Appendix S1: Overview of a number of community assembly studies that explicitly address scaling. Main findings are summarized together with information on whether organismic scales (orga.) or spatial (sp.) and environmental (env.) scales had been varied and on whether diversity (D) was estimated based on functional (f) or phylogenetic (p) information.

<table>
<thead>
<tr>
<th>Orga.</th>
<th>Sp. and env.</th>
<th>D</th>
<th>Main results</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phylogenetic and strata classes</td>
<td>Environmental extent of communities</td>
<td>p</td>
<td>More clustering at larger scales due to a shift in niche evolution</td>
<td>(Cavender-Bares et al., 2006)</td>
</tr>
<tr>
<td>Phylogenetic</td>
<td>Spatial extent of species pools</td>
<td>p</td>
<td>More clustering at larger scales</td>
<td>(Swenson et al., 2006)</td>
</tr>
<tr>
<td>Phylogenetic and size classes</td>
<td>Spatial extent of communities</td>
<td>p</td>
<td>More overdispersion at finer scales</td>
<td>(Swenson et al., 2007)</td>
</tr>
<tr>
<td>None</td>
<td>Spatial extent of communities</td>
<td>p</td>
<td>Almost no scaling effect (slightly clustered to random signal for increasing scale) but different patterns in different habitats</td>
<td>(Kembel &amp; Hubbell, 2006)</td>
</tr>
<tr>
<td>Phylogenetic</td>
<td>None</td>
<td>p</td>
<td>More overdispersion at finer scales</td>
<td>(Slingsby &amp; Verboom, 2006)</td>
</tr>
<tr>
<td>None</td>
<td>Spatial and environmental extent of communities</td>
<td>P</td>
<td>More clustering at larger scales</td>
<td>(Willis et al., 2010)</td>
</tr>
<tr>
<td>None</td>
<td>Spatial extent of communities</td>
<td>p, f</td>
<td>More overdispersion at finer scales</td>
<td>(Kraft &amp; Ackerly, 2010)</td>
</tr>
<tr>
<td>Size classes</td>
<td>Spatial extent of communities</td>
<td>f</td>
<td>Mixed</td>
<td>(Swenson &amp; Enquist, 2009)</td>
</tr>
<tr>
<td>Ecologically informed species pools</td>
<td>Environmental extent of species pools</td>
<td>f</td>
<td>Overall clustering, stronger at larger scale (and in temperate regions)</td>
<td>(Lessard et al., 2012)</td>
</tr>
<tr>
<td>None</td>
<td>Spatial extent of communities</td>
<td>p</td>
<td>Mixed</td>
<td>(Murria et al., 2012)</td>
</tr>
<tr>
<td>None</td>
<td>Spatial extent of species pools</td>
<td>p</td>
<td>No effect (suggested that environmental extent is more important)</td>
<td>(Wang et al., 2013)</td>
</tr>
<tr>
<td>None</td>
<td>Spatial extent of communities</td>
<td>p</td>
<td>From overdispersion to clustering for increasing scales</td>
<td>(Carboni et al., 2013)</td>
</tr>
<tr>
<td>Phylogenetic</td>
<td>None</td>
<td>p</td>
<td>Mixed</td>
<td>(Villalobos et al., 2013)</td>
</tr>
<tr>
<td>None</td>
<td>Spatial extent and environmental extent of species pool</td>
<td>f</td>
<td>More clustering at larger environmental scales; no additional spatial scale effect</td>
<td>(Belmaker &amp; Jetz, 2013)</td>
</tr>
<tr>
<td>None</td>
<td>Environmental extent of species pool</td>
<td>f</td>
<td>More clustering at larger scales</td>
<td>(Kraft et al., 2008)</td>
</tr>
<tr>
<td>Phylogenetic</td>
<td>Environmental extent of species pool</td>
<td>f</td>
<td>Trend towards less clustering at smaller scales</td>
<td>(Chalmandrier et al., accepted)</td>
</tr>
<tr>
<td>None</td>
<td>Spatial extent of communities and species pools</td>
<td>p, f</td>
<td>No effect for “p”; mixed for “f”</td>
<td>(Harmon-Threat &amp; Ackerly, 2013)</td>
</tr>
</tbody>
</table>
References


Appendix S2: Details for the method description.

**Merging of two databases**

To ensure consistency between the two merged databases (Alps Vegetation Database and French National Alpine Botanical Conservatory database), we applied the following set of four filters: 1- we kept only geo-referenced community plots with a precision higher than 500 m. 2- we discarded community plots for which the sampling date was prior to 1980 in order to keep contemporary data only. 3- we restricted the analyses to community-plots for which an estimation of abundance-dominance was available (Braun-Blanquet, 1946) in order to use abundance-weighted diversity metrics. Within each community-plot, species abundances were recorded using a cover scheme with six classes (1: less than 1%; 2: from 1 to 5%; 3: from 5 to 25%; 4: from 25 to 50%; 5: from 50 to 75%; 6: more than 75%; Braun-Blanquet, 1946) and were converted to estimated abundances using the mean percentage within a class (i.e. 0.5, 3, 15, 37.5, 62.5 and 87.5%). 4- we kept only community plots with more than one species and for which the species that contributed 80% or more to the total abundance cover were represented in the phylogenetic tree (see below). The outcome of such a filtering procedure led us to select a total of 18,919 community plots and 3,081 species belonging to 773 genera and 135 families.

**Land cover type classification**

Land cover classification for each of the selected community plot was extracted from the Corine Land Cover database (CORINE 2006, http://www.epa.ie/whatwedo/assessment/land/corine/) at a 250-m resolution. CORINE is a European map of the environmental landscape based on interpretation of satellite images. It provides comparable digital maps of land cover for most European countries. Because CORINE was not available for Switzerland, a reclassification of the Swiss land cover map at the same resolution was carried out to match the definition of CORINE. To restrict the number of different land cover types and to have a classification better adapted to the Alpine context (better delineation of sparsely-vegetated or bare-ground land cover types) we re-classified the CORINE land cover data (details in Table 2). The final classification for the entire Alps thus consisted of 145,683 homogenous and continuous polygons representing 11 land cover types (Table 2).

**Phylogeny**

The genus-level phylogeny of the Alpine plants was constructed following the workflow proposed by Roquet et al. (2013). We downloaded from Genbank three conserved chloroplastic regions (rbcL, matK and ndhF) plus eight regions for certain families or orders (atpB, ITS, psbA-trnH, rpl16, rps4, rps4-trnS, rps16, trnL-F), which were aligned separately by taxonomic clustering. All sequences were aligned with three methods ('MUSCLE', Edgar, 2004; 'MAFFT', Katoh et al., 2005; 'Kalign', Lassmann & Sonnhammer, 2005), then the best alignment for each region was selected and depurated with TrimAl (Capella-Gutiérrez et al., 2009) after being visually checked. Phylogenetic inference by maximum-likelihood (ML) was conducted with RAxML (Stamatakis et al., 2008) applying a supertree constraint at the family-level based on Davies et al. (2004) and Moore et al. (2010). The best ML tree was dated by penalized-likelihood using r8s (Sanderson, 2003) and 25 fossils for calibration extracted from Smith et al. (2010) and Bell et al. (2010).
Assessing statistical significance in community structure

Different randomization schemes ("null models" in the following) are necessary for different species pools when the distribution of frequencies of occurrence and/or abundances is not random in the phylogenetic tree of the species pool. We used the abundance phylogenetic divergence index (APD) to decide whether species frequencies of occurrences or abundances should be taken into account when simulating random communities (Hardy, 2008). For each species pool, we calculated the APD index on the basis of species frequencies of occurrences to detect a phylogenetic signal of frequently vs. rarely occurring species (APD₀) and on the basis of mean local relative abundances (APDₐ) to detect a phylogenetic signal of locally highly abundant vs. rare species (see Appendix S3). If neither APD₀ nor APDₐ were significant we simply randomized all species of the species pool in the phylogenetic tree (see Hardy, 2008, null models 1s). If APD₀ was significant we randomized species in a constrained way so that only species with similar frequencies of occurrence were permuted. If APDₐ was significant we only permuted species with similar mean local relative abundances. If APD₀ and APDₐ were both significant we randomized only species with similar summed relative abundances across the species pool. To constrain the randomizations as detailed above, species were grouped into frequency-of-occurrence classes, mean-local-relative-abundance classes or summed-relative-abundance classes and we applied randomizations within these classes. Class boundaries were changed for each of the 999 repetitions of the null model to avoid that similar species at different sides of borders between classes would always be in different classes (see Hardy, 2008, null model 1a for the algorithm; Pavoine et al., 2009 for the basic R-code which we adapted to the three different constraints).

To test whether 999 repetitions were sufficient for stable results, we conducted a power analysis by repeating the null model analysis for grassland community plots and the largest scale choice and thus the largest species pool, 30 times. We found that α-diversity-percentiles varied little within community plots (see Appendix S3) and thus concluded that potential differences between different species pools could be attributed to the species pool characteristics and not to the inherent uncertainties in a single randomization scheme.

References


Münkemüller, T., et al. - Scale decisions can reverse conclusions on community assembly processes.


Appendix S3: Distribution of $\alpha$-diversity-percentiles within grassland community plots across 30 repetitions of the same scale choice, i.e. the largest spatial and environmental extents and the broadest organismic scale (one species pool). Each boxplot shows the distribution of $\alpha$-diversity-percentiles across the 30 repetitions. Community plots are ranked according to the median position of their observed $\alpha$-diversity-percentiles.
**Appendix S4:** Overview of species pool structures (resulting from the different scale choices) with their number of species (no species), and the abundance phylogenetic deviation both for occurrence frequency (APD\(_O\)) and average abundance (APD\(_A\)) ('0': random, ‘-’: clustered, \(p<0.025\), ‘+’: over-dispersed, \(p<0.975\)).

<table>
<thead>
<tr>
<th></th>
<th>Lower stratum</th>
<th>All strata</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>All species</td>
<td>Only herbaceous</td>
</tr>
<tr>
<td>All data</td>
<td>no species</td>
<td>3043</td>
</tr>
<tr>
<td>APD(_O)</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>APD(_A)</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Grassland</td>
<td>no species</td>
<td>2540</td>
</tr>
<tr>
<td>All polygons</td>
<td>APD(_O)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>APD(_A)</td>
<td>0</td>
</tr>
<tr>
<td>Focal polygon</td>
<td>no species</td>
<td>695</td>
</tr>
<tr>
<td></td>
<td>APD(_O)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>APD(_A)</td>
<td>0</td>
</tr>
<tr>
<td>Bare-rock</td>
<td>no species</td>
<td>1168</td>
</tr>
<tr>
<td>All polygons</td>
<td>APD(_O)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>APD(_A)</td>
<td>-</td>
</tr>
<tr>
<td>Focal polygon</td>
<td>no species</td>
<td>257</td>
</tr>
<tr>
<td></td>
<td>APD(_O)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>APD(_A)</td>
<td>0</td>
</tr>
<tr>
<td>Sparsely</td>
<td>no species</td>
<td>1604</td>
</tr>
<tr>
<td>vegetated</td>
<td>APD(_O)</td>
<td>0</td>
</tr>
<tr>
<td>All polygons</td>
<td>APD(_A)</td>
<td>-</td>
</tr>
<tr>
<td>Focal polygon</td>
<td>no species</td>
<td>268</td>
</tr>
<tr>
<td></td>
<td>APD(_O)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>APD(_A)</td>
<td>-</td>
</tr>
</tbody>
</table>
Appendix S5: Regression and partial regression analyses to explain the influence of scale choices: (a) all scale choices (accordingly 18 species pools) and (b) removing the organismic scale choices that only include Asteraceae species (no family-only scale choices to show remaining effects after removing the most influential scale choice, 12 species pools remain). Organismic scale reduction includes phylogenetic constraints (phylogeny), growth form constraints (growth form) and vegetation stratum constraints (veg. stratum). Environmental and spatial scale reductions include a decrease in environmental extent (focus on one land cover type) and a decrease in spatial extent (space). In a first step, we calculated observed-diversity-residuals ($Q_{c, \alpha \text{res}}$: residuals of the regression of observed alpha diversity, $Q_{c, \alpha}$, against community ID, ID$_{com}$) and percentile-residuals (perc-res.: residuals of the regression of $\alpha$-diversity-percentiles against community plot ID, ID$_{com}$). In a second step, we regressed community delimitation and scales on the gamma diversity in the regional species pool ($Q_{c, \gamma}$) and on the observed-diversity-residuals. In a final step, we studied the influence of all variables on percentile-residuals.

(a) All scale choices

<table>
<thead>
<tr>
<th>Resp. variable</th>
<th>Explanatory variables</th>
<th>Grassland</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>$Q_{c, \alpha}$</td>
<td>ID$_{com}$</td>
<td>5066</td>
<td>0.9</td>
<td>0.1</td>
<td>1355</td>
<td>0.69</td>
<td>0.24</td>
<td>3446</td>
</tr>
<tr>
<td>perc_res.</td>
<td>ID$_{com}$</td>
<td>5066</td>
<td>0.24</td>
<td>0.53</td>
<td>1355</td>
<td>0.19</td>
<td>0.56</td>
<td>3446</td>
</tr>
<tr>
<td>perc_res.</td>
<td>(phylogeny + growth form + veg. stratum)$^2$</td>
<td>5364</td>
<td>0.23</td>
<td>0.02</td>
<td>1446</td>
<td>0.16</td>
<td>0.29</td>
<td>3666</td>
</tr>
<tr>
<td>perc_res.</td>
<td>space + land cover</td>
<td>5367</td>
<td>0.23</td>
<td>0.02</td>
<td>1449</td>
<td>0.18</td>
<td>0.02</td>
<td>3669</td>
</tr>
<tr>
<td>$Q_{c, \gamma}$</td>
<td>(phylogeny + growth form + veg. stratum)$^2$</td>
<td>5364</td>
<td>0.31</td>
<td>0.98</td>
<td>1446</td>
<td>0.23</td>
<td>0.98</td>
<td>3666</td>
</tr>
<tr>
<td>$Q_{c, \gamma}$</td>
<td>space + land cover</td>
<td>5367</td>
<td>2.05</td>
<td>0</td>
<td>1449</td>
<td>1.68</td>
<td>0.01</td>
<td>3669</td>
</tr>
<tr>
<td>$Q_{c, \alpha \text{res}}$</td>
<td>(phylogeny + growth form + veg. stratum)$^2$</td>
<td>5364</td>
<td>0.53</td>
<td>0.63</td>
<td>1446</td>
<td>0.41</td>
<td>0.61</td>
<td>3666</td>
</tr>
<tr>
<td>perc_res.</td>
<td>$Q_{c, \alpha \text{res}}$</td>
<td>5368</td>
<td>0.23</td>
<td>0</td>
<td>1450</td>
<td>0.16</td>
<td>0.27</td>
<td>3670</td>
</tr>
<tr>
<td>perc_res.</td>
<td>$(Q_{c, \alpha \text{res}} + Q_{c, \gamma})^2$</td>
<td>5368</td>
<td>0.21</td>
<td>0.15</td>
<td>1450</td>
<td>0.14</td>
<td>0.41</td>
<td>3670</td>
</tr>
<tr>
<td>perc_res.</td>
<td>$(Q_{c, \gamma} + Q_{c, \alpha \text{res}})^2$</td>
<td>5366</td>
<td>0.19</td>
<td>0.35</td>
<td>1448</td>
<td>0.14</td>
<td>0.41</td>
<td>3668</td>
</tr>
<tr>
<td>perc_res.</td>
<td>$(Q_{c, \gamma} + Q_{c, \alpha \text{res}} + Q_{c, \alpha \text{res}})^2$</td>
<td>5345</td>
<td>0.18</td>
<td>0.41</td>
<td>1427</td>
<td>0.14</td>
<td>0.44</td>
<td>3647</td>
</tr>
</tbody>
</table>
Münkemüller, T., et al. - Scale decisions can reverse conclusions on community assembly processes.

(b) No family-only scale choice

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Qc,α</td>
<td>ID: res</td>
<td>3344</td>
<td>0.12</td>
<td>0.75</td>
<td>1049</td>
<td>0.02</td>
<td>0.97</td>
<td>2486</td>
<td>0.03</td>
<td>0.9</td>
</tr>
<tr>
<td>perc</td>
<td>ID: res</td>
<td>3344</td>
<td>0.14</td>
<td>0.87</td>
<td>1049</td>
<td>0.08</td>
<td>0.91</td>
<td>2486</td>
<td>0.11</td>
<td>0.79</td>
</tr>
<tr>
<td>perc_res.</td>
<td>(growth form + veg. stratum)^2</td>
<td>3644</td>
<td>0.12</td>
<td>0.09</td>
<td>1142</td>
<td>0.08</td>
<td>0.14</td>
<td>2708</td>
<td>0.1</td>
<td>0.04</td>
</tr>
<tr>
<td>perc_res.</td>
<td>space + land cover</td>
<td>3645</td>
<td>0.12</td>
<td>0.11</td>
<td>1143</td>
<td>0.07</td>
<td>0.14</td>
<td>2709</td>
<td>0.09</td>
<td>0.26</td>
</tr>
<tr>
<td>Qc,γ</td>
<td>(growth form + veg. stratum)^2</td>
<td>3644</td>
<td>0.06</td>
<td>0.55</td>
<td>1142</td>
<td>0.07</td>
<td>0.13</td>
<td>2708</td>
<td>0.07</td>
<td>0.21</td>
</tr>
<tr>
<td>Qc,α_res</td>
<td>space + land cover</td>
<td>3645</td>
<td>0.07</td>
<td>0.39</td>
<td>1143</td>
<td>0.04</td>
<td>0.71</td>
<td>2709</td>
<td>0.04</td>
<td>0.71</td>
</tr>
<tr>
<td>Qc,α_res</td>
<td>(growth form + veg. stratum)^2</td>
<td>3644</td>
<td>0.1</td>
<td>0.28</td>
<td>1142</td>
<td>0.02</td>
<td>0.13</td>
<td>2708</td>
<td>0.03</td>
<td>0.3</td>
</tr>
<tr>
<td>perc_res.</td>
<td>Qc,γ</td>
<td>3646</td>
<td>0.13</td>
<td>0</td>
<td>1144</td>
<td>0.07</td>
<td>0.09</td>
<td>2710</td>
<td>0.09</td>
<td>0.18</td>
</tr>
<tr>
<td>perc_res.</td>
<td>Qc,α_res</td>
<td>3646</td>
<td>0.11</td>
<td>0.32</td>
<td>1144</td>
<td>0.07</td>
<td>0.01</td>
<td>2710</td>
<td>0.09</td>
<td>0.23</td>
</tr>
<tr>
<td>perc_res.</td>
<td>(Qc,γ + Qc,α_res)^2</td>
<td>3644</td>
<td>0.1</td>
<td>0.35</td>
<td>1142</td>
<td>0.07</td>
<td>0.11</td>
<td>2708</td>
<td>0.07</td>
<td>0.51</td>
</tr>
<tr>
<td>perc_res.</td>
<td>(space + land cover + growth form + veg. stratum + Qc,γ + Qc,α_res)^2</td>
<td>3630</td>
<td>0.1</td>
<td>0.46</td>
<td>1128</td>
<td>0.07</td>
<td>0.19</td>
<td>2694</td>
<td>0.06</td>
<td>0.62</td>
</tr>
</tbody>
</table>
Appendix S6: Distribution of $\alpha$-diversity-percentiles within bare-rock community plots across (a) all scale choices and accordingly 18 species pools and (b) removing the organismic scale choices that only include Asteraceae species (no family-only scale choices to show remaining effects after removing the most influential scale, 12 species pools remain). Each boxplot shows the distribution of $\alpha$-diversity-percentiles across the tested scale choices. Outliers are not plotted. Community plots are ranked according to the median position of their observed $\alpha$-diversity-percentiles. In (a) 2% (15%) of community plots show a median of $\alpha$-diversity-percentiles above 0.95 (below 0.05); in (b) 3% (15%) of community plots show a median of $\alpha$-diversity-percentiles above 0.95 (below 0.05).
Appendix S7: Distribution of α-diversity-percentiles within sparsely vegetated community plots across (a) all scale choices and accordingly 18 species pools and (b) removing the organismic scale choices that only include Asteraceae species (no family-only scale choices to show remaining effects after removing the most influential scale, 12 species pools remain). Each boxplot shows the distribution of α-diversity-percentiles across the tested scale choices. Outliers are not plotted. Community plots are ranked according to the median position of their observed α-diversity-percentiles. In (a) 1% (10%) of community plots show a median of α-diversity-percentiles above 0.95 (below 0.05); in (b) 1% (11%) of community plots show a median of α-diversity-percentiles above 0.95 (below 0.05).
Appendix S8: Distribution of α-diversity-percentiles within scale choices across bare-rock community plots. Each dot in a violin plot represents one of the focal community plots; black dots identify community plots with significant high or low α-diversity-percentiles, small numbers below (and above) the violin plots give the percentage of community plots with significant patterns of clustering (or over-dispersion). The width of each violin plot refers to the density of data points. The colored dots help to visualize the magnitude of change. Each color identifies one community across different scale choices. Organismic scale constraints on the x-axis include phylogenetic constraints (all vs. only Asteraceae family), growth form constraints (all vs. herbaceous species only) and vegetation stratum constraints (all vs. only lowest stratum). Environmental and spatial extent constraints on the y-axis include reduced environmental extent (all bare-rock polygons) and reduced spatial extent (focal bare-rock polygon).
Appendix S9: Distribution of $\alpha$-diversity-percentiles within scale choices across sparsely vegetated community plots. Each dot in a violin plot represents one of the focal community plots; black dots identify community plots with significant high or low $\alpha$-diversity-percentiles, small numbers below (and above) the violin plots give the percentage of community plots with significant patterns of clustering (or over-dispersion). The width of each violin plot refers to the density of data points. The colored dots help to visualize the magnitude of change. Each color identifies one community across different scale choices. Organismic scale constraints on the x-axis include phylogenetic constraints (all vs. only Asteraceae family), growth form constraints (all vs. herbaceous species only) and vegetation stratum constraints (all vs. only lowest stratum). Environmental and spatial extent constraints on the y-axis include reduced environmental extent (all sparsely vegetated polygons) and reduced spatial extent (focal sparsely vegetated polygon).
Münkemüller, T., et al. - **Scale decisions can reverse conclusions on community assembly processes.**

**Appendix S10:** Interactive effect of $\alpha$-diversity-residuals and phylogenetic constraints (organismic scale choices that only include *Asteraceae* species) on percentile-residuals in grassland communities.
Appendix S11: Visual presentation of the regression and partial regression analyses for bare-rock community plots with arrows representing the effect of explanatory variables on response variables and numbers representing adjusted $R^2$ values of the respective models (cf. Appendix S8 for more details): (a) includes all scale choices (accordingly 18 species pools) and (b) includes all scale choices besides the choices that only include Asteraceae species (no family-only scale choices to show remaining effects after removing the most influential scale choice, 12 species pools remain). Organismic scale constraints include phylogenetic constraints (all vs. only Asteraceae family), growth form constraints (all vs. herbaceous species only) and vegetation stratum constraints (all vs. only lowest stratum). Environmental and spatial constraints include land cover types and spatial extent (cf. Table 1 for more detail). In a first step, we studied the influence of scale choices on the species pool diversity ($Q_{c, y}$) and on the $\alpha$-diversity-residuals ($\text{resid}(Q_{c, a} \sim \text{ID}_{\text{com}})$, i.e. residuals of the regression of observed $\alpha$-diversity, $Q_{c,a}$, against community plot identity, $\text{ID}_{\text{com}}$). In a second step, we studied the influence of all variables on percentile-residuals ($\text{resid}(\text{perc} \sim \text{ID}_{\text{com}})$, i.e. residuals of the regression of $\alpha$-diversity-percentiles against $\text{ID}_{\text{com}}$).
Appendix S12: Visual presentation of the regression and partial regression analyses for sparsely vegetated community plots with arrows representing the effect of explanatory variables on response variables and numbers representing adjusted R² values of the respective models (see Appendix S8 for more details): (a) includes all scale choices (accordingly 18 species pools) and (b) includes all scale choices besides the choices that only include Asteraceae species (no family-only scale choices to show remaining effects after removing the most influential scale choice, 12 species pools remain). Organismic scale constraints include phylogenetic constraints (all vs. only Asteraceae family), growth form constraints (all vs. herbaceous species only) and vegetation stratum constraints (all vs. only lowest stratum). Environmental and spatial constraints include land cover types and spatial extent (cf. Table 1 for more detail). In a first step, we studied the influence of scale choices on the species pool diversity ($Q_{c,γ}$) and on the $α$-diversity-residuals ($\text{resid}(Q_{c,α} \sim ID_{com})$, i.e. residuals of the regression of observed $α$-diversity, $Q_{c,α}$, against community plot identity, ID_{com}). In a second step, we studied the influence of all variables on percentile-residuals ($\text{resid}(\text{perc} \sim ID_{com})$, i.e. residuals of the regression of $α$-diversity-percentiles against ID_{com}).
Münkemüller, T., et al. - Scale decisions can reverse conclusions on community assembly processes.

**Appendix S13**: Spearman rank correlations between the median of all α-diversity-percentiles for a community plot (without the focal scale choices) and the α-diversity-percentiles under focal scale choices for bare-rock communities.
Appendix S14: Spearman rank correlations between the median of all α-diversity-percentiles for a community plot (without the focal scale choices) and the α-diversity-percentiles under focal scale choices for sparsely vegetated communities.
Appendix S15: The greatest range of $\alpha$-diversity-percentiles for each community plot across all scale choices (open circles), removing the scale choices that only include Asteraceae species (no family-only scale choices, filled triangles) and for the scale choices that include only Asteraceae species (family-only designs, filled squares) plotted against the minimum number of species observed (note that species number may decrease with the reduction of organismic scales) and the difference in number of species (when comparing the two sampling designs that led to the highest and lowest $\alpha$-diversity-percentiles). These plots show that the influence of scale choices on $\alpha$-diversity-percentiles is not mainly driven by species richness in the community plots.
Appendix S16: The greatest range in $\alpha$-diversity-percentiles for each community plot (within the three focal polygons) across all scale choices plotted in space. The size of points relates to the greatest difference in $\alpha$-diversity-percentiles. These graphics show that the uncertainty in $\alpha$-diversity-percentiles is not mainly driven by the location of community plots.