Ecography

Supplementary material

Appendix 1. Derivation of the partitioning framework

1.1 The three-level variability equations (eqns 9 & 10)

Based on the definitions by equations 2, 4, and 8 in the main text, we have:

$$CV_{S,L} \cdot \varphi_{S \to C,L} = \frac{\sum_{i,k} \sqrt{v_{ii.kk}}}{\mu_{\Sigma.\Sigma}} \cdot \sum_k \omega'_k \cdot \varphi_{S \to C,k}$$

$$= \frac{\sum_{i,k} \sqrt{v_{ii.kk}}}{\mu_{\Sigma.\Sigma}} \cdot \sum_k \frac{\sum_i \sqrt{v_{ii.kk}}}{\sum_{i,k} \sqrt{v_{ii,kk}}} \cdot \frac{\sqrt{v_{\Sigma,kk}}}{\sum_i \sqrt{v_{ii,kk}}}$$

$$= \frac{\sum_k \sqrt{v_{\Sigma.kk}}}{\mu_{\Sigma.\Sigma}} = CV_{C,L} \tag{S1}$$

Based on equations 3, 4, and 6, we have:

$$CV_{S,L} \cdot \varphi_{S,L \to R} = \frac{\sum_{i,k} \sqrt{v_{ii.kk}}}{\mu_{\Sigma.\Sigma}} \cdot \sum_i \omega_i \cdot \varphi_{i,L \to R}$$

$$= \frac{\sum_{i,k} \sqrt{v_{ii.kk}}}{\mu_{\Sigma.\Sigma}} \cdot \sum_k \frac{\sum_k \sqrt{v_{ii,kk}}}{\sum_{i,k} \sqrt{v_{ii,kk}}} \cdot \frac{\sqrt{v_{ii,\Sigma}}}{\sum_k \sqrt{v_{ii,kk}}}$$

$$= \frac{\sum_i \sqrt{v_{ii,\Sigma}}}{\mu_{\Sigma.\Sigma}} = CV_{S,R} \tag{S2}$$

Similarly, based on equations 1, 2, 3, 5 and 7, we have:

$$CV_{C,L} \cdot \varphi_{C,L \to R} = \frac{\sum_k \sqrt{v_{\Sigma.kk}}}{\mu_{\Sigma.\Sigma}} \cdot \frac{\sqrt{v_{\Sigma,\Sigma}}}{\sum_k \sqrt{v_{\Sigma,kk}}} = \frac{\sqrt{v_{\Sigma,\Sigma}}}{\mu_{\Sigma.\Sigma}} = CV_{C,R} \tag{S3}$$

$$CV_{S,R} \cdot \varphi_{S \to C,R} = \frac{\sum_i \sqrt{v_{ii,\Sigma}}}{\mu_{\Sigma,\Sigma}} \cdot \frac{\sqrt{v_{\Sigma,\Sigma}}}{\sum_i \sqrt{v_{ii,\Sigma}}} = \frac{\sqrt{v_{\Sigma,\Sigma}}}{\mu_{\Sigma.\Sigma}} = CV_{C,R} \tag{S4}$$

Combining equations S1-S4, we have the two three-level variability equations.

1.2 Partitioning variability across more than three hierarchical levels

In the main text, we have developed a theoretical framework that partitions metacommunity variability into three lower-level components, i.e. the three-level variability equation. Our framework clarified that, to make the three-level variability equation hold, the key is to average the lower-level variability by weighting with their relative contribution to the total biomass of the

metacommunity and to average the lower-level synchrony by weighting with their relative contribution to the summed standard deviation of populations within the metacommunity (see Table 1). Indeed, based on similar methods, our framework can be easily adapted to partition metacommunity variability into an arbitrary number of hierarchical levels (Figure S3). To illustrate this, below we partition metacommunity variability into four lower-level components that correspond to the pathway from subpopulations to metacommunities in Figure S3.

We consider a metacommunity that includes a number of species (1, …, i, …) and consists of a number of local patches (1, …, k, …); each local patch k consists of a number of subplot (k_1, … k_m, …). We denote $X_{i,k\_m}(t)$ as the biomass of species i in the subplot m of patch k at time t, μ_{i,k_m} as the temporal mean biomass of species i in the subplot m of patch k, and v_{ij,kl_mn} as the temporal covariance between species i in the subplot m of patch k and species j in the subplot n of patch l. Both μ_{i,k_m} and v_{ij,kl_mn} can be easily calculated from time-series data: $\boldsymbol{\mu_{i,k\_m}} = \frac{\sum_{t=1}^{T} X_{i,k\_m}(t)}{T}$ and $\boldsymbol{v_{ij,kl\_mn}} = \frac{\sum_{t=1}^{T}(X_{i,k\_m}(t) - \mu_{i,k\_m})(X_{j,l\_n}(t) - \mu_{j,l\_n})}{T-1}$. Note that $\mu_{i,k\_m} = v_{ij,kl\_mn} = 0$ if species i is never recorded in the subplot m of patch k during the study period. Based on μ_{i,k_m} and v_{ij,kl_mn}, we similarly define a number of variability and synchrony indices that correspond to different spatial scales and organizational levels.

Defining variability at multiple hierarchical levels

First, we define the variability of species i in the subplot m of patch k as $CV_{i,k\_m} = \frac{\sqrt{v_{ii,kk\_mm}}}{\mu_{i,k\_m}}$, and the subplot-scale average species variability as the weighted average of subpopulation variability across species, patches and subplots:

$$CV_{S,B} = \sum_{i,k,m} CV_{i,k\_m} \cdot \frac{\mu_{i.k\_m}}{\mu_{\Sigma.\Sigma\_\Sigma}} = \frac{\sum_{i,k,m} \sqrt{v_{ii.kk\_mm}}}{\mu_{\Sigma.\Sigma\_\Sigma}}$$

where $\mu_{\Sigma.\Sigma\_\Sigma} = \sum_{i,k,m} \mu_{i,k\_m}$ is the total biomass of the metacommunity.

Second, we define the variability of species i in patch k as $CV_{i,k} = \frac{\sqrt{v_{ii,kk\_\Sigma}}}{\mu_{i,k\_\Sigma}}$, where $\mu_{i,k\_\Sigma} = \sum_m \mu_{i,k\_m}$ and $v_{ii,kk\_\Sigma} = \sum_{m,n} v_{ii,kk\_mn}$ are the mean and variance of the total biomass of species i in patch k, respectively. We then define the local-scale average species variability as the weighted average of local population variability ($CV_{i,k}$) across species and patches:

$$CV_{S,L} = \sum_{i,k} CV_{i,k} \cdot \frac{\mu_{i.k\_\Sigma}}{\mu_{\Sigma.\Sigma\_\Sigma}} = \frac{\sum_{i,k} \sqrt{v_{ii.kk\_\Sigma}}}{\mu_{\Sigma.\Sigma\_\Sigma}}$$

Third, we define the variability of total community biomass in patch k as $CV_{C,k} = \frac{\sqrt{v_{\Sigma,kk\_\Sigma}}}{\mu_{\Sigma.k\_\Sigma}}$, where $\mu_{\Sigma,k\_\Sigma} = \sum_{i,m} \mu_{i,k\_m}$ and $v_{\Sigma,kk\_\Sigma} = \sum_{i,j,m,n} v_{ij,kk\_mn}$ are the mean and variance of the total community biomass in patch k, respectively. We then define the local-scale average community variability as the weighted average of local community variability ($CV_{C,k}$) across patches:

$$CV_{C,L} = \sum_k CV_{C,k} \cdot \frac{\mu_{\Sigma.k\_\Sigma}}{\mu_{\Sigma.\Sigma\_\Sigma}} = \frac{\sum_k \sqrt{v_{\Sigma,kk\_\Sigma}}}{\mu_{\Sigma.\Sigma\_\Sigma}}$$

Finally, we define the variability of the total metacommunity as:

$$CV_{C,R} = \frac{\sqrt{v_{\Sigma,\Sigma\_\Sigma}}}{\mu_{\Sigma,\Sigma\_\Sigma}} = \frac{\sqrt{\sum_{i,j,k,l,m,n} v_{ij.kl\_mn}}}{\mu_{\Sigma,\Sigma\_\Sigma}}$$

where $v_{\Sigma,\Sigma\_\Sigma} = \sum_{i,j,k,l,m,n} v_{ij.kl\_mn}$ is the variance of the total metacommunity.

Defining synchrony at multiple hierarchical levels

First, we define spatial synchrony among subpopulations of species i in patch k as $\varphi_{i,k,B \to L} = \frac{\sqrt{v_{ii,kk\_\Sigma}}}{\sum_m \sqrt{v_{ii,kk\_mm}}}$. We then define species-level average spatial subpopulation synchrony

as the weighted average of spatial subpopulation synchrony across species and patches (arrow ① in Figure 1):

$$\varphi_{S,B\to L} = \sum_{i,k} \omega_{i,k} \cdot \varphi_{i,k,B\to L} = \sum_{i,k} \frac{\sum_m \sqrt{v_{ii,kk\_mm}}}{\sum_{i,k,m} \sqrt{v_{ii,kk\_mm}}} \cdot \frac{\sqrt{v_{ii,kk\_\Sigma}}}{\sum_m \sqrt{v_{ii,kk\_mm}}} = \frac{\sum_{i,k} \sqrt{v_{ii,kk\_\Sigma}}}{\sum_{i,k,m} \sqrt{v_{ii,kk\_mm}}}$$

where the weight is given by the contribution of local species to the total sum of standard deviation of all subpopulations within the metacommunity.

Second, we define the species synchrony within patch k as $\varphi_{S\to C,k} = \frac{\sqrt{v_{\Sigma,kk\_\Sigma}}}{\sum_i \sqrt{v_{ii,kk\_\Sigma}}}$. We then define local-scale average species synchrony as the weighted average of local species synchrony across patches (arrow ② in Figure 1):

$$\varphi_{S\to C,L} = \sum_k \omega'_k \cdot \varphi_{S\to C,k} = \sum_k \frac{\sum_i \sqrt{v_{ii,kk\_\Sigma}}}{\sum_{i,k} \sqrt{v_{ii,kk\_\Sigma}}} \cdot \frac{\sqrt{v_{\Sigma,kk\_\Sigma}}}{\sum_i \sqrt{v_{ii,kk\_\Sigma}}} = \frac{\sum_k \sqrt{v_{\Sigma,kk\_\Sigma}}}{\sum_{i,k} \sqrt{v_{ii,kk\_\Sigma}}}$$

Finally, we define the spatial synchrony of total community biomass (arrow ③ in Figure 1):

$$\varphi_{C,L\to R} = \frac{\sqrt{v_{\Sigma,\Sigma\_\Sigma}}}{\sum_k \sqrt{v_{\Sigma,kk\_\Sigma}}}$$

Linking variability and synchrony across hierarchical levels

Based on above definitions, we can easily derive:

$$CV_{S,L} = CV_{S,B} \cdot \varphi_{S,B\to L}$$

$$CV_{C,L} = CV_{S,L} \cdot \varphi_{S\to C,L}$$

$$CV_{C,R} = CV_{C,L} \cdot \varphi_{C,L\to R}$$

These three equations correspond to the scaling indicated by the arrows ①, ② and ③ in Figure 1, respectively. Based on these equations, the metacommunity variability can be partitioned into four lower-level components:

$$CV_{C,R} = CV_{S,B} \cdot \varphi_{S,B \to L} \cdot \varphi_{S \to C,L} \cdot \varphi_{C,L \to R}$$

Appendix 2. The R function "var.partition" to calculate variability and synchrony across hierarchical levels.

```
var.partition <- function(metacomm_tsdata){

## The function "var.partition" performs the partitioning of variability
## across hierarchical levesl within a metacommunity.
## The input array "metacomm_tsdata" is an N*T*M array. The first dimension represents N species,
## the second represents time-series observations of length T, and the third represents M local communities.
## The output includes four variability and four synchrony metrics as defined in the main text.
## Note that, to be able to handle large metacommunities, this code has avoided calculating all covariance.

    ts_metacom <- apply(metacomm_tsdata,2,sum)
    ts_patch <- apply(metacomm_tsdata,c(2,3),sum)
    ts_species <- apply(metacomm_tsdata,c(1,2),sum)

    sd_metacom <- sd(ts_metacom)
    sd_patch_k <- apply(ts_patch,2,sd)
    sd_species_i <- apply(ts_species,1,sd)
    sd_species_patch_ik <- apply(metacomm_tsdata,c(1,3),sd)

    mean_metacom <- mean(ts_metacom)

    CV_S_L <- sum(sd_species_patch_ik)/mean_metacom
    CV_C_L <- sum(sd_patch_k)/mean_metacom
    CV_S_R <- sum(sd_species_i)/mean_metacom
    CV_C_R <- sd_metacom/mean_metacom

    phi_S_L2R <- CV_S_R/CV_S_L
    phi_C_L2R <- CV_C_R/CV_C_L
    phi_S2C_L <- CV_C_L/CV_S_L
    phi_S2C_R <- CV_C_R/CV_S_R

    partition_3level <- c(CV_S_L=CV_S_L, CV_C_L=CV_C_L, CV_S_R=CV_S_R, CV_C_R=CV_C_R,
                    phi_S_L2R=phi_S_L2R, phi_C_L2R=phi_C_L2R, phi_S2C_L=phi_S2C_L,
phi_S2C_R=phi_S2C_R)
    return(partition_3level)
}
```

Appendix 3

**Table A1.** Basic information of the plant community data from the Jornada LTER site.

No	Plot	Vegetation type	Local scale (quadrat)		Regional scale (plot)		
			Quadrat size (m²)	Alpha diversity	Plot size (m²)	Number of quadrats included	Gamma diversity
1	CALI	Creosotebush	1*1	4	70*70	49	25
2	GRAV	Creosotebush	1*1	7	70*70	49	40
3	SAND	Creosotebush	1*1	8	70*70	49	44
4	BASN	Grassland	1*1	8	70*70	49	53
5	IBPE	Grassland	1*1	11	70*70	49	60
6	SUMM	Grassland	1*1	11	70*70	49	58
7	NORT	Mesquite Dune	1*1	3	70*70	49	19
8	RABB	Mesquite Dune	1*1	6	70*70	49	29
9	WELL	Mesquite Dune	1*1	5	70*70	49	25
10	COLL	Playa	1*1	6	30*60	48	20
11	SMAL	Playa	1*1	4	70*70	49	18
12	TOBO	Playa	1*1	4	70*70	49	15
13	EAST	Tarbush	1*1	6	70*70	49	33
14	TAYL	Tarbush	1*1	4	70*70	49	28
15	WEST	Tarbush	1*1	5	70*70	49	31

Figure A1. Relationship between local species richness and species variability (a), species synchrony (b), and community variability (c). Each grey point represents one quadrat. Each thin line represents the linear regression across 49 (or 48) quadrats within each of the 15 plots. The thick black lines represent linear regression across all quadrats from all 15 plots. Solid lines are statistically significant ($p < 0.05$) and dashed lines are not ($p > 0.05$).
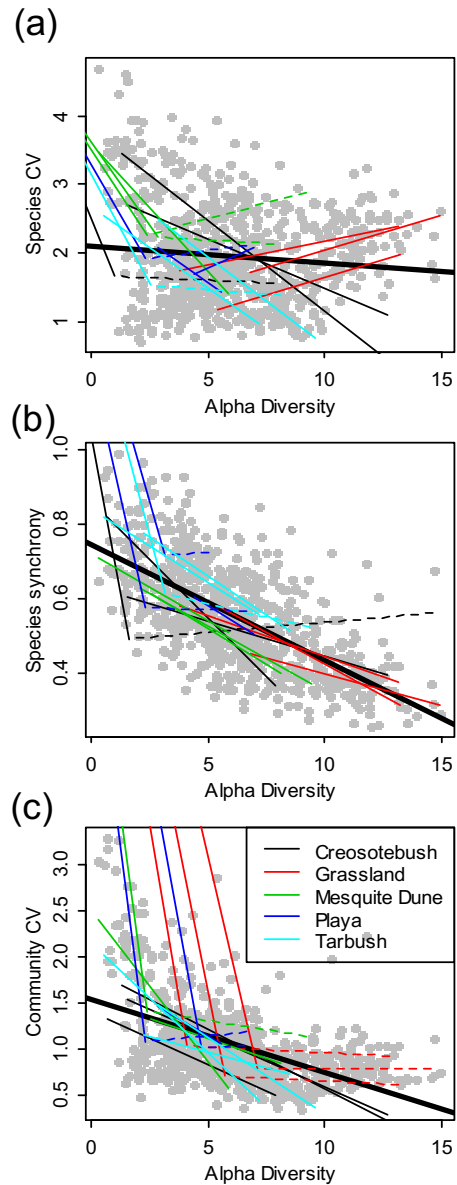
Figure A2. Relationship between local species richness (average across 49 or 48 quadrats) and regional species richness.
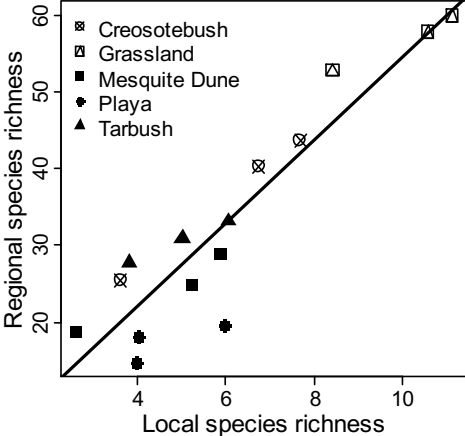
Figure A3. Ecological stability or variability can be measured at different hierarchical levels, e.g. different spatial scales and organizational levels. Across hierarchical levels, the scaling of variability is achieved through synchrony. Our framework shows that the variability at a higher level can be expressed as the product of the variability at a lower level and a series of synchrony metrics at corresponding scales and organizational levels along the pathway from low to high hierarchical levels. For instance, the metacommunity variability equals the product of sub-population variability, subpopulation-level spatial synchrony ((①)), local-scale species synchrony ((②)), and community-level spatial synchrony ((③)) (see Appendix 1).