Appendix S2

Statistical comparisons of distributions in Figure 4.

Table of Contents

Appendix S2 Table S1.

Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
736	20.81159	NA	NA	NA	NA
738	35.42466	-2	-14.61307	258.395	0

Appendix S2 Table S1. ANOVA table comparing ordinary linear models of the form abs_log_ratio ~ syndrome and abs_log_ratio ~ 1. The fit incorporating syndrome is superior to the intercept-only model (p < 0.0001).

Appendix S2 Table S2

categorical_fit	emmean	SE	df	lower.CL	upper.CL
Coupled trend	0.2007265	0.0089755	736	0.1831058	0.2183472
Decoupled trends	0.5587675	0.0137759	736	0.5317228	0.5858123
No trend	0.2211238	0.0108771	736	0.1997699	0.2424777

Appendix S2 Table S2. Estimates (calculated using emmeans (Lenth 2021)) for the mean absolute log ratio of mean mass for routes whose dynamics for biomass were best-described by different syndromes of change. Routes with decoupled long-term trends between biomass and individuals-driven dynamics have higher absolute log ratios (mean .56, 95% credible interval .53-.58) than routes with covarying trends in biomass and individual abundance (mean of .2; 95% interval .18-.22) or no detectable temporal trend (mean of .22; .2-.24).

Appendix S2 Table S3

contrast	estimate	SE	df	t.ratio	p.value
Coupled trend - Decoupled trends	-0.3580410	0.0164419	736	-21.776134	0.0000000
Coupled trend - No trend	-0.0203973	0.0141022	736	-1.446391	0.3176979
Decoupled trends - No trend	0.3376437	0.0175524	736	19.236285	0.0000000

Appendix S2 Table S3. Contrasts for absolute log ratio of mean mass, calculated using emmeans (Lenth 2021). There is a significant contrast between routes with decoupled trends and the other two syndromes of dynamics (both contrasts, p < 0.001), but not between routes showing the "no trend" and "coupled trend" syndromes (contrast p = .31).

Appendix S2 Table S4

Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
736	14.09312	NA	NA	NA
738	14.28236	-2	-0.1892428	0.9097173

Appendix S2 Table S4. ANOVA table comparing binomial generalized linear models of the form ISD_turnover ~ syndrome and ISD_turnover ~ 1. The model incorporating syndrome is not superior to the intercept-only model (p = .9).

Appendix S2 Table S5

Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
736	20.10447	NA	NA	NA
738	22.11983	-2	-2.015363	0.3650643

Appendix S2 Table S5. ANOVA table comparing binomial generalized linear models of the form Bray_Curtis_dissimilarity ~ syndrome and Bray_Curtis_dissimilarity ~ 1. The model incorporating syndrome is not superior to the intercept-only model (p = .37).

References

Lenth, R. V. 2021. Emmeans: Estimated Marginal Means, aka Least-Squares Means.