**Supplementary Material**

**Materials and Methods**

The function *hclustvar* in the package ‘ClustOfVar’ (Chavent et al. 2012a) in R (R Core Team, 2020) is a clustering algorithm that can be used to find clusters of variables that are strongly related to each other within datasets that contain a mixture of quantitative and qualitative variables.

ClustOfVar is based on the Singular Value Decomposition (SVD) approach (Chavent et al. 2012b) of PCAMIX (Kiers 1991), a principal component method for mixtures of qualitative and quantitative variables. The clustering algorithm determines the partition of variable clusters (*PK*) in a dataset that best maximizes homogeneity (*H*) within clusters, as:

$H\left(P\_{K}\right)=\sum\_{k=1}^{K}H\left(C\_{k}\right)=λ\_{1}^{1}+..λ\_{1}^{K} $ (eqn. 1)

In eqn. 1, $λ\_{1}^{1}...λ\_{1}^{K} $ are the first eigenvalues of PCAMIX applied to the *K* clusters (*Ck*) of *PK*, and the homogeneity (*H*) of a cluster (*Ck)* is a measure of relatedness between the variables in the cluster and its central synthetic quantitative variable, *yk* (see Chavent et al. 2012a for further details):

$H\left(C\_{k}\right)=\sum\_{\left(x\_{j\in C\_{k}}\right)}^{}r\_{x\_{j,}y\_{k}}^{2}+\sum\_{\left(z\_{j\in C\_{k}}\right)}^{}η\_{y\_{k,}z\_{j}}^{2}$ (eqn. 2)

The first term in eqn. 2 measures the relationship between the quantitative variables (*x*) in *Ck* and *yk* and is based on the squared Pearson correlation r2. The second term measures the relationship between the qualitative variables (*z*) in *Ck* and *yk* and is based on the correlation ratio η2. Cluster homogeneity is at a maximum when all variables in a cluster convey the same information, i.e., when all the quantitative variables are correlated to *yk* and all the correlation ratios of the qualitative variables are equal to 1.

In the hierarchical clustering algorithm, *hclustvar*, an iterative process is used to determine a set of nested partitions of variables, *p*, that maximizes *H* across all clusters. First, the data is partitioned into *p* clusters, where *p* denotes the total number of variables (quantitative and qualitative) in the dataset. Then clusters of variables are iteratively aggregated by determining levels of dissimilarity between clusters, where dissimilarity (*d*) is measured as the loss of homogeneity when two clusters (*A* and *B*) are merged

$d\left(A,B\right)=H\left(A\right)+H\left(B\right)-\left(A∪B\right)=λ\_{A}^{1}+λ\_{B}^{1}-λ\_{A∪B}^{1}$ (eqn. 3)

Clusters are assessed and merged until a new partition is obtained that maximizes *H*. Results are plotted as a dendrogram, where the height of each cluster denotes the dissimilarity (see eqn. 3) between clusters:

height(C) = *d(A, B).*



**Figure S1**. Clusters of related functional plant traits in our non-native, noxious weed dataset as determined by hierarchical clustering algorithm. Height of the branches in the dendrogram is a measure of the dissimilarity between different variables or variable clusters.

**Literature Cited**

Chavent, M., V. Kuentz-Simonet, B. Liquet, and J. Saracco. (2012a). ClustOfVar: An R package for the clustering of variables. Journal of Statistical Software 50 (13):1–16.

Chavent M, Kuentz V, Saracco J (2012b). Orthogonal Rotation in PCAMIX. Advances in Data Analysis and Classification, 6, 131-146.

Kiers H (1991). Simple Structure in Component Analysis Techniques for Mixtures of Qualitative and Quantitative Variables. Psychometrika, 56, 197–212.