

**Appendix C from J. G. Kingsolver et al., “Genetic Variation, Simplicity,
and Evolutionary Constraints for Function-Valued Traits”
(Am. Nat., vol. 185, no. 6, p. 000)**

Supplementary Table

Table C1: Description of the 10 data sets, including the types of analyses conducted in the original published study and how the analyses were handled for the results presented here

	<i>Ambystoma macrodictylum</i>	<i>Mus domesticus</i>	<i>Tribolium castaneum</i>	<i>Pieris rapae</i>	<i>Aphidius ervi</i>	G4 phage	<i>Escherichia coli</i>	<i>Salmonella</i>	<i>Impatiens capensis</i>	<i>Pinus taeda</i>
Original analysis:										
Data transform	None	None	Log	LM resids	None	In	Log base 2	Log base 2	None	None
Type of index	Age	Age	Age	Temp	Temp	Temp	Temp	Temp	Age	Age
No. index values	7	80	24	7	7	9	11	11	6	7
Registration of index	Metamorphosis	Birth	Hatch	NA	NA	NA	NA	NA	Germination	Planting
Analysis	FV	UNI	FV	FV, MV	FV, MV	TMV/splines	TMV/splines	UNI	Curve fit	Curve fit, MV
Model	LMM	RM	LMM	LMM	LMM	LMM	LMM	LMM	Bayesian	LMM
Variance components	VG	None	VA	VG	VG	None	None	None	VG	VG
Software	dfREML	SAS	Wombat	dfREML	Shaw	Matlab	SAS	SAS	R, Matlab, SAS	ASReml
Current analysis:										
Same as original?	No	No	No	Yes	Yes	No	No	No	No	No
Data transform	None	None	Log	LM resids	None	In	Log base 2	Log base 2	None	None
No. traits	7	7	6	7	7	9	11	11	6	7
Model	LMM	LMM	LMM	LMM	LMM	SBA	SBA	SBA	LMM	None
Software	Wombat	Wombat	Wombat	dfREML	Shaw	Prinsimp	Prinsimp	Prinsimp	SAS	Excel

Note: dfREML = quantitative genetic software by Karin Meyer, replaced by Wombat; FV = function valued; LM = linear model; LMM = linear mixed model; LM resids = linear model residuals; MV = multivariate; NA = not available; RM = repeated measures; Shaw = quantitative genetic software by Ruth Shaw; Temp = temperature; TMV = template modes of variation; UNI = univariate; VA = narrow-sense genetic variance; VG = broad-sense genetic variance; Wombat = quantitative genetic software by Karin Meyer.