

1 **Climate influences the response of community functional traits to local conditions**

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75 **Abstract**

76 Functional traits determine an organism's performance in a given environment and as
77 such determine which organisms will be found where. Species respond to local
78 conditions, but also to larger scale gradients, such as climate. Trait ecology links these
79 responses of species to community composition and species distributions. Yet, we often
80 do not know which environmental gradients are most important in determining
81 community trait composition at either local or biogeographical scales, or their interaction.
82 Here we quantify the relative contribution of local and climatic conditions to the structure
83 and composition of functional traits found within bromeliad invertebrate communities. We
84 conclude that climate explains more variation in invertebrate trait composition within
85 bromeliads than does local conditions. Importantly, climate mediated the response of
86 traits to local conditions; for example, invertebrates with benthic life-history traits
87 increased with bromeliad water volume only under certain precipitation regimes. Our
88 ability to detect this and other patterns hinged on the compilation of multiple fine-grained
89 datasets, allowing us to contrast the effect of climate vs. local conditions. We suggest
90 that, in addition to sampling communities at local scales, we need to aggregate studies
91 that span large ranges in climate variation in order to fully understand trait filtering at
92 local, regional and global scales.

93 Introduction

94 Ecologists are reformulating long-held perspectives on biodiversity using functional traits.
95 Since organisms interact with their environment through their traits, patterns in species
96 distribution should be a direct function of their traits. Traits directly affect community
97 assembly and species interactions, such that any snapshot of a community is the result of
98 i) physiological tolerances (Winemiller et al. 2015, Pianka et al. 2017), ii) species
99 interactions (Chesson 2000, Chase and Leibold 2004, Estes et al. 2011), iii) dispersal and
100 priority effects (MacArthur and Wilson 1967, Diamond 1975, Hanski 1999), iv) demographic
101 stochasticity (Lande et al. 2003, Hubbell 2011), and v) phylogenetic constraints (Vellend
102 2016, Pianka et al. 2017). Most of these mechanisms are, to some degree, driven by
103 functional traits (mechanisms i-iii) or determine the distribution of traits (mechanism v),
104 and their prevalence and diversity modulate the relationship between biodiversity and
105 ecosystem function rather than species *per se* (Schmitz et al. 2015). Similarly, the
106 redundancy of functional traits in a community can maintain ecosystem function and
107 stability in the face of environmental change and species loss (Loreau et al. 2001). By
108 shifting our focus away from taxonomic diversity to the diversity of functional traits within
109 a community or metacommunity, we strengthen our ability to detect the mechanisms that
110 underlie observed patterns in species distribution and biodiversity (McGill et al. 2006). In
111 particular, functional traits have been associated with broad biogeographic patterns, such
112 as the latitudinal gradient in biodiversity, leading to new insights into the processes and
113 causes of global biodiversity (Chave et al. 2009, Ricklefs 2012, Lamanna et al. 2014).

114 This trait-based paradigm recasts community ecology's central question about species
115 diversity and coexistence as: which processes determine the functional trait composition
116 of ecological communities? Spatial scale is implicit in this question, as different processes
117 are expected to act at different scales (Levin 1992, Chave 2013). For example, species
118 interactions are expected to be strongest at small spatial scales, whereas environmental
119 filtering often occurs at spatial scales large enough for environmental gradients to
120 exceed physiological thresholds (Kraft and Ackerly 2010). Finally, processes like dispersal
121 limitation and biogeographical constraints to the species pool often operate at the
122 largest spatial scales (Ricklefs and Schluter 1993). The grand challenge of integrating
123 these multiple scale processes on traits can only be resolved by a synthesis of traditional
124 small-scale ecology with macroecology and biogeography (Violle et al. 2014).

125 Environmental conditions could have cross-scale effects on functional traits in several
126 ways. First, local factors (e.g. resource availability) could scale up to affect the geographic
127 distribution of functional traits, or, local conditions such as microclimate may compensate
128 apparently limiting climatic conditions. Second, climatic and biogeographic factors could
129 constrain the local distribution of functional traits and thereby impact local processes. A
130 practical difficulty of including large scale environmental factors or biogeography into
131 syntheses of local scale studies is that some variables will be spatially pseudo-replicated
132 and others will not. That is, several field studies that fall within a single climatic zone or
133 geographic region may not represent independent measures, yet a large number of
134 sampling units are needed to detect local effects on community functional trait

135 composition. These issues can be partially resolved by a spatially structured hierarchical
136 analysis.

137 The theory and motivation for our study could be applied to almost any ecological
138 community. Yet, the data required to test this theory requires extensive information on
139 species composition, functional traits, local conditions and climate for multiple
140 georeferenced occurrences of a defined community across a broad geographic range;
141 such data are rarely available for multitrophic communities. Here we use the aquatic
142 macroinvertebrates in tank bromeliads as a model system to understand community
143 structure. The invertebrate communities in tank bromeliads have proven to be useful
144 systems for testing ecological theory, as they are easily manipulated and censused and
145 are naturally highly replicated. Previous work has related ecosystem functions, trophic
146 structure and system resilience to a variety of invertebrate functional traits (Dézerald et
147 al. 2015, 2018, de Omena et al. 2019). To date, researchers of this system have primarily
148 focused on local-scale explanations for community composition and ecosystem function,
149 detailing how bromeliad size (volume of aquatic habitat), detrital inputs, and canopy
150 cover affect community composition (Petermann et al. 2015, Kratina et al. 2017). However,
151 much of the geographic variation in invertebrate composition remains unexplained, and
152 consequently begs for more explicit incorporation of broad-scale variables like climate.
153 For example, extreme rainfall events lead to an inversion of the trophic pyramid of
154 macroinvertebrates in bromeliads across seven study sites broadly distributed across the
155 neotropics (Romero et al. 2020).

156 Here, we used fine-grain data on the functional traits of aquatic macroinvertebrates
157 sampled in more than 1600 tank bromeliads across 18 climate zones throughout the
158 Neotropics to partition the separate and combined effects of local conditions and climate
159 on community trait composition. Based on previous studies of bromeliad
160 macroinvertebrate ecosystems, we expect that both local conditions and climatic
161 gradients affect trait composition (Céréghino et al. 2011, 2018, Dézerald et al. 2015). We
162 tested three hypotheses of how trait variation could be partitioned between local and
163 biogeographical environmental gradients: (i) Variation in trait composition is primarily
164 explained by variation in the environment at the biogeographic scale. This would occur
165 when climatic factors, which vary only at biogeographic scales, determine the cost and
166 benefits of different functional traits. For example, temperature determines development
167 rates (Damos and Savopoulou-Soultani 2012) and predation pressure (Romero et al.
168 2018), while precipitation determines the mortality rates due to desiccation (Amundrud
169 and Srivastava 2015). (ii) Variation in trait composition occurs primarily along regional
170 environmental gradients, or the interaction between local conditions and the climate at a
171 given region. This would occur when heterogeneity in local conditions determines life
172 history traits. For example, traits may vary as a response to the availability of resources
173 within a bromeliad (Srivastava et al. 2008) and the avoidance of negative species
174 interactions (Hammill et al. 2015). (iii) Neither local nor regional conditions determine trait
175 composition. This would occur at the regional scale if strong biogeographic constraints
176 dampen any effect climate may have on traits. For example, geographic dispersal
177 barriers on particular clades (Amundrud et al. 2018), coupled with deep phylogenetic

178 signal on some traits override the effects of climatic conditions. Similarly, at a local scale,
179 stochasticity in colonization coupled with noise added by a generalist predator can
180 overwhelm any signal caused by environmental gradients (Srivastava and Bell 2009). We
181 used hierarchical analyses to distinguish between these three hypotheses by testing the
182 effects of local conditions, climate, and their interaction on the community functional
183 traits of bromeliad invertebrates at local and bioclimatic scales.

184 **Methods**

185 *Invertebrate traits*

186 We used as functional trait values the species scores on four main axes of invertebrate
187 trait variation identified by Cereghino et al. (2018), which represent life-history strategies
188 along trophic, habitat, defence and life-history niche axes describing ca. 852 aquatic
189 invertebrate taxa occurring in Neotropical tank bromeliads, mostly identified to species
190 or morphospecies (hereafter “species”). For completeness, in the following we explain
191 the method used by Cereghino et al. (2018) to identify such a synthetic traits: Each of
192 these species was characterized by 12 nominal traits: maximum body size, aquatic
193 developmental stage, reproduction mode, dispersal mode, resistance forms, respiration
194 mode, locomotion mode, food, feeding group, cohort production interval, morphological
195 defence, and body form. Each nominal trait had a number of modalities, or states. For
196 example, the states for the trait “feeding group” were “deposit feeder”, “shredder”,
197 “scraper”, “filter-feeder”, “piercer” and “predator”. A full description of traits and states
198 can be found in Céréghino et al. (2018). Information on these traits was structured using a

199 fuzzy-coding technique (Chevenet et al. 1994): scores ranged from “0” indicating “no
200 affinity”, to “3” indicating “high affinity” of the species for a given trait state. Scores were
201 based on observations of specimens (Dézerald et al. 2017), on the scientific literature
202 (e.g. Merritt and Cummins 1996, Céréghino et al. 2011) and expert opinion (see Céréghino
203 et al. 2018 for list of traits, modalities, and their definitions) the species x trait matrix is
204 available at <https://doi.org/10.5281/zenodo.1200194>. Principal Component Analysis (PCA)
205 was used to reduce trait dimensionality to significant axes of trait variation. The
206 rank-transformed [species x trait] matrix was used to compute Spearman’s rank
207 correlations between trait modalities, which then underwent PCA with bootstrap
208 resampling (Pillar, 1999). This procedure allowed us to test ordination stability and to
209 interpret the significant ordination axes in light of correlations with trait states. We
210 identified a robust set of four orthogonal and important axes of trait variation, namely
211 trophic position, habitat use, morphological defence, and life cycle complexity (Céréghino
212 et al. 2018). The species scores for these four PCA axes (available at
213 <https://doi.org/10.5281/zenodo.1200194>) thus represented continuous trait values, or
214 synthetic traits, which we then used in analyses of the processes underlying functional
215 diversity across different spatial scales in relation to environmental factors (this study).

216 *Site sampling*

217 The data for the present study consists of the abundance of macroinvertebrates found
218 within 1436 bromeliads in 18 field sites in 8 countries (Bromeliad Working Group BWG
219 database, Table A1). While the Bromeliad Working Group has sampled more countries

220 and field sites, we only use the sites where more than 15 bromeliads were sampled.
221 Some of these field sites were visited in multiple years (Table A1), while others were
222 visited only once. While we acknowledge there are temporal trends in community
223 abundance and composition, all of our sampling units (each sampled bromeliad) are a
224 snap-shot of the community structure, so we made the simplifying assumption to treat all
225 sampling units within a site the same, regardless of the year in which they were
226 collected. Examining temporal trends in trait composition, would be an interesting follow
227 up study.

228 The full suite of 19 bioclimatic variables was extracted from WorldClim using the latitude
229 and longitude of each sampled site (Fick and Hijmans 2017). Some of our sampling
230 locations were within 1 km² of one another. As such, these locations had the same
231 climatic conditions since this is the smallest resolution in WorldClim. We decided to group
232 the data collected from these locations, instead of attempting to downscale the climatic
233 conditions to a smaller resolution. After grouping the data from these locations, we
234 ended up with 18 sites, which we refer to as bioclimatic zones.

235 *Bromeliad sampling*

236 The following bromeliad genera were sampled across all sites: *Neoregelia*, *Quesnelia*,
237 *Tillandsia*, *Guzmania*, *Vriesea*, *Aechmea* and *Catopsis*. Each tank bromeliad was
238 exhaustively sampled either by dissecting the rosette, or by pipetting out all of its
239 contents. The bromeliad macroinvertebrate community is defined as all the aquatic

240 invertebrates found by the naked eye (> 0.5 mm) within a single plant. A total of 637
241 morpho-species were found.

242 Three local conditions were collected for each plant: water volume at time of sampling
243 (mL), total amount of detritus (mg), and canopy cover (either open or closed canopy). The
244 data on total amount of detritus and the water volume at the time of sampling were
245 log-transformed before the analyses. These variables are proxies of habitat size and
246 energy inputs, which are key drivers of food web structure (Oertli et al. 2002, Moore et
247 al. 2004). The total amount of detritus was calculated by adding the amount of small,
248 medium and large detritus. In 25.8% of bromeliads, total detritus was not measured
249 directly, instead we imputed total detritus with allometric relationships using other size
250 categories of detritus, and in a few cases with the number of leaves and the diameter of
251 the plant. In 50.4% of bromeliads, total water volume was not measured directly and
252 instead we imputed total water volume using leaf size, plant species, plant height, plant
253 diameter, and number of leaves. When either of these variables were missing, we used
254 generalized linear models with a Gaussian error distribution to impute missing values.
255 Thus, the dataset was a combination of directly measured and estimated values.

256 *Spatial scale of environmental variation*

257 To better understand the spatial scale of environmental variation, we partitioned the
258 variation in local environmental conditions of a bromeliad into site and bioclimatic scales
259 using three nested hierarchical models, one for each response. All three models used

260 the same structure of random effects, but different likelihoods according to the
261 environmental variable. The environmental variables partitioned in this way included log
262 detritus (normal likelihood) log water volume (normal) and canopy cover (binomial). By
263 using nested random effects, we can partition the variation of each local environmental
264 condition by spatial scale and determine at which spatial scale most of the variation is
265 explained. For each environmental variable, we estimated random effects for the field
266 visit (site by year combination) within bioclimatic zone, and bioclimatic zone. We also
267 calculated the correlation between all local conditions both within and across all
268 bioclimatic zones.

269 *Trait analysis*

270 Since our unit of analysis is the bromeliad invertebrate community, it was necessary to
271 quantify the presence and abundance of the animals and their traits for each bromeliad.
272 To do this, we calculated the community weighted means (CWM) of each synthetic trait
273 for each bromeliad (local scale analysis). Community weighted means (CWM) was given
274 by:

$$275 \quad CWM = \sum_{i=1}^n p_i x_i, \quad (1)$$

276 where p_i is the proportion of species abundance, x_i is the trait value of that species and n
277 is the number of species in that community (Garnier et al. 2004, Swenson 2014). To
278 reduce the effect of highly abundant species on the analysis, we applied a square root

279 transformation of the proportional abundance of invertebrates within a bromeliad (i.e. a
280 Hellinger transformation). This transformation was necessary since we used abundance
281 and not biomass, and the most abundant species were orders of magnitude (up to 100s
282 of individuals) more abundant than the least abundant species (1 or 2 individuals)
283 (Legendre and Gallagher 2001). The square root transformation de-emphasizes
284 superabundant species (gave a more equal weight to rare species), and the community
285 weighted means (CWM) allowed us to characterize the relative abundance of traits in the
286 sampled bromeliad.

287 Community weighted means were obtained using the data version 0.7.7 extracted from
288 the BWG database in July 2017.

289 To determine the effects of environmental conditions on the CWM computed using the
290 species scores on the four synthetic traits, we used a permutational multivariate analysis
291 of variance - PERMANOVA (vegan R package; Anderson 2001). This method is based on
292 within- and between-group sums of squares computed on pairwise dissimilarities, in this
293 case, of bromeliad communities considering the CWM trait values. However, instead of
294 permuting the site matrix (bromeliads or bioclimatic zones), we adapted the method to
295 permute among the species vectors in the trait matrix and recomputed the CWMs, to
296 reduce the risk of type I error (Peres-Neto and Kembel 2015, Hawkins et al. 2017, Zelený
297 2018). Since each bioclimatic zone differs in the number of bromeliad communities
298 sampled (Table A1), and sample size may bias the relative amount of variance explained,
299 we devised a sub-sampling scheme where we randomly selected 15 bromeliads from a

300 randomly selected field visit within a bioclimatic zone (18 zones, Figure 1). Note that the
301 minimum number of bromeliads per site is 18 (Table A1), therefore for some sites, most
302 bromeliads are selected in every sub-sampling procedure. We found that 15 bromeliads
303 is the minimum number that still provides a comprehensive sample of the community
304 within a field visit. Every time we performed this sub-sampling procedure, we ran the
305 multivariate statistical analysis and compiled the main results (sum of squares). We
306 repeated this process 1000 times. We used the marginal sum of squares in the analysis
307 without interactions and the sequential sum of squares in the analysis with interactions to
308 the variation explained by the main effects. From these runs, we obtained a distribution
309 of P-values and sums of squares. We do not report P-values of individual runs, because
310 they do not represent valid independent tests, however, we do report the P-values of a
311 non-sub-sampled analysis in the appendix (Tables A3 and A4). Some of the distributions
312 of sums of squares were skewed, while some were normally distributed (Figure A5). To
313 summarize this variation, we first calculated the mean of the sum of squares explained by
314 each predictor across all sub-samplings, and then calculated the total contribution of
315 local conditions, climate variables, and their interaction. This procedure allowed us to
316 take advantage of the central limit theorem to ensure that the addition occurs on
317 normally distributed means.

318 We performed the multivariate analysis of variance for each spatial scale to replicate a
319 'fine-grained analysis' (Figure 1a), a 'coarse-grained analysis' (Figure 1b) and a
320 fine-grained analysis with resource-climate interactions (Figure 1c). Thus, we are able to

321 compare the explanatory power of these models to explain functional trait composition if
322 we only had local conditions, climate information or both. (i) For the fine-grained analysis,
323 we used each bromeliad as the sampling unit and only tested the effects of local
324 conditions (that is the environmental conditions that were measured for every bromeliad:
325 water level, detritus amount, and canopy cover). We restricted the sub-sampling to field
326 visits (site by year combination) to ensure that macroinvertebrate traits relating to species
327 that only occurred in a single bioclimatic zone (most species) were not mixed between
328 countries or years (Figure 1 - fine-grained analysis). Analysis using bromeliads as
329 sampling units and only climatic variables as predictors were used to filter the 19
330 bioclimatic variables to a smaller subset. We retained climatic variables that explained a
331 significant proportion of variation in at least 5% of the runs (BC2, 4, 15 and 17), and which
332 were then used in subsequent analyses. In 1000 randomizations we expect at least 5% of
333 runs to appear significant by chance (type I error), so we only report explanatory
334 variables that are significant in >5% of runs. (ii) For the coarse-grained analysis, we used
335 the 'bioclimatic zone' as units for which we calculated the species pool CWM by
336 summing the abundance of all the morphospecies across the sub-sampled 15 bromeliads
337 and only tested the effects of climatic variables (Figure 1 - coarse-grained analysis). (iii) To
338 test for the interactions between climate and local conditions, we used the bromeliad as
339 the sampling unit, and tested the effect of local conditions, climate and their interactions
340 (Figure 1 - fine-grained analysis with resource-climate interactions). We did not include
341 the interaction between canopy cover and climatic conditions because few bioclimatic

342 zones had both open and closed canopy, and consequently canopy cover would be
 343 confounded with bioclimatic zone.

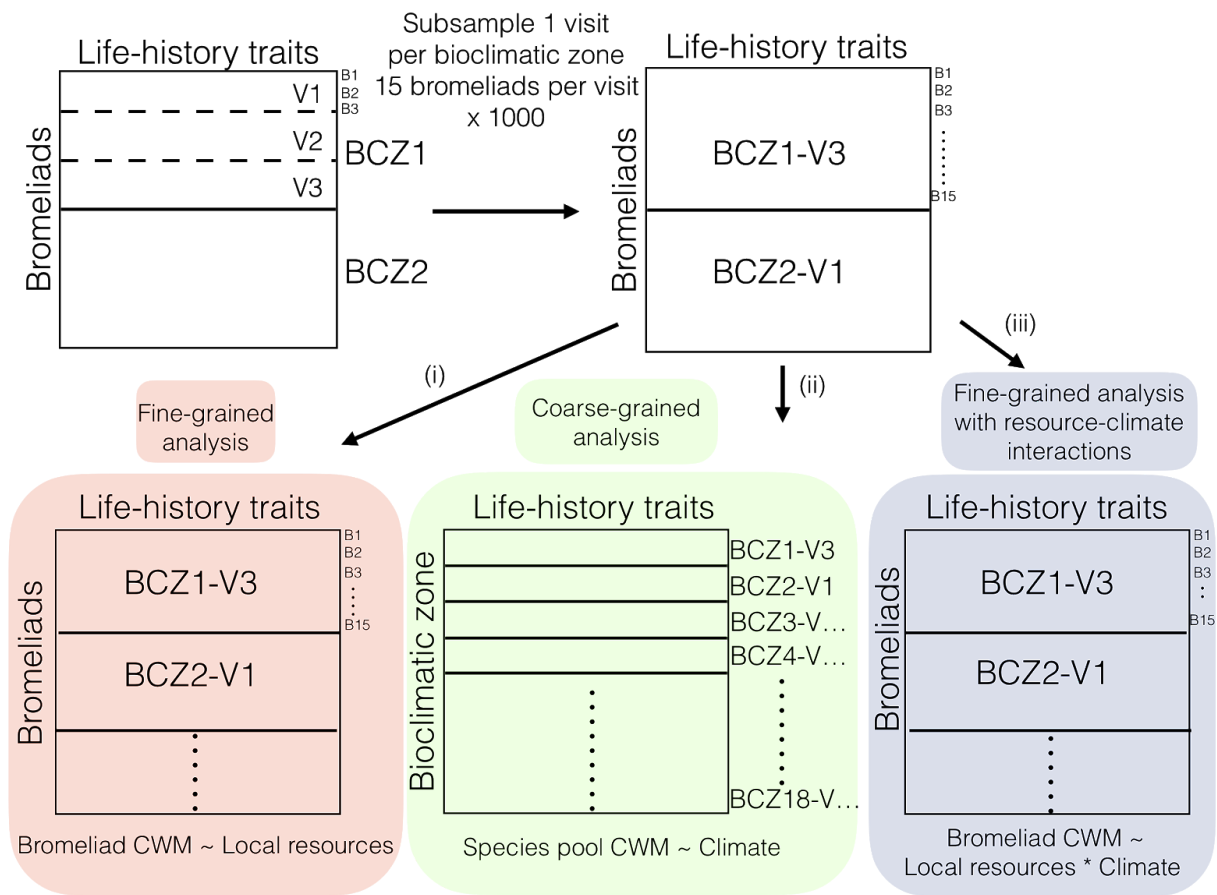
344 All multivariate analyses were performed using the vegan package (Oksanen et al. 2017).

345 Mixed effect models were performed using *lme4* R package (Bates et al. 2015) and all

346 analyses were done using the R programming language (R Core Team 2016). The code

347 for the sub-sampling and statistical analysis, as well as the adaptation of the

348 PERMANOVA can be found in: https://github.com/lmguzman/Climate_invertebrate_traits.



349 **Figure 1:** Schematic representation of the analysis. We tested for the effect of environmental conditions on
350 trait composition in three main analyses. BCZ1, BCZ2, BCZ... represent the bioclimatic zone, which can
351 contain multiple visits V1, V2, V3, V... We sampled one visit for each bioclimatic zone represented by
352 BCZ1-V3, that is, bioclimatic zone 1, visit 3. (i) At the fine grained (red area) analysis, we tested for the effect
353 of local conditions on bromeliad weighted means (CWM). (ii) At the coarse-grained analysis (green area),
354 we tested for the effect of climate on species pools CWM. (iii) We tested the interaction between climate
355 and local conditions in determining bromeliad CWM (blue-gray area).

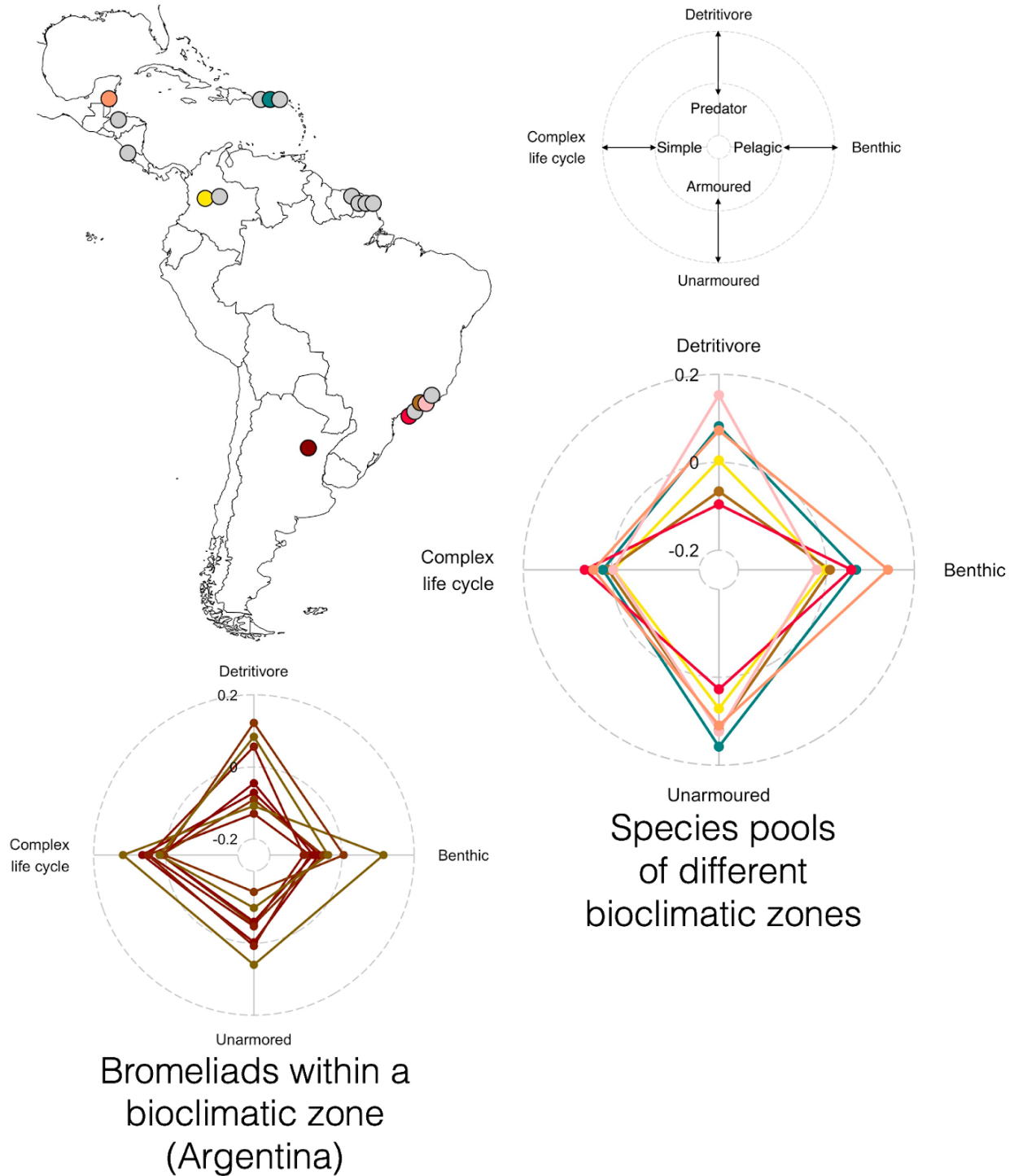
356 **Results**

357 *Spatial scale of environmental variation*

358 We determined the spatial scale of variation in our three local conditions: total detritus,
359 water volume at time of sampling, and whether the canopy was open or closed. This
360 analysis gave some indication of the potential power of each variable to explain variation
361 in synthetic trait composition (i.e. little variation at a given scale indicates a lower
362 likelihood of a significant effect at that given scale). Variation in total detritus was greatest
363 at the level of the bioclimatic zone (39.2% of variation) but also was high at the local scale
364 of the field site (31%). Variation in water volume was greatest at the local scale of field
365 visits (42.6%) and minimal at the level of bioclimatic zone (2.7%). Finally, variation in
366 canopy cover was highest at the level of bioclimatic zone (73.5%) and lowest at the level
367 of field visit (26%) (Figure A3). We also found that these three local conditions were only
368 weakly correlated across and within zones. The correlation values across bioclimatic
369 zones ranged between -0.01 and 0.35, while the correlation values within bioclimatic
370 zones ranged between -0.32 and 0.28 (Table A2).

371 *Fine-grained analysis*

372 Invertebrate traits varied among every bromeliad within a field visit (Figure 2). We found
373 that only a small amount of trait variation in CWMs (6.1%) could be explained by local
374 conditions, and that no single local condition explained most of this variation. The
375 amount of variation explained ranged from zero to 19.7% depending on the subset of
376 bromeliads selected, and the distribution of variation explained was skewed (Figure A1,
377 Table 1 - Fine-grained analysis).



378 **Figure 2:** Invertebrate traits at the level of bromeliads and at the level of species pools, for bromeliads
379 sampled in bioclimatic zones throughout the Neotropics (map, top left). Empty spider plot (top right) shows
380 all the four trait axes and their directions, and forms a key for the two filled spider plots (bottom). Filled

381 spider plots summarize the CWM of the four trait axes in a single bromeliad (bottom left) and the CWM in
382 some example species pools (bottom right). Colours on spider plots correspond to bioclimatic zones on
383 map, with those zones not shown in spider plots indicated in grey on the map.

384 **Table 1.** Synthetic trait composition (CWM) explained by local conditions in the fine-grained analysis and by
385 climatic variables in the coarse-grained analysis. The analysis using the local conditions uses the CWM for
386 each bromeliad. This analysis is blocked within each bioclimatic zone. The analysis using the
387 biogeographic climatic variables uses the CWM for the species pool for each bioclimatic zone.

Fine-grained analysis		
Predictor	Percentage of total sum of squares	
	Mean	Median
Canopy cover	2.68	2.19
Detritus	2.30	1.92
Water volume	1.18	0.99
Full model	6.16	5.1
Coarse-grained analysis		
Mean Diurnal Temperature Range	14.7	14.7
Temperature Seasonality	10.2	10.1
Precipitation of Driest Quarter	7.64	7.69
Precipitation Seasonality	7.39	7.25
Full model	39.93	39.44

388 *Coarse-grained analysis*

389 Species pools differed in the relative proportions of invertebrate traits (Figure 2). In the
390 coarse-grained analysis we found that climatic variables explained on average 39.9% of
391 the variation in the trait composition of species pools (Table 1 - Coarse-grained analysis).
392 The range of explained variation was large (14 to 47%) depending on the subset of
393 bromeliads selected (Figure A2). The amount of variation explained in this analysis is not
394 necessarily directly comparable to that in the fine-grained analysis because the scale of
395 the response variable (CWMs) is different; for this analysis, we aggregated species at the
396 site rather than bromeliad level. This aggregation changes the mean by weighting
397 bromeliads with more individuals more heavily, and also reduces the number of
398 observations, which tends to raise the R² values. Four out of 19 bioclimatic variables
399 explained substantial variation in trait composition of the macroinvertebrates across the
400 Neotropics: mean diurnal range in temperature (BC2), temperature annual seasonality
401 (BC4), precipitation annual seasonality (BC15), and precipitation of the driest quarter
402 (BC17) (Figure A4; Table 1). Species pools from zones with high mean diurnal temperature
403 range and high precipitation seasonality tended to be dominated by armoured
404 invertebrates (Figure A5d, A7d). These climatic variables also differed in their effect on
405 trophic traits: detritivores were favoured in zones with high precipitation in the driest
406 quarter (Figure A8c), whereas predators were favoured in zones with high precipitation
407 seasonality and mean diurnal range (Figures A5c, A7c).

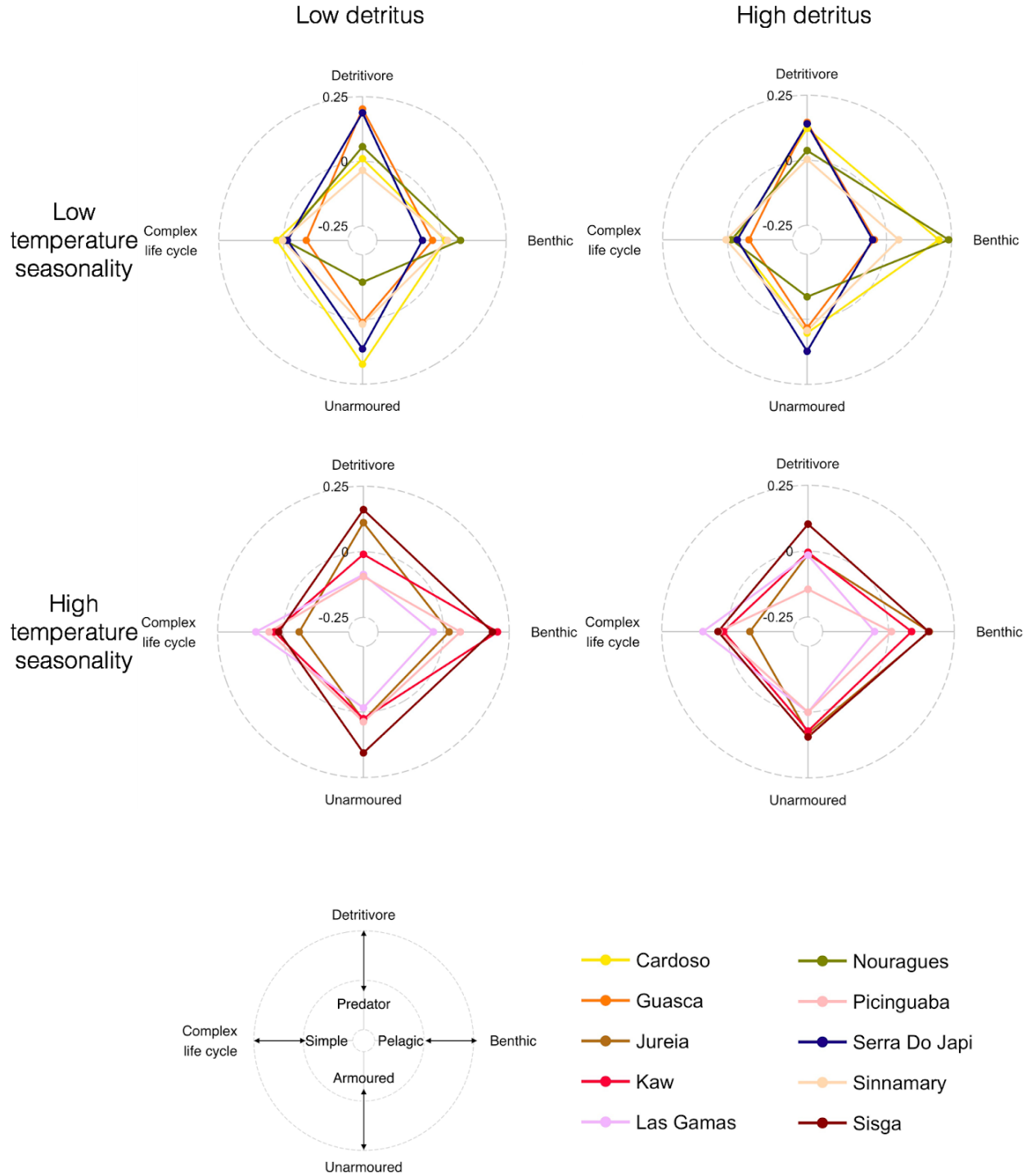
408 *Fine-grained analysis with resource-climate interactions*

409 The full model - using both the climatic and local resource environmental gradients to
410 explain traits within individual bromeliads - explained between 27.2 and 44.1% of trait
411 variation, when all the explanatory variables were included, with an average of 36.5% of
412 the variation explained (Figure A9). We found that the local conditions explained 8.7%,
413 climate explained 17.7%, and their interaction explained 10% of the variation in community
414 weighted functional traits (CWMs) on average across all runs. Among the local conditions
415 tested, detritus explained more variation than canopy cover or water volume. Of the
416 climatic conditions tested, mean diurnal range in temperature (BC2) explained more
417 variation than did the other climatic variables. Bromeliads with high mean diurnal range in
418 temperature typically had more complex and unarmoured invertebrates (Figure A10). The
419 cross-scale interaction that explained the most variation was detritus amount and
420 temperature seasonality (BC4; Figure 3-4, Figures A11, Table 2). Specifically, detritus-rich
421 bromeliads in zones with seasonal temperatures tended to contain more unarmoured
422 invertebrates, predators, and invertebrates with complex life cycles (Figure 4). No single
423 explanatory variable consistently explained the most variation in CWMs, rather, each
424 variable contributed a small amount to the total amount of variation explained by the full
425 model, which taken together explained more than a third of the variation in functional
426 traits.

427 **Table 2:** Synthetic trait composition explained by local conditions, biogeographic climatic variables and
428 their interactions. This analysis used the CWM for each bromeliad. We did not include the interaction
429 between canopy cover and climatic conditions because few bioclimatic zones had both open and closed
430 canopy, therefore canopy cover would be confounded with bioclimatic zone.

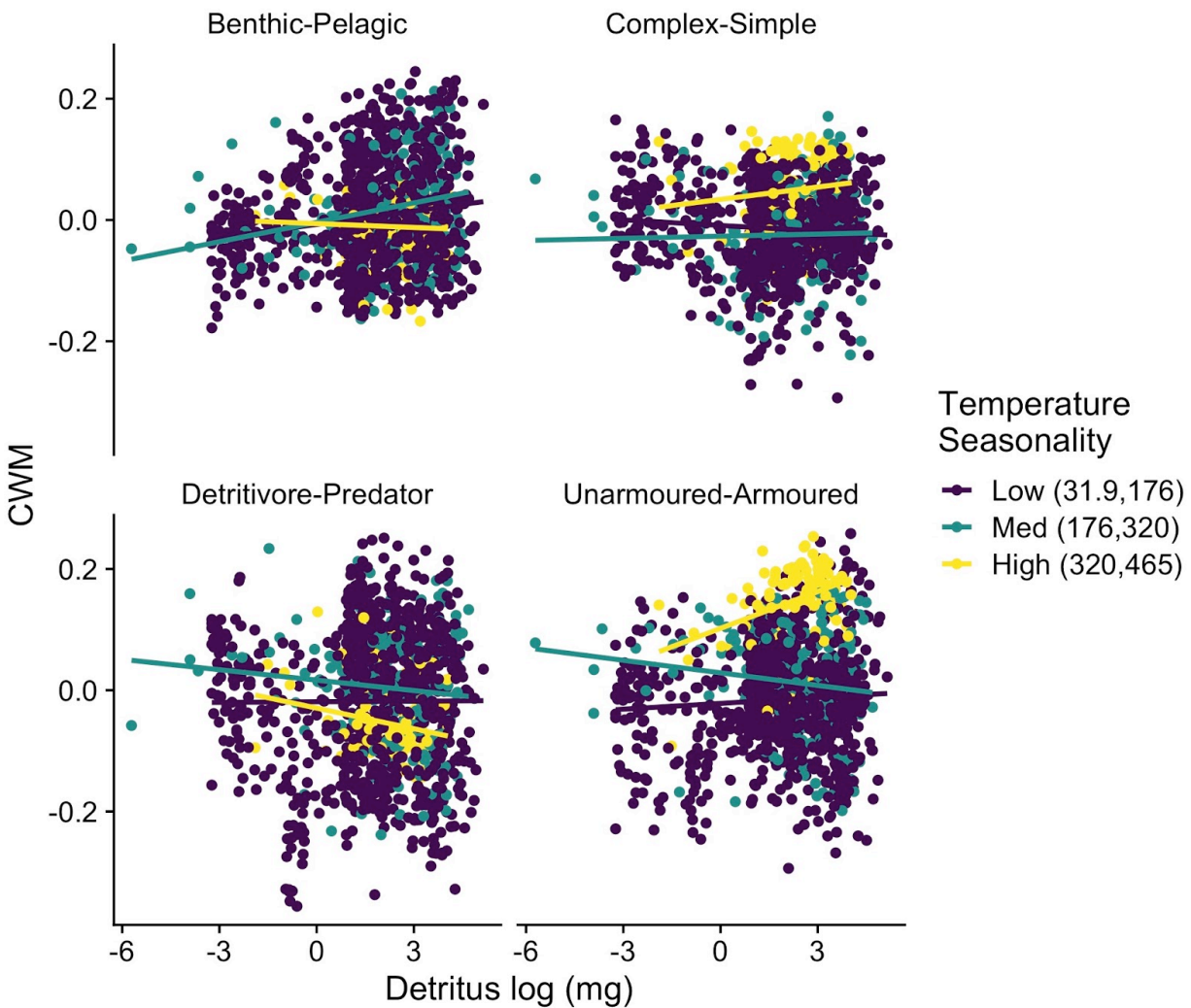
	Percentage of total sum of squares	
	Mean	Median
<i>Local conditions</i>		

Canopy cover	2.43	1.86
Detritus	4.95	4.86
Water volume	1.35	1.09
<i>Climatic variables</i>		
Mean Diurnal Temperature Range	5.55	5.55
Temperature Seasonality	3.55	3.31
Precipitation of Driest Quarter	4.66	4.57
Precipitation Seasonality	3.97	3.99
<i>Interactions between local conditions and climatic variables</i>		
Detritus : Mean Diurnal Temperature Range	1.23	1.0
Detritus : Temperature Seasonality	2.22	2.12
Detritus : Precipitation of Driest Quarter	1.33	1.25
Detritus : Precipitation Seasonality	1.56	1.39
Water volume: Mean Diurnal Temperature Range	0.84	0.68
Water volume: Temperature Seasonality	0.95	0.86
Water volume: Precipitation of Driest Quarter	1.37	1.20
Water volume: Precipitation Seasonality	0.52	0.44
<i>Total sum of squares</i>		
Full model	36.49	36.62



431 **Figure 3:** Bromeliads are characterized by their community-weighted mean traits for bioclimatic zones with
 432 low and high detritus, and high and low temperature seasonality. Detritus affects particularly the

433 Benthic-Pelagic axis: bromeliads with high detritus have more benthic organisms (i.e. high Benthic-Pelagic
434 axis values). Bioclimatic zones with high temperature seasonality have more organisms with complex life
435 cycles (i.e. higher values in the Complex life cycle – Simple axis).



436 **Figure 4:** The four trait axes differ in their relationship with the total amount of detritus which is also
437 mediated by temperature seasonality. Each point is the community weighted mean of a single bromeliad.
438 The coloured lines are simple linear regressions intended only to improve the visualization of the data and
439 not meant to be used for formal analysis since the CWM are multivariate.

440 Discussion

441 Our analyses demonstrate the importance of climate and cross-scale interactions of
442 climate with local conditions on the functional traits of macroinvertebrate communities.
443 Climate explained 40% of the trait variation in regional species pools, corroborating the
444 hypothesis that trait composition is primarily explained by the environment at the
445 biogeographic scale. Climate also explained a substantial amount (28%) of trait variation
446 at the scale of individual bromeliads, both directly (18%), and by modifying the response
447 of traits to local conditions in cross-scale interactions (10%) (Figure A9). By contrast, local
448 conditions of bromeliads, by themselves, explained only 6-9% of trait variation depending
449 on the model used. The fact that we were able to explain trait variation with both climate
450 and local conditions means that functional traits are not entirely determined by stochastic
451 factors, historical contingency and phylogenetic constraints. Although stochastic and
452 biogeographic factors no doubt affect trait distribution, they are not strong enough to
453 completely overwhelm or erase the effects that climate and local conditions have on the
454 functional traits of bromeliad macroinvertebrate communities. The implication is that local
455 adaptation and/or filtering occurs in response to both local and climatic conditions, and
456 ultimately shapes the ecological communities of bromeliad macroinvertebrates and their
457 suite of traits.

458 The most important climatic factor in explaining trait variation was mean diurnal range of
459 temperature. Combinations of precipitation and temperature were also important.

460 Detritus and canopy cover were the most important local conditions, but only explained
461 6.1 % of the variation in invertebrate trait composition. In general, not a single predictor
462 (either local conditions or climate) explained very large amounts of variation in trait
463 composition. Instead, the aggregated effects of each predictor contributed to the total
464 variation explained.

465 Our fine-grained analysis with cross-scale interactions allowed us to conclude that
466 climate explains more variation in macroinvertebrate trait composition than local
467 conditions. There are several possible explanations for this pattern. First, our synthetic
468 trait axes may have captured fundamental differences in the strategies of species for
469 tolerating climate-related stress, but not for exploiting local habitat heterogeneity. One of
470 the most important stresses in the bromeliad system is hydrologic variability, including
471 periods of drought. Some species are able to withstand drought with drought-resistant
472 eggs (e.g. *Wyeomyia* spp.: Dézerald et al. 2015), whereas others have drought-tolerant
473 larvae (e.g. Tipulidae larvae: Amundrud and Srivastava 2015). Many mosquito larvae are
474 sensitive to drought because their legless larvae require water to move (e.g. *Culex* spp.:
475 Amundrud and Srivastava 2015). However, odonates – a dominant predator in the food
476 web – are vulnerable to drought because of their long larval stage (Guzman et al. 2019,
477 Srivastava et al. 2020a). Therefore, multiple trait axes, as used in our study, are needed
478 to capture traits relevant to drought tolerance, including resistant life forms, larval
479 duration (i.e. cohort production interval), and pelagic requirements. Geographic patterns
480 in drought predict the distribution of invertebrate families that comprise the species pool

481 of bromeliad invertebrates (Srivastava et al. 2020b) and families often have unique
482 functional traits (Céréghino et al. 2018). Climate is likely a better predictor of such
483 geographic patterns in drought prevalence than bromeliad water volume, as water
484 volume is only measured on the particular day of sampling and is very dynamic between
485 days. Invertebrate mortality rarely follows a single day of drought; instead mortality
486 ranges from 11-73% after 18 days without water (Amundrud and Srivastava 2015). Similarly,
487 experimental exclusion of rainfall from French Guiana bromeliads led to changes in
488 functional trait composition of invertebrates only after six weeks without rain (Dézerald et
489 al. 2015). Although no single climate variable dominated the effects on traits, many of the
490 top climate variables were related to variation (daily or seasonal) in temperature and
491 precipitation as might be anticipated if climate affected traits via drought prevalence.
492 Our conclusion that temperature seasonality was an important determinant of trait
493 composition is similar to Swenson et al. (2012).

494 A second explanation is that deterministic filtering by local conditions is largely
495 overwhelmed by stochasticity in the colonization and emergence rates of invertebrates
496 from bromeliads. The majority of invertebrates in bromeliads are insects and thus have
497 complex life cycles, meaning that only the egg to larval or pupal stages are aquatic.
498 Larval development can be as fast as two weeks for mosquitoes, and the majority of
499 insects (except odonates) have cohort production intervals of less than 30 days (Dézerald
500 et al. 2017). This is a relatively short period for the amount of detritus, water or light to
501 limit their abundances, and suggests that abundances may be more affected by

502 oviposition and predation – both of which have an important stochastic component.
503 Furthermore, because low abundances of species in bromeliads can indicate either
504 insufficient oviposition, successful completion of the larval stage and emergence, or
505 larval mortality, even deterministic effects of local factors may result in a complex array of
506 positive and negative effects on abundance. Given that the population dynamics of
507 species with complex life cycles (i.e. insects) occurs at scales larger than the bromeliad
508 (LeCraw et al. 2014), we might expect stronger trait-environment correlations to be found
509 at these larger scales, scales which are based on the bioclimatic zone and /or the
510 species pool.

511 A third possibility is that the suite of synthetic trait axes and local variables we used for
512 analysis somehow pre-determined greater matching of traits with climatic variables than
513 with local conditions. However, both the traits and local conditions used in this study
514 have been identified in previous studies as important factors determining community
515 composition (Richardson 1999, Usseglio-Polatera et al. 2000, Dézerald et al. 2014). The
516 four synthetic trait axes represent major fundamental niche dimensions such as trophic
517 position, habitat, life history and defence (Céréghino et al. 2018), and explained 45% of
518 the total variance in species traits from the 12 traits we assembled. Although the main
519 goal of this study was to explain variations in those four main ecological strategies or four
520 PCA axes, other important ecological strategies (PCA5, PCA6, PCA7, . . .) could also be
521 influenced by local and bioclimatic conditions, however, these other axes were not
522 significant in (Céréghino et al. 2018)) and did not have biological interpretations. The four

523 ecological strategies we studied here, have previously been identified as basic niche
524 dimensions in other systems and in other clades (Winemiller et al. 2015), suggesting that
525 they may be general across different types of communities, and perhaps, broadly
526 applicable to aquatic invertebrates in other ecosystems. Extensive research on bromeliad
527 communities has demonstrated that local conditions such as water volume, detrital
528 amount and canopy cover affects bromeliad community structure, including
529 predator:prey ratios and species richness in bromeliads (Richardson et al. 2000,
530 Srivastava et al. 2008, Dézerald et al. 2014). There are well-known mechanistic reasons
531 behind these relationships. The amount of light available to a bromeliad (i.e. canopy
532 cover) determines algal productivity, and therefore, the relative importance of detritus
533 versus algae in the diet of different macroinvertebrates (Farjalla et al. 2016). In general,
534 detritus is the main source of nutrients in the bromeliad food web, and its quantity is
535 related to overall macroinvertebrate biomass (Richardson et al. 2000). The amount of
536 water found in a bromeliad at the time of sampling is related to the amount of habitat
537 available to invertebrates, the risk of drought, and whether it is colonized by predators,
538 and as such, habitat size is an important predictor of species richness, species
539 composition and trophic structure (Srivastava et al. 2008, Amundrud and Srivastava
540 2015, Petermann et al. 2015). In an experiment where many of these factors were
541 controlled for, local variation in rainfall impacted the community structure of bromeliad
542 macroinvertebrates (Srivastava 2020b), and in extreme cases, caused an inversion of the
543 trophic pyramid (Romero et al. 2020). So a combination of local conditions will have
544 some effect on community dynamics and the distribution of traits.

545 Our conclusion that climate overwhelms local conditions in driving community trait
546 structure contrasts to studies on plant communities by Bruelheide et al. (2018) who found
547 that micro-environmental gradients were more influential than climate. This may be
548 because two of the three local scale factors we analyzed varied more at biogeographical
549 than local scales (Table A2).

550 An important conclusion of our analysis is that there are cross-scale interactions between
551 environmental drivers of trait composition. That is, the effect of local conditions depends
552 on the regional climate. Specifically, the effect of either detrital amount or water volume
553 depended on temporal variation in precipitation and temperature at the field site. This
554 may reflect the ability of large detrital-filled bromeliads to buffer the effects of climate
555 variation on drought prevalence (Srivastava et al. 2020a). Studies of functional traits that
556 use coarse-grained data such as range maps or remote sensing data cannot test for such
557 cross-scale effects of the response of the community to local and climatic conditions.
558 However, there is a growing number of fine-grained datasets with a complete census of
559 the community for which interactions between local conditions and larger scale
560 environmental constraints can be tested. Such datasets are particularly well represented
561 by plants (e.g. Blonder 2018, Bruelheide et al. 2018), but also freshwater invertebrates
562 (e.g. Aspin et al. 2019), fish (e.g. Winemiller et al. 2015), intertidal organisms (e.g. Menge
563 et al. 1999) and marine coastal fishes (e.g. Hemingson and Bellwood 2018). The
564 challenge for analyzing cross-scale effects in these studies is not the large-scale climatic

565 data, but rather the fine-grained environmental data that matters for resource acquisition,
566 competition, predation and facilitation. Fine-grained microenvironmental data, only some
567 of which was available in our study, is likely to be critical in determining the relative
568 importance of environmental filtering and biotic interactions as well as the degree of
569 context dependence (Blonder 2018). A particular advantage of our study was that we
570 were able to measure the entire aquatic macroinvertebrate community at a fine scale at
571 multiple locations across a wide biogeographic range, which then were assembled into a
572 large database, through the support of the French data synthesis centre, CESAB. The
573 randomized sub-sampling procedure was used to control for uneven sampling effort
574 between sites, and gave robust estimates of variance explained between sites. Although
575 sub-sampling reduces statistical power, we gained confidence in our among site
576 comparisons.

577 Overall, we found that climate explained more variation than local conditions, and that
578 the two scales interactively determine the functional traits of bromeliad
579 macroinvertebrate communities across their Neotropical range. Our ability to contrast the
580 effects of climatic vs. local conditions hinged on the compilation of multiple fine-grained
581 datasets. We argue that in addition to sampling communities at local scales, ecologists
582 should aggregate studies that span large ranges in climate variation in order to fully
583 understand trait filtering at local, regional and global scales.

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