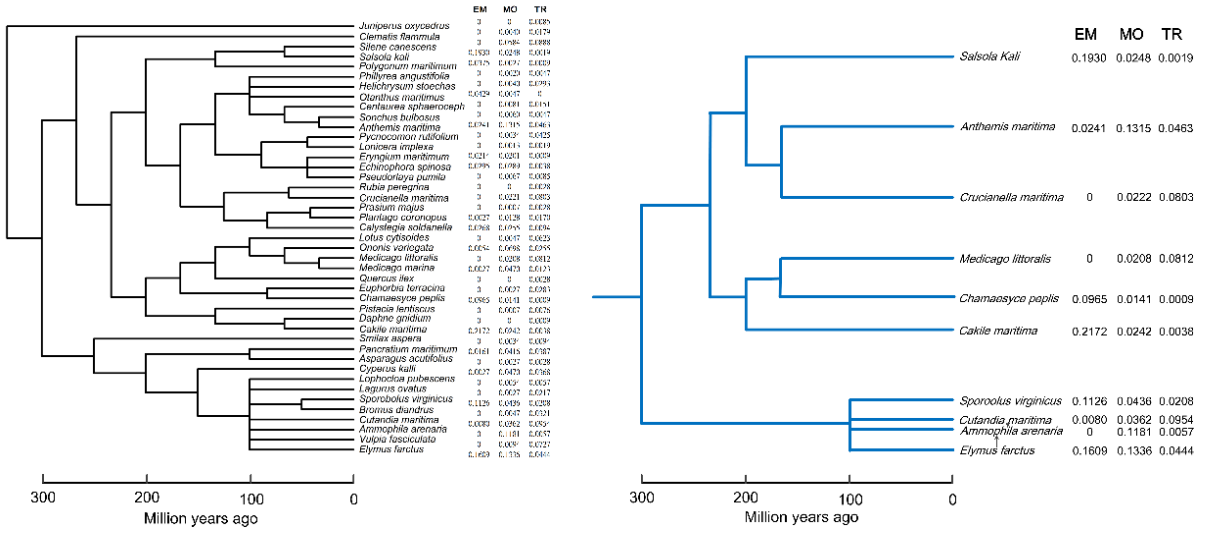
SUPPLEMENTAL APPENDIX 5: AN ILLUSTRATIVE EXAMPLE

We applied various diversity and similarity/differentiation measures to the real data discussed in Ricotta et al. (2012) and Chiu & Chao (2014). The full data contain a total of 43 vascular plant species collected from 272 random vegetation plots of 2 x 2 m in size during the period 2002-2009 in three successively less extreme fore dune habitats: embryo dunes (EM; 17 species in 70 plots), mobile dunes (MO; 39 species in 131 plots) and transition dunes (TR; 42 species in 71 plots) along the Tyrrhenian coast, where EM is closest to the sea, MO is between EM and TR, and TR is farthest from the sea; see Carboni et al. (2010, 2011, 2013) for details. There are 17 shared species (out of a total of 39 species) between EM and MO, 16 shared species (out of a total of 43 species) between EM and TR, and 38 shared species (out of a total of 43 species) between MO and TR.

In each habitat, we pooled species abundance over plots and obtained species relative abundances (see **Supplemental Figure 5.1**). All our analyses were based on the three sets of species *relative* abundances. We also constructed the phylogenetic tree (shown in **Supplemental Figure 5.1**) of the 43 species by using the software PHYLOMATIC (Webb & Donoghue 2005). The age of the root for these 43 species is around 325 million years (Myr).

All species were described by a set of sixteen functional traits which include seven quantitative variables: plant height, leaf size, leaf thickness, seed mass, seed shape, leaf dry mass and specific leaf area, together with nine categorical variables: life form, growth form, leaf texture, dispersal mode, leaf persistence, plant life span, pollination system, clonality and flowering phenology. Based on these sixteen traits, the species distance matrix was calculated by a Gower mixed-variables coefficient of distance (Pavoine et al. 2009) with equal weights for all traits. The Gower distance matrix of the pooled assemblage is provided in Chiu & Chao (2014, their Appendix S6). The matrix and the three sub-matrices (corresponding to those of three habitats) are all non-ultrametric.



Supplemental Figure 5.1
(*Left panel*) The phylogenetic tree of 43 vascular plant species and the species relative abundances in three habitats: embryo dunes (EM), mobile dunes (MO), and transition dunes (TR). A zero relative abundance means that the species does not exist in that assemblage. The age of the root is $T = 325$ Myr. (*Right panel*) A subtree contains only the dominant species (those with relative abundance >8% in at least one habitat). All dominant species in MO and TR are shared by these two habitats. In the EM habitat, the two most dominant species *Salsola kali* and *Cakile maritime* cover about 41% of the individuals and have been in isolated lineages for 200 Myr.

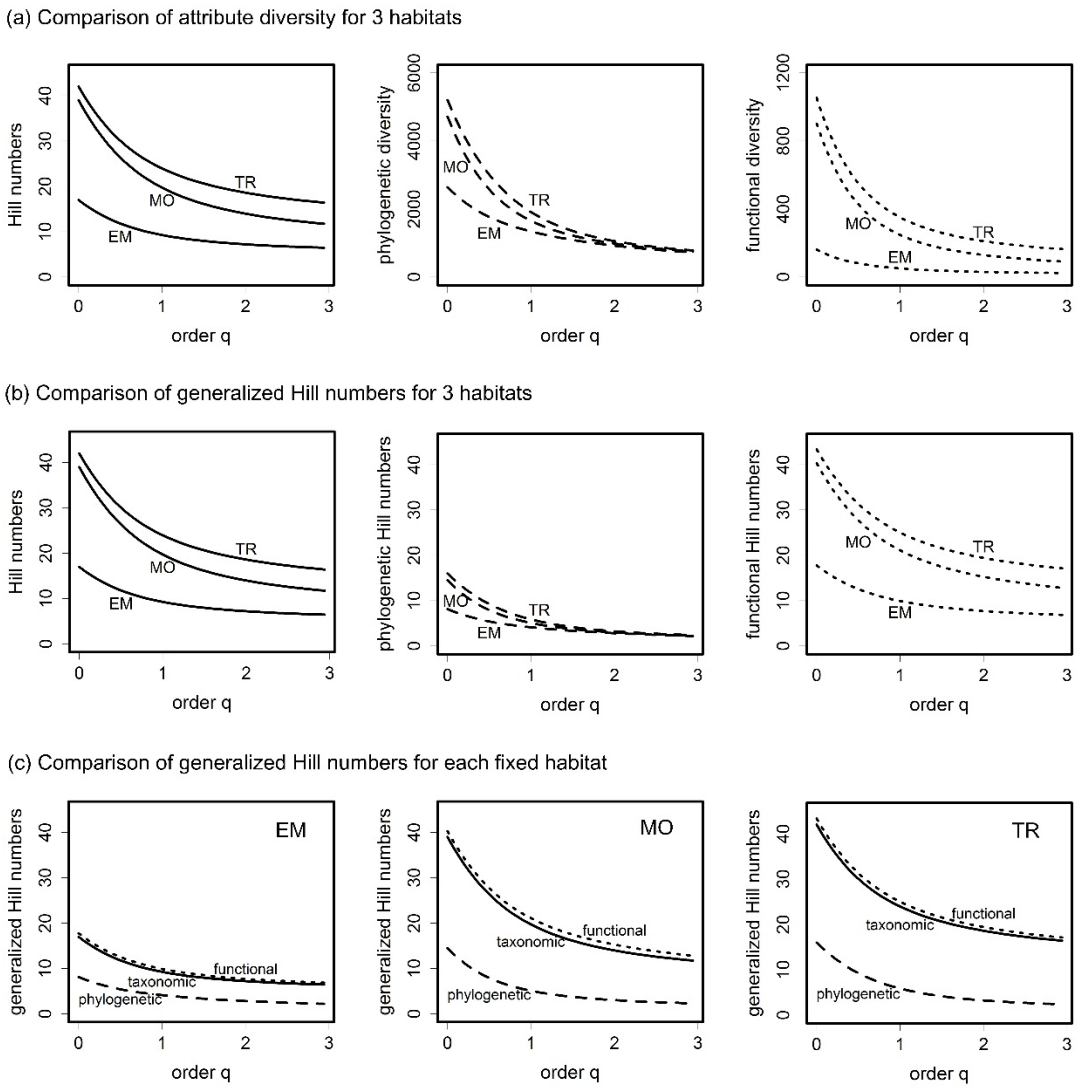
In **Supplemental Figure 5.2*a***, diversity profiles as a function of order q ($0 \le q \le 3$) of the following attribute diversities for three habitats (TR, MO, and EM) are presented: the ordinary Hill number ${}^{q}D$, the phylogenetic diversity ${}^{q}PD(\overline{T})$, and the functional diversity ${}^{q}FD(Q)$. The three attribute diversities are in different units. In **Supplemental Figure 5.2*b***, we show the corresponding profiles for three generalized Hill numbers: the ordinary Hill numbers ${}^{q}D$, phylogenetic Hill numbers ${}^{q}\overline{D}(\overline{T})$, and functional Hill number ${}^{q}D(Q)$. All these generalized Hill numbers are in the same units of "effective number of species". Thus, these three generalized Hill numbers can be compared within each habitat as shown in **Supplemental Figure 5.2*c***.

A consistent pattern is revealed for both the attribute diversity and the generalized Hill numbers: TR has the highest diversity, EM has the lowest diversity, and MO is in between. This pattern is valid for all orders of q, and is expected from ecologists' perspectives (Ricotta et al. 2012). The EM is closest to the sea, and hence exposed to wind disturbance, flooding, and salt spray, while

the vegetation of the MO is less exposed, and the vegetation of the TR is the least exposed to these harsh environmental factors. Therefore, the assemblage in the EM habitat is mainly composed of a few very abundant, specialized phylogenetically related pioneer species with similar functional traits to adapt the extreme environmental filter, leading to lowest diversities in all three dimensions (taxonomic, phylogenetic and functional). The species richness and evenness in TR are the highest among the three habitats, and the vegetation of the TR is the least affected by harsh environment factors, so the vegetation presents more functionally and evolutionarily diverse species composition, resulting in the highest value in all three dimensions. The MO habitat is between EM and TR, so the diversity in each dimension is between the two extremes.

The pairwise species functional distances (see Chiu & Chao 2014, their Appendix S6) do not vary greatly. Therefore, within each fixed habitat, the functional Hill numbers are very close to the ordinary Hill numbers, as shown in **Supplemental Figure 5.2*c***. However, there is appreciable difference between Hill number and the phylogenetic Hill number in the EM habitat. The difference becomes more pronounced in the MO and TR habitats. The difference between the ordinary Hill number and the phylogenetic Hill number arises because the ordinary Hill numbers represent the species diversity for the current assemblage, whereas the phylogenetic Hill numbers consider evolutionary histories; the latter can be expressed as a time-average of a tree's Hill numbers from the present time to the root (see Chao et al. 2010 for details) and Hill numbers decreases when the time perspective moves towards the root. Hence these differences reflect both the tree structure and node abundances.

To assess the effect of species evolutionary history or species functional distances on the differentiation among habitats, we compare in **Supplemental Table 5.1** various species compositional, phylogenetic and functional differentiation measures between any two habitats for three pairs of habitats (EM vs. MO, EM vs. TR, MO vs. TR). The measures include some previous commonly-used differentiation measures, along with the local attribute differentiation measure $1-C^{*}_{qN}(\overline{V})$, and the regional attribute differentiation measure $1-U^{*}_{qN}(\overline{V})$. See Table 2 of the main text for formulas.

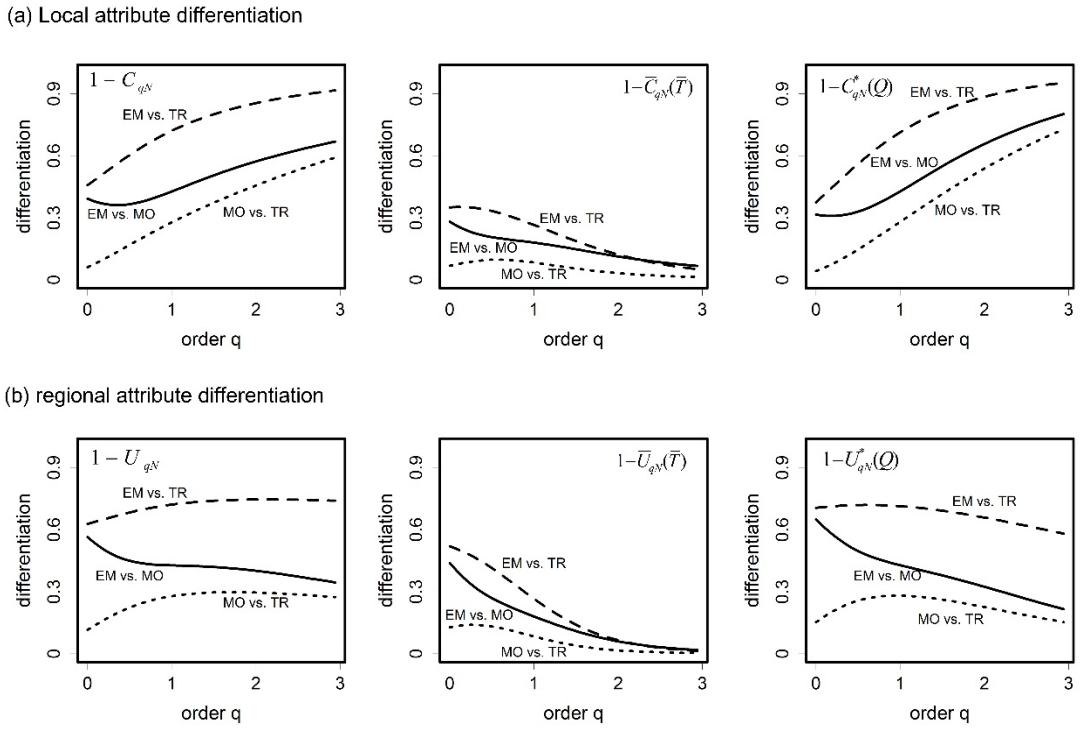


Supplemental Figure 5.2

(*a*) Diversity profiles as a function of order q ($0 \le q \le 3$) of the attribute diversity for three habitats (TR, MO, and EM): the ordinary Hill number ${}^{q}D$ (*left panel*), the phylogenetic diversity ${}^{q}PD(\overline{T})$ (middle panel), and the functional diversity ${}^{q}FD(Q)$ (*right panel*). (*b*) The corresponding diversity profiles of the generalized Hill numbers: the ordinary Hill number ${}^{q}D$ (*left panel*), the phylogenetic Hill number ${}^{q}\overline{D}(\overline{T})$ (*middle panel*), and the functional Hill number ${}^{q}D(Q)$ (*right panel*). (*c*) Comparison of diversity profiles of three generalized Hill numbers within each habitat: EM (left panel), MO (*middle panel*), and TR (*right panel*). See **Table 1** for formulas of all measures.

Supplemental Table 5.1. Comparison of various species compositional, phylogenetic and functional differentiation measures between any two habitats for three pairs

Measure	Order	EM vs. MO	EM vs. TR	MO vs. TR
(1) Species compositional differentiation measures				
(1a) Differentiation measure based on additively decomposing the generalized entropy ${}^{q}H$; see Eq. 1c of the main text				
$\frac{{}^{q}H_{\gamma} - {}^{q}H_{\alpha}}{{}^{q}H_{\gamma}}$	$q = 0$	0.2895	0.3214	0.0595
	$q = 1$	0.1022	0.1562	0.0591
	$q = 2$	0.0325	0.0435	0.0150
(1b) Differentiation measure based on decomposing Hill numbers ${}^{q}D$				
$1 - C_{qN}$	$q = 0$	0.3929	0.4576	0.0617
	$q = 1$	0.4275	0.7212	0.2788
	$q = 2$	0.5729	0.8544	0.4568
$1 - U_{qN}$	$q = 0$	0.5641	0.6279	0.1163
	$q = 1$	0.4275	0.7212	0.2788
	$q = 2$	0.4014	0.7459	0.2960
(2) Phylogenetic differentiation measures				
(2a) Differentiation measure based on additively decomposing the phylogenetic generalized entropy ${}^{q}I$; see Eq. 2c of the main text				
$\frac{{}^{q}I_{\gamma} - {}^{q}I_{\alpha}}{{}^{q}I_{\gamma}}$	$q = 0$	0.2199	0.2598	0.0640
	$q = 1$	0.0168	0.0244	0.0077
	$q = 2$	0.00006	0.00006	0.00002
(2b) Differentiation measures based on decomposing the phylogenetic diversity ${}^{q}PD(\overline{T})$				
$1 - \overline{C}_{qN}(\overline{T})$	$q = 0$	0.2818	0.3509	0.0684
	$q = 1$	0.1804	0.2659	0.0839
	$q = 2$	0.1135	0.1228	0.0328
$1 - \overline{U}_{qN}(\overline{T})$	$q = 0$	0.4397	0.5195	0.1280
	$q = 1$	0.1804	0.2659	0.0839
	$q = 2$	0.0602	0.0654	0.0167
(3) Functional differentiation measures				
(3a) Differentiation measure based on additively decomposing quadratic entropy; see Eq. 2a of the main text				
$Q^{*}_{\beta} = \frac{Q_{\gamma} - Q_{\alpha}}{Q_{\gamma}}$	$q = 2$	0.0279	0.0421	0.0257
(3b) Differentiation measure based on multiplicatively decomposing the effective number of species with maximum distance; see Section 2.3 of the main text				
$Q^{*}_{e,\beta} = \frac{1 - 1/Q_{e,\beta}}{1 - 1/N}$	$q = 2$	0.0659	0.1021	0.0669
$Q^{**}_{e,\beta} = \frac{Q_{e,\beta} - 1}{N - 1}$	$q = 2$	0.0341	0.0538	0.0346
(3c) Differentiation measures based on decomposing the functional diversity ${}^{q}FD(Q)$				
$1 - C^{*}_{qN}(Q)$	$q = 0$	0.3162	0.3751	0.0430
	$q = 1$	0.4283	0.7137	0.2815
	$q = 2$	0.6575	0.8854	0.5386
$1 - U^{*}_{qN}(Q)$	$q = 0$	0.6490	0.7059	0.1524
	$q = 1$	0.4283	0.7137	0.2815
	$q = 2$	0.3243	0.6588	0.2259



Supplemental Figure 5.3.

(*a*) Differentiation profiles as a function of order q ($0 \le q \le 3$) for local attribute differentiation measure $1-C^{*}_{qN}(\overline{V})$, including the taxonomic differentiation measure $1-C_{qN}$ (*left panel*), the phylogenetic differentiation measure $1-\overline{C}_{qN}(\overline{T})$ (*middle panel*), and the functional differentiation measure $1-C^{*}_{qN}(Q)$ (*right panel*), for three pairs of habitats (EM vs. MO, EM vs. TR and MO vs. TR). (*b*) The corresponding differentiation profiles for the regional attribute differentiation measure $1-U^{*}_{qN}(\overline{V})$, including the taxonomic differentiation measure $1-U_{qN}$ (*left panel*), the phylogenetic differentiation measure $1-\overline{U}_{qN}(\overline{T})$ (*middle panel*), and the functional differentiation measure $1-U^{*}_{qN}(Q)$ (*right panel*).

In **Supplemental Figure 5.3*a***, we show the differentiation profiles as a function of order q ($0 \le q \le 3$) of the local attribute differentiation measure $1-C^{*}_{qN}(\overline{V})$ for three pairs of habitats. The corresponding plots for the regional attribute differentiation measure $1-U^{*}_{qN}(\overline{V})$ are shown in **Supplemental Figure 5.3*b***. These profiles characterize species compositional, phylogenetic and functional differentiation among assemblages based on decomposing the attribute diversity.

All the profiles in **Supplemental Figure 5.3** reveal that EM vs. TR has the highest differentiation, MO vs. TR has the lowest differentiation, and EM vs. MO is somewhat in

between for any order q. This ordering is valid for species compositional, phylogenetic and functional differentiation. As discussed earlier, there are few shared species between EM and TR: 37.2% (16 out of 43), and also between EM and MO: 43.6% (17 out of 39). However, 88.4% (38 out of 43) of the species are shared between TR and MO. This explains the ordering of the three pairs for $q = 0$ based on the species incidence data. Moving along the profiles to $q >1$, the two species compositional differentiation measures $1-C_{qN}$ and $1-U_{qN}$ are both dominated by the relatively common species; the two phylogenetic differentiation measures $1-\overline{C}_{qN}(\overline{T})$ and $1-\overline{U}_{qN}(\overline{T})$ are dominated by the "very important lineages" (those with high node abundances) and "evolutionarily deep" species (long branch lengths). From **Supplemental Figure 5.1**, those dominant species (with relative abundance > 8% in at least one habitat) are all are shared by TR and MO, but three were not shared by the other two pairs of habitats. The most two abundant species in EM, *Cakile maritime* (21.7%) and *Salsola kali* (19.3%) cover 41% of the individuals, but these two species become less abundant in both habitats MO (4.9%) and TR (0.57%); moreover, these two species began to diverge around 200 Mya and had been in isolated lineages since then. That helps explain why the species compositional and phylogenetic differentiation in EM vs. MO (and EM vs. TR) is higher than that in MO vs. TR.

For functional differentiation measures, as discussed above, the vegetation within EM is composed of a few specialized plants (*Cakile maritime* and *Salsola kali*) with similar ecological functions to adapt to the extreme environmental stress. However, these traits are unique to species in EM when compared with species in the other two habitats. There are also fewer shared species between EM and TR (also EM and MO). In contrast, the vegetation in MO and TR are both more diverse and most species in these two habitats are shared. These explain why MO vs. TR exhibits the lowest functional differentiation, whereas EM vs. TR (also EM vs. MO) exhibit higher functional differentiation. Comparisons of our differentiation measures and the traditional approaches are given below.

(1) Species compositional differentiation measures (Supplemental Table 5.1; Supplemental Figure 5.3, *left panels*)

Due to the difference among the species relative abundance sets (shown in **Supplemental Figure 5.1**) between EM and MO (and between EM and TR) for dominant species, the compositional differentiation measures $1-C_{2N}$ and $1-U_{2N}$ correctly reflect moderate to high differentiation for $q = 2$. **Supplemental Table 5.1** show that the differentiation measure $1-C_{2N}$ for the three pairs (EM vs. MO, EM vs. TR and MO vs. TR) is respectively 0.5729, 0.8544 and 0.4568, and the corresponding differentiation measure $1-U_{2N}$ is respectively 0.4014, 0.7459 and 0.2960. The left panels of **Supplemental Figure 5.3** show that our differentiation measure $1-C_{qN}$ and $1-U_{qN}$ $(0 \le q \le 3)$ yield moderate to high differentiation for the three pairs of assemblages. In sharp contrast, some of the previously-favored abundance-sensitive

differentiation measures lead to low differentiation. The differentiation measure obtained by additively decomposing the Gini-Simpson index (which is the generalized entropy of $q = 2$) gives only 0.0325, 0.0435 and 0.0150 for the three pairs of habitats.

(2) Phylogenetic differentiation measures (Supplemental Table 5.1; Supplemental Figure 5.3, *middle panels*)

The phylogenetic differentiation measure based on additively decomposing Rao's quadratic entropy (which is the phylogenetic generalized entropy of $q = 2$) for EM vs. MO, EM vs. TR and MO vs. TR are respectively 0.00006, 0.00006 and 0.00002, indicating almost no differentiation. Although our phylogenetic differentiation measures $1-\overline{C}_{qN}(\overline{T})$ and $1-\overline{U}_{qN}(\overline{T})$ are lower than the corresponding species compositional differentiation measures (comparing the left panel with the middle panel in **Supplemental Figure 5.3**), they show for $q > 0$ much higher differentiation than the traditional measures based on additively decomposing the phylogenetic generalized entropies.

(3) Functional differentiation measures (Supplemental Table 5.1; Supplemental Figure 5.3, *right panels*)

The differentiation measures based on the additive decomposition of quadratic entropy for EM vs. MO, EM vs. TR and MO vs. TR are respectively 0.0279, 0.0421 and 0.0257, implying very low differentiation. For the two differentiation measures based on the effective number of species with maximum distance (**Equation 3c** of the main text) for the three pairs are respectively (0.0659, 0.1021, 0.0669) and (0.0341, 0.0538 and 0.0346); both sets give a counterintuitive ordering in that EM vs. MO exhibits the lowest functional differentiation. **Supplemental Table 5.1** shows that for $q = 2$, the differentiation measure $1-C^{*}_{2N}(Q)$ for each of the three pairs is respectively 0.6575, 0.8854 and 0.5386, and the corresponding differentiation measure $1-U^{*}_{2N}(Q)$ is respectively 0.3243, 0.6588 and0.2259. Thus, similar contrast is also shown for functional differentiation.

The diversity profiles in **Supplemental Figure 5.3** for the species compositional and functional differentiation measures exhibit similar patterns (comparing the *left panel* with the *right panel* in **Supplemental Figure 5.3**). The profiles for the phylogenetic differentiation show different patterns. For example, the phylogenetic differentiation measures decline with the order q, whereas the other two types of differentiation do not show this trend. This is because the node abundances near roots (where the differentiation values are near zero) are relatively high and dominant in the whole tree for large value of q, leading to substantially lower phylogenetic differentiation than the corresponding species compositional differentiation (and functional differentiation). **Supplemental Table 5.1** reveals that the difference between the abundance-based taxonomic differentiation measure and the corresponding functional differentiation measure (considering both abundance and function) is little for $q = 1$, and is

limited for $q = 0$ and for $q = 2$. This reflects that species abundance is the major factor that determines the differentiation between two habitats.

As we have proved theoretically and empirically (Jost 2007, Chiu et al. 2014, Chiu & Chao 2014), the low species compositional, phylogenetic and functional differentiation between any two habitats as obtained from previous approaches do not reflect biological reality but are inescapable consequences of a mathematical property of these measures. This example demonstrates that our attribute diversity measures and the associated differentiation measures (summarized in **Table 2** of the main text) yield the expected results and ecologically sensible interpretations.

LITERATURE CITED

Carboni M, Acosta AT, Ricotta C. 2013. Are differences in functional diversity among plant communities on Mediterranean coastal dunes driven by their phylogenetic history? *J. Veg. Sci.* 24:932–41

Carboni M, Santoro R, Acosta A. 2010. Are some communities of the coastal dune zonation more susceptible to alien plant invasion? *J. Plant Ecol.* 3:139–47

Carboni M, Santoro R, Acosta AT. 2011 Dealing with scarce data to understand how environmental gradients and propagule pressure shape fine-scale alien distribution patterns on coastal dunes. *J. Veg. Sci.* 22:751–65

Chao A, Chiu C-H, Jost L. 2010. Phylogenetic diversity measures based on Hill numbers. *Phil. Trans. R. Soc. B* 365:3599–609

Chiu C-H, Chao A. 2014. Distance-based functional diversity measures and their decomposition: a framework based on Hill numbers. *PLoS One* 9(7):e100014

Chiu C-H, Jost L, Chao A. 2014. Phylogenetic beta diversity, similarity, and differentiation measures based on Hill numbers. *Ecol. Monogr.* 84: 45–67

Jost L. 2007. Partitioning diversity into independent alpha and beta components. *Ecology* 88:2427–39

Pavoine S, Vallet J, Dufour AB, Gachet S, Daniel H. 2009. On the challenge of treating various types of variables: application for improving the measurement of functional diversity. *Oikos* 118:391–402

Ricotta C, Pavoine S, Bacaro G, Acosta AT. 2012. Functional rarefaction for species abundance data. *Methods Ecol. Evol.* 3:519–25

Webb CO, Donoghue MJ. 2005. Phylomatic: tree assembly for applied phylogenetics. *Mol. Ecol. Notes* 5:181–83