012). Taken together this leads
96 to a general prediction: adaptive plasticity, genetic variation (**G**), and selection surfaces
97 should all be aligned in multidimensional trait space. Understanding the alignment among
98 these three components (Figure 2) can also help explain why genetic variation sometimes
99 acts as an evolutionary constraint and emphasizes the importance of plasticity for
100 adaptation.

101 The only empirical test of the general prediction of alignment among **G**, plasticity,
102 and selection that we are aware of was with *Daphnia pulex* that were exposed to cues of
103 one of two predators, after which **G**, selection responses, and plasticity were estimated
104 (Lind et al. 2015). **G** matrices and the expression of plasticity differed between predatory
105 regimes but the difference between the expressions of plasticity was greater than that
106 observed for **G** matrices. Plasticity and **G** were also only aligned in one of the two predator
107 exposure treatments.

108 While further tests of this general prediction are needed, two important questions
109 about such testing remain: *i*) how do we test for this alignment; and *ii*) to what degree
110 should we expect plasticity—manifested as environmental variation (**E**)—to be aligned

111 with either **G** or selection? Here we describe statistical methods for empirically testing
112 alignment among genetic variation, plasticity, and the selection surface, as well as an
113 overview of contributors to **G** and **E**, and what implications these contributors have for the
114 general prediction of alignment. The lack of testing this prediction is unfortunate and our
115 motivation for discussing these issues here is because alignment, or lack thereof, is
116 informative as to whether, how, and how quickly populations might respond to selection.
117 The relative alignments of **E** and **G** with **β** or **ω** might also lead to hypotheses about current
118 versus past selective pressures (Table 1).

119 **i. Testing for alignment**

120 Alignment, as operationally defined by Arnold et al. (2008, defined therein as shared
121 eigenvectors), can be mathematically defined in terms of orientation in space, specifically
122 as the angle between two vectors in *n* dimensional space (see also Lind et al. 2015). This
123 can be calculated as the inner dot product of two vectors, (e.g. the dominant eigenvectors of
124 **G** and the dominant eigenvectors of a matrix describing the shape of the selection surface
125 (**ω**, Table 1), i.e. the vector correlation:

126 $$r^\circ = \frac{\boldsymbol{V_A^T V_B}}{\|\boldsymbol{V_A}\| \, \|\boldsymbol{V_B}\|} \qquad \text{(equation 1)}$$

127 where $\mathbf{V_A}$ and $\mathbf{V_B}$ are the two vectors being compared. For this application the absolute
128 value of the vector correlation, $|r^\circ|$, is of interest and can also be converted to degrees:

129 $$arccos(|r^\circ|) \times \frac{180}{\pi} \qquad \text{(equation 2)}$$

An $|r°|$ statistically indistinguishable from 1, i.e. the angle is indistinguishable from 0°, would then mean that matrices or matrices and the selection surface are aligned, or that there is insufficient power to detect differences. Alternatively, vector correlations significantly different from 1 would demonstrate misalignment.

Correlations are typically evaluated against a null expectation of 0 (corresponding to an angle of 90° between vectors), but here we are interested in whether alignment differs from a vector correlation of 1. As such, conventional approaches to calculating p-values are not appropriate. Moreover, because we are comparing vectors and matrices *within* the same population, randomization approaches described by Roff et al. (2012) and Aguirre et al. (2014) to generate null expectations for vector correlations between groups are not appropriate either as there are no groups over which randomization could be conducted. Given these limitations, and until better alternatives can be developed, two approaches exist for testing the significance of alignment. First, when only point estimates of covariance matrices and/or vectors are available, standard approaches to comparing correlation coefficients can be used. Specifically, $|r°|$ can be converted to a Z value by taking its inverse hyperbolic tangent and testing its difference from null expectations (e.g. $r^{o}_{null} = 0.975$; if set to 1, equation 3 goes to -∞). The difference between the Z values is then divided by the pooled standard deviation and compared to a normal distribution (mean = 0, standard deviation = 1) to determine significance:

$$z = \frac{arctanh(|r°|) - arctanh(r^{\circ}_{null})}{\sqrt{\frac{2}{n-3}}} \qquad \text{(equation 3)}$$

where n is an estimate of the sample size after controlling for non-independence (see also Noble et al. 2017). n can be estimated as the sample size at the highest level of the data's hierarchical structure (e.g. number of families or number of parent-offspring pairs rather than the total number of individuals sampled) or via adjusting for trait repeatability (Noble et al. 2017). Since r°_{null} does not have an associated sample size it is here assumed to have the same uncertainty as r° leading to the specified denominator (Zar 1999). `R` functions for equations 1 to 4 are provided in Supplemental Text S1.

As an example of the calculation of vector correlations and the Z-value based testing approach, consider two matrices:

$$\text{M1} = \begin{bmatrix} 30 & -15 & 0 \\ -15 & 40 & 0 \\ 0 & 0 & 50 \end{bmatrix} \text{ and M2} = \begin{bmatrix} 25 & 0 & 0 \\ 0 & 40 & 20 \\ 0 & 20 & 55 \end{bmatrix}$$

The dominant eigenvector for M1 is $\begin{bmatrix} 0.58 \\ -0.81 \\ 0 \end{bmatrix}$ and the dominant eigenvector for M2 is $\begin{bmatrix} 0 \\ 0.57 \\ 0.82 \end{bmatrix}$. Based on equation 1 $|r^{\circ}|$ is 0.46. Following equation 3, with an n of 25 Z is then -5.60. From this we would then conclude that M1 and M2 have an angle of 62.48 and that this angle significantly differs from 1 ($p = 2.19 \times 10^{-8}$).

Two main caveats to this approaches should be noted. First, the relationship between the vector correlation r° and the angle in degrees is not linear (Figure 3A). Since r° is estimated with uncertainty, this non-linearity results in uncertainty that is not uniform over the 0 : 90 degrees by which vectors might differ (Figure 3B). Because this uncertainty is highest around $r^{\circ} = 0.7$, estimation of intermediate angles and angles approaching 0 will be more imprecise than larger angles. Second, this approach is dependent on the degree to

which $\sqrt{\frac{2}{n-3}}$ accurately estimates the uncertainty in r°. Given that estimates of **G** are typically made with considerable uncertainty, more uncertainty than is expected for correlation coefficients, equation 3 will be anticonservative for **G**. When possible, more appropriate standard errors should be used in the denominator. Given these concerns significance—or lack thereof—of r° should be interpreted with caution despite its biological importance.

A second approach is possible if posterior distributions from Bayesian analyses are available instead of just point estimates of matrices and vectors. Following Ovaskainen et al. (2008) and Lind et al. (2015), the posterior distributions of two matrices or vectors (**A** and **B**) can be compared based on the distribution of the observed vector correlation between **A** and **B** versus a null expectation of this angle (**A** versus **A** and **B** versus **B** across two estimates within the posterior):

$$\psi_{r^{\circ}}(\lambda^A, \lambda^B) = \left[r^{\circ}\left(\lambda_i^A, \lambda_j^A\right) + r^{\circ}\left(\lambda_i^B, \lambda_j^B\right)\right] - \left[r^{\circ}\left(\lambda_i^A, \lambda_j^B\right) + r^{\circ}\left(\lambda_i^B, \lambda_j^A\right)\right] \quad \text{equation (4)}$$

where λ^A and λ^B are the posterior distributions of the dominant eigenvectors of matrices **A** and **B** (i.e. an estimate of **G**, plasticity, or selection surfaces) or the posterior estimate of a selection gradient. *i* and *j* correspond to two different posterior samples from the posterior distribution of either *A* or *B*. The distribution of $\psi_{r^{\circ}}$ can then be assessed versus 0 and, if 95% of $\psi_{r^{\circ}}$ estimates are greater than 0, **A** and **B** can be deemed significantly misaligned.

ii. Expectations for the alignment of E

As previously discussed, several lines of theoretical research lead to the prediction that selection surfaces, **G**, and the direction in phenotypic space in which plasticity manifests will be aligned. However, it is important to ask what this means for natural systems and how alignment will be expressed in populations. From the perspective of quantitative genetics, another way to ask this question is: how do we expect particular variance-covariance matrices and vectors to be aligned?

Starting from the simplest conceptualization of variances and covariances, we can model the (co)variances of quantitative traits of an organism as stemming from the additive contribution of genetic and environmental (co)variances:

$$\mathbf{P} = \mathbf{G} + \mathbf{E} \qquad \text{(equation 5)}$$

where **P**, **G**, and **E** are symmetrical matrices containing phenotypic, genetic, and environmental variances, respectively, along the diagonal and covariances off the diagonal. While **E** is often dismissed as random or residual variation, it is necessarily phenotypic plasticity as, under equation 5, all variation expressed among genotypes due to experiencing different environments will be partitioned into the **E** matrix (Whitman and Agrawal 2009). While plasticity expressed in response to known environmental influences may be directly estimated by estimating equation 5 using mixed-effect animal models (Kruuk 2004), plasticity—adaptive or otherwise—in response to unknown or otherwise unmodeled environmental influences will still be captured by **E**.

Given this, we can predict that **G** and **E** should be "aligned" insofar as **E** captures adaptive plasticity and, following equations 1 – 4, the significance of departure from this

alignment can be assessed. However, in real organisms, both **G** and **E** subsume considerable and important biology. **G** can be further decomposed to the unique effects of additive, dominance, and other epistatic effects. All the contributors to **G** (e.g. dominance and other epistatic effects) might be predicted to be aligned with a selection surface or gradient, although this has been examined primarily for additive effects alone (Arnold et al. 2008). Likewise, **E** contains numerous sources of environmental influences each of which can be considered "plasticity" according to the operational definition given earlier. More specific contributors to **E** can be defined by collapsing categories from Westneat et al. (2015) and include:

Active irreversible plasticity (AI; West-Eberhard 2003): the phenotype of an organism changes in response to an environmental cue indicative of selective pressures. These changes are persistent—at least over the entire time period of measurement, i.e. permanent environmental effects (Lynch and Walsh 1998).

Active reversible plasticity (AR): reversible changes in an individual's phenotype expressed in response to environmental cues indicative of selective pressures and for which variability can occur within an individual (also termed phenotypic flexibility; Piersma and Drent 2003, Piersma and Van Gils 2011).

Passive plasticity: phenotypic changes in response to environmental conditions rather than cues of selective pressures. This includes passive responses to abiotic conditions, such as hypoxic conditions (Whitman and Agrawal 2009), and thus includes developmental instability. This passive plasticity can take the form of either *passive irreversible* (PI) or *passive reversible plasticity* (PR).

232 *Organismal error*: changes to an organism's phenotype due to a failure to process a
233 cue correctly. This error can take the form of either *irreversible* (OI) or *reversible*
234 *organismal error* (OR).

235 While this list of six contributors to **E** is hardly comprehensive (see also Whitman
236 and Agrawal 2009, Forsman 2015, Westneat et al. 2015), it illustrates the point that the
237 prediction that **E** will align with selection surfaces and **G** is imprecise: not all of these
238 sources of environmental variation are expected to align with selection surfaces or **G**.
239 Specifically, we would only predict that active irreversible (**AI**) and active reversible
240 plasticity (**AR**) are aligned with selection surfaces or **G**. Passive plasticity and organismal
241 error are expected to be largely independent of selection and thus to produce variation
242 orthogonal or otherwise misaligned with selection.

243 We can include these concerns within equation 5 by incorporating the relevant
244 contributors to variances and covariances:

245 $$\mathbf{P} = \mathbf{G} + \underbrace{\mathbf{AI} + \mathbf{PI} + \mathbf{OI}}_{\text{Permanent Environmental Effects (PE)}} + \underbrace{\mathbf{AR} + \mathbf{PR} + \mathbf{OR}}_{\text{Temporary Environmental Effects (TE)}}$$

246 (equation 6)

247

248 If individual organisms are measured across environmental conditions or
249 individuals are measured multiple times specific contributors to **PE** can be estimated
250 (Taylor et al. 2012, Thomson et al. 2018, discussed below), potentially distinguishing
251 among some of the matrices of equation 6. Unfortunately for our prediction of matrix

alignment, it will often be impossible to distinguish all active plasticity from passive plasticity and organismal error. Thus **AI**, **PI**, and **OI** will be conflated as general "permanent environmental effects" (**PE**) and AR, PR, and OR effects will typically be conflated as general "temporary environmental effects" (**TE**). As a result, matrix alignment of **G** and **E** will be reduced by the degree of misalignment of passive plasticity and organismal error and their relative contributions to trait correlations.

Following Roff (1997) and Dingemanse and Dochtermann (2014) the combined contributions of these contributors to permanent and temporary environmental effects and to environmental correlations (i.e. the pair-wise correlation coefficients corresponding to the off-diagonal elements of **E** and its components) are:

$$r_{PE} = r_{AI}\sqrt{\frac{V_{AI_y}}{V_{PE_y}}\frac{V_{AI_z}}{V_{PE_z}}} + r_{PI}\sqrt{\frac{V_{PI_y}}{V_{PE_y}}\frac{V_{PI_z}}{V_{PE_z}}} + r_{IO}\sqrt{\frac{V_{IO_y}}{V_{PE_y}}\frac{V_{IO_z}}{V_{PE_z}}} \quad \text{equation 7}$$

$$r_{TE} = r_{AR}\sqrt{\frac{V_{AR_y}}{V_{TE_y}}\frac{V_{AR_z}}{V_{PE_z}}} + r_{PR}\sqrt{\frac{V_{PR_y}}{V_{TE_y}}\frac{V_{PR_z}}{V_{TE_z}}} + r_{RO}\sqrt{\frac{V_{RO_y}}{V_{TE_y}}\frac{V_{RO_z}}{V_{TE_z}}} \quad \text{equation 8}$$

$$r_E = r_{PE}\sqrt{\frac{V_{PE_y}}{V_{E_y}}\frac{V_{PE_z}}{V_{E_z}}} + r_{TE}\sqrt{\frac{V_{TE_y}}{V_{E_y}}\frac{V_{TE_z}}{V_{E_z}}} \quad \text{equation 9}$$

where V_{y} and V_{z} correspond to the variance of traits *y* and *z* due to a particular factor (_, above). Likewise, the correlation coefficients on the right hand side of equations 7 – 9 are the correlations between traits *y* and *z* due to each of the factors described above. These correlation coefficients are calculated by variance-standardizing the covariances in each matrix in equation 6. With this framework we can begin to understand how the prediction

of alignment will be manifested. Importantly, given equations 6 – 9, the alignment between **G** and **E** can be quite different than expected, even if active plasticity (**AI** and **AR)** and genetic variation (**G**) are perfectly aligned.

As a simple worked example, assume that three traits each have a heritability of 0.3 (Mousseau and Roff 1987, Stirling et al. 2002, Dochtermann et al. in review), that the phenotypic variance of the three traits differ (here 0.60, 4.27, and 4.13, randomly drawn from a uniform distribution), that the genetic correlation between traits is 0.57 (Dochtermann 2011), and that the magnitude of alignment ($|r°|$) is 1 among active irreversible plasticity (**AI**), active reversible plasticity (**AR**), and genetic variation (**G**, Table 1). For demonstration purposes we will also assume that organismal error results in an environmental correlation that is orthogonal to that observed for active plasticity and that passive plasticity is uncorrelated among traits (Table 2). If all the components contributing to V_{TE} and V_{PE} do so equally (Table 2), the end result is that $r_E = 0$ because active plasticity and organismal error offset each other. Given $r_G = 0.57$, $r°$ is then 0.70 (45.4°) and **G** and **E** are partially misaligned.

As the relative contribution of active plasticity to **E** increases, so too will alignment between **G** and **E**, if active plasticity and **G** are both aligned with the population's selection surface. For example, under the same conditions as above except without passive plasticity and with active plasticity contributing twice as much to permanent and temporary environmental variation as organismal error, r_E now equals 0.19, and $r°$ is 0.99 (6.3°), indicating alignment. The ability to detect alignment therefore depends, in part, on the

291 relative contribution of each component in equation 6 and the contribution to **E** from
292 factors besides active plasticity will lead to an underestimate of r°.

293 Because environmental (co)variances are frequently ignored or moved to the
294 denominator of effect sizes and test statistics, the relative contributions of each source of
295 variation described in equation 6 is currently unknown. Fortunately, common approaches
296 to estimating **G** also allow estimation of permanent environmental effects on phenotypic
297 covariances. When groupings of individuals that may have experienced similar
298 environmental effects are known, a multiple-matrix animal model approach allows
299 estimation of permanent environmental covariances (Thomson et al. 2018). Using a
300 multiple-matrix animal model, Taylor et al. (2012) estimated the contribution of additive
301 genetic effects and three sources of permanent environmental (co)variation to phenotypic
302 covariance in North American red squirrels (*Tamiasciurus hudsonicus*). The three, possibly
303 adaptive, sources of permanent environmental effects considered were: *i*) environmental
304 effects unique to individuals (based on repeated measures), *ii*) cohort determined
305 permanent environmental effects (based on birth year), and *iii*) maternal effects, although
306 maternal effects also have a heritable component (Räsänen and Kruuk 2007). In these red
307 squirrels Taylor et al. (2012) found that the magnitude of these permanent environmental
308 effects on phenotypic variation were of similar magnitude to the magnitudes estimated for
309 additive genetic effects. More relevant to our discussion here, permanent environmental
310 and maternal covariances were also of a similar magnitude and sign to the estimated
311 additive genetic covariances (Taylor et al. 2012). This suggests that aspects of **AI** (equation
312 6) were indeed aligned with **G**.

Conclusions

Although previous research has suggested that **G** (e.g. Arnold et al. 2008) and **E** (e.g. Draghi and Whitlock 2012, Lind et al. 2015) should align with selection surfaces, this has not previously been detailed in the context of *both* theoretical models of the evolution of **G** and vis-à-vis plasticity. Moreover, previous research did not consider this issue specifically in terms of the **E** matrix. Considering the general prediction of alignment in terms of **E** emphasizes the generality of the prediction of alignment. While alignment of **G** and relevant contributors to **E** will be obscured due to the considerable biology each of these matrices subsumes (equation 6), we still consider the estimation of alignment to be an interesting and important pursuit. Alignment informs us of the ability of populations to respond to selection and the relative contribution of active plasticity to fitness. When selection surfaces have been estimated for natural populations, alignment also informs us of the effects of the structure of **G** and **E** on fitness and possible rates of adaptation. Moreover, detection of misalignment generates evolutionarily interesting hypotheses. For example, if **E** and **β** are aligned with each other but **G** is misaligned with both, one possible reason would be that current selection pressures (**β**) differ from those that shaped **G**. The genetic correlations will in this case be quantitively constraining evolutionary responses, but phenotypic expression may still match a fitness optimum through plasticity, i.e. **E** still aligns with the new fitness surface. Finally, estimation of alignment with current selective surfaces versus projected selective surfaces may provide indications of the ability of populations to respond to the increasing effects of humans on natural populations.

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Data Availability

R functions to conduct the above analyses and examples are available on GitHub (github.com/DochtermannLab/MatrixAlignment) and archived online at both Dryad (DOI AWAITING GENERATION) and Zenodo (DOI AWAITING GENERATION).

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442 Tables and Figures

443 Figure 1. **A**. Response of a population under stabilizing selection where the population's
444 mean is at the optimum (θ). Over successive generations, if the optimum does not change,
445 variation around the mean is lost. **B**. An example of a selection surface (ω) for which fitness
446 increases as traits approach intermediate values for both traits, i.e. when trait
447 combinations are along the adaptive ridge. **C**. If a population's multivariate mean is at an
448 optimum, variation will be depleted over successive generations so as to mirror the
449 selection surface (B)—note that under stabilizing selection the distribution of variation is
450 visualized as being similar to the topography of the selection surface and that, as a result,
451 most variation is present in the direction of weakest selection (i.e. under stabilizing
452 selection **G** is orthogonal to **ω**).

453 Figure 2. Relationship among **G**, **E**, **P**, and **β** in two populations (A and B). In both
454 populations the main axes of genetic and environmental variation (i.e. the dominant
455 eigenvector of **G** and **E**) are closely aligned with a minimal angle (r°) between them.
456 Consequently, phenotypic variation is similarly oriented (**P**). However, in A, variation at all
457 levels (**G**, **E** and **P**) is misaligned with the direction of selection (**β**) by ~45°. In contrast, in
458 B, **G**, **E**, **P**, and **β** are all approximately aligned. Assuming the same amount of variation is
459 present in each population and that the strength of selection is the same, this difference in
460 alignment with **β** between the two populations means that population B will more rapidly
461 respond to selection than will population A.

462 Figure 3. **A**. Relationship between a vector correlation and the degree of the angle between
463 two vectors in multivariate space. The shaded area represents a 95% confidence interval
464 around the degree of the angle for constant uncertainty of the vector correlation. **B**. The
465 breadth of the 95% CI (A) around the degrees of the angle relative to the magnitude of a
466 vector correlation. Uncertainty around r° was held constant but because of the non-linear
467 relationship (A), the uncertainty in the angle is greatest at high values of r°.

468 Table 1. Relevant evolutionary alignments and some of their biological significance.

	Biological Significance	Relevant references
G || **ω** or **β**	Alignment between the dominant eigenvector of **G** ($\mathbf{g}_{max}$) and the direction or shape of selection. This alignment results in populations more rapidly responding to selection and suggests the possibility that the geometry of **G** has responded to selection and is itself adaptive.	Schluter (1996), Arnold et al. (2008)
E || **ω** or **β**	Alignment between the dominant eigenvector of **E** ($\mathbf{e}_{max}$) and the direction or shape of selection. With this alignment plasticity is adaptive in that the expression of plasticity produces phenotypes approaching the optima.	this paper and Draghi and Whitlock (2012), Lind et al. (2015)
G || **E**	Alignment between the dominant eigenvectors of **G** ($\mathbf{g}_{max}$) and of **E** ($\mathbf{e}_{max}$). If these are misaligned, and we assume plasticity is adaptive, it might suggest that current selective pressures are different than those in the past.	this paper and Draghi and Whitlock (2012), Lind et al. (2015)

469

Table 2. Components contributing to phenotypic variation with example expected values and corresponding correlations. Equations 5 – 7 can also be represented as covariances. Correlations are presented to simplify equations.

Variances and correlations	Expected value	Rationale	
V_P			
V_G	$0.3 \times V_P$	Average heritability of life-history, physiological, and behavioral traits is approximately 0.3	(Mousseau and Roff 1987, Stirling et al. 2002)
V_{PE}	$0.3 \times V_P$	V_G and V_{PE} are of similar magnitude for behavior, although this relationship is unknown for other traits	(Dochtermann et al. 2015)
V_{AI}	$0.1 \times V_P$		
V_{PI}	$0.1 \times V_P$	Assumes these three components contribute equally to V_{PE}.	
V_{OI}	$0.1 \times V_P$		
V_{TE}	$0.4 \times V_P$	$V_{TE} = V_P - V_G - V_{PE}$	
V_{AR}	$0.1\bar{3} \times V_P$		
V_{PR}	$0.1\bar{3} \times V_P$	Assumes all three components contribute equally to V_{TE}	
V_{OR}	$0.1\bar{3} \times V_P$		
V_E	$0.7 \times V_P$	Equation 5	
r_G	0.57	Absolute average of genetic correlations for behaviors	(Dochtermann 2011)
r_{PE}	Equation 6		
r_{AI}	0.57	Assumes perfect alignment between $\mathbf{g}_{max}$ and plasticity	
r_{PI}	0	Assumes that passive plasticity is agnostic to selection	(Whitman and Agrawal 2009)
r_{OI}	-0.57	Assumes that errors result in phenotypes orthogonal to $\mathbf{g}_{max}$	
r_{TE}	Equation 7		
r_{AI}	0.57	Assuming perfect alignment between $\mathbf{g}_{max}$ and plasticity	
r_{PI}	0	Assumes that passive plasticity is agnostic to selection	(Whitman and Agrawal 2009)
r_{OR}	-0.57	Assumes that errors result in phenotypes orthogonal to $\mathbf{g}_{max}$	

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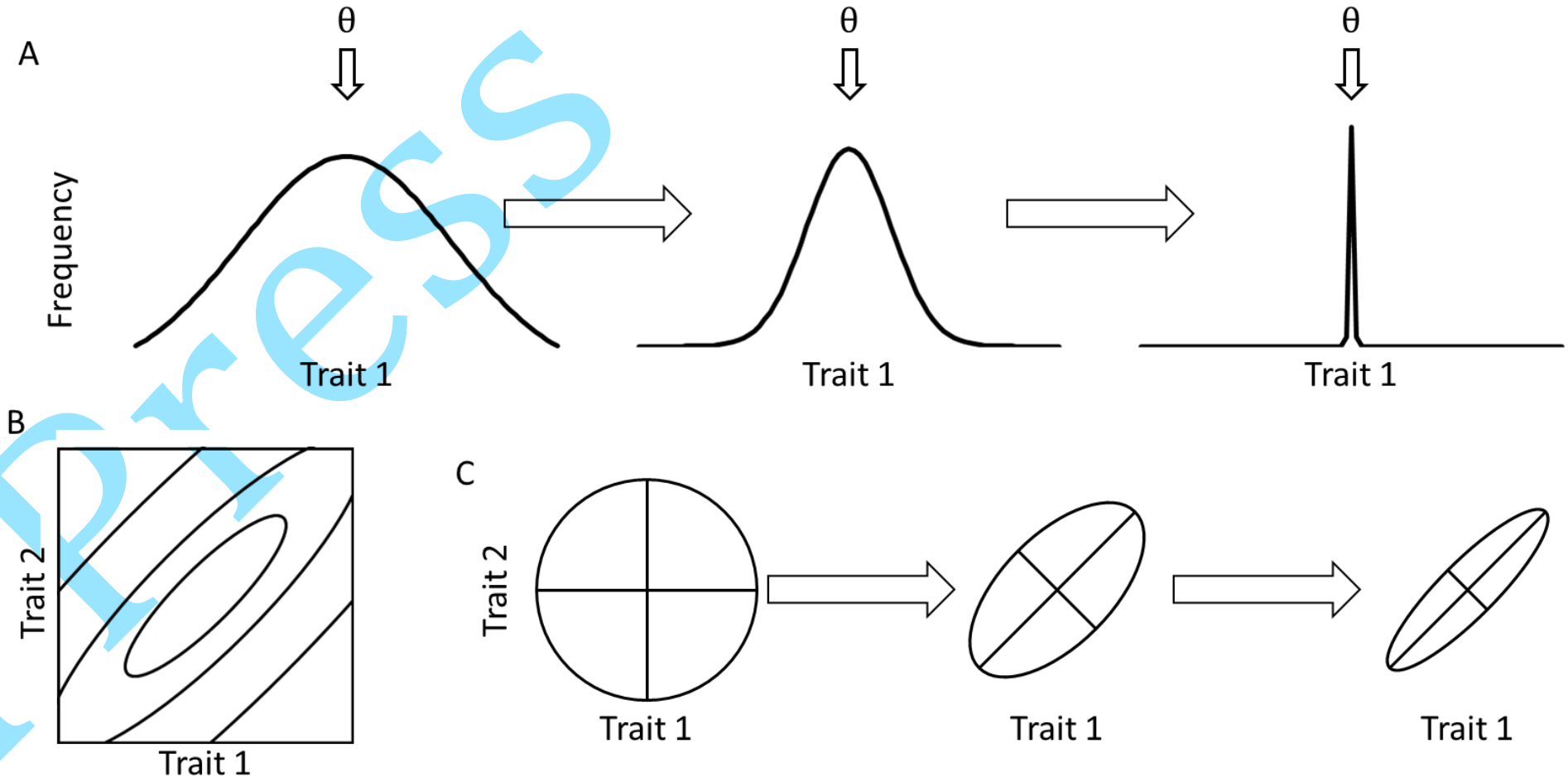

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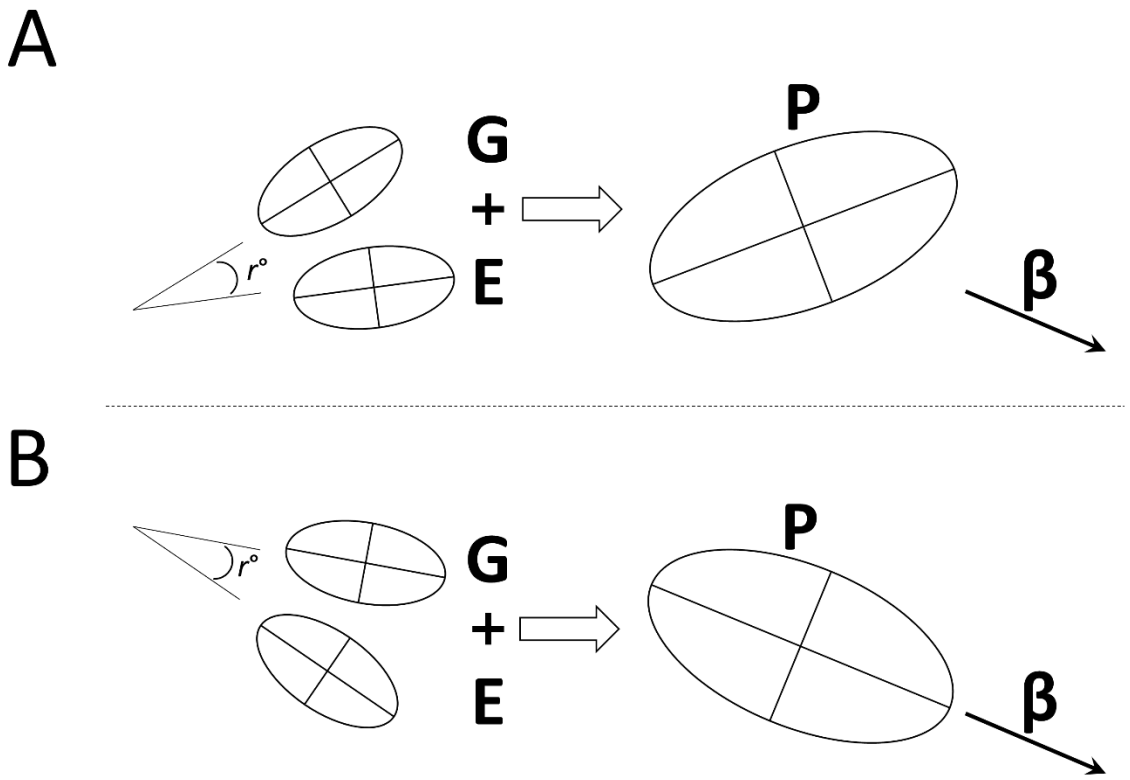
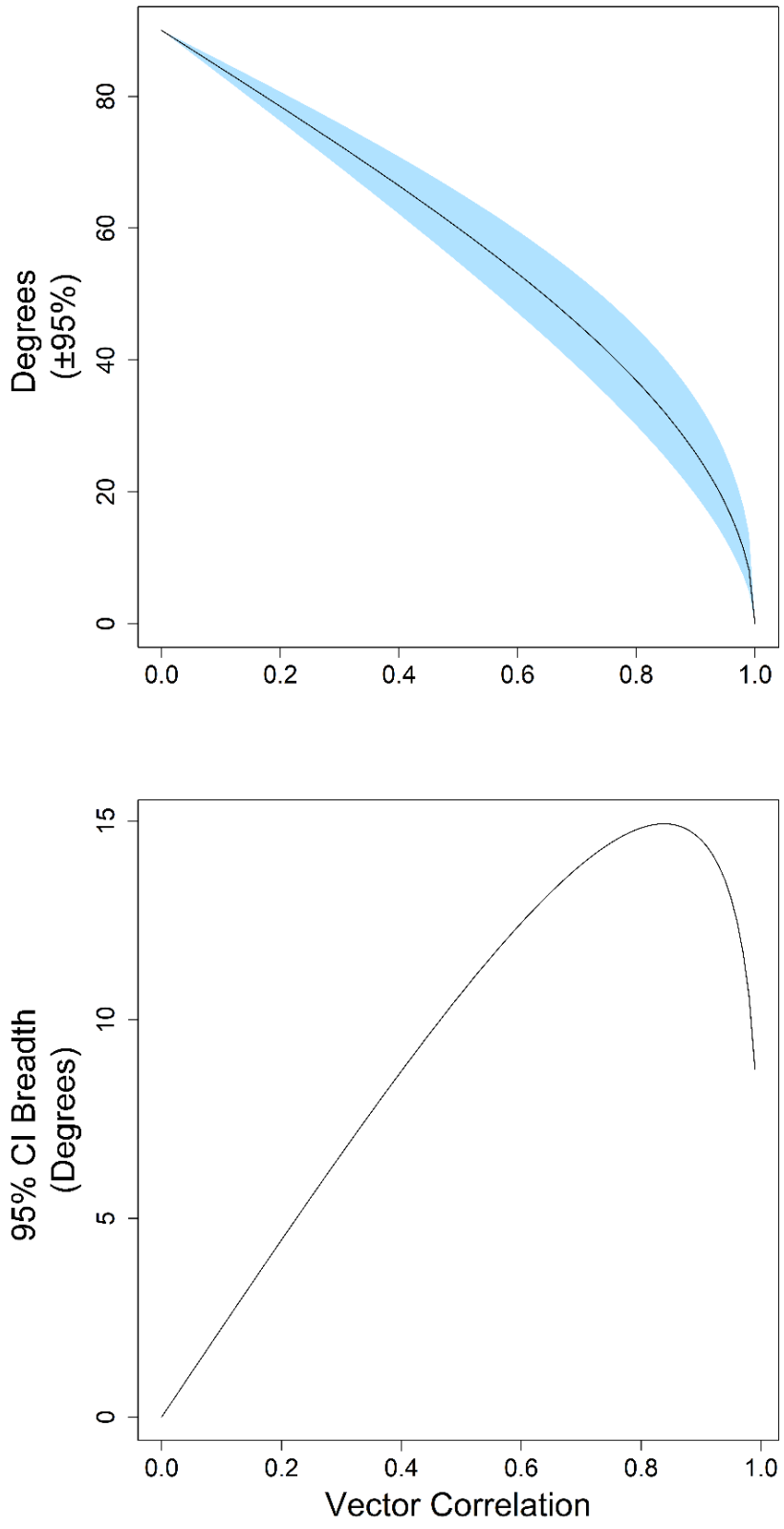
475 Figure 1.



476
477 Figure 2.


Degrees
(±95%)
0
20
40
60
80
0.0
0.2
0.4
0.6
0.8
1.0
95% CI Breadth
(Degrees)
0
5
10
15
0.0
0.2
0.4
0.6
0.8
1.0
Vector Correlation

478
479 Fig 3