

# Appendix for the manuscript:

## Selection and the direction of phenotypic evolution

François Mallard<sup>1\*</sup>, Bruno Afonso<sup>1</sup>, Henrique Teotónio<sup>1\*</sup>

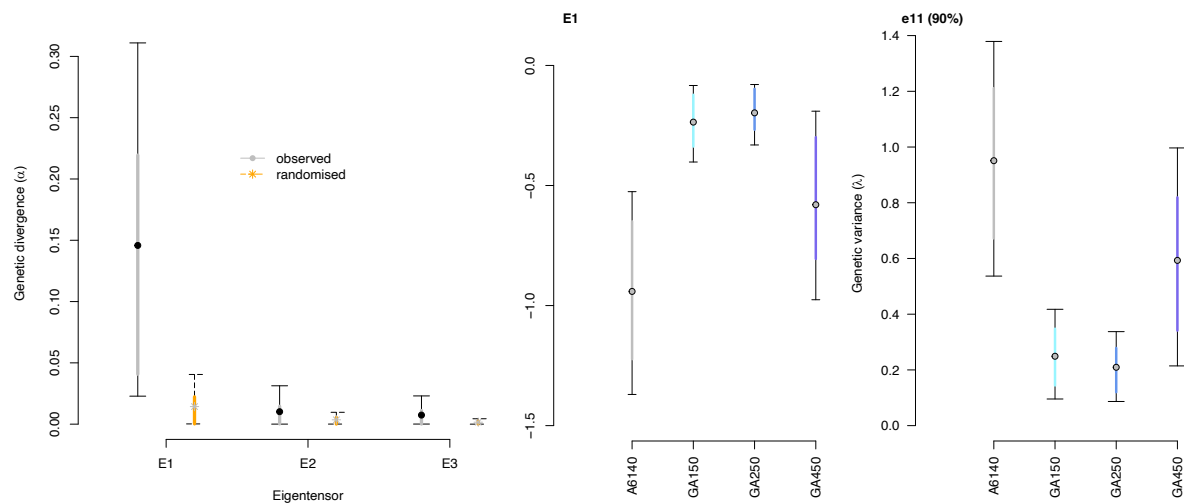
### Tensor analysis to detect genetic evolution

#### Methods

To describe the genetic divergence during experimental evolution we performed eigentensor analysis of the four A6140, GA[1,2,4]50 **G**-matrices in high salt (Aguirre et al., 2014; Hine et al., 2009). To produce a null distribution, we generated a randomized distribution of **G**-matrices while accounting for sampling variance. In brief, we created data sets of our experimental sample size based on the observed **G**-matrices as done in Aguirre et al. (2014) and then randomized the line ID across populations. Following Morrissey and Bonnet (2019), we added random environmental variance to our synthetic phenotypic data set before estimating each population **G**-matrix using *MCMCglmm*. We then repeated this procedure 1000 times and extracted the posterior mode of each 1000 set of 4 matrices that are then used to create a null distribution of genetic divergence (see Figure A left panel). Eigentensors are 4-dimensional objects describing differences among the four **G**-matrices. Each eigentensor was decomposed into eigenvectors to describe the dimensions maximizing genetic differentiation between four **G**-matrices. The first eigenvector of the first eigentensor is here called the vector of genetic divergence ( $e_{11}$ ) because the A6140 ancestral population drives most differentiation.

#### Results

Eigentensor analysis confirms that genetic divergence mainly occurs through the loss of genetic variance along one canonical dimension, a result similar to the random skewers analysis. Eigentensor analysis shows that the first eigentensor explains most differences between the four **G**-matrices in high salt (98%, Figure A, left panel), and its coordinates indicate that it is the ancestral population that drives most differentiation (Figure A, middle panel). Eigendecomposition of the first eigentensor then shows that genetic divergence during experimental evolution occurs along the first canonical dimension for all GA replicates (90% for  $e_{11}$ ; Figure A - right panel). Not surprisingly,  $e_{11}$  and  $e_{\max}$  are highly colinear ( $e_{11}$ : -0.38; -0.48; 0.29; 0.50; 0.14; 0.47; -0.2) with a small angle between them (8.4°, well below the random estimates shown in the main texts, see Figure 3B for an example).



**Figure A.** G-matrix evolution in high salt. A. Eigentensor analysis of all four ancestral and derived G-matrices. Left: Shown are the first three eigentensor values encompassing most of the differences between G-matrices, with only the first one E1 containing more genetic variation than expected with our sample sizes. Middle: Coordinates of each population in the first eigentensor. Right: For the first eigentensor E1, further decomposition shows that its first eigenvector ( $e_{11}$ ) explains 90% of the genetic differences between all populations (eigenvalues in the y-axis). Colored bars show 83% and 95% credible intervals of the posterior distribution, dots the mean.