# Unveiling the temporal signatures of demographic stochasticity from populations to metacommunities

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**Abstract:** The temporal stability of ecological properties tends to increase with spatial scale and levels of biological organization, which is mostly associated with deterministic processes. However, random fluctuations caused by demographic stochasticity in small populations might extend to communities and metacommunities, potentially affecting stability propagation across biological levels and spatial scales. Here, we tested this hypothesis by combining process-based simulations and statistical modeling of 468 sites distributed across 39 regions, sampled from 1981 to 2019, to investigate how fish communities and metacommunities changed over time at local and regional scales. We found that more communities with more species and in more seasonal environments were more variable. However, the major driver of compositional temporal variability was community size. Communities comprising smaller populations were more temporally variable than those comprising larger populations. This relationship was weaker at the regional scale, suggesting a dampening effect at the metacommunity level. Our results suggest that the potential effects of demographic stochasticity, which are undoubtedly stronger in small populations, might extend beyond populations, leaving different signals in the temporal variability of ecological properties. These effects appear to be stronger and consistent within small communities and weaker in metacommunities. Our study advances the knowledge of how populational-demographic stochasticity might affect biodiversity temporal dynamics across scales.

**KEYWORDS**: random demography; community size; compositional variability; environmental variability; spatial scale; temporal variability

## Introduction

Theoretical and observational research posit that the temporal variability of ecological properties (e.g., coefficient of variation of biomass) decreases with the increase of spatial scale, levels of biological organization, and trophic levels (Kéfi et al. 2019; Wang et al. 2019; Hammond et al. 2020; Siqueira et al. 2024). The explanations for these relationships are mainly based on deterministic processes, such as compensatory dynamics (Gonzalez and Loreau 2009, Brown et al. 2016), the role of mobile predators (McCann et al. 2005), and the Moran effect (Steiner et al. 2013). Small populations experience high temporal variability due to random demographic events (Reed and Hobbs 2004; Melbourne and Hastings 2008). Thus, as a process that unfolds over time, could demographic stochasticity increase the temporal variability of communities and metacommunities? Or do its effects also weaken from populations to metacommunities? Understanding how random demographic events may affect biodiversity temporal variability at larger scales is important to better forecast how ecosystems will respond to global changes.

Demographic stochastic events such as birth, death, and emigration are inherent elements of population dynamics (Lande 1988; 1993; Otto and Whitlock 1997; Whitlock 2004; Willi, van Buskirk, and Hoffmann 2006; Melbourne and Hastings 2008). While various forces influence population demography, their impacts are consolidated into population size. Small populations are more susceptible to the effects of random events, making them more temporally variable than larger populations (Otto and Whitlock 1997; Reed and Hobbs 2004; Whitlock 2004). Expanding on this understanding, recent research suggests that the effects of local demographic stochastic events might extend to larger spatial scales and levels of biological organization. For example, there is mounting evidence indicating that demographic stochasticity increases spatial beta diversity among local communities comprised of small populations (small communities; (Orrock and Watling 2010; Gilbert and Levine 2017; Siqueira et al. 2020) and weakens community-environment relationships (Jacobi and Siqueira 2023).

Although there is limited research about the effects of demographic stochasticity on the temporal variability of multispecies communities, most studies suggest that small communities tend to exhibit greater temporal variability (temporal beta diversity) compared to larger ones because small populations have few individuals to buffer against random fluctuations in their demography (Orrock and Fletcher 2005; Pedruski, Fussmann, and Gonzalez 2015; Gilbert and Levine 2017; Legault, Fox, and Melbourne 2019). One possible explanation for such relationship is that when demographic stochasticity plays a strong role in community assembly, niche differences become less important, as the likelihood of any demographic event happening is similar for all individuals, regardless of their fitness differences (Orrock and Watling 2010, Legault et al. 2019). For this reason, it is reasonable to expect that small local communities should have higher temporal variability in their species composition (i.e. high temporal beta diversity) than large communities. However, stochastic variability in species composition might be also caused by an interaction between trait-diversity, dispersal and population size (Arim et al. 2023). Thus, further empirical research still needed to understand the effects of demographic stochasticity in the temporal assembly of ecological communities.

Considering that small communities may experience high temporal variability in species composition, it is possible that metacommunities formed by small communities may also be highly variable in time. Simulations and experiments analyzing biodiversity variability have found that metacommunity size is a key factor shaping species composition temporal variability (LeCraw, Srivastava, and Romero 2014; Suzuki and Economo 2024). Thus, large temporal fluctuations in species composition within the metacommunity should happen if random extinctions (or abundance changes) of species occur independently across different sites within the metacommunity. Alternatively, if demographic stochasticity is not widespread within the metacommunity, its effects might be negligible compared to the influence of deterministic processes like compensatory dynamics (Andrew Gonzalez and Loreau 2009; Loreau 2010; Brown, Downing, and Leibold 2016).

In light of the ongoing declines in population sizes and the elevated rates of species extinction (McCallum 2015; He et al. 2019; Almond, Grooten, and Petersen 2020), we ask whether the effects of population-level demographic stochasticity propagate to higher levels of biological organization and influence biodiversity temporal dynamics at larger spatial scales. To do so, we analyzed how temporal variability in species composition was related to the size of communities at local and regional scales. If small communities are more variable than large ones simply due to their size, this would indicate a stronger influence of demographic stochasticity on these communities. However, analyzing this relationship is challenging as, aside from the need for a significant amount of independent temporally and spatially replicated data across a gradient of community size, it is crucial that the metrics used to quantify temporal variation in species composition are not inherently affected by differences in community size. Thus, we first used a process-based simulation model to test if metrics commonly used to quantify variation in species composition could indicate the effects of demographic stochasticity via their relationship with community size. We then applied these metrics to time-series observational data and statistical models to understand the relationships of temporal variability in species composition at both the community and metacommunity levels with community size and other potential predictors, including temporal variation in environmental conditions, time series length, the number of samples in the time series, and species richness.

We expected to find a negative relationship between temporal variability in species composition within local communities and community size, suggesting that local species composition vary more over time within small communities. At the metacommunity level, we had two competitive expectations: (1) either a negative relationship between temporal variability in spatial beta-diversity and regional community size (2) or no relationship between temporal variability in spatial beta-diversity and regional community size. Evidence supporting the latter would indicate that the effects of local demographic stochasticity are weakened over time at the regional scale.

## Material and methods

### Data

We ran our empirical analyses using data from two large databases. From RivFishTIME (Comte et al. 2021), we obtained time series count data of riverine fish. TerraClimate (Abatzoglou et al. 2018) provided high-resolution monthly data for environmental variables, from which we calculated annual averages for precipitation, maximum air temperature, and minimum air temperature (a good proxy for water temperature; Stefan and Preud'homme 1993).

We defined a metacommunity as the set of sites within basin delineations (HydroBASINS level 7 – Lehner and Grill 2013) and assigned a Strahler stream order for each sampled site using information from the HydroRIVERS network (Lehner and Grill 2013). After that, we selected metacommunities that met the following criteria: (1) were composed of at least five communities in first to third-order streams, (2) were sampled at least four times in different years, and (3) had at least five species. When dealing with metacommunity data comprising multiple sampling events per year, we selected the sampling date with the highest number of sampled sites. These steps resulted in 468 communities distributed within 39 metacommunities, sampled from 1981 to 2019, located in the Australasia (12), Nearctic (12), and Palearctic (15) biogeographical realms (Figure S1). These metacommunities are composed on average of 12 communities (standard deviation = 9) sampled, on average, 11 times in the time-series (standard deviation = 5) with an average temporal extent of 14 years (standard deviation = 5). All data selection and manipulation were made in R v. 4.2.1 (www.r-project.org) using the packages ncdf4 (Pierce 2023), mapview (Appelhans et al. 2022) raster (Hijmans 2023), sf (Pebesma 2018; Pebesma and Bivand 2023), sp (Pebesma and Bivand 2005, Bivand et al. 2013), tidyverse (Wickham et al. 2019).

## Representing the signature of demographic stochasticity

Because the effects of demographic stochasticity are negatively correlated with population size, we used the median of community size over time as a proxy to represent the signature of demographic stochasticity. We measured the size of each community as the median number of individuals over time (local community size), considering that communities composed of fewer individuals are also composed, on average, of smaller populations than communities with more individuals. Finally, to represent the signature of demographic stochasticity at the regional scale, we measured the size of each metacommunity as the median community size within each metacommunity over time (regional community size).

## Metrics of temporal variability

A major challenge involved in the use of community size as a proxy for the signature of demographic stochasticity is that many community metrics can be mathematically related to sample size regardless of the underlying assembly process (Beck, Holloway, and Schwanghart 2013; Chase and Knight 2013; Barwell, Isaac, and Kunin 2015; Cao et al. 2021). Thus, to select appropriate metrics of temporal variability that could be modelled against community size, we first developed a process-based simulation model according to the following steps.

We first simulated a purely neutral dynamics in 39 metacommunities of varying sizes over 1000-time steps with the mcbrnet package (Terui and Pomeranz 2023). These simulations were performed using different levels of dispersal within the metacommunities, which mirrored the empirical dataset in terms of community and species numbers. Given that the assembly of the simulated metacommunities was entirely neutral, there should be no relationship between temporal variability in species composition and community size. If any metric of temporal variability was related with size, we understood it as unsuitable for our objective. Secondly, we selected 10 time steps and measured temporal variability at both local (within each community) and regional (among communities) scales using different metrics: (i) temporal variability in species abundance measuring the coefficient of variation of abundance at each organizational level based on the partitioning framework developed by Wang et al. (2019); (ii) temporal variability in species composition at the local and regional scales employing the metric proposed by Lamy et al. (2021) and implemented with the ltmc package (Sokol & Lamy 2022); (iii) temporal beta diversity as the median of species rank changes (Avolio et al. 2019) within each community over time, using the RAC_change function from the codyn package (Hallett et al. 2020). Additionally, we used codyn to assess spatial beta diversity at the metacommunity level via the RAC_difference function. The median difference in species rank among communities was calculated at each time step. Finally, we regressed all these metrics of temporal variability described above against the median community size over time and compared the outcomes. The performance of each metric is informed in the Results section. Further details on the process-based simulation are available in the supplementary information.

## Predictors of temporal variability in species composition

We measured several metrics that are expected to play a role in explaining temporal variability in species composition. This included assessing the number of samples collected over time (number of samples) and the temporal extent of each sampling (time series length) for each community and metacommunity. We also measured the coefficient of variation (CV) of maximum (CV tmax) and minimum (CV tmin) temperature and of precipitation (CV ppt) as potential predictors of community variability over time. These metrics were measured by dividing the standard deviation of temperature and precipitation values at each site over time by the mean of these values. We also estimated the median asymptotic richness of each community over time to be included as a predictor of community variability. Asymptotic richness was estimated with the iNEXT package (Hsieh et al. 2022), which combines extrapolation and interpolation techniques. At the metacommunity level, we also measured environmental synchrony as a proxy for the Moran effect (Siqueira et al. 2024). We measured environmental synchrony within metacommunities by calculating the correlation of each environmental variable (syn tmax, syn tmin, syn ppt) between communities over time. A high correlation or environmental synchrony would indicate that the environmental conditions being analyzed changed similarly across sites, while a low synchrony indicates that environmental conditions vary more independently across sites. Finally, we measured the spatial connectivity within each metacommunity by calculating the mean Euclidean distance, in meters, between the central point of each metacommunity and its respective communities. The smaller the mean distance between communities, the greater the proximity centrality between them (Erős et al. 2012). We used the geosphere package to perform this calculation (Hijmans 2022).

## Statistical analysis

To investigate how temporal variability in the species composition of local communities was related to community size, we fitted a Generalized Linear Mixed Model (GLMM) with metacommunity identity as a random effect. We modeled temporal variability in the species composition as the response variable and included as fixed-effects the median of local community size over time, estimated species richness (median of estimated species richness over time), the coefficients of variation of local environmental variables over time (CV tmax, CV tmin, CV ppt), the number of samples and the time series length of each community. All variables were log transformed and we assumed a Gaussian distribution. We used the lme4 package (Bates et al. 2015) to fit this GLMM model and estimated the marginal (due to fixed effects) and the conditional (due to fixed and random effects) $R^2$ values with the MuMIn package (Bartoń 2023). We also estimated p-values associated with the fixed effects using Wald chi-square tests with the Anova function in the car package (Fox and Weisberg 2019).

To investigate whether temporal variability in species composition within metacommunities was related to regional community size, we used a Generalized Linear Model (GLM). We included regional community size (median community size within each metacommunity over time), spatial connectivity, environmental synchrony (syn tmax, syn tmin, syn ppt), number of metacommunity samples over time, and the time series length of each metacommunity as predictors. This model was also described by a Gaussian distribution and the variables were not log transformed. Model assumptions were examined via a visual assessment, utilizing the check_model function from the performance package (Lüdecke et al. 2021), and the simulateResiduals function from the DHARMa package (Hartig 2022). All analyses were performed in R version 4.2.1 (www.r-project.org). Data and codes used in this research are available at Zenodo (Jacobi 2024).

## Results

### Metrics of temporal variability in simulated metacommunities

Our process-based simulation models indicated that while the temporal variability (CV) in abundance had a consistent negative relationship with community size both at the local and regional scales, the LTMC metric exhibited a negative relationship with community size at the local scale (Table S1). Thus, these metrics of temporal variability were not adequate to be used in our study. The species rank change metric was the only metric that was not related to community size at the local scale (Table S1). The species rank difference was positively related to community size in most simulations at the regional scale; however, the explanatory power of the models ($R^2$) was consistently low across all simulation scenarios (mean $R^2 = 0.03$; Table S1). Conversely, the LTMC metric had a negative relationship with regional community size in some simulations, while in others, no such relationship was observed (Table S1). However, when a relationship was present, it exhibited a higher explanatory power compared to the metric based in species rank differences.

Thus, considering that the metrics based on change in species rank yielded the most robust results regarding community size variations in a neutral scenario, we used them to analyze the empirical data. More specifically, to represent temporal variability in species composition for each community, we used the species rank change metric. To represent temporal variability in species composition in metacommunities we used the coefficient of variation (CV) of the rank difference of each year over time.

**Relationships in the empirical dataset**

Despite a small violation of model assumptions (residuals slightly deviated from the model predicted values; Figure S2; S3), the model describing temporal variability in species composition at the local scale explained 34% of the variation in community turnover (fixed effects = 29%, random effects = 5%). Temporal variability in community composition was negatively related to local community size (Wald $X^2_{[1, 458]} = 112.4725$, p-value = 2.2e-16, Figure 1a), indicating that species change more in rank position over time in smaller communities. Such result was not observed in the null model, which reinforces the significance of observing this relationship in the real dataset. Compositional variability also increased with the increase of species richness (Wald $X^2_{[1, 458]} = 93.2697$, p-value = 2.2e-16, Figure 1b), CV of the minimum temperature (Wald $X^2_{[1, 458]} = 9.3190$, p-value = 0.002, Figure 1c), and of the CV of precipitation (Wald $X^2_{[1, 458]} = 7.8240$, p-value = 0.005, Figure 1d). These relationships indicate that more diverse communities in more variable environments were also more temporally variable in their species composition.

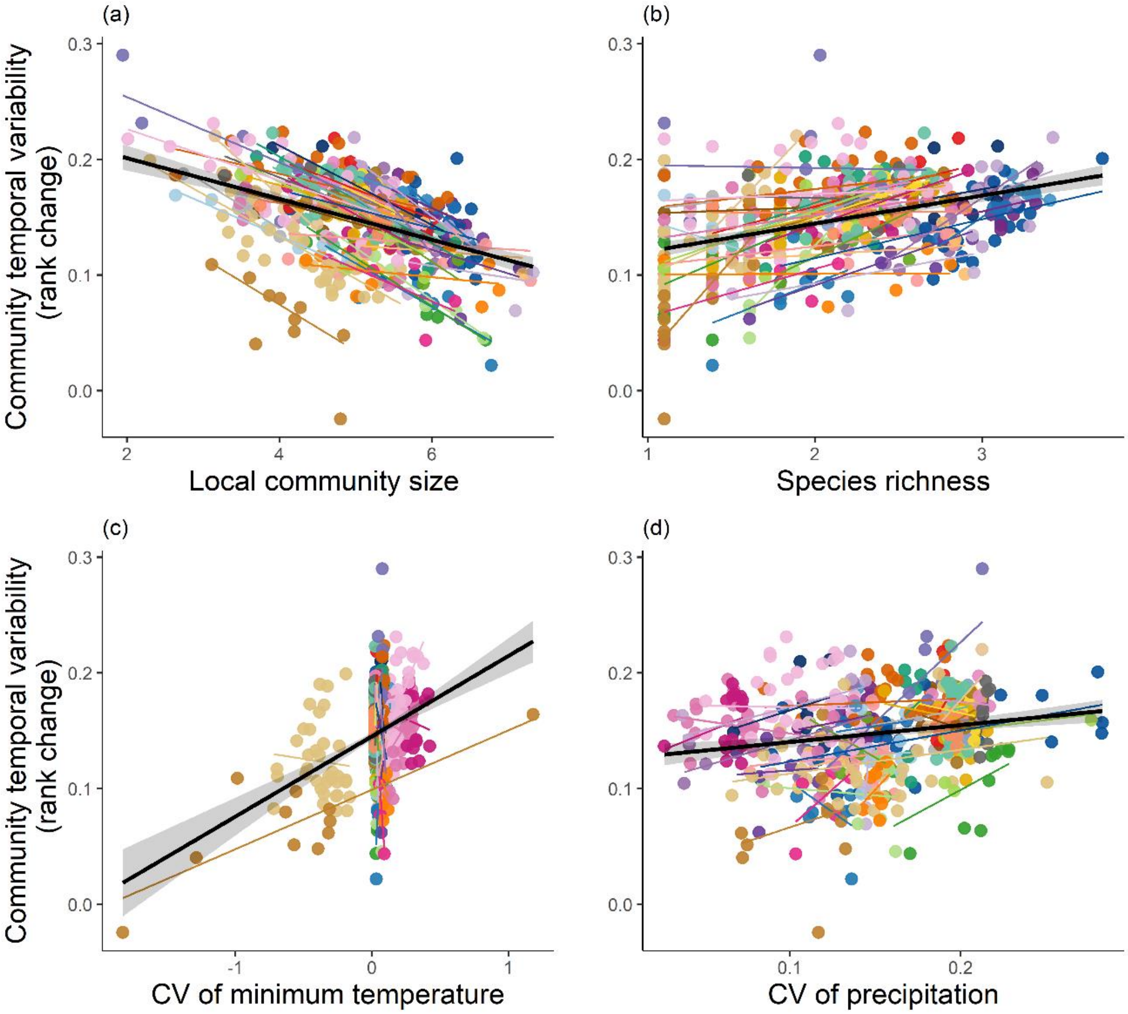

Figure 1. Relationship between temporal variability in species composition of local communities (rank change) and (a) local community size, (b) species richness, (c) coefficient of variation of minimum temperature (CV tmin), and (d) coefficient of variation of precipitation (CV ppt). Points represent local communities; colors represent the metacommunity to which the local communities belong to. All variables are in log scale. Grey bands represent the 95% confidence interval.

The model describing temporal variability in species composition at the regional scale exhibited high collinearity among the predictors of environmental synchrony. To address this issue, we refitted the model by including only one environmental synchrony variable at a time and then selected the model with the lowest Akaike information criterion value corrected for small sample size ($AIC_c$). The selected model was the one that included synchrony of precipitation as a predictor of environmental synchrony (Table S2). Following this adjustment, the model showed no issues with assumptions (Figure S4) and explained 16% of temporal variability in species composition. The only predictor variable associated with p-value < 0.05 in the model was syn ppt ($\beta = 0.0820$; std. error = 0.0367; t-value$_{[38, 33]}$ = -2.232; p = 0.0324; Figure 2a; Table S3), indicating that greater synchronicity in precipitation across communities reduces the temporal variability in regional species composition. While no relationship was found between temporal variability and regional community size, the data exhibited a slight negative trend (Figure 2b; Table S3), which may suggest that a negative relationship could emerge with a larger sample. In summary, our results indicate that the relationship between temporal variability in species composition and size was statistically strong only for the local scale.

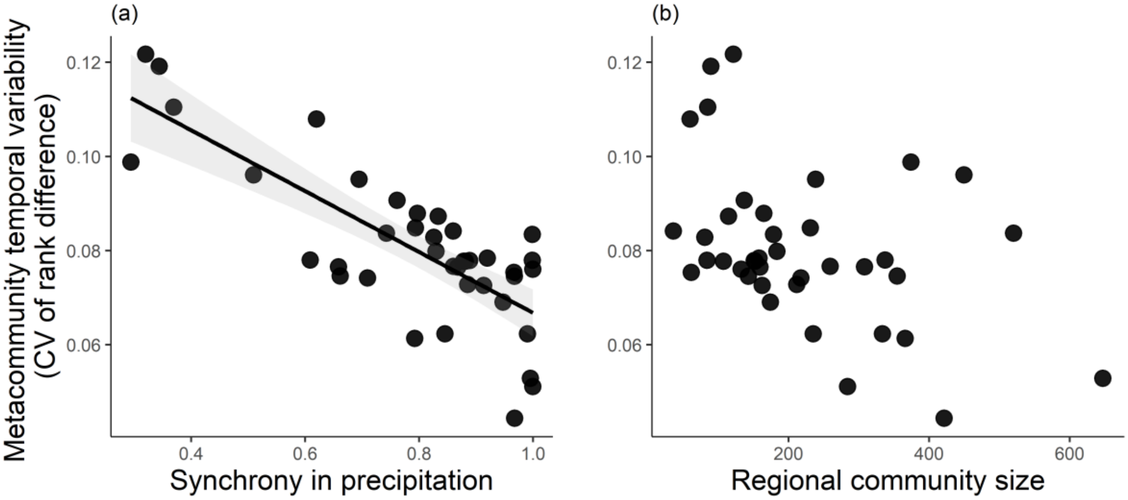

Figure 2. Relationship between temporal variability in species composition in metacommunities (CV of rank difference) and (a) synchrony in precipitation among localities, and (b) regional community size. Grey bands represent the 95% confidence interval.

## Discussion

Our research investigated the potential for random fluctuations driven by demographic stochasticity to extend beyond the population level and influence the dynamics of higher organizational levels of biological organization, such as communities and metacommunities. Agreeing with our predictions, we found a consistent negative relationship between temporal variability in species composition and community size, but mainly at the local scale. Although statistically weak, there was also a negative trend between temporal variability in species composition and community size at the regional scale. Together, our results suggest that the potential effects of demographic stochasticity, which are undoubtedly stronger in small populations, might leave different signals in the temporal variability of ecological properties, being stronger and consistent within small communities and weaker in metacommunities.

Populations comprising few individuals tend to fluctuate more over time because independent random demographic events can cause substantial changes in both their mean size and variance compared to populations with many individuals (Lande 1993; Legendre et al. 1999; Melbourne and Hastings 2008; Fauvergue et al. 2012). In line with this knowledge, our finding of a negative relationship between temporal variability in species composition and community size suggests that communities comprised of small populations are also more likely to vary in time. This means that species abundances within these communities change more over time than within larger communities, relatively to their size and number of species. This result provides empirical support to previous theoretical and experimental findings that indicated how random demographic events in small populations can lead to temporal changes in the compositional turnover of individual communities (Gilbert and Levine 2017; Legault, Fox, and Melbourne 2019). These studies suggest that communities comprising small populations undergo more pronounced demographic fluctuations, preventing any species from maintaining a constant competitive advantage over others (Orrock and Fletcher 2005). Consequently, the smaller the community, the more the effects of demographic stochasticity increase community variability over time.

Our results also indicated that the influence of demographic stochasticity on community composition weakens or even disappears over time as we move from the local to the regional scale. While at the local scale stochastic events are likely to cause major shifts in the species composition of small communities, at the regional scale they are likely to be counterbalanced by other factors such as the dispersal of individuals among patches and population spatial asynchrony (Wang and Loreau 2016; Thompson et al. 2020). To influence regional species composition, random demographic events that influence the species composition of local communities would need to occur concurrently and similarly in different communities, resulting in the loss (or change in the abundance) of the same species across the entire metacommunity. However, due to the inherently random nature of demographic stochasticity (Hubbell 2001; Lande, Engen, and Sæther 2003), its impact is unlikely to be uniform across communities. Even if demographic stochasticity were widespread within the metacommunities we studied, its effects on local communities would have been asynchronous, meaning that the species affected by its effects would vary from one community to another, thus keeping regional species composition relatively stable.

Although our analyses did not indicate a statistical relationship between temporal variability in species composition at the regional scale with metacommunity size, a visual inspection of the scatter plot suggested a negative trend between these variables. As the first study of its kind, we caution that our analyses, derived from a limited sample size (39 metacommunities), should be approached with care before dismissing the potential propagation of the effects of random demography to the metacommunity level. Further studies comprising more metacommunities, longer time-series, and different response and predictor variables might clarify this potential relationship. For example, Suzuki and Economo (2024) found that increasing the number of patches in simulated metacommunities led to less temporal variability, implying that larger metacommunities could be more temporally stable.

Beyond community size, multiple abiotic and biotic factors can influence the temporal variability of multispecies communities (Dunson and Travis 1991; Araújo and Luoto 2007; Valencia et al. 2020). After adjusting for the effect of community size, we found that communities with more species were also the ones with more compositional variability over time. Although this finding contrasts with the exiting research on the temporal stability of ecological properties, it can be explained by the type of variability being used here. The temporal variability of aggregate ecological properties, such as total biomass or abundance, is expected to decrease with the increase in the number of species due to the statistical averaging of fluctuations in species abundances (Doak et al. 1998; Xu et al. 2021). But our analyses were based on the temporal variability of species composition (rank of species abundances). As found recently by Arim et al. (2023), high functional and taxonomic diversity allows for a wider array of responses to environmental fluctuations, potentially resulting in varying levels of success for different species over time or under different conditions. Differential responses of species to stochastic fluctuations in the environment can lead to changes in species dominance over time and increase the variability in species rank abundance (A. Gonzalez and Descamps-Julien 2004). This is likely the reason why we found that the coefficient of variation (CV) of both minimum temperature and precipitation were positively related to the temporal variability in species composition of local communities.

Demographic stochastic events are a natural component of population dynamics (Otto and Whitlock 1997, Whitlock 2004, Willi et al. 2006). Our research indicates that such population-level events can have consequences for the temporal dynamics of local communities and potentially to metacommunities. So far, most previous research on this topic highlighted the effects of demographic stochasticity on either population temporal dynamics or community spatial dynamics (Lande 1993; Legendre et al. 1999; Vindenes and Engen 2017; Siqueira et al. 2020; Feng et al. 2022; Jacobi and Siqueira 2023). We extend previous findings here by showing with empirical data that demographic stochasticity can also generate greater temporal variability in species composition, but mainly at the local scale. We thus suggest that the effects of demographic stochasticity are scale-dependent, being strongest at the local scale and decreasing in intensity with the increase of spatial scale or level of biological organization.

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## Supplementary Information

### Process-based simulation model

To select temporal variability metrics that could be used to investigate the role of demographic stochasticity, we simulated neutral temporal dynamics in metacommunities of varying sizes and examined the relationship between temporal variability metrics and community size. By simulating neutral metacommunities, we eliminated niche selection effects on species composition. As communities were assembled under neutral dynamics, any relationship between temporal variability and community size would suggest that a given variability metric was not appropriate.

Initially, we simulated random branching networks using the function brnet from the mcbrnet package (Terui & Pomeranz, 2023). The branching networks were then employed in the mcsim function of the mcbrnet package to simulate our metacommunities. We generated 39 metacommunities comprising the same range of community (5-30) and species (5-48) numbers as observed in the datasets used for statistical modeling. Given that we were interested in simulating a neutral dynamic, we excluded environmental variation and niche differences from the simulation. We randomly varied the number of species among the metacommunities to generate a gradient of metacommunity sizes. We also incorporated a species carrying capacity value within communities to restrict growth and prevent excessive size increase over time. The carrying capacity of each population was consistent within communities of a given metacommunity but varied randomly among metacommunities (ranging from 50 to 150 individuals). We also introduced variability in species abundance within communities by simulating a disturbance. To achieve this, we set the disturbance probability to 1 and the intensity to 0.43 for all metacommunities. We arrived at this disturbance value by adjusting it to match metacommunity sizes similar to those in real datasets. Additionally, we conducted simulations considering different dispersal values within metacommunities (0.1, 0.5, and 1) to observe if this could impact the relationships with size. Then, we ran each simulation for a total of 1000 time steps. We selected the time-steps 100, 200, 300, 400, 500, 600, 700, 800, 900, and 1000 as our temporal samples to calculate metrics related to the temporal variability in species composition.

We started measuring the temporal variability in species abundance at both the community and metacommunity levels to subsequently relate them to the median community size. We assessed temporal variability in species abundance by measuring the temporal variability of aggregate abundance at each biological level based on the framework proposed by Wang et al. (2019). However, we excluded this metric from our future analyses as it demonstrated a negative relationship with community size, both at the local and regional scales (Table. S1). Then, we decided to test some metrics for temporal variability in species composition. We measured both community and metacommunity variability using the approach proposed by Lamy et al. (2021) with the ltmc package. We also assessed temporal variability in the rank of species (Avolio et al. 2019), measuring the rank change within each community over time and the rank difference between communities at each time point. This was done using the codyn package (Hallett et al.) Considering multiple simulations conducted with various dispersal rates and different seeds, we observed that both at the local and regional scales, the metrics of species rank variability were less influenced by community size compared to the ltmc metrics (Table S1). When the metrics of species rank variability showed an association with size, the relationship exhibited low explanatory power. In contrast, the local ltmc metric consistently showed a negative relationship with community size, while the regional ltmc demonstrated higher explanatory power when related to community size.

Table S1. Statistics obtained in the process-based simulation model by relating the metrics of temporal variability in species composition with the median community size. Simulations were conducted using different seeds and dispersal rates. The p-value represents the significance of each relationship, and the explanatory power was measured by $R^2$.

| Temporal variability metric | set.seed | Dispersal | Slope | p-value | $R^2$ | Adjusted $R^2$ |
|---|---|---|---|---|---|---|
| Local abundance (CV) | 1234 | 0.1 | -1.7E-04 | 2.5E-14 | 0.7958 | 0.7903 |
| Regional abundance (CV) | 1234 | 0.1 | -4.1E-05 | 0.0002 | 0.3084 | 0.2897 |
| LTMC local | 1234 | 0.1 | -1.2E-04 | 0.0055 | 0.1901 | 0.1683 |
| LTMC regional | 1234 | 0.1 | -6.4E-06 | 0.0985 | 0.0721 | 0.0470 |
| Rank change | 1234 | 0.1 | 1.0E-06 | 0.8411 | 6.3E-05 | -0.0015 |
| Rank difference | 1234 | 0.1 | 1.1E-05 | 0.0017 | 0.0252 | 0.0227 |
| Local abundance (CV) | 1234 | 0.5 | -1.3E-04 | 5.2E-15 | 0.8123 | 0.8072 |
| Regional abundance (CV) | 1234 | 0.5 | -4.4E-05 | 0.0006 | 0.2777 | 0.2581 |
| LTMC local | 1234 | 0.5 | -3.8E-05 | 0.0132 | 0.1549 | 0.1321 |
| LTMC regional | 1234 | 0.5 | -1.2E-06 | 0.6211 | 0.0067 | -0.0202 |
| Rank change | 1234 | 0.5 | 8.6E-06 | 0.0364 | 0.0069 | 0.0053 |
| Rank difference | 1234 | 0.5 | 4.2E-06 | 0.301 | 0.0028 | 0.0002 |
| Local abundance (CV) | 1234 | 1 | 1.1E-01 | 2.7E-13 | 0.7682 | 0.7619 |
| Regional abundance (CV) | 1234 | 1 | -5.1E-02 | 7.7E-05 | 0.3482 | 0.3306 |
| LTMC local | 1234 | 1 | -3.7E-05 | 0.0108 | 0.1632 | 0.1406 |
| LTMC regional | 1234 | 1 | -2.3E-06 | 0.405 | 0.0188 | -0.0077 |
| Rank change | 1234 | 1 | 5.0E-07 | 0.9071 | 2.2E-05 | -0.0016 |
| Rank difference | 1234 | 1 | 1.2E-05 | 0.0091 | 0.0174 | 0.0149 |
| Local abundance (CV) | 111 | 0.1 | -1.9E-04 | 4.0E-11 | 0.6967 | 0.6885 |
| Regional abundance (CV) | 111 | 0.1 | -6.0E-05 | 3.6E-05 | 0.3736 | 0.3567 |
| LTMC local | 111 | 0.1 | -1.3E-04 | 0.0001 | 0.328 | 0.3098 |
| LTMC regional | 111 | 0.1 | -9.0E-06 | 0.0021 | 0.2274 | 0.2065 |
| Rank change | 111 | 0.1 | -2.3E-07 | 0.9565 | 4.8E-06 | -0.0016 |
| Rank difference | 111 | 0.1 | 1.4E-05 | 1.5E-06 | 0.0580 | 0.0556 |
| Local abundance (CV) | 111 | 0.5 | -1.4E-04 | 9.5E-12 | 0.7192 | 0.7116 |
| Regional abundance (CV) | 111 | 0.5 | -4.8E-05 | 6.8E-06 | 0.4258 | 0.4103 |
| LTMC local | 111 | 0.5 | -4.6E-05 | 0.0003 | 0.3016 | 0.2827 |
| LTMC regional | 111 | 0.5 | -6.7E-06 | 0.0060 | 0.1868 | 0.1648 |
| Rank change | 111 | 0.5 | 6.3E-06 | 0.1187 | 0.0039 | 0.0023 |
| Rank difference | 111 | 0.5 | 2.1E-05 | 2.1E-08 | 0.0778 | 0.0754 |

| Temporal variability metric | set.seed | Dispersal | Slope | p-value | $R^2$ | Adjusted $R^2$ |
|---|---|---|---|---|---|---|
| Local abundance (CV) | 111 | 1 | -1.4E-04 | 2.7E-11 | 0.7028 | 0.6948 |
| Regional abundance (CV) | 111 | 1 | -4.7E-05 | 1.3E-07 | 0.5329 | 0.5203 |
| LTMC local | 111 | 1 | -4.3E-05 | 0.0003 | 0.3063 | 0.2875 |
| LTMC regional | 111 | 1 | -5.5E-06 | 0.0255 | 0.1278 | 0.1042 |
| Rank change | 111 | 1 | -4.8E-07 | 0.9029 | 2.4E-05 | -0.0016 |
| Rank difference | 111 | 1 | 1.7E-05 | 1.4E-05 | 0.0476 | 0.0451 |

## Supplementary Figures

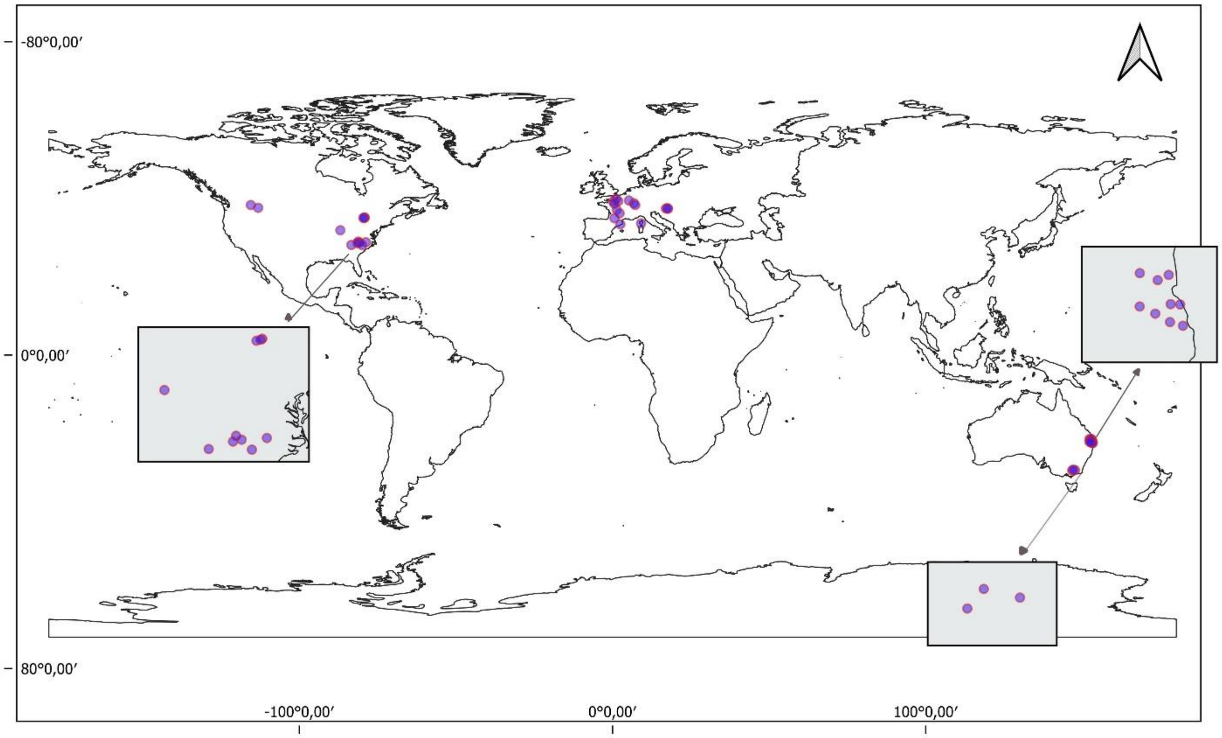

Figure S1. Geographic distribution of the 39 metacommunities selected in our study, located in Australasia (12), Nearctic (12), and Palearctic (15) biogeographical realms.

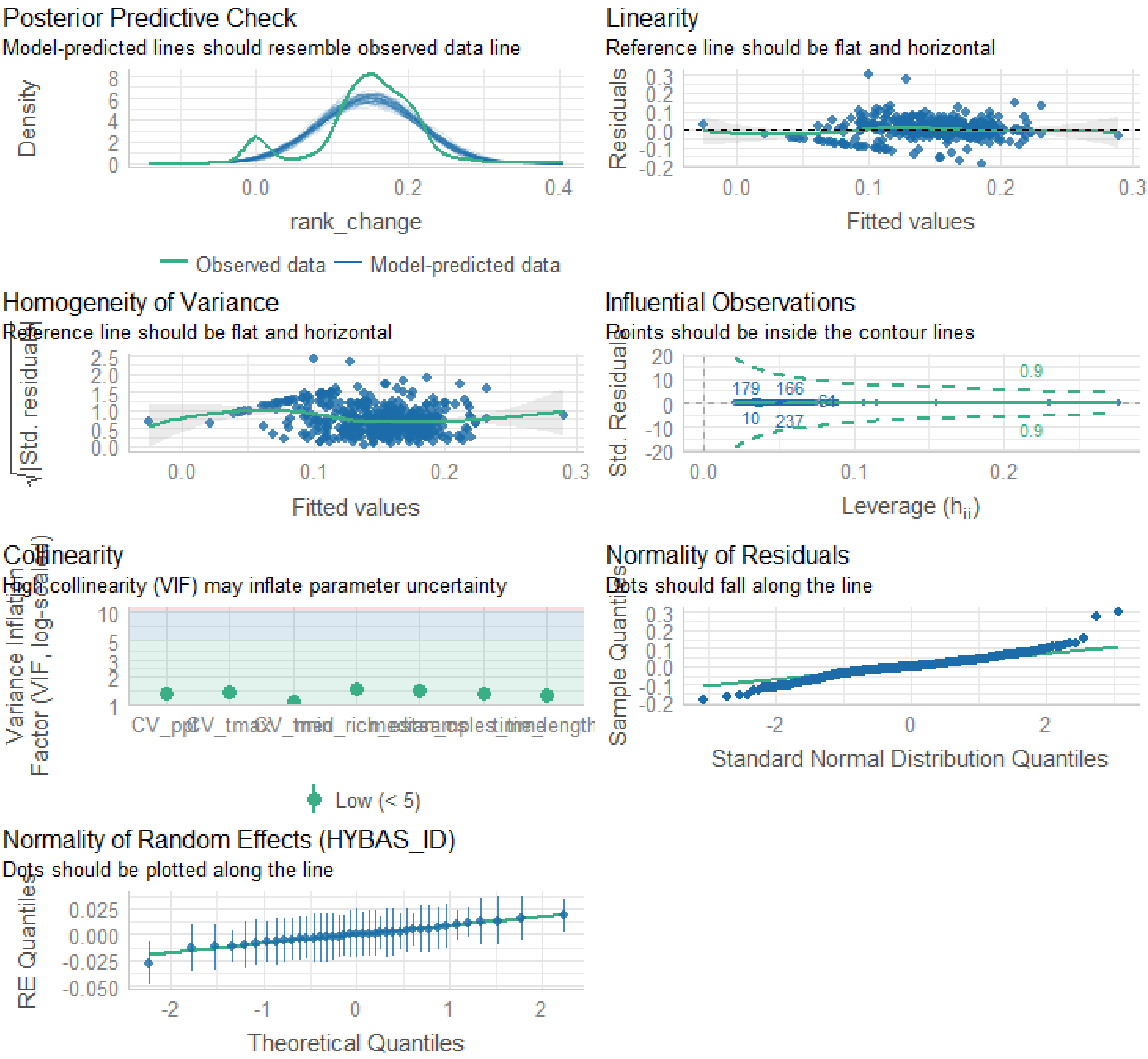

Figure S2 – Visual check of various assumptions of the model explaining temporal variability in species composition in local communities.

An alternative way to assess a GLMM is by examining the residuals from the fitted model, a process that can be done with simulateResiduals function from the DHARMa package (Hartig, 2022). This function generates a qq-plot (Fig. S3 - left panel) to identify overall deviations from the expected distribution, typically including tests for distribution correctness

(KS test), dispersion, and outliers. Additionally, it produces the plotResiduals (Fig. S3 - right panel), which generates a plot of residuals against predicted values, aiding in visualizing deviations from uniformity. We observed that the residuals deviated slightly from the model's predictions (Fig. S3; the closer the solid line to the dashed line, the better the fit). However, a residual pattern does not suggest the model is unsuitable (Hartig, 2022). With a considerable number of data points, residual diagnostics are likely to show significance, as achieving a perfectly fitting model is improbable (Hartig, 2022).

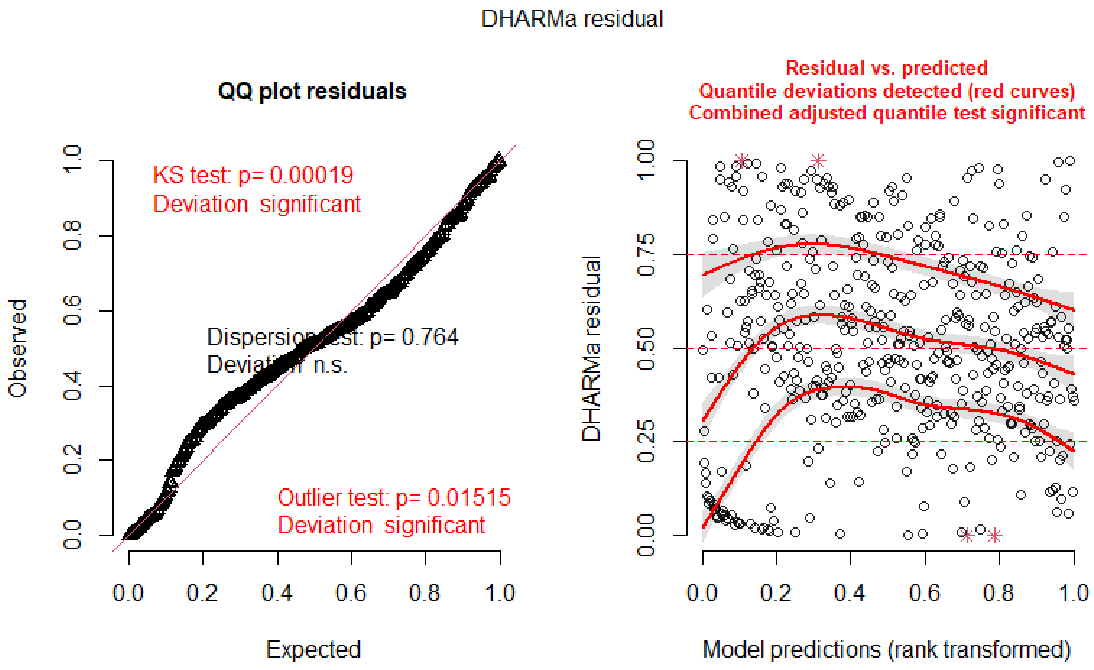

Figure S3 – Output from the simulateResiduals function of the DHARMa package, providing a visual aid in detecting deviations from uniformity for the model that explains the temporal variability in species composition in local communities (model one). Red stars represent simulation outliers.

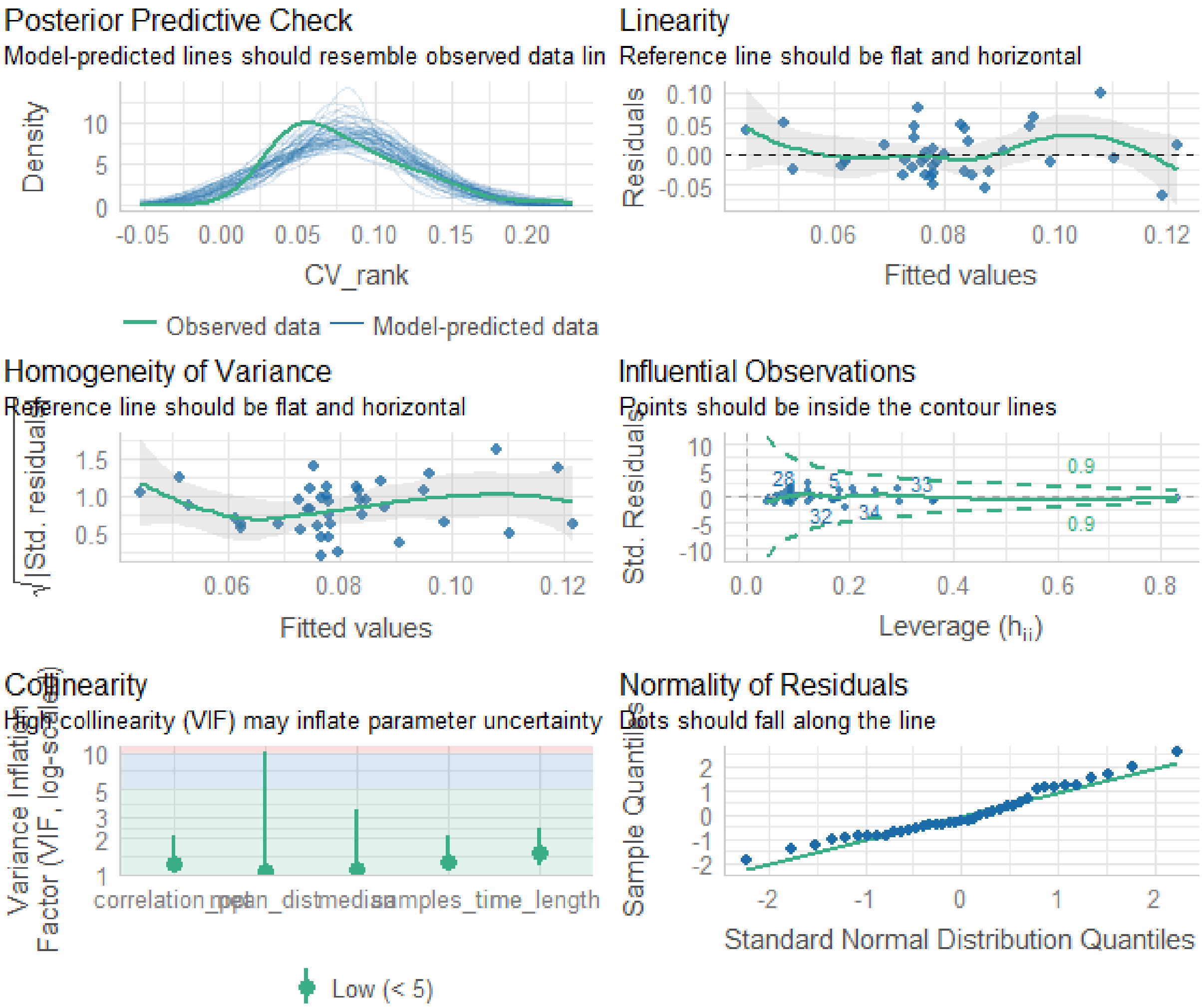

Figure S4 – Visual check of various assumptions from the model that explains the temporal variability in species composition in metacommunities.

## Supplementary Tables

Table S2. Model selection for generalized linear model of temporal variability in species composition at the regional scale (CV of rank difference) as a function of regional community size (Reg. size), spatial connectivity (Connectivity), number of metacommunity samples over time (Number of samples), time series length of each metacommunity (Time series length), synchrony in precipitation (Syn ppt), synchrony in maximum temperature (Syn tmax) and synchrony in minimum temperature (Syn tmin). AICs is Akaike's Information Criterion corrected for small sample sizes, ΔAIC indicates the difference between a model's $AIC_c$ value and the $AIC_c$ value for the best-fitting model.

| Model | Reg. size | Connectivity | Number of samples | Time series length | Syn ppt | Syn tmax | Syn tmin | $AIC_c$ | $\Delta AIC_c$ |
|---|---|---|---|---|---|---|---|---|---|
| M1 | x | x | x | x | x | | | -128.6 | 0 |
| M2 | x | x | x | x | | | x | -128.28 | 0.32 |
| M3 | x | x | x | x | | x | | -128.02 | 0.58 |

Table S3. Model statistics summary for the metacommunity GLM. Here, the response variable was the temporal variability in species composition at the regional scale (CV of rank difference). Model coefficients (and their standard errors), t-values, and p-values are reported for each predictor variable and the intercept.

| | Estimate | Std. Error | t-value | p-value |
|---|---|---|---|---|
| Intercept | 1.769e-01 | 4.538e-02 | 3.899 | 0.000447 |
| Regional size | -4.074e-05 | 5.001e-05 | -0.815 | 0.421058 |
| Connectivity | -1.387e-09 | 1.438e-07 | -0.010 | 0.992362 |
| Syn ppt | -8.202e-02 | 3.674e-02 | -2.232 | 0.032488 |
| Number of samples | 3.278e-04 | 1.521e-03 | 0.216 | 0.830645 |
| Time series length | -1.865e-03 | 1.720e-03 | -1.085 | 0.285962 |

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