### **Appendix S1: Statistical comparisons of distributions in Figure 4**

**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 |

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).

**Table S2.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Syndrome | 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 |

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).

**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 |

**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).

#### Table S4.

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

### **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).

#### Table 7.

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

### **Table 7.** 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.