CJ Patrick *et al*. – Supporting Information

WebPanel 1. Methods

Datasets

Terrestrial arthropods were previously collected in Phoenix, Arizona, with nine yearly (2006–2014) estimates of abundance of multiple taxa from 24 sites, across 20,000 km^2 (Grimm *et al*. 2018). Data consisted of pit-fall traps in groups, typically of four (mean ± standard deviation, 3.7 ± 0.7), trapped quarterly, with all individuals identified to family (~50 beetle families included in the dataset). Data were aggregated across replicates by averaging and then summed across quarters to give an annual community × abundance vector for each spatial location. Our analyses focused on beetles because they are highly abundant and diverse and often sensitive to environmental change. Covariate data included percent land use in a 500-m radius circle surrounding trapping sites, from the 2006 National Land Cover Dataset (Homer *et al*. 2004), which most closely aligned with sampling dates. Minimum and maximum temperature, and precipitation, from downscaled PRISM data (PRISM Climate Group 2016) were also included.

Submerged aquatic vegetation (SAV) was surveyed from 95 subestuaries with 30 yearly (1984–2009, except 1988) estimates of density-weighted coverage distributed across Chesapeake Bay, in Maryland and Virginia (Patrick and Weller 2015). Subestuaries in this system are estuaries with unique watersheds connected to the main stem of the Chesapeake Bay (Patrick *et al*. 2014). Data consisted of aerial imagery collected each year and weighted by SAV density. Species composition (25 taxa across bays) within each embayment was derived from ground observations collected over the study period (Patrick *et al*. 2017). Covariate data included estuary morphology, salinity, tidal range, benthic substrate, watershed land cover, and shoreline armoring and structures (see Patrick *et al*. [2017] for a complete explanation of all variables and sources). For the analyses, subestuaries were divided into two groups, upper bay and lower bay, in accordance with Chesapeake Bay Program designation (Batiuk 2000).

Stream fish were identified from 27 streams with 13 yearly (2000–2012) estimates of fish abundance distributed across Maryland (Southerland *et al*. 2005). Data consisted of fish captured via electrofishing within a 75-m bounded stream reach, with all individuals identified to species (56 species reported). Fish counts were converted to biomass (grams, g) by multiplying the mean length of each taxa by species-specific allometric scaling equations (see www.fishbase.org). Covariate data included water chemistry and quality (pH, conductivity, temperature, dissolved organic carbon, total nitrogen, total phosphorus, orthophosphate, ammonium, nitrate), habitat quality metrics, canopy cover, stream morphology (width, depth, drainage area), velocity, and watershed land cover from the 2006 National Land Cover Dataset (Homer *et al*. 2004).

Dataset construction

Datasets used in all analyses were converted into a site × environment matrix, a site × year × species matrix, and a site × coordinate matrix. Covariate information was averaged across years within sites to give a mean value for each covariate in each site. Regions were sampled by creating rings around each site ranging from a diameter of 5 km to the maximum distance observed between sites at 5-km intervals. In each replicate ring, all sites that fell within the ring were included in the calculation of a series of metrics (WebFigure 1).

Metrics

Environmental dissimilarity: mean Bray-Curtis dissimilarity in covariate values among all sites within the sampling circle.

Area (distance): diameter of the sampling circle (km).

γ-richness: total number of taxa present across all sites within the sampling circle.

$\overline{\alpha}$-richness: mean number of taxa within the sites within the sampling circle.

β-diversity: mean Bray-Curtis dissimilarity in species composition among all sites within the sampling circle.

$\overline{\alpha}$-variability: mean temporal coefficient of variation for response variable (biomass, abundance, etc) within sites through time within the sampling circle.

Synchrony: measured as the variance explained by first common mode of variation derived from empirical orthogonal function (EOF) analysis (Jassby and Powell 1990). EOF takes a multidimensional time series dataset – for example, multiple time series of the same response variable collected at different spatial locations – and extracts the major modes of temporal variation. These modes of variation are single time series that describe a portion of the shared covariation among series (Jassby *et al*. 1992). EOF analysis has been referred to as "principal components analysis" for time series and is often used by climatologists (Lorenz 1956, 1970). Climate cycles, such as the North Pacific Oscillation and the North Atlantic Oscillation, are well-known examples of EOF modes. EOFs offer several advantages over simply measuring the correlation among temporal series. Each mode of variation extracted from the multidimensional series describes a portion of the dominant shared covariation among series (Jassby *et al*. 1992). The variation explained by the first mode is comparable to mean cross-correlation among individual time series, but the modes themselves also contain information about the dominant temporal patterns common among locations. We chose this over other possible metrics of spatial synchrony where the calculations are mathematically dependent on α-variability and γ-variability (Wang and Loreau 2014) because we use all three measures in our SEM and it would be statistically inappropriate to do so were they derived from one another.

γ-variability: coefficient of variation for response variable (biomass, abundance, etc) through time for a series created by aggregating among sites within years within the sampling circle.

Statistical analysis

Data were analyzed as an SEM using data from the four systems in the three datasets. The SEM was based on an examination of the relationships representing each individual hypothesis within successively larger, randomly selected analysis rings within each region, analyzing subsampled aggregations of sites. This leads to a lack of complete independence among replicate observations. Although each group of sites is a unique combination, groups of sites may partially overlap spatially with other groups of sites. This overlap has often prevented the use of traditional statistics when analyzing patterns of temporal variability across scales (eg Schindler *et al*. 2010; Carlson *et al*. 2011). To address this problem, we combined the established procedure for dealing with spatial autocorrelation in the SEMs (Harrison and Grace 2007; Matteson *et al*.

2013), with a direct measurement of the amount of non-independence between each spatially overlapping pair of groups of sites.

The approach for dealing with spatial autocorrelation in SEMs is fully explained in a web tutorial developed by J Grace (https://www.usgs.gov/centers/wetland-and-aquatic-research-center/science/quantitative-analysis-using-structural-equation). The code for the tutorial was largely based on an unpublished function developed by J Byrnes called LavSpatialCorrect. Here we summarize the method based on that material. The general approach assumes that spatial autocorrelation results in reduced information present in the observations because nearby observations can predict one another (ie they are not fully independent). One solution for dealing with the reduced information is to reduce the sample size concordantly with the information lost to generate an "effective" sample size (Naroll 1961). This new sample size can then be used to recalculate standard errors and *P* values. Grace therefore suggests that the appropriate procedure is to measure the degree of spatially structured correlation in the dataset using Moran's *I* (Moran 1950) and then obtain the effective sample size (N_{eff}) via:

$$N_{eff} = N * \frac{(1-I)}{(1+I)} \quad \text{(Equation 1).}$$

For our datasets, we needed to add an additional step. While the centroids of each "group" are fixed in space, the radii of the groups vary among samples, and therefore the degree of spatial overlap between pairs of observations vary based on both centroid location and the grain of each sample. In response, we directly calculated the degree of spatial overlap between each pair of groups and used this to build a distance matrix based of overlap. We then performed a principal coordinate analysis and projected the observations into a Cartesian plane, where Euclidian distance between points was a measure of degree of overlap. We also randomly selected ½ of the observations from each dataset to reduce overlap. We then used the coordinates in the projected plane to calculate Moran's *I* and applied the procedure outlined above to recalculate the standard errors and adjusted *P* values. Analyses were performed using the *lavaan* package (Rosseel 2012) in the statistical program R (R Team 2015). Two separate model forms were used, one where "system" was not included as a factor (general model) and one where "system" was included as a factor (multigroup model).

Results

For the general model, we failed to reject the null hypothesis that the covariance matrix implied by the model differed significantly from the covariance matrix of the data ($\chi^2 = 0.003$, $P = 0.956$, $n = 1{,}086$), and therefore the model was deemed to be consistent with the data (WebFigure 2). For the multigroup model, we rejected the null hypothesis that the covariance matrix implied by the model differed significantly from the covariance matrix of the data ($\chi^2 = 142.404$, $P < 0.001$, $n = 1{,}086$), and therefore the model was deemed to be inconsistent with the data. The poor fit of the multigroup model indicated that while the proposed model form generally fits data (ie excellent fit of the general model), there are differences between the individual systems (WebFigure 3). See the main text for a discussion about differences among systems. Full model results are presented in WebTable 1, and raw biplots of the variables in the model are illustrated in WebFigure 4.

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