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- **Abstract**

 Species richness has long been used as an indicator of ecosystem functioning and health. Global richness is declining, but it is unclear whether sub-global trends differ. Regional trends are especially understudied, with most focused on island regions where richness is strongly impacted by novel colonizations. We addressed this knowledge gap by testing for multi-decade trends in species richness in nine open marine regions around North America (197 region-years) while accounting for imperfect observations and grounding our findings in species-level range dynamics. We found positive richness trends in eight of nine regions, four of which were statistically significant. Species' range sizes generally contracted pre-extinction and expanded post-colonization, but the ranges of transient species expanded over the long-term, slowly increasing their regional retention and driving increasing richness. These results provide more evidence that sub-global richness trends are stable or increasing, and highlight the utility of range size for understanding richness dynamics. **Solution**
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Introduction

 Biological diversity is a key determinant of ecosystem function and change. It affects food web stability (Hooper *et al.* 2005; Loreau & de Mazancourt 2013), ecosystem productivity (Tilman *et al.* 2001), and benefits human well being through ecosystem services and its social and cultural value (Millennium Ecosystem Assessment 2005; Cardinale *et al.* 2012). Anthropogenic forcings are causing rapid and long-term change in biodiversity (Newbold *et al.* 2015), but the magnitude of this change varies across the globe and is difficult to measure. Species richness, for example, is a straightforward enumeration of distinct species, but precise measurement is difficult because there are many species, most of them are rare, and observations species richness and extinction rates make it clear that global species richness is currently declining and will likely continue to do so over the next century (Pereira *et al.* 2010; Pimm *et al.* 2014). Biodiversity trends are therefore an important focus of current research and conservation efforts.

 Though declining globally, biodiversity is scale dependent, and processes like colonization and extirpation only affect sub-global diversity, potentially decoupling trends at different spatial scales (Sax & Gaines 2003). In fact, recent studies have found that, on average, net changes and multi-year trends in local-scale diversity are approximately stable (Vellend *et al.* 2013; Dornelas *et al.* 2014). These results have sparked controversy about whether diversity trends differ between local and global scales (Gonzalez *et al.* 2016; Vellend *et al.* 2016); however, relatively few studies have quantified contemporary changes in biodiversity at regional scales. Most studies of regional richness focus on islands, where richness has often increased through human introduction of novel species (Sax *et al.* 2002; Sax & Gaines 2008; Vellend *et al.* 2017). Marine systems are particularly underrepresented (McGill *et al.* 2015), with the few existing studies suggesting diversity has increased in some regions and decreased in others (Hiddink & ter Hofstede 2008; ter Hofstede *et al.* 2010; Hiddink & Coleby 2012). Conclusions of existing sub-global studies of diversity change have been criticized on grounds of their geographic representativeness and statistical methods. First, sub-global studies are not spatially comprehensive (Vellend *et al.* 2016) and are not representative of spatially heterogeneous drivers of richness (Gonzalez *et al.* 2016) like geographic connectivity, environmental change, and anthropogenic stressors (Hiddink & Coleby 2012; Burrows *et al.* 2014; Elahi *et al.* 2015). Other critiques have focused on statistical tests for richness trends and the need for multi-decade time series (Gonzalez *et al.* 2016; Vellend *et al.* 2016), although 84 measurement error is another important statistical challenge affecting trends (Dornelas *et al.*) 2013). Specifically, equipment and observation techniques often improve over time, potentially improving detection of rare species and introducing a bias to long-term richness surveys (Tingley & Beissinger 2013). Statistical methods that account for imperfect detection with community datasets have been developed (Iknayan *et al.* 2014; Guillera-Arroita 2016), but are not commonly used (Kellner & Swihart 2014). Overcoming statistical challenges and estimating diversity trends for a wider representation of ecosystems will improve understanding of global 91 diversity the declined set of different spatial scale of different spatial scale and mulder of different spatial scale and mulder of the different spatial tends differ between however, relatively 1
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 Species-level dynamics provide insight into the process of diversity change. Changes in regional species richness are primarily driven by individual species shifting their ranges into (colonization) or out of (extinction) a region. Range shifts – which can include changes in range size or location – can be driven by changes in local habitat suitability (Cheung *et al.* 2009; Elahi *et al.* 2015; Molinos *et al.* 2015) or human-facilitated changes in connectivity (Sax & Gaines 2008). Changes in range size (proportion of occupied sites within a region) often also reflect changes in population size (Fretwell & Lucas 1969; Hanski 1982; MacCall 1990), and in turn predict extinction probability, as small populations (or ranges) have short expected times to extinction (MacArthur & Wilson 1967). However, changes in range size depend on both abundance and density, and range can change rapidly after colonizations (van den Bosch *et al.* 1992; Hastings *et al.* 2004; Urban *et al.* 2008) or before extinctions (Wilcove & Terborgh 1984; Lawton 1993). Range dynamics are further complicated when different processes govern the dynamics of rare and common species (Hanski 1982; Gaston *et al.* 1997; Holt *et al.* 1997; Yenni *et al.* 2012), and by the difficulty in modeling the distribution of rare species (Lomba *et al.* 2010). Thus, range size should provide insights into richness dynamics, but quantifying range trends for rare species is challenging.

 Nonetheless, time series of range size and its related measures have been used to illustrate how changes in community structure arise from population processes. In the eastern North Sea, species-level range size trends in fished *versus* unfished populations explained increased local species richness over an eight year period (Hiddink & Coleby 2012). Similar processes contributed to changes in local richness over a longer period in the Scotian Shelf (Shackell & Frank 2003). In another part of the eastern North Sea, local species richness was generally stable, but large compositional changes were observed in the form of assemblage homogenization (Magurran *et al.* 2015), due either to range expansion or shifts in range location. Conversely, local richness and beta diversity both increased over several decades on the Scotian Shelf, likely as a consequence of fishing reducing the abundance of cod, an important predator in the region (Ellingsen *et al.* 2015). Although range size and spatial community turnover are inversely related, it is important to note that beta diversity depends on both range size and location (Harrison *et al.* 1992). These studies emphasize how changes in range size and beta *et al.* 2015; Molinos *et al.* 2015 or human-
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 Less clear is how species-level range size affects richness at regional scales. Changes in range sizes have the potential to increase regional richness via two separate processes: colonization and retention. First, a species not present in a region may expand its range, 125 eventually colonizing; this process is important for increasing island richness (Sax & Gaines 2008; Byers *et al.* 2015). In this case, prior to the colonization, no within-region change in range size would be observed. For the second process, retention, it is useful to distinguish between core species that are widespread and always present, and transient species that are sometimes present and geographically constrained (Hanski 1982; Magurran & Henderson 2003). Retention increases richness by reducing species loss, and would be expected to increase as a result of range expansions. Since they are rare, transient species have the greatest potential for increased retention. Therefore, long-term trends in species richness could be reflected in range expansion, but only if richness trends are not dominated by changes in colonization rates. There are few tests of this idea at regional and decadal scales.

 We tested for long-term changes in regional species richness and for contributions of range size dynamics to these trends. We analyzed multi-decade time series of the occupancy and geographic distribution of marine fishes and invertebrates in nine ecosystems around the North American coastline. The large area of our study regions might suggest that their richness trends should be similar to the negative global trend, but neutral or positive trends would match results from previous regional studies (Sax & Gaines 2008; Hiddink & Coleby 2012), of which only a few were in open or marine ecosystems. We hypothesized that a trend in richness should be, at least in part, driven by changes in range size. Range size should influence richness trends if 1) range size declines with increased proximity to extinction, 2) transient species have small ranges, and 3) the range size of transient species exhibits a long-term trend. The first two conditions are 145 commonly met, but we tested for their applicability to our study systems and used them to facilitate the interpretation of other results. If the third condition is also met, then changes in richness were at least partly driven by changes in the persistence of rare species. 162 2008: Byers er al. 2015). In this case, prior to the colonization, no within region change in

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Methods

Survey Data

We used data on the presence and absence of marine species sampled by scientific

 analyzed observations of 581 species, which principally included bottom-dwelling fishes and invertebrates such as flatfishes and shellfish (Supporting Information). Sampled regions were Eastern Bering Sea (1984-2014, n=31), Aleutian Islands (1983-2014, n=12), Gulf of Alaska (1984-2013, n=13), West Coast U.S. (1977-2004, n=10), Gulf of Mexico (1984-2000, n=17), Southeast U.S. (1990-2014, n=25), Northeast U.S. (1982-2013, n=32), Scotian Shelf (1970-2010, n=41), and Newfoundland (1996-2011, n=16; Table S1, Fig. S1). Measurements of bottom water temperature and bottom depth were taken for each trawl sample; these values were used as covariates in models.

 We restricted our analysis to samples from years and sites that had the most consistent sampling methods. The fundamental sampling unit is the tow, a drag of the trawl net at a given place and time. Data were restricted to tows with consistent gear, season, and site; tows within a site and year were considered repeat samples of that site. Sites were defined by binning regular intervals of longitude, latitude, and depth. We chose a spatial resolution (0.5° for longitude and latitude) that yielded a large number of sites that were sampled at least once in most years. Sites were then binned by 500 m or 100 m depth increments. In most regions we used 500 m depth increments, which rarely subdivided the 0.5º bins but guarded against large within-site differences in depth-related habitat suitability. However, sampling was relatively dense across longitude and latitude in the Aleutian Islands and the West Coast U.S., allowing us to use 100 m depth increments while still sampling the sites in most years. We only included sites in our analysis that were sampled in at least 85% of years, except in Eastern Bering Sea and Gulf of Alaska where sites had to be present in all years to avoid large interannual changes in the extremes of longitude or latitude (Supporting Information: Excluding Years). st U.S. (1990
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 Analyses were restricted to taxa identified to species and that were not known to have undergone large changes in identification accuracy. We used automated and manual procedures 177 to correct errors in taxonomy (Supporting Information: Taxonomic & Sampling Consistency). 178 After these corrections, we removed any species that were not observed in at least 10 tows over 179 the course of that region's time series. \blacktriangleleft

Species Richness

- We refer to the number of species in a sampled assemblage as the species richness of that community. Note that because sampling methods differ somewhat among regions, definitions of "community", and therefore richness values, are not entirely comparable across regions.
- 185 Species richness is rarely ascertained accurately from raw survey data (Gotelli & Colwell 2001). We calculated a naïve measure of species richness (observed species counts) and estimated true richness using a multispecies occupancy model (MSOM; (Dorazio & Royle 2005)). MSOMs accounted for imperfect detection of species, making estimates of richness more robust to possible methodological improvements in survey methods that could bias naïve trends

(Iknayan *et al.* 2014).

 MSOMs use a mixed modeling and state-space framework to separate true absences (1 - occupancy probability) from false absences (1 - detection probability), and to estimate true richness by accounting for those undetected species likely to be present at a site. Both probabilities of occupancy and detection can each be modeled as a function of *a priori* covariates. Covariate coefficients and intercepts are species-specific, but are drawn from community-wide hyper-distributions, making the model hierarchical. Model hierarchy allows observations of one species to inform parameter fits for other species, including the membership and occupancy parameters of unobserved species (Supporting Information: Occupancy Model), allowing estimated richness to exceed observed richness. This technique is known as data augmentation, and has previously been used to estimate occupancy and species richness (Royle *et al.* 2007; Kéry *et al.* 2009). We fit the MSOMs in a Bayesian framework using JAGS (Plummer 2003), and fit 197 separate models, one for each year and region. Manuscript
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Trends in Species Richness

205 Species richness trends were quantified using Kendall's τ_b , which measures the similarity in rank-order for two variables, or in this case, whether richness tended to exhibit a monotonic 207 trend over time. We used Kendall's τ_b because it is nonparametric and does not assume a linear trend, which visual inspection indicated may not be the case for several time series. Our 209 calculation of Kendall's τ_b uses the MSOM posterior samples of richness and accounts for serial correlation (Supporting Information: Trends in Species Richness).

Range Size

 Range size is the proportion of sites in a region occupied by a species in a year. To account for variation in the number of tows per site, for each site we calculated the fraction of tows that contained the species; range size was rarefied to a single tow by summing this fraction across sites. This measure of range size was used to compare changes in range size prior to extinction and after colonization, and to compare long-term changes in range size for transient and core groups of species.

 In addition to range size, we define a long-term species range index (SRI), and the cross- species average of SRI, community range index (CRI). SRI is the long-term average of a species' range size (excluding range sizes of 0). SRI is the typical range size of a species when it was present. SRI was compared with the total number of a species' colonizations and extinctions in order to relate range size to transience (transient species were expected to have a small SRI). CRI was calculated annually as the average SRI of species present in that year. We used CRI as a test for how community composition might change with richness; decreases in CRI are expected to occur as the number of transient species increases (as a proportion of richness). This means are the sense
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Species Categories

 Colonizations and extinctions were defined according to observed changes in occupancy. As a result, a species that was present but undetected would be recorded as absent since it was not observed. Furthermore, extinctions were defined regionally, not globally; therefore, a species could repeatedly colonize and go extinct.

 All species were categorized as either core or transient in each region. Core species were those that were present in a region in all years, and transient species were those that were absent from a region in at least one year (but not all years). Each transient species was further categorized according to its colonization and extinction history. *Colonizing* species colonized the region but never went extinct, *leaving* species went extinct from the region but were never observed to have colonized, and the remaining transient species, categorized as *both*, experienced at least one colonization and extinction.

Trends in Range Size

 We tested for pre-extinction contractions and post-colonization expansions of range size for transient species. For any year in which the species was present, a variable *time to absence* was defined as the number of years before an absence (*years before extinction*) or after an absence (*years after colonization*). Each transient species' time series was separated into years that were either post-colonization or pre-extinction, depending on which event type was most proximal (ties were post-colonization). No analysis included range sizes of 0 because range size is defined as 0 when *time to absence* is 0. We performed regressions separately for each region using a linear mixed effects model with *range size* as the response variable and *time to absence* as a covariate (we excluded stretches of fewer than three years); species identity was modeled as a random effect that allowed the slope parameter associated with *time to absence* and the intercept parameter to vary among species. This is the final model used for all regions, except the Gulf of Mexico, for which we did not allow intercept to vary among species because this term prevented the model from properly converging. Models that allowed slopes and intercepts to change with phase *type* did not improve fit according to AIC, except for Scotian Shelf (intercept \times *type* p = 0.005, \triangle AIC = 0.228), though improvement was minor. Henceforth we present results from the simpler models because the purpose here was to test the idea that range size changes in proximity to colonization or extinction, and this outcome did not differ among model structures. The detect of the post
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 To test for long-term changes in range sizes of transient and core species, we used mixed effects models with range size as the response variable. Predictors were year, species group (*transient* or *core*; adjustment to intercept) and its interaction with year (adjustment to slope), and species identity as a random factor that allowed the intercept parameter to vary among species. Range sizes of 0 were excluded. Regressions were fit separately for each region. All analyses aside from Bayesian model fitting were performed in R v3.3.0 (R Core

 Team 2016). In calculating richness trends we used the Kendall function in the package *Kendall* (McLeod 2011), and auto.arima in *forecast* v7.1 (Hyndman & Khandakar 2008). The mixed effects regressions were performed using lmer in *lme4* (Bates *et al.* 2015). 268 Conditional and marginal R^2 values were calculated using ${\tt sem.model}.$ fits in $piecewise SEM$ 269 (Lefcheck 2016). Conditional R^2 indicates the variation explained by both fixed and random 270 effects; marginal R^2 indicates variation explained by fixed effects (Nakagawa & Schielzeth 2013).

Results

Species Richness

275 Estimated long-term trends (Kendall's τ_b) in both observed and estimated richness were positive for most regions (Fig. 1, Table 1). Trends in MSOM estimates of species richness were significant in four of the nine regions, and all significant trends were positive: Eastern Bering 278 Sea ($\tau_b = 0.42$), West Coast U.S. ($\tau_b = 0.61$), Scotian Shelf ($\tau_b = 0.45$), and Newfoundland ($\tau_b = 0.45$) 0.73) (Table 1, Fig. 1). Any region with a significant MSOM trend also had a significant trend in naïve richness; naïve richness was significant in three additional regions, including a negative trend in the Southeast U.S. (Table S2). Although MSOM estimates of richness were greater than naïve estimates, estimates from the two methods were correlated (Fig. S2). Henceforth, we report species richness as MSOM estimates unless otherwise specified.

Colonization and Extinction

 Across regions, most species were core species: with 536 out of 863 region-species combinations being present in all years (Fig. S3). Core species were the most common group in all regions except the Northeast U.S., where transient species that *both* colonized and went extinct were the most common, followed by core species. Summed across regions, most transient species were categorized as *both* (263 region-species), followed by *colonizing* (60) and *leaving* (4). Aleutian Islands was the only region with more *colonizing* species than *both* species (Fig. S3).

 If richness increased and yet the number of *colonizing* species was less than the net change in richness, then species that *both* colonized and went extinct (possibly multiple times) from the region must also have contributed to the net change in richness. The net change in richness was calculated as the difference between the last and first predicted values of a linear trend fit to the time series of MSOM richness estimates. The number of *colonizing* species was less than the net change in richness for all regions with a significant trend in richness (Table S3): E. Bering Sea Δ = 12.5, *colonizing* = 2; Newfoundland Δ = 12.7, *colonizing* = 10; Scotian Shelf $\Delta = 7.6$, *colonizing* = 1; West Coast US $\Delta = 18.8$, *colonizing* = 12, indicating that species that had *both* entered and exited the region during the time series also contributed to increases in 276 positive for most reg

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Trends in Range Size Near Colonizations and Extinctions

 Species' range sizes contracted in the years leading up to extinction (Fig. 2A), and expanded in the years following colonization (Fig. 2B; *see* Fig. S5 for a version that is not 307 averaged). We fit separate mixed effects models for each region, and excluded points at $t=0$ years pre-extinction or post-colonization. As the number of years before extinction or after 309 colonization increased, range size also increased (across regions, $1.4 \le \beta \le 11.2$, average = 4.8 310 percent occupancy per decade, all corrected $p \le 0.036$). Proximity to colonization or extinction 311 explained a modest amount of variation in range size ($0.06 \le mR^2 \le 0.19$). Among-species 312 differences in slopes and intercepts explained much more variance $(0.63 \leq cR^2 \leq 0.95)$; Fig. S5). 313 Indeed, variation among species' slopes was similar to the average slope ($\bar{\sigma}_{\beta} = 6.5$ percent per decade), indicating that some species exhibited very steep trends in range size. In general, species were at their rarest just before extinction or just after colonization.

Richness and Range Size

 The total number of colonizations and extinctions was greatest for species with small SRIs, and many species (*both*) colonized and went extinct multiple times (Fig. S4). In mixed effects models with intercepts varying among species and transient *versus* core as a categorical predictor, transient species had range sizes that were 18 (% occupancy) smaller than the ranges 322 of core species (average intercept; all $p \le 0.02$ after correcting for multiple tests). Furthermore, species richness was negatively correlated with the community range index (CRI) in each region 324 (Fig. 3; separate linear regression for each region, for slope all corrected $p \le 0.002$, $0.36 \le R^2 \le$ 325 0.95, average $R^2 = 0.79$). These results indicate that smaller long-term averages of range size were characteristic of transient species, and richness was highest when more geographically 327
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 Richness was highest when more transient species were present, but why did transient species accumulate in regions with positive trends in richness? Range size was negatively related to the proximity of upcoming extinctions (Fig. 2, Fig. S4). We found that the range sizes of many species, but particularly transient species, expanded over time in most regions (Fig. 4). We used mixed effects models to predict range size from the main effects of survey year and the core-transient category, their interaction, and an intercept that varied randomly among species. Range

334 sizes for core species decreased in Southeast U.S. (β Y = -1.8% occupancy per decade),

335 Newfoundland (β Y = -1.7), and Scotian Shelf (β Y = -0.36), and increased in the six other regions (

336 $\beta_{Y+1.6}$; after correcting for multiple testing, all p \leq 0.045). However, the interaction term

337 indicated that the slopes of core and transient species were different in six of the regions ($p \le$

338 0.004), including positive interactions in Newfoundland ($\beta_{Y\times T=4.8}$) and Scotian Shelf ($\beta_{Y\times T}$

339 = 2.1), where the net trend $(\beta_Y + \beta_{Y \times T})$ for transient species was positive. In all regions except 340 Southeast U.S., the range sizes of transient species expanded over the course of the time series 341 (average $= 2.6\%$ occupancy per decade).

Discussion

 We found that long-term trends in regional species richness tended to be positive. Previous studies have found local trends to be stable (Dornelas *et al.* 2014; Magurran *et al.* 2015), and regional trends to increase (Sax & Gaines 2003, 2008; Hiddink & ter Hofstede 2008; ter Hofstede *et al.* 2010; Hiddink & Coleby 2012). Although most of the regions studied were islands, and only a few marine, our findings of positive trends in nine open marine ecosystems lend more support to the conclusion that regional richness trends are generally positive around the world and across ecosystems.

 Trends in species richness require careful analysis and interpretation. First, changes in richness can be context dependent, varying with space, time, and taxa (Sax & Gaines 2003; Elahi *et al.* 2015; Gonzalez *et al.* 2016; Vellend *et al.* 2017). All datasets have limited taxonomic, spatial, and temporal scope, but we analyzed many decades of observations from nine regions that encompass a large fraction of coastal North America. Second, detection probability usually increases with abundance and range size, causing the number of colonizations and extinctions to be overestimated, and range sizes underestimated; for our purposes, these imperfections would be most problematic if they were changing over time. However, our analysis of range size detected both long-term trends and short-term rises and falls near absences, patterns unlikely to be produced in nine regions by sampling artefacts alone. Furthermore, when estimating richness, 361 we accounted for possible temporal bias in detectability by using the MSOM (Tingley $\&$ Beissinger 2013; Iknayan *et al.* 2014; Guillera-Arroita 2016). While MSOMs fit to many years can infer colonization and extinction dynamics (Kéry *et al.* 2013), we fit models separately to 363

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26.1), where the net created ($\beta \gamma + \beta \gamma \times \gamma$) for transient species we positive. In all regions expondence

 MSOM results had dampened trends compared to naïve results, suggesting that the MSOM estimated more undetected-but-present species in early, low-richness years. These results demonstrate how imperfect detection can exaggerate richness trends, and highlight a benefit of using the MSOM.

 A goal of our study was to gain insight into the process by which regional species richness changes by decomposing these changes into colonizations and extinctions, which in turn should be reflected in range size dynamics. We found pre-extinction range contractions and post- colonization expansions, a pattern often reported in paleoecological, macroecological, and metapopulation studies (Hanski 1982; Jablonski 1987; Harrison 1991; Gaston 2003). However, these studies focused on select species with many consecutive years of presences, unlike the numerous rare species in our analysis whose small ranges and short time series (average duration of pre-extinction and post-colonization stretches = 4.2 years) made trend analysis challenging. 377 Nonlinear dynamics over long periods also obscure expected trends, such as for the green sea urchin in the Aleutian Islands: originally at a range of < 1%, it increased to 66% over 11 years, then declined to < 20% over 20 years before going extinct (Fig. S5, Fig. 2A). A linear trend through this time series does not reflect the pre-extinction contraction. Therefore, it is 381 unsurprising that marginal R^2 values were low, and similar challenges likely apply to other systems. Transient species are generally rare (Gaston 1994), and steep or nonlinear dynamics frequently characterize both pre-extinction (Wilcove & Terborgh 1984; Simberloff & Gibbons 2004) and post-colonization (Lewis & Kareiva 1993; Hastings *et al.* 2004) dynamics. The general rule of pre-extinction contractions and post-colonization extinctions encompasses a wide variety of complex dynamics that are typically tested with select, well-observed species. Our findings suggest that similar theory and analysis can be applied to a large number of rare and **intermints and the species whose of the species whose occupancy of members of members of members of members of the species whose occupancies species conditations should be reflected in range size dynamics. We found p**

 Trends in the range size of transient species were essential for linking range size to regional trends in richness. Richness was tightly correlated with CRI, which is readily explained by a tendency for transient species – whose occupancy defines richness change – to have small ranges (see above). These relationships, however, do not imply a trend in species richness, which results from changes in colonization or extinction rates. We found that transient species had positive, long-term trends in their range sizes, which implies decreased extinction rates. Thus, increased retention allowed species to accumulate. However, our analysis may have excluded

 some colonizing species that did not persist or were infrequently detected, and so may not be a comprehensive test of the relative roles of increased colonization *versus* retention. Species distribution models that cover multiple regions (Molinos *et al.* 2015) and include rare species (Lomba *et al.* 2010) might be useful for testing this idea. Nonetheless, the role of increased retention in these marine regions contrasts with past studies of regional richness on islands, 401 where increased connectivity and novel colonizations were important processes (Sax $\&$ Gaines 2003, 2008). Thus, marine regions and islands both experienced increased species richness, but for different reasons.

 Temperature and fishing are factors that could have contributed to the range expansion of transient species. The geographic ranges and abundances of the more common species in these data are known to be responsive to temperature changes (Mueter & Litzow 2008; Pinsky *et al.* 2013; Sunday *et al.* 2015; Morley *et al.* 2017), and temperature changes could increase the prevalence of certain species. For example, there is a biogeographic break between the Northeast U.S. and the warmer Southeast U.S., and the strength of the latitudinal diversity gradient fluctuates with climate oscillations (Fisher *et al.* 2008). During warm years, southerly fish may be introduced to the northern region, but retreat upon cooling. The Northeast U.S. has experienced long-term warming trends (Pershing *et al.* 2015), possibly enhancing the range and duration of the northern establishment of southern species. In addition, fishing resulted in the collapse of cod in the 1990's, after which many invertebrates expanded (Shackell & Frank 2003; Choi *et al.* 2004; Boudreau & Worm 2010; Ellingsen *et al.* 2015). The timing of perturbations can determine whether positive trends indicate a recovery to a "normal" state or an increase beyond baseline conditions. In this case, the effect of cod collapse did not explain differences in richness trends among the Northeast U.S. (began before the collapse, no trend), Scotian Shelf (began before, positive trend), and Newfoundland (began after, positive trend). However, we did not specifically test for the drivers of richness change. Future work should consider which drivers played a role in increased range sizes and richness, and how the timing of changes in drivers might affect what are perceived as baseline conditions. 440 ecosystem and spatial scale for the matter of equal control and spatial scale of regional richness on islands, where increased connectivity and nevel eclonizations were important processes (Sax & Gaines 2003, 2005, 20

 Long-term changes in species richness have been the subject of recent debate (Gonzalez *et al.* 2016; Vellend *et al.* 2016): do global and sub-global time series have opposing trends? We tested for multi-decade trends in regional marine species richness, an underrepresented

- that regional trends are stable or increasing, and that this result is consistent across ecosystems types. However, richness is a measure of community change that aggregates over the dynamics of many species. By decomposing richness change into the range dynamics of individual species, we also found that increases in regional richness were driven by the long-term tendency for regionally rare species to expand their geographic ranges and become more common as more sites became suitable for them, which contrasted with previous results emphasizing changes in connectivity. Our results suggest that the spatial dynamics of individual species are closely tied to richness dynamics, which might explain differences between local, regional, and global trends. Continuing to improve our understanding of these trends and their drivers is critical to the successful prediction and management of the biodiversity changes taking place around the globe. 445 van den Bosch, F., Hengeveld, R. & Metz, J.A.J. (1995). Controlling the False Discovery Rate: A Practical and Bosch, F., Hengeveld, R. & Metz, J.A.J. (1992). Analysing the Velocity of Meta-Metz is uncertained by the W
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- **Tables**
- 694 **Table 1.** Trends in MSOM estimates of richness. Kendall's τ_b , which accounts for ties, was
- calculated after removing serial correlation in each resampled time series of the posterior. P-
- values were corrected for multiple comparisons in order to maintain a false discovery rate of
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700 **Figure Legends**

701 **Fig. 1.** Time series of MSOM estimates of regional richness. Each point is the posterior mean of 702 regional richness in a year. Lines indicate long-term trends from fitted values of linear regression 703 models predicting richness from time. Solid lines indicate that τ_b was significant, dashed lines 704 insignificant (Table 1).

705

 Fig. 2. Range size versus years before extinction (A) and years after colonization (B). The horizontal axis is the number of years to the nearest absence, separated into either a pre- extinction or post-colonization phase. A species might experience repeated pre-extinction and post-colonization phases in the same time series. For visualization, range sizes within a region were averaged across each species-phase combination for a given number of years to absence. Statistics (see main text) use unaggregated data (*see* Fig. S5). By definition, range size is 0 when years to event is 0, and we excluded points at (0,0) from all figures and analyses. Lines are trends 713 from linear regressions fit to aggregated range sizes. Exico 0.098

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715 **Fig. 3.** Regional species richness (estimated from MSOM) versus community range index (CRI). 716 CRI is the community average of each species' typical range size. There is one point per region

717 per year. Solid lines are linear regression fits. Colors represent different regions (Figs. 1,2).

718

Fig 4. Changes in range sizes (rarefied) for the transient (red) and core (blue) members of each

of the nine regional assemblages. The shading encompasses the middle 50% of the observations,

and thick lines are at the median. The black line represents CRI, which is the same metric

represented by the horizontal axis of Fig. 3. Range sizes of zero were excluded when calculating

T23 all metrics.

Author Manuscription

