

Supplementary information

Table S1: General checks of inputs done by each *mFD* function

Inputs checks	Functions names
Species coordinates matrix does not contain NA	<i>alpha.fd.multidim, alpha.multidim.plot, beta.fd.multidim, funct.space.plot, fuse, traits.faxes.cor</i>
Species coordinates matrix has row names	<i>alpha.fd.multidim, alpha.multidim.plot, beta.fd.multidim, funct.space.plot, fuse, traits.faxes.cor</i>
Species coordinates matrix has column names	<i>alpha.fd.multidim, alpha.multidim.plot, beta.fd.multidim, funct.space.plot, fuse, traits.faxes.cor</i>
Species weight matrix does not contain NA	<i>alpha.fd.hill, alpha.fd.multidim, alpha.fd.fe, alpha.multidim.plot, asb.sp.summary, beta.fd.hill</i>
Species weight matrix has row names	<i>alpha.fd.hill, alpha.fd.multidim, alpha.fd.fe, alpha.multidim.plot, asb.sp.summary, beta.fd.hill</i>
Species weight matrix has column names	<i>alpha.fd.hill, alpha.fd.multidim, alpha.fd.fe, alpha.multidim.plot, asb.sp.summary, beta.fd.hill</i>

Species weight matrix only contains numeric values	<i>alpha.fd.hill, alpha.fd.multidim, alpha.multidim.plot, alpha.multidim.plot, asb.sp.summary, beta.fd.hill</i>
Species weight matrix does not contain negative values	<i>alpha.fd.hill, alpha.fd.multidim, alpha.multidim.plot, asb.sp.summary, beta.fd.hill</i>
All species belong at least to one assemblage	<i>alpha.fd.hill, alpha.fd.multidim, alpha.fd.fe, alpha.multidim.plot, beta.fd.hill, beta.fd.multidim</i>
All assemblage contain at least one species	<i>alpha.fd.hill, alpha.fd.multidim, alpha.fd.fe, alpha.multidim.plot, beta.fd.hill, beta.fd.multidim</i>
Names of species are the same in the species weight dataframe and the species coordinates matrix	<i>alpha.fd.multidim, alpha.multidim.plot</i>
Species traits dataframe has column names	<i>sp.tr.summary, tr.cont.fspace, tr.cont.scale, funct.dist, sp.to.fe, traits.faxes.cor</i>

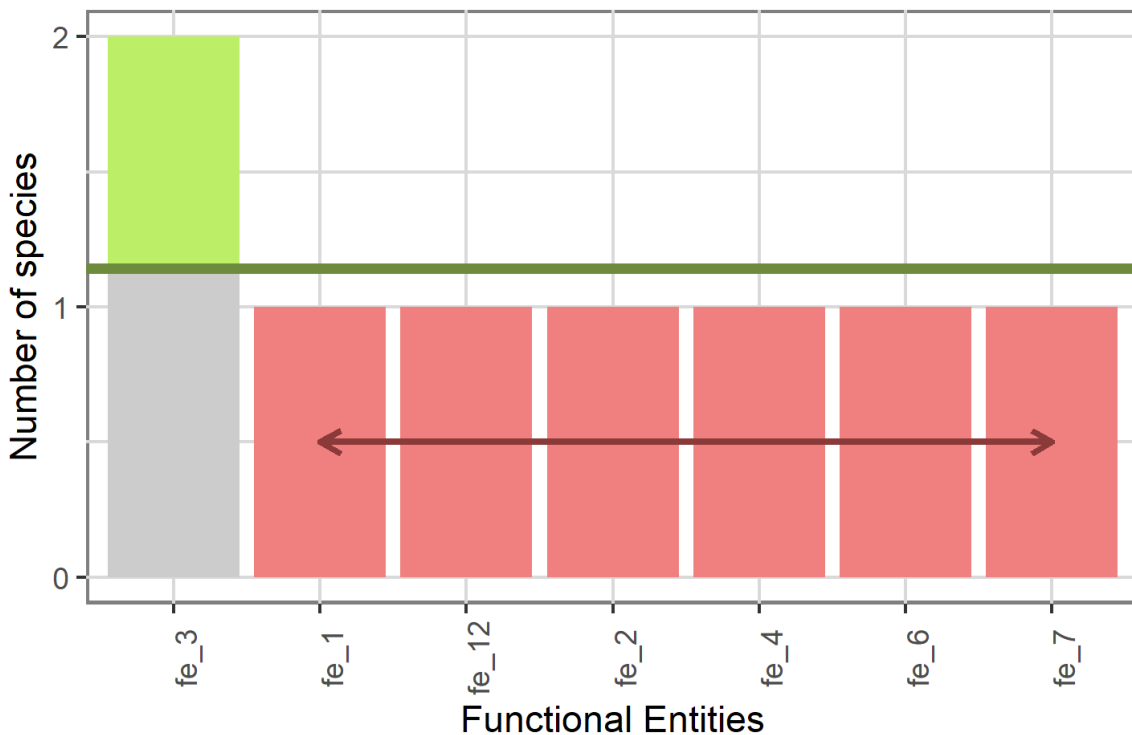
Species traits dataframe has row names	<i>sp.tr.summary, tr.cont.fspace, tr.cont.scale, funct.dist, sp.to.fe, traits.faxes.cor</i>
Species traits dataframe does not contain NA	<i>sp.tr.summary, tr.cont.fspace, tr.cont.scale, funct.dist, sp.to.fe, traits.faxes.cor</i>
Species traits dataframe and species coordinates matrix have the same species names	<i>traits.faxes.cor</i>
Traits names do not differ between species traits dataframe and traits category dataframe	<i>sp.tr.summary, funct.dist, sp.to.fe</i>
Traits types in traits category dataframe does not contain NA	<i>sp.tr.summary, funct.dist, sp.to.fe</i>
Species distance object does not contain NA	<i>alpha.fd.hill, beta.fd.hill, fuse, quality.fspaces</i>
Species names provided in the species distance object	<i>alpha.fd.hill, beta.fd.hill, fuse, quality.fspaces</i>
Species weight matrix and species distances matrix have the same species names	<i>alpha.fd.hill, beta.fd.hill</i>
Traits have the same class in traits category dataframe and data	<i>sp.tr.summary, sp.to.fe</i>
Inputs have the right format/name	<i>alpha.fd.hill, alpha.fd.multidim, alpha.fd.fe, alpha.fd.fe.plot, alpha.multidim.plot, beta.fd.hill, alpha.fd.multidim, beta.fd.multidim.</i>

	<i>beta.multidim.plot, tr.cont.fspace, funct.dist, funct.space.plot, quality.fspaces, quality.fspaces.plot</i>
Species assemblage occurrence dataframe only contains 0 or 1	<i>alpha.fd.fe, beta.fd.multidim</i>
Checking number of species	<i>beta.fd.multidim, alpha.fd.multidim (for FRic computation and MST computation)</i>

Figure S1: Illustration of FE based indices using *alpha.fd.fe.plot* function with *FRed* shown as an horizontal dark green line, *FVuln* depicted as a horizontal red double-arrow over the vulnerable entities which are further identified in orange (here, all FEs except "fe_3" contain only one species thus *FRed* and *FVuln* are close to one) and *FOR* depicted by colouring the top of the bars in light green corresponding to FE with more species than average (here only "fe_3" has more species than the average number of species thus the proportion of species in excess in FE richer than average is quite low ($FORed = 0.107$)).

FD based on FE for basket_1 :

$FRed=1.143$ $FORed=0.107$ $FVuln=0.857$



made with mFD package

Table S2: Graphical functions used in *funct.space.plot*, *alpha.multidim.plot* or *beta.multidim.plot* functions

Function name	Functionality
<i>background.plot()</i>	creates a ggplot object with customized axes range, names and background
<i>fdiv.plot()</i>	plot FDiv indice for a given pair of functional axes and one or several assemblages

<i>fdis.plot()</i>	plot FDis indice for a given pair of functional axes and one or several assemblages
<i>feve.plot()</i>	plot FEve indice for a given pair of functional axes and one or several assemblages
<i>fide.plot()</i>	plot FIde indice for a given pair of functional axes and one or several assemblages
<i>fnnd.plot()</i>	plot FNND indice for a given pair of functional axes and one or several assemblages
<i>fori.plot()</i>	plot FOri indice for a given pair of functional axes and one or several assemblages
<i>fric.plot()</i>	plot FRic indice for a given pair of functional axes and one or several assemblages
<i>fspe.plot()</i>	plot FSpe indice for a given pair of functional axes and one or several assemblages
<i>panels.to.patchwork()</i>	gathers index panels into a unique <i>patchwork</i> graph with caption
<i>pool.plot()</i>	plot all species from the study case and associated convex hull
<i>sp.plot()</i>	plot species for one to n assemblages

Table S3: Dataframe gathering fruits trait values used in the example

Species x traits dataframe based on *fruits* dataset

	Size	Plant	Climate	Seed	Sugar
apple	5-10cm	tree	temperate	pip	103.9
apricot	3-5cm	tree	temperate	pit	92.4
banana	10-20cm	tree	tropical	none	122.3
currant	0-1cm	shrub	temperate	pip	73.7
blackberry	1-3cm	shrub	temperate	pip	48.8
blueberry	0-1cm	forb	temperate	pip	100.0
cherry	1-3cm	tree	temperate	pit	128.2
grape	1-3cm	vine	temperate	pip	162.5
grapefruit	10-20cm	tree	subtropical	pip	73.1
kiwifruit	5-10cm	vine	temperate	pip	89.9
lemon	5-10cm	tree	subtropical	pip	25.0
lime	3-5cm	tree	tropical	pip	16.9
litchi	1-3cm	tree	tropical	pit	152.3
mango	10-20cm	tree	tropical	pit	136.6
melon	10-20cm	forb	temperate	pip	78.6
orange	5-10cm	tree	subtropical	pip	91.4
passion_fruit	3-5cm	vine	tropical	pip	112.0
peach	5-10cm	tree	temperate	pit	83.9
pear	5-10cm	tree	temperate	pip	97.5
pineapple	10-20cm	forb	tropical	none	98.5
plum	3-5cm	tree	temperate	pit	99.2
raspberry	1-3cm	shrub	temperate	pip	44.0
strawberry	1-3cm	forb	temperate	pip	48.9
tangerine	3-5cm	tree	subtropical	pip	105.8
water_melon	10-20cm	forb	temperate	pip	81.2

Table S4: Matrix with biomass of 25 fruits (species) in 10 baskets (assemblages) used in the example

Species x assemblages dataframe based on <i>fruits</i> dataset																										
	apple	apricot	banana	currant	blackberry	blueberry	cherry	grape	grapefruit	kiwifruit	lemon	lime	litchi	mango	melon	orange	passion_fruit	peach	pear	pineapple	plum	raspberry	strawberry	tangerine	water_melon	
basket_1	400	0	100	0	0	0	150	0	0	0	200	0	0	0	200	0	100	0	600	0	0	0	0	250	0	0
basket_2	200	0	400	0	0	0	250	0	0	0	100	0	0	0	500	0	100	0	200	0	0	0	0	250	0	0
basket_3	200	0	500	0	0	0	250	0	0	0	100	0	0	0	400	0	100	0	200	0	0	0	0	250	0	0
basket_4	300	0	0	0	0	0	0	0	0	100	100	0	0	0	0	400	0	300	400	0	200	0	0	0	200	0
basket_5	200	0	0	0	0	0	0	0	0	300	300	0	0	0	0	300	0	300	300	0	200	0	0	0	100	0
basket_6	100	0	200	0	0	0	0	0	0	0	0	200	200	500	0	100	0	0	0	500	0	0	0	0	0	200
basket_7	100	0	200	0	0	0	0	0	0	0	0	200	100	200	0	100	0	0	0	500	0	0	0	0	0	600
basket_8	0	0	0	200	300	200	200	200	0	0	100	0	0	0	0	0	0	0	0	0	0	0	400	400	0	0
basket_9	0	0	0	100	100	100	100	400	0	0	300	0	0	0	0	0	0	0	0	0	0	500	400	0	0	0
basket_10	350	200	0	0	0	0	0	300	300	0	0	0	0	0	400	0	0	0	200	0	150	0	100	0	0	0

Figure S2: Representation of relations between traits and PCoA axes (significant correlation: dark blue, non-significant correlation: light grey)

Relation between traits and PCoA axes

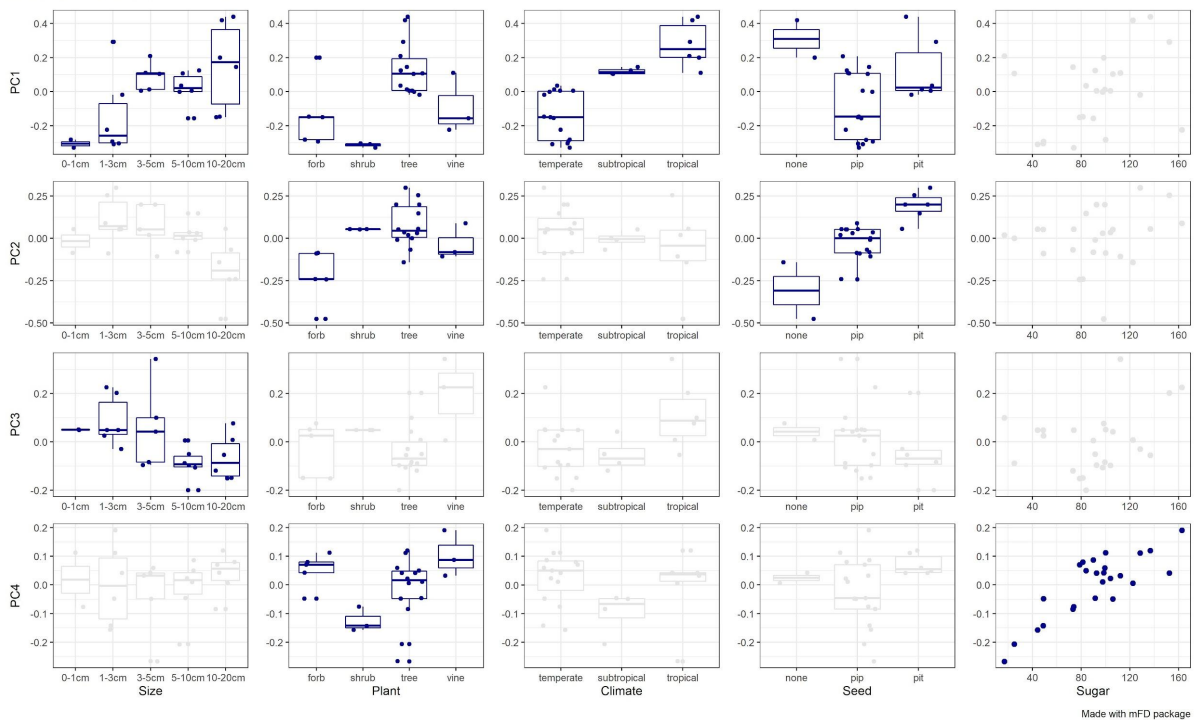


Table S5: External functions used in *mFD*

Packages name	Functionality used	Contribution in mFD package
ade4	is.euclid()	Check dist object
ape	mst (), pcoa()	compute PCoA and
betapart	beta.para.control(), functional.beta.pair(), functional.beta part.core()	Compute beta diversity indices
cluster	daisy()	compute species dissimilarity matrix
dendextend	dist_long(), is.dist()	check distance object and convert distance object to a dataframe
FactoMineR	PCA()	Compute PCA analysis
gawdis	gawdis()	Compute functional distances
geometry	convhulln()	Compute convex hull to retrieve vertices and compute FRic
ggforce	geom_circle()	Plot FDiv index
ggplot2	aes(), aes_(), aes_string(), coord_fixed(), element_blank(), element_line(), element_rect(), element_text(), expansion(), geom_abline(), geom_bar(), geom_boxplot(), geom_hline(),	Plot and save functional spaces and other plots

	geom_jitter(), geom_point(), geom_polygon(), geom_rect(), geom_segment(), geom_text(), geom_vline(), ggplot(), ggsave(), guides(), labs(), margin(), scale_color_manual(), scale_colour_gradient(), scale_colour_gradient2(), scale_fill_manual(), scale_shape_manual(), scale_size(), scale_size_manual(), scale_x_continuous(), scale_y_continuous(), theme(), theme_bw(), theme_void(), xlab(), ylab()	
ggrepel	geom_text_repel()	Aesthetics of functional plots
grid	arrow(), unit()	Draw arrows on alpha functional diversity plots
Hmisc	rcorr()	Compute correlation
patchwork	plot_annotation(), plot_layout(), plot_spacer()	Dispose individual graphs to compute output plots
reshape2	melt()	Change data format in the fuse function
rlist	list.append()	Manipulate lists
rstatix	kruskal_effsize()	

stats	as.dist(), cophenetic(), dist(), hclust(), kruskal.test(), lm(), na.omit(), reorder(), sd(), setNames()	compute euclidean distance, compute dendrogram and cophenetic distance of species, assign new names to an output object
utils	combn()	compute all possible combinations of functional axes
vegan	decostand()	Standardize