



1 **MacroTraits: a global trait data and information system for** 2 **marine benthic ecology**

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10 **Abstract.** For a long time, biological trait data have been a bottleneck in biodiversity research. Constraints of data
11 unavailability and challenging analytical implementation are still obstacles to the investigation of functional
12 biodiversity patterns. This is especially true in marine zoobenthic ecology where the use of biological traits became
13 common much later than in terrestrial and freshwater ecology. Additionally, most of trait-based marine studies have
14 dominantly been conducted in European waters while large gaps remain in other areas of the world. Therefore, this
15 paper offers a framework to fill this gap by providing the most comprehensive zoobenthic trait data compilation at the
16 global scale. Based on more than 8000 references, 1893 species of the marine macrozoobenthos are documented for life
17 history, dwelling mode, ecosystem function, habitat and biogeography through 41 traits. Next to this compilation, the
18 paper brings clarifications on research directions by means of these data within the dominant paradigms of modern
19 ecology. In particular, the dichotomous expressiveness that opposes response to effect traits (i.e., fitness components
20 versus ecosystem function) is emphasised. The data base is accessible through an R package in the repository
21 <https://doi.org/10.5281/zenodo.20555888> and that facilitates data treatment such as trait selection, cross table
22 construction and label handling.

23 24 25 **1 Introduction**

26
27 The advent of the biodiversity concept has triggered tremendous endeavours to study variations in species richness and
28 taxonomic dissimilarities in the world's biota (Gaston and Spicer, 2004). In the quest to explain numbers of species,
29 species coexistence or exclusion, organism biology has played a central role through the use of biological traits, leading
30 to the “biodiversity revolution” (Cernansky, 2017). This paradigmatic development blossomed from species community
31 ecology, a discipline considered as “the locus of exciting advances” (Simberloff, 2004). Indeed, the use of species traits
32 has given rise to functional species community ecology, nowadays the spearhead of biodiversity research. Functional
33 species community ecology bridges spatio-temporal distributions of species and traits, and ultimately enables the
34 functional characterisation of species communities through synthetic indices (“functional diversity indices”; Mouillot et
35 al., 2013; Ricotta et al., 2023). This field, highly in vogue, is strongly appealing since it can bring mechanistic
36 understanding of complex species assemblages, but, unfortunately, trait data availability and implementation remains an
37 obstacle to research advances.

38 Most of time, a biological trait is simply defined as any feature measurable in an organism (Violle et al., 2007; de
39 Bello et al., 2021). The phrasing “functional trait”, coined in the early time of functional ecology (Calow, 1987), has
40 been a puzzling concept in the literature (Violle et al., 2007). de Bello et al. (2021) concisely summarised its historical



41 relevance when trait expression impacts species fitness, what is, altogether, the ultimate goal of a biologist in search for
42 evolutionary causes and effects in living forms. Whether a trait could be considered “functional” or not is subject to
43 debate (Mlambo, 2014; Dawson et al., 2021; Susini et al., 2021). The phrase “functional trait” can be tautological
44 (Dawson et al., 2021), but, more appropriately, a trait can be considered *significantly functional* when it contributes to a
45 studied pattern (Susini et al., 2025). Depending on the addressed research objectives, different types of traits can be
46 distinguished. A direct impact on fitness is not a necessary condition to define a trait as other measurements, less or not
47 impacting the fitness of the organism on which the trait is measured, can be needed for functional diversity analysis (see
48 section 2). In marine benthic ecology, the growing interest in functional community structure has led to a boosted
49 release of trait data bases in the recent years (Chapman et al., 2019; Degen and Faulwetter, 2019; Clare et al., 2022;
50 Beauchard et al., 2023c; Lam-Gordillo et al., 2023), but still persists a lack of consensus on trait reporting (de Juan et
51 al., 2022) and gaps in data availability in many parts of the world (Costello et al., 2015).

52 In this paper, we present an extensive trait data compilation of the marine macrozoobenthos led over more than one
53 decade (2013-2026). The work started with a local focus on the European northwestern shelf as part of different
54 projects, and was progressively extended to other parts of the world once trait functionalities became discernible as
55 regards needs for ongoing researches and data availability became more and more appreciable. A trait classification is
56 firstly introduced in accordance with research directions in order to ensure a relevant scientific use of the data. Then, a
57 terminology of the documented traits provides definitions and accounts of research relevance in uni- or multivariate
58 contexts. Finally, after a description of the trait data structure and quantification, an overview shows the data
59 availability over space.

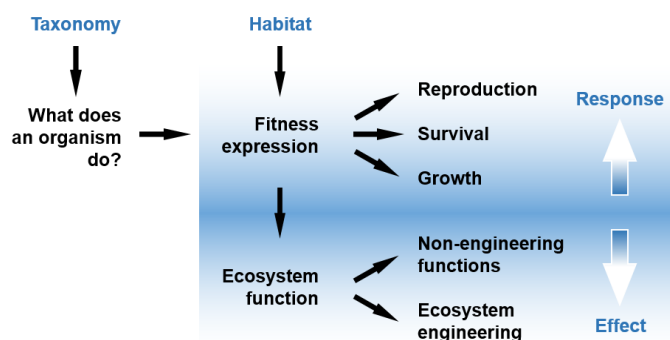
60
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62 2 Research purposes and trait data classification

63

64 Following a concise definition of a trait (see introduction), a myriad of traits can be generated as far as measurements
65 enable it, but not always with scientific pertinence. Sound scientific research is primarily induced by questions rather
66 than data availability. In modern ecology, the use of biological traits aims to test specific hypotheses related to ongoing
67 paradigms (Lavorel and Garnier, 2002; Oliver et al., 2015; de Bello et al., 2021). Some dominant paradigms that
68 currently drive functional biodiversity studies require the use of specific types of traits as described in Figure 1.

69



70
71

72 Figure 1. Organigram rationalizing the conception of biological traits as measurements on the biota. A taxon (population
73 of individual organisms sharing similar taxonomic trait modalities), under habitat forces (habitat traits), exhibit average



74 specific performances in the three fitness components (response traits), of which the expressions can lead to more or
75 less substantial effects on the ecosystem (effect traits). The vertical colour gradient underlines the possible dual nature
76 of a trait between response and effect. The use of a biological trait is necessarily paradigmatic: its relevance must be
77 based on its ability to express either response or effect (white), and less a mix of both (blue) at the risk of losing
78 functional meaning; see section 3.1 and Table 1.

79

80 *Assembly rules.* The assembly of species communities depends on four processes (Vellend, 2010): dispersal,
81 selection, drift and speciation. Every organism undergoes effects of environmental forces, both abiotic (e.g.,
82 temperature, hydrology) and biotic (e.g., predation, competition) that constrain their distributions within specific
83 environmental boundaries (niche). These forces directly act on the three components of organisms' fitness (growth,
84 survival and reproduction; Darwin, 1959; Walsh, 1996), so a habitat of specific environmental features only retains
85 species endowed with adapted trait performances (natural selection). Hence, in response to environmental forces,
86 fitness-related traits represent a first type of traits, called "response traits" (Díaz and Cabido, 2001). On the short
87 evolutionary term, response traits lie at the heart of dispersal and selection, the latter also called "environmental
88 filtering" when specifically dealing with abiotic forces (Keddy, 1992b; Stutzner et al., 1994; Townsend and Hildrew,
89 1994), and constitute the fundamental basis to explore species assembly. Within the framework of assembly rules, an
90 ultimate goal consists in identifying life-history strategies as evolutionary convergences of traits adapted to specific
91 habitats (e.g., *r*-, *K*- and *A*-strategies, or POSE concept; Southwood, 1988; Kindsvater et al., 2016). Also, the strong
92 affinity of response traits for environmental features make them primarily relevant in the development of ecological
93 indicators of species vulnerability as human-mediated pressures are also environmental forces that can mimic natural
94 ones, especially in the marine benthos (Beauchard et al., 2017). Importantly, through the ecological literature, the
95 concept of life-history strategy has been insufficiently addressed as recently stressed (Stott et al., 2024), and a more
96 flexible conception should be considered beyond the too simplistic *r*-*K* continuum. While multivariate exploration of
97 life-history strategy as a result of environmental forces has been mostly investigated in freshwater and terrestrial
98 ecology, there are only a handful of marine benthic studies (Sutton et al., 2021; Beauchard et al., 2022; Gusha and
99 McQuaid, 2025; Mendes et al., 2025; Bergagna et al., 2026).

100 *Ecosystem function.* Through fitness expression, organisms alter the abiotic and biotic components of their
101 environment through "effect traits" (Lavorel and Garnier, 2002). A typical example is a predator controlling the
102 population of a prey and maintaining an equilibrium in the ecosystem, thus contributing to ecosystem functions such as
103 fluxes of energy and materials. In this way, an effect trait participates to processes taking place beyond the life cycle of
104 the organism expressing this trait (e.g., dead shell as a microhabitat). At least two types of ecosystem functions can be
105 distinguished: (1) biomass production and dispersal, and consequent biotic interactions (mutualism, antagonism,
106 commensalism and amensalism) and (2) ecosystem engineering whereby an engineering species indirectly alter the
107 fitness of other species by modifications of the abiotic component of the environment (Jones et al., 1994). The latter is
108 particularly prominent in the marine benthos in both hard and soft bottoms where species communities ensure an
109 extraordinarily high diversity of functions beneficial to the entire ecosystem (e.g., pelagic-benthic coupling,
110 bioturbation, habitat creation; Snelgrove, 1999; Thrush and Dayton, 2002). For that reason, effect traits also indicate
111 where conservation efforts should be prioritised, especially when species ensure important services in the ecosystem
112 (Miatta et al., 2021).

113 *Ecophylogenetics.* This vast research field, investigating species community assembly based on taxonomic
114 information, has gained growing interest the last fifteen years (Cavender-Bares et al., 2009; Mouquet et al., 2012;
115 Cadotte et al., 2019). In this framework, the nested taxonomic levels of a phylogenetic tree can be considered as traits



116 whereby a distance between two taxonomic profiles can express a certain evolutionary difference between two taxa
117 (Pavoine and Ricotta, 2013). By this way, such a distance can be related to the distance induced by non-taxonomic
118 traits; while the two previous research directions imply specifically response or effect traits, ecophylogenetics can
119 proceed with any type of trait. Part of ecophylogenetic applications involve species traits for several purposes such as
120 speciation, species co-evolution, disentangling ecological from evolutionary processes or identifying labile traits.

121 *Habitat traits.* They represent another type of species descriptors that may not necessarily be specific of research
122 directions. Rather, their use takes place in particular contexts when research challenges are limited by pure data
123 exploration and theoretical predictions (Statzner et al., 1997; Usseglio-Polatera et al., 2000; Willby et al., 2000; Pavoine
124 et al., 2004). Habitat traits can be useful to mimic unrealistic in-situ contexts such as pristine state or combining
125 different faunal components requiring different sampling designs (e.g., macro- versus megabenthos). Their
126 combinations can produce theoretical versions of real habitats to explore potential response or effect trait distributions
127 (Statzner et al., 1997; Beauchard et al., 2023c). In more applied contexts, especially at the biogeographic scale, habitat
128 traits can be relevant response traits when environmental drivers of community composition are well recognized to
129 induced specific adaptations to physiological stress (e.g., salinity, intertidal elevation; Gusha and McQuaid, 2025).

130

131

132 **3 Trait relevance and terminology**

133

134 **3.1 Trait relevance in functional biodiversity studies**

135

136 The use of multiple biological traits in functional biodiversity studies is necessarily paradigmatic since fitness or
137 ecosystem function must be characterised by specific traits (Fig. 1). However, the possible dual nature of traits, in
138 expressing both (Lavorel and Garnier, 2002), may appear disconcerting in this respect, especially in the marine benthos
139 where this duality can be prominent. For instance, the ability of burrowing into sediments can express both response
140 (survival, escaping to epibenthic or demersal predators) and effect (sediment mixing and irrigation as biogeochemical
141 functions). In fact, this duality is variable as exemplified in the concept of fitness: the ultimate goal of an organism in its
142 life time is to achieve reproductive success, not ecosystem function. Translated by traits, the reproductive component of
143 fitness affects only an individual organism and its progeny, over time (age at maturity, reproductive frequency and
144 reproductive life span), through specific modes (fertilisation and offspring release) and environmentally neutral
145 numbers (e.g., fecundity as a pure response trait that only discriminates life strategies). Hence, ecosystem functions are
146 poorly expressed in most reproductive traits that are largely independent on species biomass and dwelling modes in the
147 marine benthos (McHugh and Rouse, 1998). On the contrary, growth and survival, acting in concert to ensure
148 reproductive success, are more at the basis of ecosystem function as a side effect of fitness expression, and can strongly
149 exhibit a dual nature. In the marine benthos, several traits related to growth and survival (body size and dwelling mode)
150 can express ecosystem function, especially ecosystem engineering through bioturbation (sediment mixing and
151 irrigation; Kristensen et al., 2012) and habitat creation (Thrush and Dayton, 2002). While a mix of both specific
152 response and effect traits in a same analysis can be functionally meaningless (Beauchard et al., 2023a), the use of
153 unspecific traits (i.e., dual nature) may make sense, but may also be at the expense of functional precision.
154 Conclusively, when investigating habitat occupancy, reproductive traits represent the key of response traits as they
155 provide a direct mechanism of long-term population persistence in different environments (Stearns, 1992). Other traits,
156 more related to growth and survival, can provide an important complement to explore short-term or local persistence,



157 and are indispensable to study ecosystem function, including some of them that can be considered fully independent
158 from fitness (e.g., bioturbation; see sections 3.2.36-37).

159

160 **3.2 Trait terminology and affinities for trait types**

161

162 The MacroTraits data base includes 7 habitat traits and 34 other traits (Table 1). All traits were selected when direct
163 implication in fitness expression or ecosystem function was well-established in the literature of marine biology as
164 reported below. A trait can take different states (modalities) for which a species can differently perform; see section 4
165 for technical details. So, in this section, the terminology includes a description of each trait and its modalities, including
166 labels. For each trait, arguments were provided regarding its affinities for response and effect, assessed in Table 1.

167

168 Table 1. List of the documented traits in the MacroTraits data base and their expressiveness from no affinity (empty
169 cell) to low (+) and high affinity (+++); see text (sections 3.2.1 to 3.2.41) and Figure 7 for degree of specificity. The
170 table provides a summary of trait theoretical relevance to research questions; for instance, degree of attachment is
171 highly specific to response (+++; e.g., surviving to shear stress in exposed shore habitats) but poorly expressive of effect
172 (+; e.g., can be an advantage in space occupation, without more information). Substratum depth occupancy is an
173 exception as this trait also expresses both response (e.g., burrowing as survival to predation) and effect (e.g.,
174 bioturbation). Trait ID: identifier in the data base.

175



Trait ID	Trait	Expressiveness		
		Habitat	Response	Effect
1	Biome	+++	+	
2	Salinity	+++	+	
3	Water depth	+++	+	
4	Sea floor affinity	+++	+	+
5	Substratum	+++	+	
6	Substratum depth occupancy	++	+++	+++
7	Epi-bioconstruction occupancy	+++		
8	Life span		+++	
9	Age at maturity		+++	
10	Voltinism		+++	
11	Sexuality		+++	
12	Reproductive frequency		+++	
13	Fertilisation		+++	+
14	Annual fecundity		+++	
15	Offspring type		+++	
16	Offspring size		+++	
17	Offspring protection		+++	
18	Offspring development		+++	
19	Offspring benthic stage duration		+++	
20	Offspring pelagic stage duration		+++	
21	Offspring settlement size		+++	
22	Body resistance		+	+
23	Body mass		+++	+++
24	Body length		+++	+++
25	Motility		++	++
26	Mobility		++	++
27	Rafting		+++	
28	Degree of attachment	+	+++	+
29	Sociality		+++	+
30	Epi-bioconstruction type		++	+++
31	Epi-bioconstruction extension		++	+++
32	Epi-bioconstruction size		++	+++
33	Endo-bioconstruction type		+	+++
34	Endo-bioconstruction depth		+	+++
35	Endo-bioconstruction width		+	+++
36	Ventilation/Pumping	+	++	+++
37	Sediment mixing type	+		+++
38	Bioerosion	+		+++
39	Biostabilisation	+		+++
40	Feeding type		+	+++
41	Foraging depth		+	++

176

177

178 **3.2.1 Biome**

179

180 Spalding et al. (2007) defined contours of biogeographic provinces and ecoregions within polar, temperate and tropical
 181 realms. These divisions can provide a native thermal niche when the geographic range of a species is known. In general,
 182 information on species geographic range was not accurate enough for a delineation at the ecoregion level, so
 183 occurrences were inventoried per realm at the province level, resulting in three realm modalities. However, this
 184 classification is limited to shelves (< 200 m deep) while species distributions can extend deeper, with species being
 185 exclusively found on slopes or abyssal plains. Also apart, hydrothermal vents and cold seeps (HVCS), found
 186 systematically below shelves, consist in separate systems in terms of temperature and salinity. Therefore, the modalities
 187 “Deep” and “HVCS” were added.

188

189 Modalities

190

- 191 • Polar
- 192 • Temperate
- 193 • Tropical
- 194 • Deep



195 • HVCS

196

197 3.2.2 Salinity

198

199 Salinity is the most prominent feature that makes marine habitats distinct from other aquatic environments (Remane,
200 1934). Similar to freshwater organisms, marine organisms have to cope with osmotic gradients, but in an opposite way:
201 from the external environment (salt water, high ionic concentration) to the internal environment (body, lower ionic
202 concentration) (Podbielski et al., 2022). However, marine organisms can face another physiological constraint in coastal
203 environments where salinity can vary due to freshwater inputs, especially in estuaries (Little et al., 2017). Hence,
204 tolerance to salinity variation (euryhalinity, opposed to stenohalinity) can be a stronger marker of habitat preference
205 than average salinity (Lim et al., 2025). Some migratory species transit seasonally to freshwaters for reproduction
206 (catadromous species) or foraging (amphidromous), which requires a physiological switch (Anger, 2003). Under its
207 presently coded form, salinity slightly expresses response from a stenohaline to a euryhaline profile (affinity from only
208 one to several modalities).

209

210 Modalities (in psu)

211

- 212 • Oligohaline. < 5, considered freshwater.
- 213 • Mesohaline. 5 – 18, estuarine habitats and landlocked seas.
- 214 • Polyhaline. 18 – 30, estuarine habitats, river mouths and landlocked seas.
- 215 • Euhaline. 30 – 40, typically marine.
- 216 • Hyperhaline. > 40, coastal lagoons, hydrothermal vent and cold seep brines.

217

218 3.2.3 Water depth

219

220 Water depth is a simple vertical delineation of space, but following prominent zones associated to important
221 environmental determinants of benthic life (Etter and Mullineaux, 2001). Water depth can be strongly correlated to light
222 availability and benthic primary productivity, salinity, temperature and oxygen. Very often, deeper areas undergo
223 seasonal or permanent vertical stratification whereby water masses of different densities modulate the transfer of upper
224 organic matter from planktonic and nektonic sources to the sea floor that sustain a large part of benthic biomass
225 production. Horizontally, hydrological dynamics through tidal velocity and wave energy increases toward coasts (Hall,
226 1994). In the upper part, along the intertidal gradient, organisms are periodically exposed to air, which represent another
227 type of stress and selective force of adaptation (Peterson, 1991; Tomanek and Helmuth, 2002).

228

229 Modalities

230

- 231 • Extralittoral. Terrestrial environment.
- 232 • Supralittoral. Higher intertidal zone, presence of salt water only through splash and or occasionally during storms.
- 233 • Mediolittoral. Fully intertidal.
- 234 • Shore. 0 – 20 m deep.
- 235 • Shelf. 20 – 200 m deep.
- 236 • Slope. 200 – 4000 m deep.



- 237 • Abyss. > 4000 m deep.

238

239 Remark: no species documented in the hadal zone (> 6000 m).

240

241 **3.2.4 Sea floor affinity**

242

243 By definition, the marine zoobenthos includes the species that live near the sea floor, on or in the substratum. Sea floor
244 affinity is a soft trait that informs on broad aspects of species dwelling modes at the adult stage. In general, from above
245 the substratum (hyperbenthic) to inside (endobenthic), there is a decline in mobility with many consequences (dispersal,
246 micro-habitat specificity, ecological interactions, ecosystem engineering). Also, a benthic species can perform for
247 different modalities of this trait; for instance, most crabs are mainly hyperbenthic but bury themselves for short periods
248 (occasionally endobenthic). Hence, this trait can tell whether some ecosystem engineering (e.g., biomixing,
249 bioirrigation) are continuously or intermittently sustained.

250

251 Modalities

252

- 253 • Mainly hyperbenthic
- 254 • Occasionally hyperbenthic
- 255 • Epibenthic
- 256 • Occasionally endobenthic
- 257 • Mainly endobenthic

258

259 **3.2.5 Substratum**

260

261 Substratum is a key habitat descriptor on the sea floor as it represents the environmental medium that hosts benthic life
262 (Johnson, 1971; Gray, 1974; Sebens, 1991; Snelgrove and Butman, 1994). A major feature among substrata is the soft-
263 hard gradient that strongly determines organism dwelling modes. On the one hand, hard substrata are typically
264 colonised by firmly anchored species, and rubbles offer shelters to mobile ones. On the other hand, soft substrata are
265 represented by mobile and malleable sediments that enable organisms to quickly bury or burrow. Although many
266 benthic substrata have a geological origin, an important component of sediments is biologically processed (Seibold and
267 Berger, 2017): organic matter (excrements and carrion remains) and hard body parts (carbonate shells and skeletons) are
268 mixed with various mineral components. In any case, in sedimentary environments, grain size is a strong proxy for
269 hydrodynamics (tidal current speed and wave energy) as the higher the hydrodynamic forces, the coarser the sediment
270 grains (Creutzberg et al., 1984; Barmuta, 1990; Seibold and Berger, 2017). In general, the stiller the waters, the more
271 organic-rich are the sediments (Wildish, 1977; Wildish and Peer, 1983; Snelgrove and Butman, 1994).

272 In MacroTraits, the chosen substratum modalities may not provide the most accurate description of sediment
273 compositions due to limited information in the literature and possibly the ample substratum niche in many species, but,
274 nevertheless, their semi-categorical nature follows relatively well the reference gradient proposed by Wentworth (1922).

275

276 Modalities

277

- 278 • Mud – Sandy-mud. Finest and organically richest substratum type.



- 279 • Muddy sand. Less muddy, with a substantial fraction of coarser particles.
- 280 • Sand. Dominantly mineral, often representative of surf zone and beach subject to wave action.
- 281 • Mixed gravel
- 282 • Gravel
- 283 • Mixed soft-hard. Combination of any of the previous categories with “Hard”; see below.
- 284 • Hard. Homogeneous composition of hard and relatively immobile elements from pebble-cobble to boulder and
- 285 uniform bedrock.

286

287 **3.2.6 Substratum depth occupancy**

288

289 Vertical position of an organism within the sea floor. Endobenthic occupancy is an evolutionary response to epibenthic
290 and demersal predation (Brett et al., 2002), with major effects of bioturbation on ecosystem functioning (Meysman et
291 al., 2006). This trait is complementary to the trait “Sea floor affinity” for endobenthic species (modalities “Occasionally
292 endobenthic” and “Mainly endobenthic”). It is an important trait in benthic ecology as it expresses (micro-) habitat,
293 response (sheltering from predation) and effect (bioturbation). However, this particular and unspecific expressiveness
294 makes this trait not easily relevant to identify the processes to which it contributes (i.e. response or effect) in the
295 absence of other traits.

296

297 Modalities

298

- 299 • 0 cm. Epibenthic level.
- 300 • 0 – 5 cm. Occupied by permanently buried species, but also temporarily by many mobile epibenthic species.
- 301 • 5 – 15 cm. Deeper layer than enable the construction of more sustainable burrows.
- 302 • 15 – 30 cm. Characteristic of important bioturbators.
- 303 • > 30 cm. Depths of the deepest burrowers, mostly mobile burrowing crustaceans with a few other species that have a
- 304 bulldozing effect on the sediment matrix.
- 305 • Crevice/Den. Specific to hard and mixed soft-hard substrata, and not necessarily vertical. A den can be dug in a soft
- 306 substratum below a hard layer (e.g., *Hommarus* spp.).

307

308 **3.2.7 Epi-bioconstruction occupancy**

309

310 Biogenic structures significantly occupied by the species. This trait can discriminate habitat occupancy in shallow areas
311 as most documented structures rarely occur in the deep, except corals and sponges. Its slight expression of response can
312 be expected in some modalities for the hyperbenthos through predation avoidance, and ecosystem effect in grazing
313 specialists.

314

315 Modalities

316

- 317 • None
- 318 • Terrestrial plant/Helophyte
- 319 • Mangrove



- 320 • Wrack
- 321 • Seagrass
- 322 • Kelp
- 323 • Other seaweed
- 324 • Coral/Sponge
- 325 • Maerl
- 326 • Shell

327

328 Remark: tube lawn could represent another modality, but given the high frequency of this kind of biogenic structure, it
329 is difficult to know whether a species can avoid it for any reason.

330

331 **3.2.8 Life span**

332

333 Duration of the life cycle following settlement in the sea floor. Life span is associated with environmental cycles
334 (Powell and Cummins, 1985; Gage, 1986): the longer the cycle, the longer the life in order to ensure a minimum
335 number of reproductive successes over years during which recruitment conditions are not always suitable (e.g.,
336 predation on propagules, limited food resource). So, life span does not express a precise characteristic of the life cycle,
337 but its link with recruitment success frequency makes it a prominent response trait (Grassle and Sanders, 1973;
338 Robertson, 1979; Powell and Cummins, 1985; Beukema, 1989; Montero-Serraet et al., 2018; Beauchard et al., 2022):
339 the longer the life span, the safer the adult longevity.

340

341 Modalities

342

- 343 • < 6 months
- 344 • 6 months – 1 year
- 345 • 1 – 3 years
- 346 • 3 – 10 years
- 347 • 10 – 20 years
- 348 • 20 – 50 years
- 349 • 50 – 100 years
- 350 • > 100 years

351

352 Remark. Life span and the following traits from section 3.2.9 to section 3.2.21 are descriptors of organism's ontogeny
353 and multiplication over time, most typical of life history and revealing how a population can persist in specific
354 environmental conditions (Stearns, 1992). These traits purely express response to environment, without clear effects on
355 the organism's environment (Table 1).

356

357 **3.2.9 Age at maturity**

358

359 Time before reproducing. In general, age at maturity is strongly correlated to life span, the relationship being clade-
360 dependent (Charnov, 1993). Increase in life span induces multiple cohorts of which some of the first ones might not be



361 sexually mature. In some species, the onset of reproduction is delayed such that the individual organism be large enough
362 to allocate a sufficient amount of energy into reproduction (offspring size or fecundity). In this respect, age at maturity
363 is inversely proportional to the intrinsic rate of natural increase that accounts for population recovery time following
364 disturbance (Savage et al., 2004). As to life span, age at maturity is a pure response trait expressing an important facet
365 of life strategy. When combined with reproductive allocation, a mechanistic understanding of the implications of life
366 span and age at maturity in life strategies can be found in the concept of pace-of-life syndrome that defines trade-offs
367 between reproductive schedule and success, and determined by environmental conditions (Ricklefs and Wikelski, 2002;
368 Dammhahn et al., 2018).

369

370 Modalities (in years)

371

- 372 • < 6 months
- 373 • 6 months – 1 year
- 374 • 1 – 3 years
- 375 • 3 – 5 years
- 376 • 5 – 7 years
- 377 • > 7 years

378

379 **3.2.10 Voltinism**

380

381 Except in some tropical contexts, most ecosystem processes are rhythmized by marked seasonal cycles, and most large-
382 bodied and long-lived species are perennial iteroparous that comply with seasonal dynamics to achieve reproductive
383 success. However, many small and short-lived species have found evolutionary solutions to circumvent the problem of
384 periods unfavorable to reproduction. While such periods prevent population growth through reproduction, individual
385 survival and growth remain possible. Hence, multiplying the number of generations at the expense of adult survival
386 during favorable periods is a solution to persist in fluctuating environments and maximize adaptation (San Vicente,
387 2018). Therefore, in those short-lived species, voltinism, the number of generations per year, is a trait complementary to
388 the understanding of reproductive schedules.

389

390 Modalities

391

- 392 • Semivoltine (life span > 1 year)
- 393 • Univoltine (annual life span)
- 394 • Bivoltine (2 generations per year)
- 395 • Multivoltine (> 2 generations per year)

396

397 **3.2.11 Reproductive frequency**

398

399 Reproductive schedules are central matters in life history. Traditionally, biologists consider a general dichotomy
400 (“parity”) between semelparity whereby an organism reproduces only once before dying and iteroparity when the
401 reproductive effort is spread over several events. The one or the other strategy is adopted to ensure reproductive success
402 depending on environmental assets and constraints such as population density or abiotic fluctuations (Varpe and



403 Ejsmond, 2018). Therefore, a trait simply consisting of the two modalities could express important parts of fitness.
404 However, this discrete consideration of parity may not be so relevant as more complicated reproductive schedules
405 appear in reality. While strict semelparity is frequent in small crustaceans that achieve life cycle in less than a year
406 (“annual semelparity”) or some cephalopods after a few years (“perennial semelparity”) after releasing offspring at
407 once, others extend the release over successive events before dying (i.e., over a few weeks or months). Since various
408 combinations exist from strict semelparity to pure perennial iteroparity, parity should be viewed as a continuum
409 (Hughes, 2017). In fact, using several traits in concert can implicitly account for parity. The combination of life span
410 and age at sexual maturity provides a first piece of the puzzle. Here, sexual reproductive frequency indicates whether
411 reproductive outputs are released in a relatively restricted period of the year or more continuously.

412 Asexual reproduction is another way for organisms to multiply, without the involvement of gametes or breeding
413 partners. This can be an advantage to rapidly colonise open environments or to compensate for depletions in individual
414 densities by ensuring genotype persistence in the face of extinction (Williams, 1975). Body fragmentation and
415 parthenogenesis (development of a new individual from an unfertilized oocyte) represent the principal processes.
416 Although the latter is known to occur in various clades (corals, mollusk, annelids, sipunculids, crustaceans,
417 echinoderms; Lively and Johnson, 1994), its documentation may not be exhaustive at the species level. On the contrary,
418 the former is prominent in starfish, polychaetes and cnidarians. Therefore, fragmentation was solely considered as
419 asexual reproduction.

420

421 Modalities

422

- 423 • Sexual seasonal
- 424 • Sexual continuous
- 425 • Asexual seasonal
- 426 • Asexual continuous

427

428 Remark. “Sexual seasonal” can be relatively prolonged (e.g., 6 months), the attribution of the modality being
429 determined by minimum annual variations in reproductive activity due to oscillations in external requirements (e.g.,
430 temperature, food resources...). In case of more than one generation per year (see “Voltinism”), continuous
431 reproduction can occur during the summer while a period of inactivity takes place during winter with a longer-lived
432 generation that lately reproduces. In that case, both modalities can be attributed.

433

434 3.2.12 Sexuality

435

436 Type of gametes released by an individual organism. Gonochorism, when a single type is released (sperm or ovum) is
437 the dominant mode. Some species can produce and release both types (“hermaphroditism”), in different ways:
438 homogamy when both types are permanently present and functional (“simultaneous hermaphroditism”), with or without
439 self-fertilisation, and sequential hermaphroditism when individuals born one sex and change to the opposite sex in the
440 course of the life cycle. In this latter, two modes can be distinguished: protandry when individuals are born male and
441 switch to female after additional growth that multiplies ovum production; protogyny is the switch from female to male,
442 for instance when male reproductive success is ensured by large body size that gives advantage in between-male
443 competition.

444



445 Modalities

446

447 • Gonochorism

448 • Homogamy

449 • Protandry

450 • Protogyny

451

452 3.2.13 Fertilisation

453

454 Fertilisation is the union of male and female gametes that can be released in different ways. A key expression of this
455 trait is the proximity of parental organisms on which a successful cross-fertilization depends. Through broadcasting, the
456 simplest way, gametes are released in the water column where fertilization takes place. This is the main mode on most
457 sessile or weakly mobile species; individuals can be distant when spawning, at the expense of success. Spermcasting,
458 generally overlooked (Bishop and Pemberton, 2006), is the broadcast of only spermatozoa (allosperm), free or through
459 spermatophores, that must reach the recipient organism where fertilization is either internal or external and usually
460 followed by embryonic brooding before offspring release. Spermcasting is frequent in sponges, hydroids, ascidians,
461 sessile annelids, less in some corals and bivalves. Other fertilisation modes through direct contact between mating
462 organisms include copulation (internal fertilisation) as encountered in cephalopods, most crustaceans, part of
463 gastropods, and, more rarely, external fertilisation accompanied by protection (brooding, gel or capsule). Internal or
464 external fertilisation, the necessary direct contact between breeding mates was categorised as “pairing”. This way of
465 coding fertilization can somehow express mobility, with a slight indirect expression of ecosystem function (Table 1).

466

467 Modalities

468

469 • Broadcasting

470 • Spermcasting

471 • Pairing

472

473 Remarks. Internal fertilization is regularly found in trait coding; however, as explained above, it is not discriminated
474 between spermcasting and pairing which can be related to contrasting dwelling modes. Also, self-fertilisation (in
475 simultaneous hermaphrodites) could have been an additional modality but it was omitted due to the lack of information.

476

477 3.2.14 Annual fecundity

478

479 Annual fecundity was defined as the number of offspring per mother and per year. Fecundity is a trait of central
480 importance in energy allocation trade-offs within the reproductive component of an organism’s fitness. In general,
481 fecundity is inextricably associated to offspring type (section 3.2.15) and offspring size (section 3.2.16). While
482 offspring type determines offspring size, fecundity decreases with offspring size (Stearns, 1992). Fecundity was shown
483 to be a strong determinant of bioenergetics and life history strategies in the marine benthos (Ramirez Llodra, 2002).

484

485 Modalities (number of offspring per year)

486



- 487 • $< 10^2$
- 488 • $10^2 - 10^3$
- 489 • $10^3 - 10^4$
- 490 • $10^4 - 10^5$
- 491 • $10^5 - 10^6$
- 492 • $> 10^6$

493

494 **3.2.15 Offspring type**

495

496 Among the four assembly rule processes, dispersal can be relevantly investigated by using offspring traits (McEdward,
497 1997; Pechenik, 1999; Burgess et al., 2015). First of all, offspring type is the development stage of the offspring once
498 released by parent organisms. From gamete to settled juvenile, offspring can be released under different developmental
499 stages. Eggs arise from shed gametes in the water column where fertilization takes place, while larvae are brooded
500 before being released at a more advanced stage. Juvenile, resulting from internal incubation, consists in the most
501 elaborate form, as an adult miniature. An advanced stage shortens the development before settlement on the sea floor
502 and increases survival (Strathmann, 1990). These three different offspring types may induce similar energetic costs for
503 the parents (Giangrande et al., 1994), yet some variations within egg and larval types must be considered to better
504 account for a complete developmental strategy (see sections 3.2.17 and 3.2.18).

505

506 Modalities

507

- 508 • Egg
- 509 • Larva
- 510 • Juvenile

511

512 **3.2.16 Offspring size**

513

514 Offspring size is complementary to annual fecundity, especially to determine reproductive investment (Marshall and
515 Keough, 2007). Besides, this trait is substantially variable within each offspring type as size depends on several aspects,
516 including taxonomy, species body size, development type and duration (see sections 3.2.18 to 3.2.20).

517

518 Modalities (mm)

519

- 520 • < 0.1
- 521 • $0.1 - 0.5$
- 522 • $0.5 - 1.5$
- 523 • $1.5 - 5.0$
- 524 • > 5.0

525

526 **3.2.17 Offspring protection**

527



528 When released, offspring propagules are generally more vulnerable than adult stage, undergoing physico-chemical
529 stress or predation. Therefore, offspring can be endowed with various types of protections that optimise survival until
530 settlement on the sea floor. The absence of protection is specific to numerous gametes broadcasted in the water column;
531 sometimes, broadcasting is accompanied by gel surrounding the gametes. However, gel is more typical when offspring
532 are released on the bottom, either for completing development in absence of pelagic phase, or temporarily before a
533 pelagic phase. The benthic release of egg capsules is frequent in gastropods, and combination of encapsulated eggs
534 within a jelly matrix is typical of nudibranchs. Burying into the sediment also ensures a matrix protecting against
535 epibenthic and demersal threats (e.g., horseshoe crabs, lugworms). Direct parental cares can be either larval bearing
536 such as in decapods or external egg or larval brooding (tubicolous worms, some snails). Finally, internal development
537 that lead to the release of juvenile represent the most achieved form of protection to ensure optimal offspring survival.

538

539 Modalities

540

- 541 • None
- 542 • Gel
- 543 • Capsule
- 544 • Burying
- 545 • Bearing/Brooding
- 546 • Internal

547

548 **3.2.18 Offspring development**

549

550 Offspring development provides a key expression of ontogeny and more consequently life-history strategy (Vance,
551 1973; Strathmann, 1977; McHugh and Rouse, 1998). In the literature, trait coding usually overlooks this important
552 aspect through simplistic trait coding such as benthic/pelagic or direct/planktotrophic/lecithotrophic. However, early
553 works had already revealed the more complicated reality in the marine benthos (Fauchald, 1983; Jablonski and Lutz,
554 1983; Bhaud and Duchêne, 1996). An essential fact is the possible combination of benthic and pelagic phases within a
555 same development called “mixed development” (Jablonski and Lutz, 1983). Below, a synthetic description is provided
556 to each modality.

557

558 Modalities

559

- 560 • Planktotrophic. Purely pelagic, feeding on planktonic organisms.
- 561 • Lecithotrophic. Either benthic or pelagic, non-feeding.
- 562 • Mixed planktotrophic. Benthic phase, with parental cares or not, followed by pelagic feeding phase.
- 563 • Mixed lecithotrophic. Benthic phase, with parental cares or not, followed by pelagic non-feeding phase.
- 564 • Internal. Incubated within the adult, necessarily released as juvenile.

565

566 Remark. Some species exhibit a developmental polymorphism whereby planktonic or benthic offspring on the one
567 hand, and feeding or non-feeding on the other hand, are produced, likely depending on environmental conditions
568 (“poecilogony”; Chia et al., 1996). In that case, all possible types of development were considered.

569



570 **3.2.19 Offspring benthic stage duration**

571

572 In the previous section, the need for separating benthic and pelagic offspring developmental phases naturally leads to
573 phase durations as two complementary traits. Benthic stage duration indicates the developmental time under parental of
574 other protective forms on the sea floor; there is no such a phase in directly broadcasted gametes in the water column
575 (modality “Null”).

576

577 Modalities (days)

578

579 • Null

580 • < 15

581 • 15 – 30

582 • 30 – 60

583 • 60 – 180

584 • > 180

585

586 **3.2.20 Offspring pelagic stage duration**

587

588 This trait, complementary of the previous one, indicates the offspring development time in the water column. While it is
589 quite predictable in some clades such as bivalves (ca 3-4 weeks), it can be highly variable in some others such as
590 annelids that exhibit various developmental types, but also in corals, that, although less variable in development with a
591 pelagic phase in most species, can delay metamorphosis and settlement until finding a suitable habitat; this phase is
592 called “larval competence” and can extend from a few hours to several months in a same species (Pechenik, 1990;
593 Gleason and Hofmann, 2011).

594

595 Modalities (days)

596

597 • Null

598 • < 15

599 • 15 – 30

600 • 30 – 60

601 • 60 – 180

602 • > 180

603

604 **3.2.21 Offspring settlement size**

605

606 This trait, generally not encountered in the literature, can be complementary to investigate ontogeny, and especially
607 offspring growth across various pelagic stage durations in broadcasting species.

608

609 Modalities (mm)

610

611 • < 0.5



- 612 • 0.5 – 1.5
- 613 • 1.5 – 5.0
- 614 • 5.0 – 10.0
- 615 • 10.0 – 20.0
- 616 • > 20.0

617

618 3.2.22 Body resistance

619

620 This is a subjective measurement to approximate resistance to physical damage, as encountered sometimes in the
621 literature. From an evolutionary perspective, body resistance may not be always associated to survival (e.g., sessile and
622 hard shell versus soft-bodied and highly mobile organisms) while stony organisms exhibit systematic habitat
623 opportunity to fouling ones. Therefore, this trait may equally express both response and effect without clear indication.

624

625 Modalities

626

- 627 • Gelatinous (e.g., some oweniid worms, impossible to remove from their tube without damaging them)
- 628 • Brittle (e.g., requiring care to be manipulated such as tellinid bivalves)
- 629 • Intermediate (wide range of organisms, from some degree of softness to relatively firm; e.g., intermediate to large-
630 bodied worms and shrimps)
- 631 • Firm/Hard (can be manipulated without cares such as large crustaceans, cephalopods or relatively thick shellfishes)
- 632 • Stony (necessarily endowed with very hard or thick shell, typically oysters)

633

634 3.2.23 Body mass

635

636 Body size is the most prominent feature of an organism. Body mass is a first way to quantify it and was documented
637 here in terms of ash-free dry mass (AFDM). This is the best quantification of the amount of living tissues in an
638 organism. Besides, half of AFDM is generally the carbon content of the organism's body (Salonen et al., 1976; Clarke,
639 2008). Body size is associated to many biological and ecological aspects, from individual organism to ecosystem. While
640 it cannot be specifically related to life strategies (Strathmann and Strathmann, 1982; Warwick, 1984), implications in
641 population density (White et al., 2007; Yamanaka et al., 2012) and carbon fluxes (Blanchard et al., 2017) are more
642 explicit for this trait. AFDM was recorded when directly available, otherwise, if available as wet or dry mass,
643 conversion into AFDM was done according to Ricciardi and Bourget (1998).

644 The quantitative information carried by body size makes the use of this trait in concert with others a necessity to
645 relevantly express engineering functions involving biogeochemistry (Beauchard et al., 2023c). Hence, body size,
646 including mass and length (next section), is involved in so many processes that it fully expresses both response and
647 effect. However, possible expressiveness in species community analysis might not be generally clear, especially as
648 regards selection in which growth rate can make more sense (Beauchard et al., 2022).

649

650 Modalities (g AFDM)

651

- 652 • < 0.001
- 653 • 0.001 – 0.010



- 654 • 0.010 – 0.100
- 655 • 0.100 – 1.000
- 656 • 1.000 – 10.000
- 657 • > 10.000

658

659 **3.2.24 Body length**

660

661 Body length, as a second quantification of body size, was considered as the length of the prominent part of the
662 organism's body, avoiding appendices of negligible mass such as palps or antennae and of which the size can exceed the
663 size of the remaining part. Note that the correlation between body length and mass can be limited, which makes length a
664 complementary trait. This is especially the case for biogenic structures such as in corals.

665

666 Modalities (cm)

667

- 668 • < 1
- 669 • 1 – 3
- 670 • 3 – 10
- 671 • 10 – 20
- 672 • 20 – 50
- 673 • > 50

674

675 **3.2.25 Motility**

676

677 Motility is the way of moving at the adult stage, and, with sea floor affinity, substratum depth occupancy and mobility
678 (next section), an important descriptor of dwelling mode. It roughly indicates whether the organism moves or not, and,
679 if motile, an indication on the organism's ecology as its physical relationship with the substratum. Like mobility,
680 motility largely contributes to both fitness components and ecosystem function.

681

682 Modalities

683

- 684 • Sessile. Fixed on or in the substratum (e.g., mussel).
- 685 • Tubicolous. Lives in a biogenic tube, possible moves within the tube (e.g., spionid worms, some amphipods).
- 686 • Crawler. No specialized appendages for moving (e.g., worm, snail, slug).
- 687 • Walker. Moves with appendages (e.g., most crustaceans).
- 688 • Swimmer. Substantial ability to swim (e.g., squid), not exclusively (e.g., lobster).

689

690 **3.2.26 Mobility**

691

692 Mobility is closely related to motility, at least in distinguishing sessile-immobile from non-sessile and fast moving
693 species. More than motility, mobility is the most concise way to express adult dispersal ability through foraging,



694 migration or predator avoidance. It is particularly useful for building composite trait indicators of ecosystem functions
695 in which it integrates time within the process of interest (Swift, 1993; Supplement S3).

696

697 Modalities

698

699 • Immobile (necessarily sessile)

700 • Limited (e.g., many bivalves and tubicolous worms)

701 • Slow (most crawling organisms)

702 • Fast (at least small swimming species)

703 • Very fast (large swimming species, but also large walking ones; e.g., crabs)

704

705 3.2.27 Rafting

706

707 Whatever its motility, benthic organisms can sometimes disperse over very long distances by means of floating objects.

708 This ability, called “rafting”, is an important dispersal mechanism and therefore a clear response trait (Thiel and Gutow,

709 2005a; Thiel and Gutow, 2006). Rafting has been observed in many species, occasionally or frequently (Thiel and

710 Gutow, 2005b). Debris or any substratum of human origin are especially involved in rafting and strongly contribute to

711 non-native species invasions (Rech et al., 2025).

712

713 Modalities

714

715 • Not reported

716 • Likely/Occasional

717 • Frequent

718

719 Remark. “Not reported” does not exclude possible rafting ability; this includes either species with no obvious ability

720 (e.g., burrowing fauna) or absence of tangible evidences.

721

722 3.2.28 Degree of attachment

723

724 Various abiotic and biotic forces constrain the dwelling modes of animal life on the sea floor. Hydrodynamics is a

725 prominent physical constraint with which highly mobile species can easily cope. By contrast, sessile or slowly motile

726 organisms exposed to strong water movements must strongly anchor to the substratum, permanently with cement or

727 temporarily with adhesive film or suckers (Flammang, 1996; Dodou et al., 2011). Except on mobile sand that requires

728 some degree of mobility, soft sediment habitats do not undergo such physical constraints, so most hosted species are

729 freely sessile or motile; some exceptions include anemones that anchor on buried shell or stone (e.g., *Cylista*

730 *trogodytes*). Degree of attachment, as a dwelling function, surely contributes to fitness, but is also indicative of

731 microhabitat; besides, the strong attachment through cementation or perforation can have engineering effects on the

732 substratum (e.g., oysters, limpets).

733

734 Modalities

735



- 736 • Null (hyperbenthic or free in soft sediment)
737 • Slight (grabbed, not necessarily attached or slightly attached)
738 • Strong (generally on hard substrata)

739

740 **3.2.29 Sociality**

741

742 Sociality is defined as the propensity to which individual organisms of a same species aggregate (Jacoby et al., 2022).
743 This has important implications in habitat occupancy (Webb et al., 2009) and sea floor biogenic engineering (Sebens,
744 1991). Sociality is particularly critical to reproduction and dispersal (Mazzei and Rubenstein, 2021), limited by
745 fertilization success that decreases with individual organism isolation (Levitan, 1995). The adopted coding especially
746 reflects this last point, opposing the modalities “solitary” to “aggregated” while “colonial” refers to individual colonies
747 such as encountered in Cnidaria and composed of different interbreeding genotypes. Therefore, sociality is mainly a
748 response trait, but when sessile and depending on morphology, it can also express ecosystem function (see following
749 sections).

750

751 Modalities

752

- 753 • Solitary
754 • Aggregated
755 • Colonial

756

757 Remark. In colonial species, it is always specified whether individual colonies are solitary or aggregated.

758

759 **3.2.30 Epi-bioconstruction type**

760

761 According to Ingrosso et al. (2018), “bioconstruction” refers to tridimensional structures rising above the sea floor. In
762 the present and following sections, we separate epi- from endo-bioconstruction as structures engineered by benthic
763 species above and below the substratum surface, respectively. The traits described in sections 3.2.30-39 were firstly
764 used in Beauchard et al. (2023c) and strongly express ecosystem functions. Epi-bioconstruction types are either
765 biogenic such as in corals and shelly species or engineered based on abiotic elements such as mound or tube from
766 sedimentary materials. This is the only trait that includes morphological aspects for obvious effects of habitat creation
767 (Roberts et al., 2006); however, morphological adaptations to environmental conditions can express response (Darling
768 et al., 2012).

769

770 Modalities

771

- 772 • None
773 • Mat
774 • Mound
775 • Shell
776 • Tube/Tubular protrusion
777 • Stalk/Feather



778 • Protuberance/Lobe

779 • Arborescence

780

781 **3.2.31 Epi-bioconstruction extension**

782

783 This trait describes how the type of epi-bioconstruction spreads above the substratum. The more complex the
784 bioconstruction, the higher the potential in habitat opportunities for various organisms (Buhl-Mortensen et al., 2010;
785 Kovalenko et al., 2012).

786

787 Modalities

788

789 • None

790 • Simple. No noticeable 3D-complexity (e.g., tube, or flat or spherical shell).

791 • Horizontally flattened. Large coverage, no prominent erected structure (e.g., continuous mat or dense and
792 homogeneous tube lawn).

793 • Horizontally erect. Large coverage, with prominent vertical structuration (e.g., oyster or coral reef).

794 • Vertically complex. Vertical structuration, basic degree of morphological complexity (e.g., shelly reef).

795 • Vertically highly complex. Vertical structuration, high degree of morphological complexity (e.g., arborescent coral
796 structure).

797

798 **3.2.32 Epi-bioconstruction size**

799

800 Largest dimension between horizontal and vertical extent. When present, epi-bioconstructions are generally produced
801 by sessile species with variable degrees of aggregations. Therefore, this trait does not always capture the size of the
802 individual organism, but the size of its effect. For instance, in the case of a large aggregation of mussels, the
803 corresponding modality is the extent of the reef rather than the individual shell length (e.g., > 50 cm).

804

805 Modalities (cm)

806

807 • < 1

808 • 1 – 3

809 • 3 – 10

810 • 10 – 20

811 • 20 – 50

812 • > 50

813

814 **3.2.33 Endo-bioconstruction type**

815

816 Type of bioconstruction within the substratum matrix. While endo-bioconstructions exist in hard substrata (Bromley,
817 1978), they are usually more common in soft sediments. Endo-bioconstructions can express different effects such as
818 biogeochemical through bioirrigation (Kristensen et al., 2012) and habitat creation (Woodin, 1978; Lackschewitz and



819 Reise, 1998; Anker et al., 2005; Callaway, 2006; Tseng et al., 2019). Burrows in sedimentary substrata can be
820 permanent or semi-permanent.

821

822 Modalities

823

824 • None/Surficial

825 • Rugosity/Pit. Exclusively in hard substrata.

826 • Chimney/Funnel

827 • Tube. Engineered biological or mineral materials.

828 • IJ-shaped burrow

829 • UY-shaped burrow

830 • Branched burrow

831 • Anastomosed burrow

832

833 Remark. This trait is of utmost importance when investigating bioirrigation. All the listed modalities may not be
834 relevant in that case. The flushing potential of a burrow is increased with more than one opening (otherwise, closed;
835 Kristensen and Kostka, 2005). Changing the listed modalities above enables a relevant way to express it (same order
836 than above): Null/Null/Closed/Closed/Closed/Open/Closed/Open (Supplement S1).

837

838 **3.2.34 Endo-bioconstruction depth**

839

840 Maximum vertical extent of endo-bioconstruction. While substratum depth occupancy (section 3.2.6) considers the
841 deepest layer where the upper part of the organism can occur, endo-bioconstruction depth takes the entire extent of the
842 bioconstruction, so the two traits can differ.

843

844 Modalities (cm)

845

846 • None/Surficial

847 • 0 – 5

848 • 5 – 15

849 • 15 – 30

850 • > 30

851

852 **3.2.35 Endo-bioconstruction width**

853

854 Size of the transversal section of the endo-bioconstruction. It is usually related to inhabitant's body width (Kristensen
855 and Kostka, 2005). Bioirrigation and habitat potentials increase with width.

856

857 Modalities (mm)

858

859 • None



- 860 • < 5
- 861 • 5 – 10
- 862 • > 10

863

864 3.2.36 Ventilation/Pumping

865

866 Ability to induce water transports into soft substrata. It is particularly useful to investigate bioirrigation potential. As
867 experimental water flux measurements are available only for a few soft sediment species, this trait expresses solely the
868 presence of ventilation/pumping ability through sea floor affinity and motility, independently of other traits such as
869 body size or burrowing depth. Information is not directly available for all burying species, but modalities can be
870 attributed based on strong assumptions. “Null” was systematically attributed to hard substratum, epi- or hyperbenthic
871 species. Species attributed “High” were generally documented (e.g., lugworms, mudshrimps), especially for deeply
872 buried suspension feeders (Kristensen 1981, Christensen et al. 2000, Kristensen and Kostka 2005, Kristensen et al.
873 2012). “Potential/Low” means either observed or supposed given the necessary oxygen demand when deeply buried
874 (Lindroth, 1941) or induced through local pore water transports when sediment particles are displaced by organism
875 movements, especially near the sediment-water interface (Aller, 1982; Kristensen, 1988; Berg et al., 2001; Volkenborn
876 et al., 2012; Volkenborn et al., 2016). Besides, this is why the term “bioturbation”, often wrongly used, implies that
877 sediment particle reworking is necessarily accompanied by water diffusion (Kristensen et al., 2012). Hence,
878 “Potential/Low” indicates rather passive bioirrigation whereas “High” holds for more active organism movements to
879 generate water fluxes, generally through permanent or semi-permanent burrows.

880

881 Modalities

882

- 883 • Null
- 884 • Potential/Low
- 885 • High

886

887 3.2.37 Sediment biomixing type

888

889 Specific to soft substratum habitat, sediment biomixing is the reworking of sediment particles through organism
890 movements, ingestion and defecation (Kristensen et al., 2012). It is a clear effect trait closely related to dwelling mode,
891 especially organism motility, sediment depth occupancy and mobility that condition sediment particle local and non-
892 local displacements (François et al., 1997). In general, a meaningful use of this trait makes sense in combination with
893 other traits such as pioneered by Swift (1993) and further developed by others (Solan et al., 2004; Queirós et al., 2013).

894

895 Modalities

896

- 897 • None
- 898 • Diffusion
- 899 • Upward conveying
- 900 • Downward conveying
- 901 • Regeneration



902

903 Remark. One biomixing type does not necessarily exclude another one; for instance, a large crab can induce substantial
904 biodiffusion when walking, while regenerating the sediment matrix when burying itself.

905

906 **3.2.38 Bioerosion**

907

908 Bioerosion is the alteration of hard substrata by organisms through boring, abrasion or biochemical effects (Trudgill,
909 1987, 1988). This is a prominent effect trait that enables the construction of refuges such as pits or deep burrows (e.g.,
910 urchins, annelids, sipunculids, bivalves), or destruction through firm anchoring (e.g., corals, sponges) (Bromley, 1978).

911

912 Modalities

913

914 • None

915 • Scraping (e.g., barnacle fixation, snail or limpet grazing)

916 • Scarring/Perforating (e.g., limpet home scar, sponge perforations)

917 • Boring (e.g., urchin pits, pholadid burrow)

918

919 **3.2.39 Biostabilisation**

920

921 This trait is specific to soft sediments where some species, through morphological or aggregative aspects, can prevent
922 substratum erosion from water hydrodynamics. Typical examples appear through organism aggregations, including
923 shelly structures such as shallow mussel or oyster beds (Meyer et al., 1997; Meadows et al., 1998; Ysebaert et al., 2019)
924 and tube lawns (Young and Rhoads, 1971; Luckenbachs, 1986; Friedrichs et al., 2000). Free shells from free species
925 (e.g., bivalves, snails), alive or dead, can also have a stabilizing effect on sediments (Cheng et al., 2021), but it depends
926 on local organism density, which requires field expertise. Therefore, biostabilisation ability was attributed when well
927 documented (modality “High”) or likely (“Low”) when organism aggregation was not systematic.

928

929 Modalities

930

931 • Null

932 • Low

933 • High

934

935 **3.2.40 Feeding type**

936

937 Historically, feeding type has been one of the most studied traits given the important role of trophic relations in
938 ecosystem structuring (Walker and Bambach, 1974). Also, in the second part of the twentieth century, human-induced
939 organic disturbances were dominant drivers of benthic community structures and successions, and represented a central
940 research focus in marine coastal waters (Pearson and Rosenberg, 1978; Rhoads et al., 1978; Diaz and Rosenberg, 1995;
941 Levinton and Kelaher, 2004). Effects of organic enrichment on sea floor functioning are now well evidenced, especially
942 their propensity to favour deposit feeding. Hence, feeding type, as a single trait or combined with a few others related to
943 dwelling mode, was considered a trait of utmost importance in benthic ecology. Nowadays, it should be less the case



944 given the multiplicity of research directions that require multiple traits (e.g., evolutionary aspects, life history,
945 functional diversity) and the numerous reasons according to which feeding type, besides organic disturbance, is
946 generally a poor predictor of species persistence in habitats undergoing various regimes of physical disturbance or stress
947 (i.e., plurality of fitness components). Nevertheless, feeding type remains an important effect trait, often indispensable
948 when focusing on ecosystem functions.

949 Technically, a major issue has been the attribution of specific and meaningful categories to species due to the
950 constraint of omnivory. Indeed, seasonality and spatial heterogeneity limit feeding specialization (Clarke, 1988; Herman
951 et al., 1999; Jumars et al., 2015). A necessary simplification is possible and lies in the close relation between diet and
952 feeding mechanism that can be identified on organism anatomy (Yonge, 1928), which has given rise to influential works
953 on trophic guilds (Fauchald and Jumars, 1979; Gaston, 1987). Here, we considered the most general feeding types
954 encountered in the literature (essentially since Walker and Bambach (1974); see modalities below). Omnivory, an
955 important aspect in benthic studies, was not considered as a separate modality. In fact, the selected modalities already
956 express a certain degree of omnivory. Deposit feeding consists in ingestion of organic materials in deposited sediments
957 originating from multiple sources and of varying state of decomposition, but also the associated micro-organisms
958 (Lopez and Levinton, 1987; Herman et al., 1999). Suspension-feeders prey upon particles in the water column, which
959 can include phytoplankton, zooplankton, decaying planktonic materials or re-suspended deposit, and whereby particle
960 selection can passively or actively operate to exclude low quality or irrelevant materials (Ward and Shumway, 2004).
961 Carnivory and scavenging are difficult to separate as both consist in consuming live or dead animal materials that can
962 remain alike in the marine environment (Beasley et al., 2012), and have been usually grouped within the same category
963 (Walker and Bambach, 1974; Fauchald and Jumars, 1979; Ambrose, 1984).

964 To summarise, the first four modalities of feeding type can indicate the origin of food resource (water column or
965 sea floor), the liability of the material (deposit or living) and the trophic level (herbivory or carnivory). Among the two
966 last ones, parasitism (Pa) was represented by a few species, either as exclusive modality (e.g., on anemone or sponge) or
967 complementary of another modality (e.g., temporary ectoparasitism on fish). Lastly, “Sy” indicates obligatory
968 association with endosymbionts; this mainly includes shallow corals and giant clams (zooxanthellae, zoochlorellae),
969 some slugs (chloroplasts in the gut), and hydrothermal vent species and shipworms (bacteria).

970

971 Modalities

972

- 973 • De (deposit feeding)
- 974 • Su (suspension feeding)
- 975 • HeGr (herbivory – grazing)
- 976 • CaSc (carnivory – scavenging)
- 977 • Pa (parasitism)
- 978 • Sy (symbiont-associated)

979

980 Remarks. A species can be attributed more than one modality (e.g., very often, De and Su). Considering the modalities
981 as a basis of specialization (at least, one cannot do better), omnivory appears for species that are attributed at least two
982 modalities; then, the total number of attributed modalities can express the degree of omnivory. Also, suspension
983 feeding, combined with body mass, can be used to quantify biodeposition, an important engineering function of the sea
984 floor in pelagic-benthic coupling (Graf and Rosenberg, 1997; Gili and Coma, 1998).

985



986 **3.2.41 Foraging depth**

987

988 The vertical position of an organism within the substratum is not always indicative of the origin of food resource
989 (Pearson, 2001). So, complementary to feeding type, foraging depth indicates the spatial origin of food resource and can
990 inform on the transfer of fresh organic materials into the substratum. This regards mainly deposit feeding and carnivory
991 in soft substrata whereby the same food type can be consumed at various sediment depths. Hence, the modality “De” in
992 feeding type (deposit feeding) can be subdivided into surface (0 cm) and sub-surface (> 0 cm) deposit feeding; besides,
993 deep sub-surface deposit feeding may suggest the consumption of organic matter of low quality compared to the high
994 quality of planktonic material freshly deposited on the sediment surface. Also, defecation following sub-surface
995 carnivory provides labile organic inputs (Gontikaki et al., 2011).

996

997 Modalities (cm)

998

999 • 0

1000 • 0 – 5

1001 • 5 – 15

1002 • > 15

1003

1004

1005 **4 Trait quantification**

1006

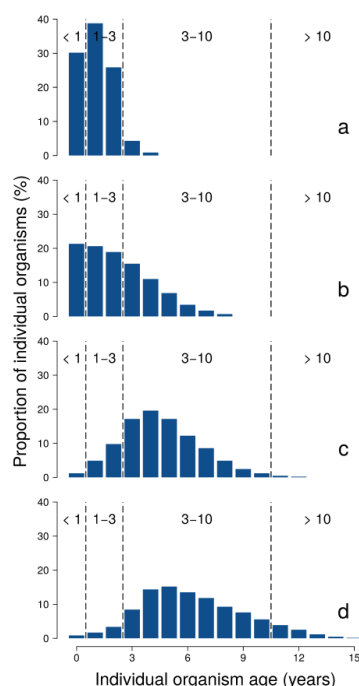
1007 In situ trait measurement is always laudable, but it is more idealistic than realistic when working on many species.
1008 Therefore, a priori or a posteriori documentation from the literature is generally required. Historically, in marine studies,
1009 Swift (1993) pioneered biological trait quantification by attributing discrete scores to species as a degree of affinity. In
1010 the meantime, Chevenet et al. (1994) popularized the fuzzy coding technique in freshwater ecology, an improved
1011 version of complete disjunctive coding (Tenenhaus and Young, 1985), more elaborate and relevantly designed for
1012 multivariate ordinations. In MacroTraits, species were attributed 1 when their affinity for a given trait modality was
1013 likely, 0 otherwise. By this way, a fuzzy coding can be implemented; for example, the scoring profile of a suspension-
1014 feeding species for feeding type (De/Su/HeGr/CaSc/Pa/Sy) is 0/1/0/0/0/0 and remains as such following fuzzy coding;
1015 for a deposit and suspension-feeding species, the profile is 1/1/0/0/0/0 and becomes 0.5/0.5/0.0/0.0/0.0/0.0, and
1016 generally, such that scores sum to 1 within any trait profile. Very often, in existing trait data sets, raw scores can vary
1017 between 0 and 3, or even 0 and 5. However, the attribution of scores greater than 1 requires a strong background of
1018 organism biology and a very detailed literature, conditions rarely met. For instance, some traits are variable over time
1019 (e.g., large body length in long wintering generation, small in short summer generations) or space in species distributed
1020 over large geographic extents whereby local biogeographic influences can exacerbate variations in population biology
1021 (e.g., growth rate: early sexual maturity and short life span in warm waters, later maturity and longer life span in cold
1022 ones). Even basic habitat descriptors like sediment type can induce noticeable variations on important traits of dominant
1023 species such as substratum depth occupancy (Enderlein, 2004; Gilbert et al., 2021; Wiesebron et al., 2021). In fact, in
1024 many data sets providing 0-3 scorings, score distributions are dominated by values 0 and 3, making them similar to 0-1
1025 through fuzzy coding. This underlines the fact that trait data designers do not escape to those inherent constraints of
1026 fuzzy coding when attempting to establish precise trait profiles. While the method of Chevenet et al. (1994) truly
1027 enables the expression of within-species trait variations (e.g., 0/0/2/5/3/1 for body size), current data availability in the



1028 marine benthos is unrealistic for this purpose. Therefore, in MacroTraits, we opted for simplification with a scoring
1029 limited to 0-1 as in Chevalier et al. (2025); its reliability is exemplified in Appendix A. Note that complete disjunctive
1030 coding, a more restrictive way of coding, was successfully used in Beauchard et al. (2022).

1031 In general, scoring qualitative traits (e.g., offspring type, Egg/Larva/Juvenile) is straightforward while it can be less
1032 intuitive for quantitative traits (e.g., body size, life span, fecundity...). As variability is naturally inherent to population
1033 biology, the quantification of a trait cannot be fully objective when working on multiple traits and species. The
1034 attribution of discrete modality scores has been so far the least bad solution, even though unknown associated
1035 uncertainties seem inevitable. Thus, a certain degree of subjectivity, which can vary among trait data designers, is
1036 generally accepted in fuzzy coding. In the absence of clear rule, one can advocate for a principle: when studying a
1037 species pool, a trait is technically worth to consider if the modalities within the trait are variable enough over the pool.
1038 Therefore, trait profiles among species must differ as much as possible. Based on life span, Figure 2 exemplifies how a
1039 parsimonious scoring enables the distinction of different species. Mortality occurs in both juvenile and adult individuals
1040 for various and unexpected reasons (e.g., predation, disease, disturbance), unpredictable over space and time, and that
1041 can be differently experienced across cohorts. Thus, in absence of unpredictable mortality and by excluding outliers, the
1042 last cohort indicates a potential life span beyond age at sexual maturity. By considering maturity within 1-3 years in the
1043 four different cases in Figure 2, score profiles can be unambiguous in some cases (0/0/1/0 or 0/0/0/1; Fig. 2b and 2d),
1044 and multiple score attribution may be more careful in other cases (0/1/1/0 or 0/0/1/1; Fig. 2b and 2d). When multiple
1045 scores are attributed, the flexibility of fuzzy coding ensures an average scoring. In MacroTraits, this way of scoring was
1046 applied either to cope with natural uncertainty or under clear evidence of human pressure (Ramón and Richardson,
1047 1992; Fallon et al., 2013). Additionally, as previously stressed, the attribution of several categories can be due to
1048 biogeographic implications; for instance, life span in *Macoma balthica* varies from 1-3 to 20-50 years depending on the
1049 population from temperate to Arctic waters (Gilbert, 1973); hence, for local investigations, the trait profile must be
1050 accordingly adjusted.

1051



1052

1053

1054 Fig. 2. Virtual examples of quantitative trait coding. From a to d, distributions of individual organism ages in four
1055 populations, all reaching maturity within 1-3 years. The trait is composed of four modalities: < 1, 1-3, 3-10 and > 10
1056 years. a) Many individuals reach the third cohort (2-3 years) before massive mortality at 3 years, but some individuals
1057 survive until 4 years; a profile of 0/1/1/0 is attributed to the species. b) As a large part of the population reaches the third
1058 modality without reaching the fourth one, a profile of 0/0/1/0 is attributed without ambiguity. c) 3-10 years also seems
1059 to make sense, so 0/0/1/0 can be attributed; however, either the sampling period failed in catching the oldest cohorts or
1060 human exploitation or disturbance limits individual growth; therefore, 0/0/1/1 may be more careful. d) Cohorts older
1061 than 10 years are clearly discernable; 0/0/0/1.

1062

1063 When detailed distributions of quantitative traits were not available, information was derived from explicitly
1064 documented ranges or single values, or estimated according to the data source. In few cases, in short-lived clades,
1065 absence of age data was compensated by estimations based on visual analysis of size distribution. More generally,
1066 missing information was dealt with taxonomic proximity, mostly the genus level. In traits highly related to phylogeny
1067 such as offspring type or development, and more subjective traits such as body resistance, epi- and endo-
1068 bioconstruction types, data were referred to books of general biology when the information was not explicitly provided
1069 by specific sources.

1070 Fuzzy data are organised at two levels: numerical scores are attributed to biological modalities, themselves nested
1071 within traits. The R package “fuzR” was built to easily handle fuzzy data, and hosts the MacroTraits data base (see next
1072 section). Trait data are typically used through a species × traits matrix (i.e., autecology × comparative ecology)
1073 according to Keddy (1992a). In MacroTraits, since the biological data are provided in a long format table and given the
1074 heavy vertical partition of fuzzy data matrices (i.e., trait as blocks of modality-columns), the function “fuz.tab()”



1075 enables the conversion from long to wide format (Supplement S1); it returns a species × trait modalities matrix and a
 1076 data frame listing the trait and modality labels that enables easy data manipulation.

1077

1078

1079 **5 Data overview**

1080

1081 The MacroTraits data base is available at <https://doi.org/10.5281/zenodo.20555888>, and organised in four separate
 1082 objects (Fig. 3). The first one is a taxonomic table with 1893 species as rows and columns as 13 taxonomic levels,
 1083 starting from subkingdom (attributing Eumatozoa or Porifera), followed by six successive clades, and continuing from
 1084 phylum to species (Fig. 3a). The second one is a long-format table with the following fields: species, trait ID, modality
 1085 ID, score and reference ID (Fig. 3b). The third one is the list of trait and modality labels (Fig. 3c). The fourth one
 1086 contains the species occurrences among biogeographical units that include realm, biome and province according to
 1087 Spalding et al. (2007) (Fig. 3d). The characteristics of each biogeographic unit are listed in a fifth object (Fig. 3e). The
 1088 last one is the list of 8280 references indexed in the second and fourth tables (Fig. 3f). It contains reference ID, the
 1089 reference itself and the type of reference: peer-reviewed article (7410), proceedings (72), book (196, including book
 1090 chapter), thesis (366; BSc, MSc or PhD), other academic dissertation (13), report (209) or website (14). For the sake of
 1091 authenticity and transparency, reference to websites or existing data sets were avoided as much as possible in order to
 1092 provide original sources. As a result, articles, books, theses and reports represent 98 % of the record documentation (72,
 1093 16, 7 and 3 %, respectively).

1094

Subkingdom	Clade1	Clade2	Clade3	Clade4	Clade5	Clade6	Phylum	Class	Order	Family	Genus	Species	AphiaID	Realm	Biome	Province	Longitude	Latitude
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Arctic	Temperate	1	-83.908	70.543
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	2	7.235	60.120
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	3	-10.980	34.527
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	4	16.528	36.467
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	5	-68.123	44.764
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	6	-88.277	30.166
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	7	35.180	43.948
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	8	140.073	50.710
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	9	127.414	30.812
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	10	-142.393	52.475
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	11	-112.780	28.093
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	12	-77.025	17.772
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	13	-52.128	10.959
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	14	-35.452	-11.344
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	15	-5.719	-15.997
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	16	20.372	19.248
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	17	2.341	1.230
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	18	41.399	18.117
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	19	54.896	24.073
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	20	47.213	-14.723
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	21	74.372	16.370
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	22	72.442	1.199
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	23	88.845	18.847
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	24	95.567	5.718
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	25	111.165	18.624
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	26	106.436	4.080
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	27	108.727	-9.121
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	28	127.549	23.645
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	29	146.099	12.129
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	30	124.591	1.142
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	31	153.391	-8.559
Eumetazoa	Bilateria	Protostolo	Lophotrochozoa	Mollusca	Bivalvia	Cardiida	Semelida	Abra	Abra	Abra	Abra	Abra	Abra	Temperate	Temperate	32	136.034	-17.867

1095

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1097

Fig. 3. Structure of the MacroTraits data base.

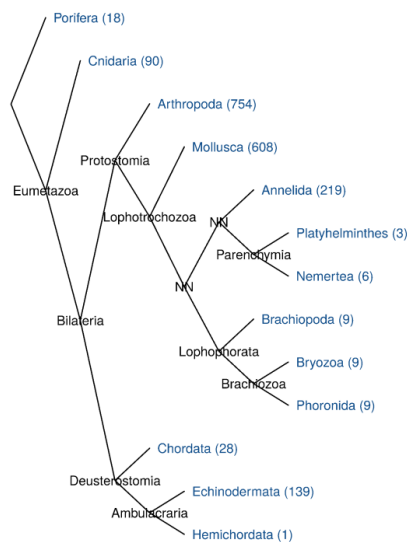


1098

1099 5.1 The documented fauna

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1101 The upper phylogeny of the species pool (Fig. 4) was rebuild according to Love (2009), Giribet (2016) and Bleidorn
1102 (2019). From phylum to species, the taxonomy was validated according to the World Register of Marine Species
1103 (WoRMS, 2025), with species indexed by their respective Aphia identifier. In general, the more diversified the clade,
1104 the larger the number of species documented for traits (Fig. 5). This is especially the case for polychaetes, bivalves,
1105 gastropods and malacostracans (from 200 to more than 700 species per class). On average, the documented fauna
1106 accounts for 7 % of the known species per class, but only 1.2 % of the total number of species.
1107

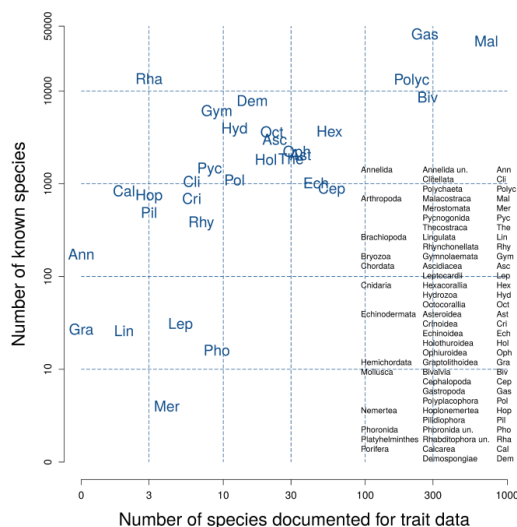


1108

1109

1110 Fig. 4. Upper phylogenic overview of the documented fauna. NN, no name attributed yet to the clade. In blue, phyla;
1111 values within parentheses indicate the numbers of species per phylum documented for traits.

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 1114

1115 Fig. 5. Taxonomic representativeness through numbers of species per class level. Y-axis, number of species inventoried
 1116 on the WoRMS platform. Legend, “un.” for “unassigned”.

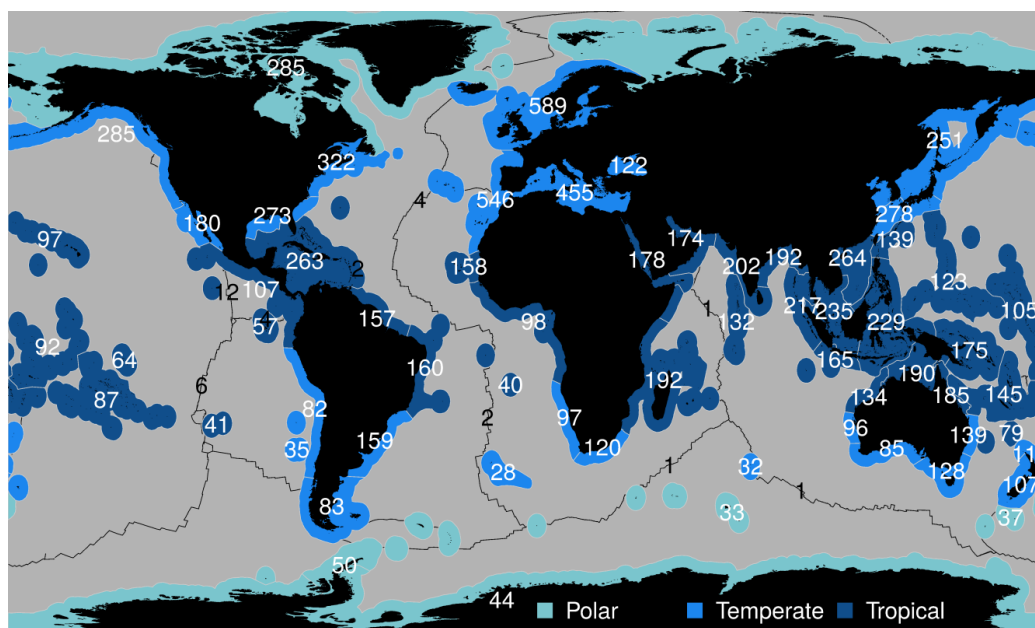
1117

1118 **5.2 Spatial representativeness**

1119

1120 9961 species occurrences in biogeographic provinces were recorded. Highest numbers of species documented per
 1121 province are clearly biased toward regions of the Western World (Fig. 6). This reflects the geography of scientific
 1122 efforts in the history of marine benthic zoology. European provinces are particularly symptomatic of the strongly
 1123 uneven data availability among the world regions. To a lesser extent, North American faunas are relatively well
 1124 documented. Although high numbers of species appear in the Indo-Pacific, many encountered species are distributed
 1125 over very large extents that overlap. By contrast, scientific deserts occurring in central Pacific and southern regions
 1126 witness of constraining remoteness. Larger documentation in the Arctic compared to Antarctica may be deceiving: many
 1127 European and northeast American species distributions range from temperate to polar waters, whereas Antarctic faunas
 1128 are more biogeographically isolated (Piepenburg, 2005; Clarke, 2008; Sirenko, 2009).

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Fig. 6. Number of documented species per geographic area. Shaded areas (within white delineations), following shelves (< 200 m deep) are biogeographic provinces following Spalding et al. (2007). Continuous black lines, tectonic plate boundaries characterised by hydrothermal vents and cold seeps. Species that occur deeper than shelves (> 200 m) were attributed the closest provinces. White, numbers of species per province, black, numbers of species along tectonic plate boundaries.

1138 5.3 Trait correlational pattern

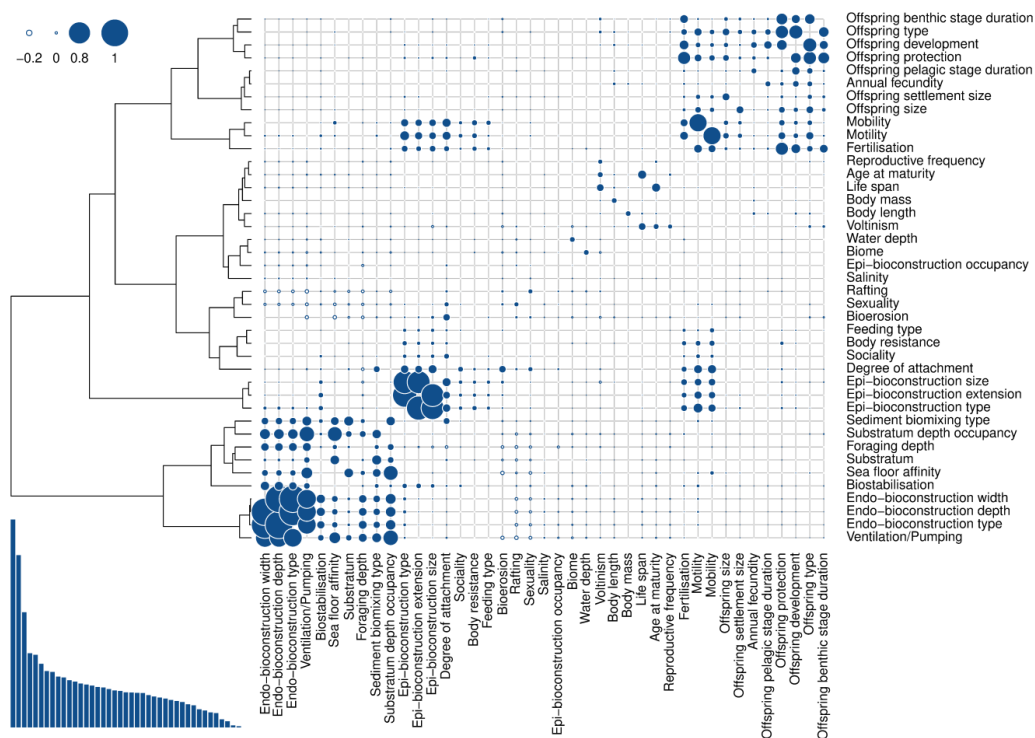
1139

1140 In order to support the statements in section 3.1 (i.e., degree of specificity for response or effect), the correlational
1141 pattern of traits was explored through Principal Component Analysis (PCA; Fig. 7). From each trait, as a species × trait
1142 modalities matrix, a species × species Euclidean distance matrix was derived (Gower, 1966) such that species pairs
1143 could be correlated following Mantel (1967); this operation converts a trait into a single vector composed of species
1144 pair distances. Then, a trait clustering based on Ward's aggregation criterion (Murtagh and Legendre, 2014) was done
1145 on trait scores along the most significant PCA axes. The analyses were performed in R 4.5.2 (R Core Team, 2025) with
1146 the ade4 package (Chessel et al., 2004; Dray et al., 2007). As a basic rule, multiple expressiveness among habitat,
1147 response and effect can be deducted depending on correlation strength. Specific expressiveness (e.g., only response or
1148 only effect) can be deducted from the documentation in section 3.2.

1149 On the whole, the correlation matrix displays two main areas of noticeable correlation strengths (Fig. 7). A first one
1150 includes bioconstructions, itself split into epibenthic and endobenthic bioconstructions, with traits related to spatial
1151 occupancy (sea floor affinity, substratum depth) and sediment engineering (biostabilisation, biomixing). The second
1152 cluster relates reproductive and developmental aspects. In between, fertilisation, motility, mobility, body resistance and
1153 feeding type are the only traits that exhibit substantial affinities for both response and effect. This correlation pattern
1154 supports most arguments on trait expressiveness in section 3 and Table 1. Besides, absence of correlation within a trait
1155 may indicate undetermined expressiveness such as for body mass and body length (i.e., slight involvement in



1156 everything); this may also indicate high complementarity within a same expression such as for life span and age at
 1157 maturity (i.e., within life history, independence of reproductive and developmental modes).
 1158

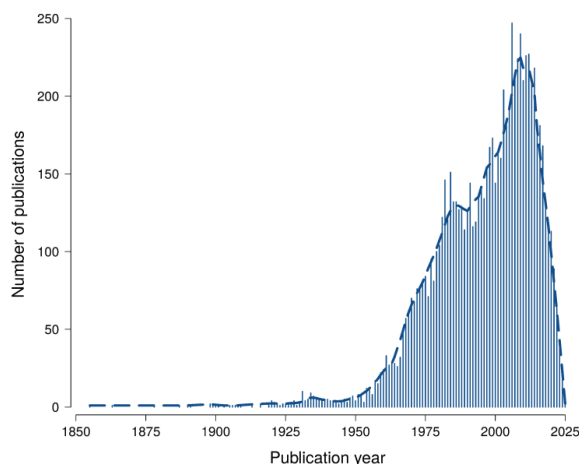


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 1160
 1161 Fig. 7. Trait pattern according to Principal Component Analysis (PCA) on Mantel's correlation matrix. Trait variables
 1162 were clustered according their positions along the three first PCA axes that accounted for 12, 9 and 6 % of total inertia,
 1163 respectively (bottom-left bar diagram). Right, correlation matrix; dot size, proportional to Mantel's correlation
 1164 coefficient between two traits; see legend in the top-left corner. Low correlations can indicate functional
 1165 complementarity, but only when trait expression is coherent with research questions (i.e., environmental selection or
 1166 ecosystem functions; see section 3.1 and Table 1).

1167 5.4 Historical considerations

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 1169
 1170 Beyond its interest for current researches on functional biodiversity, the MacroTraits data compilation provides
 1171 opportunities to assess research efforts in the field of marine benthic natural history (Fig. 8). Substantial efforts arose in
 1172 the 1970s and 1980s, with a peak of information that substantially fueled the data base around the year 2000. Then,
 1173 research activities resulted in a spectacular decline around the year 2010, dropping to almost nil in 2025.

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1178 Fig. 8. Historical publication trend in the field of marine benthic natural history. Each considered publication provided a
1179 minimum information on biological traits. A dramatic collapse, starting around the year 2010, is clearly perceptible.

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1182 6 Discussion

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1184 The wide panel of biological traits in the MacroTraits data base can foster data analyses in many places and domains of
1185 benthic ecology where a sufficient amount of taxa is documented. In case of limited documentation, ecophylogenetic
1186 applications provide solutions to trait data gaps. Nowadays, new analytical developments enable users to relate a trait to
1187 a phylogeny in order to predict trait modalities where trait information is missing (Guénard et al., 2013; Goolsby et al.,
1188 2017). In any case, MacroTraits data offer a great potential within a wide panel of analytical applications, the data
1189 quality being already supported by successful uses of part of the data in response and effect trait pattern analyses
1190 (Beauchard et al., 2021; Beauchard et al., 2022; Beauchard et al., 2023b; Beauchard et al., 2023c; Bergagna et al.,
1191 2026). Updated or refined version of the present data release can improve the use or development of community
1192 disturbance (Beauchard et al., 2017) or ecosystem function indices (Queirós et al., 2013; Wrede et al., 2018); see
1193 Supplement S3. The unusual consideration of habitat traits could also benefit developments that are currently limited by
1194 availability of ecological information at the species level. For instance, in European waters, the EUNIS marine habitat
1195 classification (Galparsoro et al., 2012) was built in the absence of species information, except a few iconic ones, which
1196 hampers its performance when related to changes in community composition (Cooper et al., 2019). Additionally, the use
1197 of habitat traits enables analyses for theoretical predictions when sampling constraints prevent the combination of endo-
1198 and epibenthos or in the absence of historical reference due to severe changes induced by human pressures (Beauchard
1199 et al., 2023c).

1200 Morphological descriptors were not considered in the data base as their expressiveness regarding fitness
1201 components or ecosystem function can be too subjective. Indeed, morphological analogues are rarely functional
1202 analogues (Weiss and Courtenay, 2019). Although epibenthic species that form biogenic structures (autogenic
1203 engineers) represent an exception (Darling et al., 2012; Fernandez et al., 2020), morphological traits in other groups
1204 consist in too soft traits to be significantly helpful in expressing life strategies or precise ecosystem functions. In the
1205 marine benthos, there is still no empirical support for using morphological traits as accurate proxies of fitness. In the



1206 absence of hard response traits, instead of morphology, anatomical traits are more explicit descriptors of some
1207 functional aspects (Mendes et al., 2025).

1208 In marine benthic ecology, several efforts were recently made to classify traits, discern different types of
1209 achievements or envision new directions (Costello et al., 2015; Lam-Gordillo et al., 2020; Lam-Gordillo et al., 2020;
1210 Martini et al., 2021; de Juan et al., 2022; Lam-Gordillo et al., 2023; Morim et al., 2023; Gimenez et al., 2024).
1211 According to the terminology from previous works and synthesized here, it is obvious that a trait can have multiple
1212 expressions. However, our correlative analysis showed that sets of independent traits can be distinguished (Fig. 7). On
1213 the one hand, traits linked to reproduction and ontogeny, typically inter-related through trade-offs, can be distinctly
1214 considered as deprived of significant expression of ecosystem function, and probably represent the purest descriptors of
1215 population persistence in response to specific environmental variations. On the other hand, traits linked to substratum
1216 relations and bioconstructions have clear expressions of sea floor engineering functions. In between, trait correlated to
1217 these two extreme clusters, mostly associated to dwelling mode and adult dispersal, seem complementary for relevant
1218 trait selections in respect to research questions. Alterations of the highlighted pattern in Figure 7 are not excluded when
1219 focusing on more local species pools, but important deviations are unlikely given strong phylogenetic implications in
1220 trait correlations (McHugh and Rouse, 1998). Hence, our analysis provides robust baselines to limit some confusions
1221 persisting within the scientific community whereby some traits are said to be of major importance without deepened
1222 justification. For instance, body size (i.e., length or mass) can be, on the one hand, considered *important* as regards its
1223 physical prominence and variation among species. On the other hand, its functional expression is diffused in so many
1224 processes that this trait poorly discriminates response from effect; as a result, body size is not substantially correlated to
1225 any of the other traits. Therefore, a relevant trait selection prior to data analysis should consider two aspects, trait
1226 *expressiveness* that is the functional specificity to response or effect, and trait *expression* as the degree of functional
1227 involvement or significance in the studied process. Many traits documented in MacroTraits are very likely involved in
1228 both response and effect, while some of them are highly specific to one of the two processes (Table 1, “+++”), next to a
1229 few ones with lower expression (++ or + as a weaker proxy).

1230 These clarifications on the response-effect trait duality do not unconditionally exclude implications of the most
1231 specific response traits in ecosystem function, especially non-engineering functions (Fig. 1). While our assessment of
1232 trait relevance holds for a direct use of the response traits as they are provided in this data base (especially the
1233 reproductive ones), a combined use of those traits with others can be useful to explore potential ecosystem functions.
1234 The notion of effect is particularly related to organism body size, an auxiliary trait needed to express the level of
1235 magnitude of environmental effect induced by an individual organism. In this context, *effect* and *quantity* should be
1236 understood as synergistic. As an example, let us reconsider reproductive traits: while fecundity alone represents a simple
1237 number neutral to ecosystem function, its multiplication by offspring size generates a synthetic trait representing a
1238 potential amount of food resource for other organisms (e.g., egg dispersal in the water column). Furthermore,
1239 multiplying this new trait by pelagic stage duration of the propagule provides a dispersive dimension to potential food
1240 resource or organic carbon over space. Similarly, the combinations of body mass, mobility and life span express the
1241 same functions in the adult stage. Note that score attribution and standardisation of traits must be done prior to
1242 calculation; see Supplement S3 for examples on reproductive and bioturbation traits. Except in the special case of
1243 bioturbation (Swift, 1993; Solan et al., 2004), the use of such synthetic traits seems to be absent from current
1244 researches, but it could open new avenues for describing benthic patterns in ecosystem functions.

1245 Finally, the phrasings “trait-based ecology”, “trait-based approach” or “biological trait analysis” have emerged with
1246 the possibility of integrating species traits in the study of biodiversity (de Bello et al., 2021). While the scientific
1247 community is striving in that direction, it is important to remind that community ecology, the study of species



1248 composition in space and time, remains the key ingredient to quantify biodiversity. Community ecology is the mother
1249 discipline in which traits represent only a piece of the puzzle that also includes environmental, taxonomic and genetic
1250 information. Hence, there is no exclusive “trait science”, species distribution being the observation of central
1251 importance. However, in community ecology with functional emphasis, no significant research outcome is possible in
1252 the absence of natural history that safeguards competences in taxonomy and species autecology, and that represents the
1253 fabric of biological traits. In itself, the MacroTraits bibliography is very demonstrative of issues on scientific vision and
1254 recruitment policy within universities and public institutes, and that is extremely penalising for biodiversity research.
1255 Figure 8 clearly materialises earlier warnings from the marine domain (Dayton, 2003; Able, 2016), and more widely
1256 from general ecology regarding the dramatic decline of natural history (Gaston and May, 1992; Greene, 2005; Engel et
1257 al., 2021; Nanglu et al., 2023). We are now facing an unbelievable paradox whereby concerns on marine benthic
1258 biodiversity are accompanied by a loss of the means needed to understand those concerns. As a graphic example, the
1259 North Sea sediment macroinvertebrate fauna, within a biogeographic province among the most documented for traits
1260 (Fig. 6), encompasses more than 1000 species (Heip et al., 1992; Kunitzer et al., 1992). Nowadays, a complete
1261 biological trait documentation can be achieved for less than 300 of those species or genera (Beauchard et al., 2022;
1262 Supplement S5); although the most dominant taxa are documented, this example is particularly indicative of data
1263 deficiency in areas outside the Western World and in the deep seas. Therefore, a new scientific vision rethinking the
1264 importance of community ecology is required to counteract current and future research shortcomings in biodiversity
1265 assessments.

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1268 **7 Conclusions**

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1270 Initiated thirteen years ago, the MacroTraits data compilation has carefully evolved toward a comprehensive synthesis
1271 of trait data in marine benthic ecology. Although calls for harmonising trait data and terminology have come up in this
1272 research field (Costello et al., 2015; de Juan et al., 2022; Morim et al., 2023; Susini et al., 2025), there is still a large
1273 absence of concrete international initiative to provide and maintain a standard macrozoobenthic trait data bank, and this
1274 may persist without clear research agenda. To this end, the response-effect trait dichotomy, established long ago
1275 (Lavorel and Garnier, 2002), remains essential and no other trait classification seem to be more relevant in functional
1276 biodiversity research. Such an agenda should prioritise evolutionary aspects since they are still insufficiently addressed
1277 in community ecology of the marine benthos. The identification of response trait combinations from which specific
1278 life-history strategies emerge among the different marine environments represent a basic but crucial need to understand
1279 faunal responses to natural and human-mediated pressures, including climate change. In parallel, this could enable more
1280 relevant vulnerability analyses along gradients of effect trait composition (Oliver et al., 2015; de Bello et al., 2021).
1281 Fundamental science, at the basis of concepts and theories, is of primary importance and must take place before the data
1282 themselves in order to assess what is needed and achievable. The MacroTraits data base paves the way toward such a
1283 general consensus regarding trait data conception and utility in marine benthic ecology. A key point in this work was to
1284 show what was achievable for benthic synecology in a worldwide-comparative context and where the fauna can consist
1285 in several tens of species within a single case study. Relevant biological trait data must be congruent with a scientific
1286 vision as exposed in this paper, and the proposed system and associated terminology strongly fulfill this essential
1287 condition. The data base can evolve over time, at least when sufficient biological information on species not yet
1288 included will be available, and possibly with feed-back from further collaborations and projects.

1289



1290 **Data availability**

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1292 The MacroTraits data base is accessible within the R package fuzR in the Zenodo repository
1293 <https://doi.org/10.5281/zenodo.20555888>.

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1296 **Author contributions**

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1298 OB: conceptualisation, data compilation, R package development, data analyses and writing. KS: review and editing.

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1301 **Competing interests**

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1303 The authors have no conflict of interest to declare.

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1307

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- 1836



1837

Appendix A

1838

Are scores greater than one needed in fuzzy coding?

1839

1840

1841 The document provides analytical support to the simplification of fuzzy coding. Depending on the considered data set,
1842 quantitative scores of species affinities for trait modalities exhibit variable ranges. While 0 clearly expresses no affinity,
1843 maximum non-null values can be 1, 3, 5 or more. The precision of score attribution certainly depends on the biological
1844 background of the data designer or the available literature. Such conditions are not always met to attribute values > 1
1845 with minor subjectivity. However, to our knowledge, the relevance of values > 1 does not seem to have been
1846 questioned. Here, fuzzy-coded data sets are confronted to their simplified 0-1 versions, and we provide the accompanied
1847 R script (R Core Team, 2025).

1848 In community ecology, fuzzy coding of biological trait data was popularized by Chevenet et al. (1994) as part of a
1849 special issue of *Freshwater Biology* (Townsend and Hildrew, 1994) in which several application examples on plants and
1850 animals were provided. Such data sets, especially on stream invertebrates, were built by highly experienced biologists
1851 from the second half of the twentieth century (Statzner and Bêche, 2010). Therefore, those data sets represent a kind of
1852 reference in terms of data quality from an experimental perspective. In that special issue, Chevenet et al. (1994)
1853 exemplified the use of fuzzy coding with an ecological trait data set on aquatic Coleoptera (110 species \times 32 modalities
1854 from 9 traits; Bournaud et al., 1992); trait modality scores range from 0 (no affinity) to 6 (highest performance). The
1855 data are available in the *ade4* package (Chessel et al., 2004; Dray et al., 2007). In order to assess the relevance of
1856 scoring range in multivariate ordination of species and traits, the original data table (0-6 scores) was fuzzy coded as
1857 done in Chevenet et al. (1994) before being compared to its 0-1 version.

1858

1859

```
library(ade4)
```

1860

```
data(coleo)
```

1861

1862

```
tab1 <- coleo$stab
```

1863

```
fuz1 <- prep.fuzzy.var(df = tab1, col.blocks = coleo$col.blocks)
```

1864

1865 Then, every value greater than one was replaced by one, and the table was fuzzy coded.

1866

1867

```
tab2 <- data.frame(ifelse(tab1 == 0, 0, 1))
```

1868

```
fuz2 <- prep.fuzzy.var(df = tab2, col.blocks = coleo$col.blocks)
```

1869

1870 As the two fuzzy tables are matched by species, they can be related by the RV coefficient, an index varying between 0
1871 (no multivariate co-structure) and 1 (perfect co-structure), equivalent to Pearson's r coefficient in a multivariate space
1872 (Escoufier, 1973). The similarity of the two multivariate structures ("co-structure") can be tested against the null
1873 hypothesis by randomly permuting the rows of one data frame, which breaks the relationship between the two. By this
1874 way, a null distribution of 999 simulated RV coefficients was generated to assess the significance of the observed RV
1875 value.

1876

1877

```
RV.rtest(df1 = fuz1, df2 = fuz2, nrepet = 999)
```

1878

1879

```
Monte-Carlo test
```

1880

```
Call: RV.rtest(df1 = fuz1, df2 = fuz2, nrepet = 999)
```

1881



1882 Observation: 0.9886374

1883

1884 Based on 999 replicates

1885 Simulated p-value: 0.001

1886 Alternative hypothesis: greater

1887

1888	Std.Obs	Expectation	Variance
1889	7.599942e+01	2.569097e-02	1.605402e-04

1890

1891 The two data frames are almost perfectly similar ($RV = 0.99$, $p < 0.001$), which means that modality scores > 1 do not
1892 significantly change the species trait pattern. This can be graphically illustrated by Co-Inertia Analysis (CoIA; Dray et
1893 al., 2003). The two data frames were firstly processed by Fuzzy Correspondence Analysis (FCA; Chevenet et al., 1994),
1894 after what the two FCAs were combined into CoIA (Fig. A1).

1895

```
1896 fca1 <- dudi.fca(df = fuz1, scannf = FALSE)
```

```
1897 fca2 <- dudi.fca(df = fuz2, scannf = FALSE)
```

```
1898 coia <- coinertia(fca1, fca2, scannf = FALSE)
```

1899

```
1900 layout(matrix(c(1, 1, 2, 3), nr = 2), width = c(1, 0.5))
```

```
1901 par(bty = "n", cex.lab = 1.5)
```

```
1902 s.match(coia$mX, coia$mY, clab = 0, cpoint = 2.5, grid = FALSE,
```

```
1903         xlim = c(-1.5, 2.5), ylim = c(-2.5, 2.0),
```

```
1904         sub = "a", possub = "topleft", csub = 4)
```

```
1905 text(-1.3, 0.15, "Axis 1", cex = 2, font = 3)
```

```
1906 text(-0.15, -2.2, "Axis 2", cex = 2, font = 3, srt = 90)
```

```
1907 par(mar = c(4.5, 5, 1, 1))
```

```
1908 plot(coia$mX[,1], coia$mY[,1], xlim = c(-1.5, 2.5), ylim = c(-1.5, 2.5),
```

```
1909       bty = "n", pch = 20, cex = 1.5, xaxt = "n", yaxt = "n",
```

```
1910       xlab = "First axis score", ylab = "First axis score")
```

```
1911 axis(side = 1, seq(-1.5, 2.5, 1), cex = 0.8)
```

```
1912 axis(side = 2, seq(-1.5, 2.5, 1), cex = 0.8)
```

```
1913 mtext(side = 3, "b", cex = 2.5, adj = 0.9, line = -17)
```

```
1914 plot(coia$mX[,2], coia$mY[,2], xlim = c(-2.5, 2.5), ylim = c(-2.5, 2.5),
```

```
1915       bty = "n", pch = 20, cex = 1.5, xaxt = "n", yaxt = "n",
```

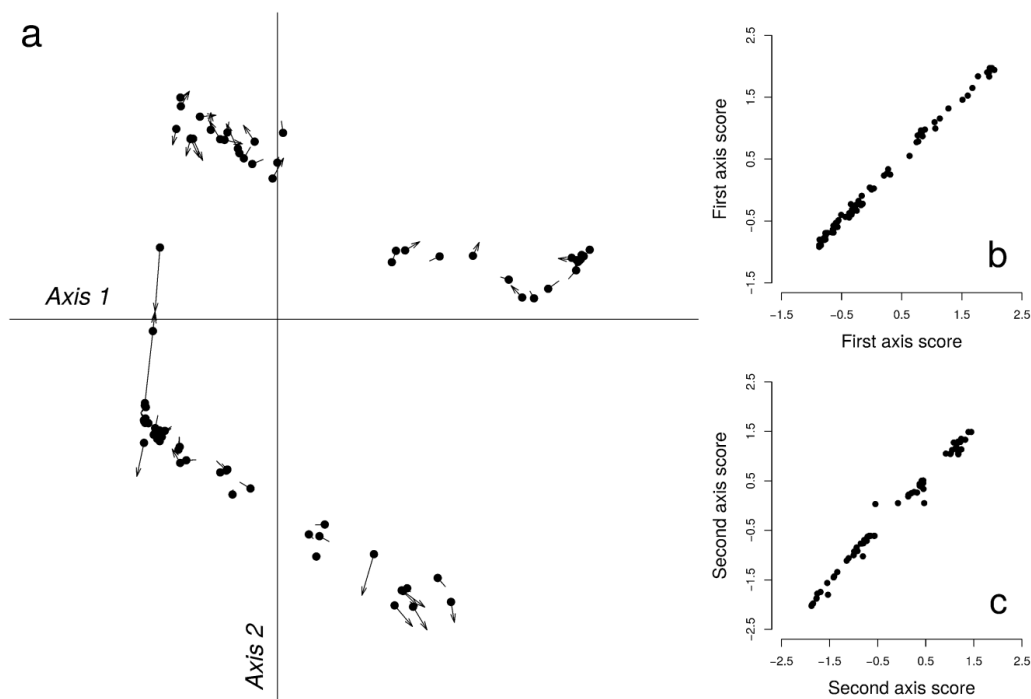
```
1916       xlab = "Second axis score", ylab = "Second axis score")
```

```
1917 axis(side = 1, seq(-2.5, 2.5, 1), cex = 0.8)
```

```
1918 axis(side = 2, seq(-2.5, 2.5, 1), cex = 0.8)
```

```
1919 mtext(side = 3, "c", cex = 2.5, adj = 0.9, line = -17)
```

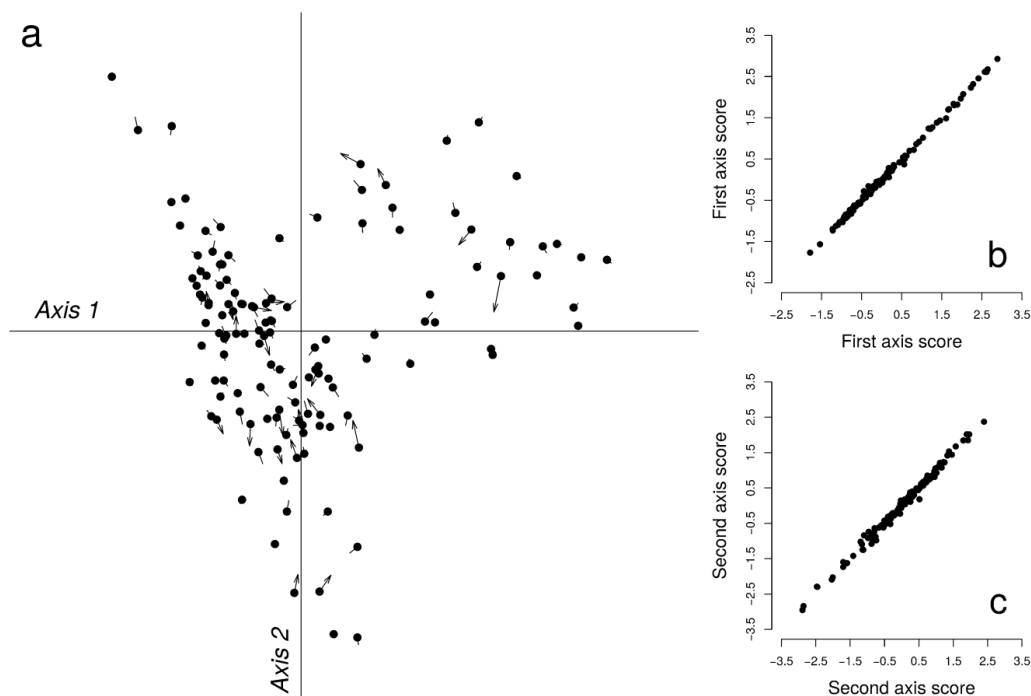
1920



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1933

Fig. A1. Co-Inertia Analysis (CoIA) on ecological trait data from Bournaud et al. (1997). a) Co-structure between the 110 species ordinated by traits according to 0-6 scoring (black dots) and according to 0-1 scoring (arrow tips). Arrow length indicates discrepancy, i.e., when the 0-1 scoring does not well reproduce the 0-6 scoring. b) Relationship between dot (x-axis) and arrow tip (y-axis) scores of the first CoIA axis. c) Relationship between dot and arrow tip scores of the second CoIA axis. Overall, the two multivariate structures are extremely similar.

Another example can be drawn from Statzner et al. (1997) that finely covers the reproductive biology of 131 aquatic insect species through the 41 modalities of ten traits documented by internationally recognised experts. The same methodology was applied, and CoIA revealed a strong co-structure between the original fuzzy-coded data frame (0-3) and the simplified one (0-1); $RV = 0.98$, $p < 0.001$ (Fig. A2).



1934
 1935

1936 Fig. A2. Co-Inertia Analysis (CoIA) on reproductive trait data from Statzner et al. (1997). a) Co-structure between the
 1937 131 species ordinated by traits according to 0-3 scoring (black dots) and according to 0-1 scoring (arrow tips). Arrow
 1938 length indicates discrepancy, i.e., when the 0-1 scoring does not well reproduce the 0-6 scoring. b) Relationship
 1939 between dot (x-axis) and arrow tip (y-axis) scores of the first CoIA axis. c) Relationship between dot and arrow tip
 1940 scores of the second CoIA axis. Overall, the two multivariate structures are extremely similar.

1941

1942 In marine benthic ecology, the data from Clare et al. (2022) have been massively used for different purposes. The
 1943 data frame documents 10 biological and ecological traits (48 modalities) of 899 genera found on the European
 1944 northwestern shelf. Given the more limited biological information in the marine environment and the attempt to cover a
 1945 taxonomic pool as large as possible, the authors carefully used a 0-3 scoring to express within-genus uncertainty in
 1946 species functional affinities. As previously observed, the 0-1 version of the data frame does not differ from the original
 1947 version, with an RV close to 1.

1948

```
1949 url <- "https://raw.githubusercontent.com/obeauchard/Fuzzy-data-sets/main/"
1950 data <- read.csv(paste(url, "FuzzyData_Clare2022_tab.csv", sep = ""), header = TRUE)
1951 blo <- read.csv(paste(url, "FuzzyData_Clare2022_blo.csv", sep = ""), header = FALSE)[,1]
1952 data <- data[data$Genus != "",]
1953 tab1 <- data[7:ncol(data)]
1954 rownames(tab1) <- data$Genus
1955 tab2 <- data.frame(iffelse(tab1 == 0, 0, 1))
1956 fuz1 <- prep.fuzzy.var(df = tab1, col.blocks = blo)
1957 fuz2 <- prep.fuzzy.var(df = tab2, col.blocks = blo)
1958 RV.rtest(fuz1, fuz2, nrepet = 999)
1959 Monte-Carlo test
1960 Call: RV.rtest(df1 = fuz1, df2 = fuz2, nrepet = 999)
```



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2012

Observation: 0.9967481

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: greater

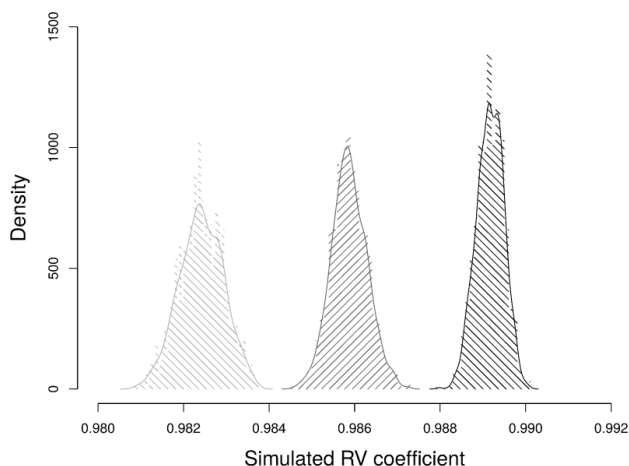
Std.Obs	Expectation	Variance
6.356538e+02	1.318734e-02	2.394203e-06

These recurring outcomes bring us to push forward the falsification of the original data set: does the attribution of random scores lead to a significantly different data set? We replaced the non-null values of the original data set by random scores according to three scorings: 1-3, 1-5 and 1-10. For each scoring, 1000 replicates were simulated, and the 1000 corresponding RV were calculated (p -value test skipped with `nrepet = 1`).

```
RV.sim3 <- numeric()
RV.sim5 <- numeric()
RV.sim10 <- numeric()
for(i in 1:1000){
  tab.sim3 <- tab1
  tab.sim5 <- tab1
  tab.sim10 <- tab1
  w <- tab1[tab1 > 0]
  w3 <- sample(x = 1:3, size = length(w), replace = TRUE)
  w5 <- sample(x = 1:5, size = length(w), replace = TRUE)
  w10 <- sample(x = 1:10, size = length(w), replace = TRUE)
  tab.sim3[tab1 > 0] <- w3
  tab.sim5[tab1 > 0] <- w5
  tab.sim10[tab1 > 0] <- w10
  fuz.sim3 <- prep.fuzzy.var(tab.sim3, col.blocks = blo)
  fuz.sim5 <- prep.fuzzy.var(tab.sim5, col.blocks = blo)
  fuz.sim10 <- prep.fuzzy.var(tab.sim10, col.blocks = blo)
  RV.sim3[i] <- RV.rtest(fuz1, fuz.sim3, nrepet = 1)$obs
  RV.sim5[i] <- RV.rtest(fuz1, fuz.sim5, nrepet = 1)$obs
  RV.sim10[i] <- RV.rtest(fuz1, fuz.sim10, nrepet = 1)$obs
}
par(mar = c(5, 5, 1, 1))
hist(RV.sim3, nclass = 20, xlim = c(0.980, 0.992), ylim = c(0, 1500),
     freq = FALSE, border = FALSE, density = 15, angle = -45, col = 1,
     xlab = "", ylab = "", main = "")
hist(RV.sim5, nclass = 20,
     freq = FALSE, border = FALSE, density = 15, angle = 45, col = "grey40", add = TRUE)
hist(RV.sim10, nclass = 20,
     freq = FALSE, border = FALSE, density = 15, angle = -45, col = "grey70", add = TRUE)
w1 <- density(RV.sim3)
w2 <- density(RV.sim5)
w3 <- density(RV.sim10)
lines(w1, lty = 1)
lines(w2, lty = 1, col = "grey40")
lines(w3, lty = 1, col = "grey70")
mtext(side = 1, "Simulated RV coefficient", line = 3, cex = 1.5)
```



2013 `mtext(side = 2, "Density", line = 3, cex = 1.5)`
 2014



2015
 2016 Fig. A3. Simulated distributions of RV coefficients between the original trait data set from Clare et al. (2022) and the
 2017 same data set in which non-null trait modality scores were replaced by random scores between 1 and 3 (right, black), 1
 2018 and 5 (center, grey) and 1 and 10 (left, light grey).

2019
 2020 Figure A3 indicates that, in spite of slight differences among the three series of simulations, the RV coefficients remain
 2021 close to one in any case. This means that the attribution of scores > 1 does not significantly differ from the attribution of
 2022 random scores, even with an unrealistic 1-10 scoring.

2023 The particularity of biological trait data sets is the species-specific biology, even at the genus level as shown in the
 2024 previous example. This is necessarily the case in data sets composed of a dominant number of qualitative traits for
 2025 which a single non-null score can be attributed (e.g., offspring type). In general, species do not have many non-null
 2026 affinities within a same trait, except, to a lesser extent, omnivores for feeding type. As a result, fuzzy-coded data sets
 2027 contain a large dominance of zeros.

```
2028
2029 nval <- nrow(tabl) * ncol(tabl)
2030 length(tabl[tabl == 0]) / nval
2031
2032 0.7293752
2033
```

2034 Here, the data frame is composed of 73 % of zeros. This probably influences correlations between trait modality
 2035 columns whereby strong relationships may not be determined by the differences between the non-null scores, but
 2036 between 0 and everything else. Below, the column-modalities of the first trait (body length) from the original data frame
 2037 are selected and correlated:

```
2038
2039 indic <- rep(1:length(blo), blo)
2040 as.dist(round(cor(fuzl[indic == 1]), 2))
2041
2042          sr_Less_than_10 sr_11_to_20 sr_21_to_100 sr_101_to_200 sr_201_to_500
2043 sr_11_to_20              -0.25
2044 sr_21_to_100            -0.49      -0.37
```



```

2045 sr_101_to_200          -0.24      -0.23      -0.22
2046 sr_201_to_500        -0.15      -0.15      -0.19      0.02
2047 sr_More_than_500     -0.06      -0.06      -0.09      -0.03      0.02
    
```

2048

2049 The same data frame after replacement of the non-null values by random scores between 1 and 10:

2050

```

2051 w <- tab1[tab1 > 0]
2052 w <- sample(x = 1:10, size = length(w), replace = TRUE)
2053 tab.sim <- tab1
2054 tab.sim[tab1 > 0] <- w
2055 fuz.sim <- prep.fuzzy.var(tab.sim, col.blocks = blo)
2056 as.dist(round(cor(fuz.sim[indic == 1]), 2))
    
```

2057

```

2058          sr_Less_than_10 sr_11_to_20 sr_21_to_100 sr_101_to_200 sr_201_to_500
2059 sr_11_to_20              -0.26
2060 sr_21_to_100            -0.49      -0.38
2061 sr_101_to_200          -0.23      -0.22      -0.22
2062 sr_201_to_500          -0.15      -0.14      -0.19      0.00
2063 sr_More_than_500      -0.06      -0.06      -0.09      -0.03      0.02
    
```

2064

2065 The correlations remain quite stable and do not seem to be substantially affected by the falsification of the original data.

2066 Other marine benthic data sets, combining different numbers of taxa and modality columns, exhibit the same numerical symptoms (Table A1).

2068

2069 Table A1. Other fuzzy-coded data sets. The column RV indicates matrix correlation between the original data table and its simplified version through 0-1 trait modality scoring.

2070

2071

Source	Number of taxa	Number of traits	Number of modalities	Scoring	RV
Beauchard et al. (2023)	812	15	68	0-3	1.00
Lam-Gordillo et al. (2020)	277	13	54	0-4	0.99
Meijer et al. (2023)	235	16	76	0-3	1.00
Pacheco et al. (2011)	40	13	54	0-3	0.99
Tillin et al. (2006)	52	10	47	0-4	0.96
Tornroos et al. (2012)	56	25	102	0-3	1.00
Wong and Dowd (2015)	48	7	28	0-3	0.99

2072

2073

2074 Conclusively, these data manipulations advocate for simplifying fuzzy coding when intended to multivariate patterns. In no case we reconsider the validity of fuzzy coding for expressing within-species biological variations in quantitative traits when sufficient information is available. However, in the marine benthos, such a perspective seems illusive for the present time.

2078

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2080

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2083



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- 2123
- 2124