

# Appendix S2

Statistical comparisons of distributions in Figure 4.

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**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

$\text{abs\_log\_ratio} \sim \text{syndrome}$  and  $\text{abs\_log\_ratio} \sim 1$ . 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 abundance-driven dynamics have higher absolute log ratios (mean .56, 95% credible interval .53-.58) than routes with covarying trends in biomass and 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  $\text{ISD\_turnover} \sim \text{syndrome}$  and  $\text{ISD\_turnover} \sim 1$ . 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.