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### Qualitative modelling of functional relationships in marine benthic communities

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#### Abstract :

In order to better understand and predict the dynamics of benthic macroinvertebrate communities, we need to first define the functional components of benthic biodiversity and then provide a mechanistic description of how they interact with their abiotic environment, their basic resources and each other. These interactions should be largely controlled by readily available biological traits, making trait-based modelling an ideal framework for the synthesis of relevant hypotheses from ecological theory and expert knowledge. With the help of benthic species traits, we derived a set of first principles regarding the role of organisms in processes of environmental filtering, consumption of algae/detritus, predation, use of space, biogenic habitat modification and trade-offs in the utilization and allocation of resources. These principles were incorporated into qualitative models in the form of functional relationships linking groups of benthic organisms in the Rance estuary (Brittany, France). The general stability of these models illustrates their potential to persist in time and to constitute a plausible representation of the natural world. Their structure provides insight into the role of various community assembly mechanisms and the direction that the system might take in response to perturbations. The results are expected to inform the development of quantitative models reproducing the spatial and temporal dynamics of marine benthic biodiversity in the Rance estuary.

#### Highlights

► We derived first principles on the role of benthic organisms in community assembly. ► These principles dictated functional relationships among groups of benthic species. ► Groups and functional relationships comprised qualitative models of benthic systems. ► Stability analysis supported the models' potential to represent benthic communities. ► Model structure offered insight into the role of some community assembly mechanisms.

**Keywords** : Benthic macroinvertebrates, Biological traits, Biotic interactions, Community assembly, Functional groups, Qualitative modelling

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39 Introduction

40 Reliable prediction of biodiversity responses to environmental change remains a 41 key challenge of ecological research (Sutherland et al., 2013). Because it involves combinations of species and environmental gradients that have not been observed 42 yet, it requires a mechanistic understanding of the processes that shape biological 43 44 communities (Kearney and Porter, 2009). Ecological theory has generated many 45 hypotheses about the maintenance of species diversity (Chesson, 2000). However, empirical investigation of these hypotheses has been mostly performed by studies of 46 47 relatively small spatial and temporal scales (Cardinale et al., 2012). This has limited the potential of their findings to be extrapolated to larger scales and has added 48 49 uncertainty to projected trends of biodiversity (Pereira et al., 2010).

In ecological systems where observation and experimentation fall short of fully revealing the drivers of biodiversity, the analysis of mechanistic models has been suggested as an alternative way of identifying the most likely community assembly mechanisms (Amarasekare, 2003). Since the role of organisms in the functioning of ecosystems is defined by their traits, the development of trait-based modelling approaches has been suggested as a fruitful avenue for models of ecological systems (Ings et al., 2009). Limited understanding of specific mechanisms should not exclude them from the modelling procedure (Queirós et al., 2015). Instead, awareness about the assumptions that are made at each step should allow models to test alternative hypotheses, elucidate domains of uncertainty and identify critical areas for research. 

The development of mechanistic models of biodiversity can be considered to be subject to two main conditions. First, the functional components of biodiversity need to be defined through rigorous and testable procedures (Petchey and Gaston, 2006). Next, a mechanistic description of the way these components interact with their environment and among themselves is necessary. These issues have traditionally been addressed in the context of food web modelling. Organisms are typically separated into groups according to their food sources, and interactions among them are assumed to represent their trophic behaviour (Yodzis and Innes, 1992). In lack of empirical information to help formulate these models, various methods have been developed for the construction of food webs, based on principles of community (e.g., Cohen and Newman, 1985; Williams and Martinez, 2000; Cattin et al., 2004) or ecosystem ecology (e.g., Fath, 2004; Morris et al., 2005; Halnes et al., 2007). Still, a disproportionate focus on trophic interactions has restricted the scope of most modelling efforts (but see Kéfi et al. (2012)). 

Predicting biodiversity patterns is particularly challenging for communities of marine benthic macroinvertebrates (Constable, 1999). The study of these systems has long suffered from a lack of empirical information (Solan et al., 2003), while non-trophic interactions often play a central role. Many of these organisms can alter the physical or chemical properties of their environment in ways that significantly impact other members of their communities (Meadows et al., 2012). These effects appear to be non-linear and form intricate feedback cycles (Herman et al., 1999), while they can greatly vary among different life stages (Pineda et al., 2009). Along with the prevalence of omnivory and facultative feeding modes, this has reduced the pertinence of classic trophic groupings of benthic macrofauna (Snelgrove and Butman, 1994). Moreover, theoretically derived allometries that have facilitated the quantification of trophic interactions appear to be less efficient for their non-trophic counterparts (Berlow et al., 2009; Petchey et al., 2008), in support of a more mechanistic representation of the latter. 

Quite independent of mechanistic modelling, an increased interest in the functioning of marine benthic communities has led to the compilation of large data bases of species traits. At the same time, theoretical and expert knowledge about potential trait associations is being continuously generated. Particularly lacking is a systematic procedure for the assignment of functional groupings and inter-group relationships on the basis of such readily available information. Recent work in the terrestrial environment led to the development of a trait-based method for the construction of functional groups for models of plant diversity (Boulangeat et al., 2012). The conceptual and methodological framework was provided by the emergent group hypothesis, which assumes functional equivalence within and functional divergence among emergent groups of species (Hérault, 2007). The adaptation of 

this framework to the benthic macroinvertebrate communities of the Rance estuary (Brittany, France) can provide the functional components for a mechanistic representation of the system (Alexandridis et al., 2017). Here we implement these components in a demonstration of a systematic procedure for the assignment of functional relationships between them. In a first conception of the system, we are restricted to the qualitative nature of the relationships. 

The objective of our study is to use mechanistic models of benthic macrofauna, in order to assess the role of different processes in shaping biodiversity patterns in the Rance estuary. To this end, we represented benthic macroinvertebrate communities through signed-directed graph (or signed digraph) models. The previously defined groups of species comprised the functional components of the system and were assigned to sub-systems based on rules of environmental filtering. In each of these sub-systems, groups were linked by functional relationships that were largely derived from ecological theory and expert knowledge regarding general community assembly mechanisms. This procedure was dictated by each group's assigned trait values and representative species. The stability analysis of the signed digraphs demonstrated the potential of the respective systems to persist in time and, therefore, to constitute a plausible representation of the natural world. The structure of the models gave some insight into the role of different community assembly mechanisms, as well as the direction of the system's response to potential perturbations. This work serves as a first step toward quantitative mechanistic models that will be able to reproduce the spatial and temporal dynamics of benthic biodiversity in the Rance estuary (Alexandridis, 2017). 

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 125 Methods

<sup>300</sup><sub>301</sub> 126 **2.1** 

303 127 Study site

The Rance estuary (Brittany, France) is situated in the southern part of the English Channel (Fig. 1). The site is characterized by the presence of a tidal power plant at its mouth. The operating constraints of the installation have reduced the tidal range in the estuary compared to the open sea. The intertidal zone has shifted from 70% of the total surface of the estuary before the construction of the power plant, to 50% after. Maximum water depth is 17 m at low tide, but the main part of the basin is 5-6 m deep. The sluice and turbine currents from the power plant have eroded parts of the riverbed. Sandbanks closest to the dam have shifted and the bed is predominantly covered with gravel or pebbles (Retière, 1994). At the same time, long periods of slack water have promoted the deposition of fine particles in coves and bays (Bonnot-Courtois and Lafond, 1991). From downstream to upstream of the estuary, pebbles and coarse sands are replaced by medium and fine sands, muddy sands and finally muds upstream of Port-St-Hubert. A similar sequence is observable from the central channel of the estuary to its banks. 

Sediment samples were collected from 113 stations on the bed of the Rance estuary in April 1995, prior to the spring recruitment (Fig. 1). The sampled stations are expected to represent the variability of benthic communities in the system. A total of 240 macroinvertebrate (i.e., retained by a 1 mm sieve) species or higher taxonomic groups belonging to 9 phyla were identified in the samples and their abundances in each station were measured (Desroy, 1998).

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Fig. 1. Map of the study site. The Rance estuary is situated on the northern coast of Brittany, France. Crosses indicate the location of the 113 stations that were sampled in the spring of 1995. The tidal power plant is located at the mouth of the estuary, south of the city of St-Malo

410 156 Functional groups

2.2

For the representation of the primary functional components of benthic macroinvertebrate communities in the Rance estuary, we employed 20 functional groups, previously built on the basis of biological trait information for the 240 species of the system in 1995 (Alexandridis et al., 2017). The collected abundance data set allowed each of the groups to be assigned with a representative species along with a value for each of the 14 biological traits (Table 1). The traits are expected to describe the role of benthic algae/detritus feeders and predators/scavengers in 7 important community assembly mechanisms (Table 2). The list of mechanisms was mostly adopted from the framework developed by Boulangeat et al. (2012) for dynamic models of terrestrial vegetation. A few adjustments were made to the original framework, in order to adapt it to marine benthic systems (Alexandridis et al., 2017). 

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Table 1. Functional groups with their assigned representative species and biological trait values (Alexandridis et al., 2017). For details about the biological traits, see Table 2. Group names starting with 'H' correspond to groups of algae/detritus feeders and those starting with 'C' correspond to groups of predators/scavengers

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482	Groups	Representative species	T1. temperature	T2. development	T3. dispersal	T4. fecundity	T5. tide/salinity	T6. substrate	T7. size (cm)	T8. area	T9. position	T10. mobility	T11. growth rate	T12. lifespan (yr)	T13. epibiosis	T14. engineering
483	H1	Morchellium argus	eurythermal	brooded	short	low	stenohaline	rock	3.3	0.1	epifauna	sessile	2.6	1.7	epibiont	neutral
484	H2	Lepidochitona cinerea	stenothermal	planktonic	short	high	stenohaline	rock	10.8	4.1	epifauna	mobile	0.9	11.6	epibiont	neutral
485	H3	Balanus crenatus	eurythermal	planktonic	long	high	euryhaline	rock	2.0	0.8	epifauna	sessile	2.5	2.0	epibiont	neutral
486	H4	Crepidula fornicata	stenothermal	planktonic	long	high	stenohaline	rock	7.6	0.0	epifauna	sessile	1.9	11.2	basibiont	neutral
487	H5	Oligochaeta	stenothermal	laid	short	low	emersed	muddy sand	4.5	5.0	infauna	mobile	3.4	2.0	neutral	destabilizer
488	H6	Thyasira flexuosa	eurythermal	planktonic	short	low	stenohaline	mud	3.6	0.8	infauna	mobile	1.0	10.0	neutral	stabilizer
489	H7	Melinna palmata	stenothermal	brooded	short	low	stenohaline	mud	7.5	0.3	interface	sessile	2.6	3.6	neutral	stabilizer
490	H8	Notomastus latericeus	stenothermal	brooded	short	low	stenohaline	muddy sand	6.0	2.9	interface	mobile	2.6	1.9	neutral	destabilizer
491	H9	Hediste diversicolor	eurythermal	laid	short	high	emersed	muddy sand	12.8	0.2	interface	mobile	2.1	3.4	neutral	destabilizer
492	H10	Malacoceros fuliginosus	eurythermal	planktonic	long	high	euryhaline	mud	8.5	1.9	interface	mobile	2.5	2.7	neutral	destabilizer
494	H11	Galathowenia oculata	eurythermal	planktonic	long	high	euryhaline	mud	11.1	0.0	interface	sessile	2.7	4.4	neutral	stabilizer
495	H12	Glycymeris glycymeris	stenothermal	planktonic	short	high	stenohaline	muddy gravel	8.0	1.4	infauna	mobile	0.8	15.0	neutral	stabilizer
496	H13	Anapagurus hyndmanni	stenothermal	planktonic	long	high	stenohaline	gravel	10.0	0.1	epifauna	mobile	0.6	10.0	neutral	neutral
497	H14	Cerastoderma edule	stenothermal	planktonic	long	high	emersed	muddy sand	8.6	0.5	interface	mobile	0.7	8.9	neutral	stabilizer
498	C1	Sphaerosyllis bulbosa	stenothermal	brooded	short	low	stenohaline	gravel	1.3	0.5	epifauna	mobile	4.7	1.9	neutral	neutral
499	C2	Marphysa bellii	stenothermal	planktonic	short	high	stenohaline	muddy sand	23.3	0.3	interface	mobile	1.1	4.7	neutral	neutral
500	C3	Nephtys hombergii	stenothermal	planktonic	long	high	stenohaline	gravel	10.5	0.3	interface	mobile	2.2	7.3	neutral	neutral
501	C4	Myrianida edwardsi	stenothermal	planktonic	long	low	stenohaline	mud	1.4	3.1	interface	mobile	5.8	1.9	neutral	neutral
502	C5	Urticina felina	eurvthermal	planktonic	short	hiah	eurvhaline	rock	16.7	10.3	epifauna	sessile	1.1	14.0	epibiont	neutral
503	C6	Svllis cornuta	stenothermal	planktonic	long	low	stenohaline	rock	7.4	5.2	epifauna	mobile	2.3	2.3	epibiont	neutral
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#### Table 2. List of community assembly mechanisms, biological traits that represent the organisms' role in them, potential trait values and comments about their assignment to the system's species, which formed the basis for the construction of the 20 functional groups (Alexandridis et al., 2017)

Mechanisms	Biological traits	Trait values	Comments				
	T1. low temperature tolerance	eurythermal/stenothermal	Species that can tolerate continued exposure to single-digit temperatures (eurythermal) were distinguished from those t cannot (stenothermal).				
Resistance to perturbation	T2. early development mode	planktonic/laid/brooded	Trait values should define a gradient of increasing ability t cope with perturbations during the early life stages, due to increasing investment in early offspring survival.				
Dispersal	T3. larval dispersal distance	short/long	Species were separated in two groups based on their maximum observed dispersal distance, with a distance of 10 km used as the breaking point.				
potential	T4. maximum fecundity	low/high	Species were separated in two groups, with the number of 1000 eggs produced by a female of each species per year used as the breaking point.				
Environmental	T5. tidal emersion/ low salinity tolerance	emersed/euryhaline/ stenohaline	Soft bottom species that can tolerate long tidal exposure should be able to tolerate low salinity (emersed). Immersec species either can tolerate salinities that differ greatly from those of the open sea (euryhaline) or cannot (stenohaline).				
filtering	T6. preferred substrate type	mud/muddy sand/ sand/muddy gravel/ gravel/rock	The assignment of one value to each species represented greatest substrate affinity, but was often too restrictive.				
Competitive	T7. maximum size	1 cm/2 cm/10 cm/20 cm/ 40 cm	Trait values should define a gradient of increasing area tha can be searched for food or distance from the substrate, wi should enhance food availability (McLean and Lasker, 2013				
effect	T8. minimum space requirement	0.003/0.1/49.5 (min./median/max.) Values are not absolute, but rather relative levels.	Species with the lowest trait value should compete best for space (Tilman, 1980). Trait values were derived from data of body mass (Robinson et al., 2010) and use of an exponent 3/4 from the metabolic theory of ecology (Jetz et al., 2004).				
Response to	T9. preferred substrate position	infauna/interface/epifauna	Living deep in the sediment (infauna), at its upper layer (interface) or on its surface (epifauna) should allow species existence in spite of established competitive hierarchies.				
competition	T10. adult mobility	mobile/sessile	Differences in the ability of species to move should lead to resource partitioning and avoidance of competition.				
Population	T11. population growth rate	0.27/2.14/6.95 (min./median/max.) Values are not absolute, but rather relative levels.	Trait values were derived from data on body mass (Robinse et al., 2010) and use of an exponent of -1/4 from the metabol theory of ecology (Savage et al., 2004).				
dynamics	T12. maximum lifespan	1 yr/2 yr/10 yr/20 yr	Different trait values should reflect differentiations in specie population dynamics.				

habitat modification Sediment destabilizing species should inhibit sessile, tube stabilizer/destabilizer/ T14. role in sediment building species (stabilizers) and vice versa (Posey, 1987). engineering neutral Neutral species do not participate in sediment engineering. 2.3 Signed digraphs The structure of the system was represented by signed digraphs (networks of interactions that portray the interactions' direction and sign but not their strength) (Levins, 1998). The functional groups and the basic resources of food (algae/detritus) and space were depicted as nodes and the signs of the direct effects among them were represented by directed links between the nodes. A link ending in an arrow signified a positive direct effect, such as births produced through the consumption of prey, whereas a link ending in a filled circle signified a negative one, such as deaths from predation. A self-effect, as in self-thinning, was depicted as a link that starts and ends at the same node. Links were drawn based on functional relationships representing general community assembly mechanisms and the expected role of each group in them. This role was defined by the groups' assigned trait values and representative species (Table 1). The functional relationships encompass processes of 1) environmental filtering, 2) consumption of algae/detritus, 3) predation, 4) use of space, 5) food-space competition trade-off, 6) early survival-colonization trade-off, 7) biogenic habitat modification and 8) intra-group inhibition. Predation of benthos by fish and birds was not included, because the former plays a limited role in the Rance estuary,

basibiont/epibiont/neutral

T13. role in epibiosis

Biogenic

Species that can grow on other organisms (epibiont) were

distinguished from those that also provide biotic substrate

(basibiont). Neutral species do not participate in epibiosis.

- while the latter is highly seasonal and mostly restricted to the intertidal zone.

In addition to the explicit representation of space as a basic resource (see section 2.3.4), implicit spatial considerations were required for the representation of a few other processes (see sections 2.3.5–2.3.7). The modelled functional relationships represent interactions among populations of functional groups within an area that is adequately large for the processes that shape these inter-group interactions to occur. Intra-group spatial interactions were addressed independently (see section 2.3.8). 

<sup>649</sup> 207 **2.3.1** 

651 208 Environmental filtering

Epifaunal (T9) organisms with a preference for rock or gravel (T6) are clearly distinguished from infaunal or interface-positioned organisms (T9) that prefer finer sediment types (T6), with respect to both their functional characteristics (Alexandridis et al., 2017) and their distribution patterns in the Rance estuary (see section S1 in the Supplementary Material). This observation led to the drawing of two separate signed digraphs for these two groups of organisms, signed digraph 1 (SD1) for the former, epifaunal (Fig. 2a) and signed digraph 2 (SD2) for the latter, infaunal (Fig. 3a). Only group C6 is part of both models, because of the high mobility (T10) and ambiguous substrate preference (T6) of its species. The two sub-systems might co-occur but the way in which they interact is not addressed here. 

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677 220 **2.3.2** 

679 221 Consumption of algae/detritus

681<br/>682222Algae/detritus feeders along with predators/scavengers with the smallest682<br/>683<br/>684223maximum size (T7) among all functional groups (groups C1 in SD1 and C4 in SD2)685<br/>686224are assumed to consume the basic food resource, either from the water column or

through deposit feeding. This interaction was represented by a negative effect on food and a positive effect on consumers (Fig. 2b, 3b). Group H2 in SD1 was excluded from the consumption of the basic food resource, because of the grazing behaviour of its representative species. The bulldozing effect of this behaviour, which is expected to deprive other organisms of the free use of space (Pascual, 1997), was represented by a consumption interaction with this resource.

<sup>708</sup> 232 **2.3.3** 

710 233 **Predation** 

The majority of predators appear to be larger than their prey, and predator size generally increases with the size of prey (Cohen et al., 1993). This general observation formed the assumption that groups of predators/scavengers (except for the smallest groups C1 and C4) can only feed on groups that are smaller or similar in maximum size (T7). Prey groups were, still, not allowed to be smaller than 1/3 of the maximum size of the predator/scavenger groups themselves. The reason is that predator-prev body-size ratios are generally the lowest, just over 2 on average, for marine invertebrate predators, compared to predators of other taxonomic groups and habitat types, probably due to the energetic costs of prey capture and consumption (Brose et al., 2006a). 

Predation was represented by a negative effect on prey and a positive effect on predators (Fig. 2c, 3c). The predator/scavenger group C5 in SD1 is represented by a sea anemone and its adult mobility (T10) is restricted, hence, only mobile functional groups were considered as its potential prey. Since all predator/scavenger groups are characterized as epifauna or interface-related (T9), infaunal functional groups (groups H5, H6 and H12 in SD2) along with groups whose representative species are 

protected by plates (groups H2 and H3 in SD1), shells (groups H4, H13 in SD1 and
H14 in SD2) or tubes (groups H7 and H11 in SD2) were excluded from predator–prey
interactions.

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  - 3 255 Use of space

2.3.4

Just like food, space is assumed to be a basic resource that is "consumed" or used by groups of algae/detritus feeders. Predators/scavengers (including sessile group C5) are, instead, expected to only have their prey as their basic resource. In addition to the aforementioned group H2, space in SD1 is also used by algae/detritus feeders that are characterized as sessile (T10), since mobile organisms probably do not have such a strong interaction with space.

In SD2, we expect the role of organisms in sediment engineering (T14) to play a central role in their interaction with space, with sediment stabilizers being primarily limited by it. Organisms are also assumed to partition space, by occupying different positions with respect to the substrate (T9). Since the two-dimensional nature of the interface renders space particularly limiting for organisms that occupy this position, we set space as a resource only for stabilizing groups of the interface. The use of space by these organisms was represented by a negative effect on space and a positive effect on its consumers (Fig. 2d, 3d).

- 95 270
- 97 271 2.3.5
- 99 272 Food-space competition trade-off

In order to better represent differences in the functional roles of benthic
 organisms in a way that is consistent with the general trade-offs that are expected to

characterize these functional roles, we resorted again to the trait of maximum size (T7). Higher levels of this trait are expected to confer a competitive advantage for limited food resources, due to a larger area that can be searched for food or distance from the substrate, which enhances the availability of food from the water column (McLean and Lasker, 2013). On the other hand, maximum size (T7) appears to be positively associated with the trait of minimum space requirement (T8) among benthic macroinvertebrates of the Rance estuary (see section S2 in the Supplementary Material). Higher values of the latter trait should confer a competitive disadvantage for limited available space (Tilman 1980). We, thus, assumed that larger maximum size (T7) represents a competitive advantage for food and disadvantage for space. 

Based on this assumption, we divided the functional groups of each signed digraph that consume the basic food resource in two categories, the small and the big. We did so, by making sure that groups with similar sizes are placed in the same category and that there are more small than large groups (Blackburn and Gaston, 1994). The members of each category are expected to be limited by the resource for which they have a competitive disadvantage, while being able to efficiently reduce the levels of the resource for which they are competitively superior. This set of interactions was represented by an alteration of the existing resource consumption interactions, so that a functional group receives a positive effect from its limiting resource, while having a negative effect on the resource that it can efficiently reduce (Fig. 2e, 3e). This rule was not applied to any groups that would otherwise appear not to be limited by any of the basic resources, along with group H2 in SD1, whose relationship with space represents its bulldozing effect on macroinvertebrate recruits. 

860 298

- 299 2.3.6

Early survival-colonization trade-off

We used three traits to represent life history trade-offs: early development mode (T2), larval dispersal distance (T3) and maximum fecundity (T4). High levels for the last two traits appear to be associated with planktonic early development (T2) among benthic organisms in the Rance estuary, whereas low levels are associated with brooded early development (T2) and high population growth rates (T11) (see section S2 in the Supplementary Material). The former trait associations are expected to result in higher colonization potential, whereas the latter can be linked to higher early survival rates. The distinction between these groups of trait values represents a trade-off among benthic organisms in the allocation of resources toward early survival versus colonization potential (Tilman, 1990). 

Functional groups with planktonic early development, long dispersal distance and high fecundity are the only groups expected to effectively interact with the resource of space, because of their high dispersal potential. The mobility of group H2 in SD1 and its special relationship with space again excluded it from this rule. On the other hand, functional groups with brooded early development should be able to resist a variety of perturbations and, at least locally, reach high levels of abundance. They were, therefore, depicted as able to reduce the resource of food, even if their size did not qualify them to do so (Fig. 2f, 3f). 

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913 320 **2.3.7** 

915 321 Biogenic habitat modification

917322The organisms that are represented by SD1 are distinguished from the rest by918919323their epifaunal position (T9) and requirement for hard substrate (T6) (see section S2920921324in the Supplementary Material). Their occurrence in the Rance estuary can be at

least partly attributed to the phenomenon of epibiosis (T13), regardless of the basibiotic organisms being alive or not (Wahl and Mark, 1999). The provision of hard substrate by the single functional group that is described as basibiont (group H4) was represented by a positive effect on all algae/detritus feeders of the system and the sessile predator/scavenger group C5 (Fig. 2g). 

Substrate preferences among the organisms of SD2 (T6) appear to match their effect on the sediment (T14) (see section S2 in the Supplementary Material), in support of the mobility mode hypothesis and, hence, the separation of organisms into stabilizers and destabilizers (Posey, 1987). Sediment destabilization in the form of bioturbation should constitute the main mechanism of sediment engineering in estuarine soft bottoms (Meadows et al., 2012). Due to its high dispersal potential (T2, T3 and T4) and its role as a sediment destabilizer (T14), group H10 is expected to be mostly responsible for it. This group was, therefore, allowed to reduce the available space for stabilizing organisms of the interface and have a direct negative impact on infaunal stabilizers (groups H6 and H12). On the other hand, the ensuing bioirrigation is expected to generate favourable conditions for infaunal destabilizers and was depicted as a positive effect on group H5 (Fig. 3g). 

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968 343 **2.3.8** 

970 344 Intra-group inhibition

Negative self-effects were added to all variables of SD1 and SD2, representing a variety of processes (Fig. 2h, 3h). In the case of the two basic resources, negative self-effects are mostly indicative of the existence of intrinsic limitations in the amounts that are available to their consumers. Negative self-effects for the rest of the variables can be the result of, among other things, crowding, behavioural inhibition of 

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 950 reproduction, territoriality or accumulation of waste products (Levins, 1998). These or

similar processes appear to be wide-spread in ecological systems (Connell, 1983).

b а C5 C5 C6 **C**3 C1 C6 C3 **v**(C1) food (H4) space ...**⊳**(H4) space ····· НЗ (H1 (H1) (H2) НЗ (H13) (H2) d С (C6) (H4 space НЗ H13 (H2) (H2) (H13) e f (H2) (H13) (H13 h g 353

Fig. 2. Stepwise drawing of signed digraph 1 (SD1, epifauna). The steps represent processes of a) environmental filtering, b) consumption of algae/detritus, c) predation,d) use of space, e) food–space competition trade-off, f) early survival–colonization trade-off, g) epibiosis and h) intra-group inhibition. The nodes represent functional

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groups (see Table 1) or the basic resources of food and space. Links ending in arrows and filled circles represent positive and negative direct effects, respectively. Dashed and dotted lines represent links that are added and removed, respectively, at each step. See text for details 



Fig. 3. Stepwise drawing of signed digraph 2 (SD2, infauna). The steps represent processes of a) environmental filtering, b) consumption of algae/detritus, c) predation,

d) use of space, e) food-space competition trade-off, f) early survival-colonization trade-off, g) sediment engineering and h) intra-group inhibition. The nodes represent functional groups (see Table 1) or the basic resources of food and space. Links ending in arrows and filled circles represent positive and negative direct effects, respectively. Dashed and dotted lines represent links that are added and removed, respectively, at each step. See text for details 

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374 Feedback analysis

The concept of feedback in qualitatively specified systems, such as signed digraphs, can be defined at different levels of a system, depending on the number of interactions that are considered to participate in feedback cycles (i.e., closed paths of interactions linking a subset of a system's variables without crossing any of them twice). Feedback cycles at level 1 are self effects, at level 2 they comprise pair-wise interactions, such as predator-prey, with the highest level of feedback involving n interactions in a model with *n* variables. A cycle can consist of positive and negative interactions and the product of their signs sets the overall sign of the cycle. In general terms, negative feedback cycles provide stability and positive feedback cycles act to destabilize a system (Puccia and Levins, 1985). 

We assessed the potential for stability of our qualitative models as an indication of the likelihood of the respective systems to exist in nature. To this end, we followed the approach of Dambacher et al. (2003), who derived two criteria for the stability of qualitative models, classified conditionally stable models accordingly and developed stability metrics for each of the two model classes. The stability of class I models is jeopardized by positive feedback dominating feedback at the highest level of a 

system. Instability in class II models is characterized by overcompensation, which leads to oscillations, due to feedback at higher levels in a system overwhelming feedback at lower levels. The latter case can be assessed by measuring the relative balance of feedback at different system levels. 

Most biological systems appear to be represented by class I models and their potential for stability is determined by their maximum weighted feedback (Dambacher et al., 2003). This metric is calculated by counting all feedback cycles (both positive and negative) at the highest level of a system and computing the ratio of their net to absolute sums. It portrays the contribution of negative and positive feedback cycles to the overall system feedback. Values that tend toward -1 indicate a high potential for the variables of a system in equilibrium to converge toward their original levels following a pulse perturbation. Values that tend toward 1 indicate a high potential for post-perturbation divergence from these levels. Values near 0 show high ambiguity with respect to the system's stability potential. 

1195 405 The classification of the models and the calculation of the stability metrics were based on qualitatively specified community matrices, which are equivalent to signed digraphs as a representation of a system. With the help of tools specifically designed for their analysis (Dambacher et al., 2002), we assigned the gualitative models to one of the two stability classes. Based on this classification, we calculated the metric that quantifies each model's potential for stability. 

Signed digraphs were drawn, and from them qualitatively specified community matrices were derived using the digraph editor software PowerPlay version 2.0 (Westfahl et al., 2002). The stability analysis of the qualitative mathematical models was performed with a program for the qualitative and symbolic analysis of community was performed with a program for the qualitative and symbolic analysis of community

 416 matrices (*esapubs.org/archive/ecol/E083/022*) using the technical computing
417 software Maple version 18.0 (Maplesoft, 2014).

Building the signed digraphs of benthic macroinvertebrate communities in the Rance estuary left the epifaunal SD1 with 9 functional groups and the infaunal SD2 with 12, as group C6 participates in both models. In spite of having fewer groups, SD1 has 3 of them acting as predators, compared to only 2 predatory groups in SD2. Only 5 groups interact with algae/detritus in SD1 and 10 groups in SD2, while 3 groups interact with the basic resource of space in both models. The representation of the trade-off in competitive ability for food and space appears to have a deeper impact on the structure of the models than the trade-off between early survival and colonization potential. Incorporating the latter often resulted in a reversal of changes made to the models to represent the former. Biogenic habitat modification is of facilitating nature in SD1, taking the form of epibiosis, and of mostly inhibiting nature in SD2, where it represents bioturbation.

The qualitatively specified community matrices that correspond to SD1 (Table 3) and SD2 (Table 4) offer a detailed description of the interactions that comprise the two models. Of the 121 possible interactions in SD1 and the 196 possible interactions in SD2, only 36 occur in the former model and 41 in the latter. As a measure of system complexity, the proportion of possible interactions among each system's variables that are actually realized is equal to 0.29 in SD1 and 0.21 in SD2. SD1

comprises 21 negative and 15 positive interactions, while SD2 has the same number of positive interactions as SD1 and 26 negative. 

Table 3. Qualitatively specified community matrix corresponding to SD1 (see Fig. 2). Values along each column indicate negative (-), positive (+) or absent (0) direct effects of the respective variable on the variables of the rows. The variables 1294 446 1296 447 represent functional groups (see Table 1) or the basic resources of food and space

	food	space	H1	H2	H3	H4	H13	C1	C3	C6	C5
food	-	0	-	0	0	-	-	-	0	0	0
space	0	-	0	-	-	0	0	0	0	0	0
H1	+	0	-	0	0	+	0	0	0	-	0
H2	0	+	0	-	0	+	0	0	0	0	0
H3	+	0	0	0	-	+	0	0	0	0	0
H4	0	+	0	0	0	-	0	0	0	0	0
H13	+	0	0	0	0	+	-	0	0	0	0
C1	+	0	0	0	0	0	0	-	0	0	0
C3	0	0	0	0	0	0	0	0	-	+	-
C6	0	0	+	0	0	0	0	0	-	-	-
C5	0	0	0	0	0	+	0	0	+	+	-

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Table 4. Qualitatively specified community matrix corresponding to SD2 (see Fig. 3). Values along each column indicate negative (-), positive (+) or absent (0) direct effects of the respective variable on the variables of the rows. The variables represent functional groups (see Table 1) or the basic resources of food and space

	food	space	H5	H9	H14	H8	C2	C6	H6	H7	H10	H11	H12	C4
food	-	0	0	-	0	-	0	0	0	-	0	-	0	0

1340																
1341																
1342																
1343		space	0	-	0	0	-	0	0	0	0	0	-	0	0	0
1344		ЦБ		0		0	0	0	0	0	0	0		0	0	0
1345		115	т	0	-	0	0	0	0	0	0	0	Ŧ	0	0	0
1346		H9	+	0	0	-	0	0	-	0	0	0	0	0	0	0
1347		-		-	-		-	-		-	-	-	-	-	-	-
1348		H14	+	0	0	0	-	0	0	0	0	0	0	0	0	0
1349																
1350		H8	+	0	0	0	0	-	0	-	0	0	0	0	0	0
1351		C2	0	0	0	+	0	0	-	0	0	0	+	0	0	0
1352		02	0	0	0	•	Ū	0		Ū	Ū	Ū	•	Ū	0	Ū
1353		C6	0	0	0	0	0	+	0	-	0	0	+	0	0	0
1354																
1300		H6	+	0	0	0	0	0	0	0	-	0	-	0	0	0
1350		LI7		0	0	0	0	0	0	0	0		0	0	0	0
1358		Π/	÷	0	0	0	0	0	0	0	0	-	0	0	0	0
1359		H10	+	0	0	0	0	0	-	-	0	0	-	0	0	0
1360		-		-	-	-	-	-			-	-		-	-	-
1361		H11	0	+	0	0	0	0	0	0	0	0	0	-	0	0
1362		140		0	0	0	0	0	0	0	0	0		0		0
1363		HIZ	+	0	0	0	0	0	0	0	0	0	-	0	-	0
1364		C4	+	0	0	0	0	0	0	0	0	0	0	0	0	-
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1366	454															
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1370	456	3.2														
1371																
1372	457	Feedb	ack a	analys	sis											
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1374	458	Т	he re	esults	of th	ne sta	ability	analy	sis fo	or the	quali	tative	ly spe	ecified	com	munity
13/5											_					_
1370	459	matrice	es th	at co	rresp	ond to	o SD1	l and	SD2	ares	showr	n in T	able	5. Th	e pat	tern of
1378																
1379	460	increas	sing	weigh	ited fe	edba	ck wit	h incr	easing	g syst	em le	vel fo	r both	mod	els ind	dicates
1380																
1381	461	that the	eir st	ability	could	be c	ompro	omise	d by p	ositiv	e feed	lback	domir	nating	feedb	back at
1382			_													
1383	462	the hig	phest	level	of the	e syst	em ra	ther t	han b	y ove	rcomp	pensa	tion; S	SD1 a	nd SE	02 are,
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1385	463	therefo	ore, o	class	l mo	dels	(sens	u Dai	mbacl	her e	t al.	(2003	)). Co	onseq	uently	, their
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1387	464	potent	ial fo	or sta	bility	is de	termir	ned b	y the	ir ma	ximun	n wei	ghted	feed	back,	which
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1389	465	quantif	fies t	he co	ontribu	ution	of neg	gative	and	positi	ve fe	edbac	k cyc	les to	the	overall
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168	lev	el of a	mbigu	ity with	n respe	ect to th	ne stat	pility po	otentia	l of the	e syste	m.			
1.0															
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170	Tak	Table 5 Results of the stability analysis for the systems represented by SD1 (see													
+/U	Table 5. Results of the stability analysis for the systems represented by SDT (See														
171	Fig. 2) and SD2 (see Fig. 3). Values along each row correspond to weighted														
T/1	ing. 27 and 502 (see ing. 3). values along each row correspond to weighted														
172	feedback (wE) calculated at the system level that is indicated by the ensuing number														
			()								,		3		
173	The	e value	e of ma	aximur	n weig	hted fe	edbad	ck for e	each m	nodel is	s indica	ated by	/ an as	terisk	
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		wF1	wF2	wF3	wF4	wF5	wF6	wF7	wF8	wF9	wF10	wF11	wF12	wF13	wF14
-															
	SD1	-1	-1	-0.99	-0.97	-0.94	-0.9	-0.83	-0.75	-0.66	-0.57	-0.5*	-	-	-
	SD2	-1	-1	-1	-0 99	-0.98	-0.95	-0.9	-0 84	-0 77	-0 69	-0.6	-0 51	-0 42	-0 33*
	002	1	1	•	0.00	0.00	0.00	0.0	0.04	0.11	0.00	0.0	0.01	0.42	0.00
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170			1111	л апо	SD2	the ha	sic res	ources	s of for	nd and	space	are n	ап ог г	OSITIVE	ć
				Ji and	SD2, 1	the ba	sic res	ources	s of foo	od and	space	are p	art of p	ositive	9
177	fee	dback	cvcle	s of le	SD2, t ength f	the ba our. Ir	sic res n the c	ources case o	s of foc of SD1	od and , the r	space oositive	are p feed	art of p back c	vcle is	6
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477 478	fee forr	dback med w	cycle	s of le	SD2, f ength f 13 and	the ba our. Ir I H4 (I	sic res n the c Fig. 4a	ources case o a). The	s of foo of SD1 e forme	od and , the p er, bei	space positive ng sma	are p e feed all, is	art of p back c enhan	ced by	9 6 /
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1 1 1 1 1 1 1 1 1	67 68 69 70 71 72 73 - 74 75 75 76	67 dor 68 lev 69 70 Tak 71 Fig 72 fee 73 The 5D1 5D2 74 75 76	<ul> <li>67 dominance</li> <li>68 level of an end</li> <li>69</li> <li>70 Table 5.</li> <li>71 Fig. 2) a</li> <li>72 feedback</li> <li>73 The value</li> <li>wF1</li> <li>SD1 -1</li> <li>SD2 -1</li> <li>74</li> <li>75</li> <li>76 In be</li> </ul>	67 dominance of 1 68 level of ambigu 69 70 Table 5. Resul 71 Fig. 2) and S 72 feedback (wF) 73 The value of ma wF1 wF2 SD1 -1 -1 SD2 -1 -1 74 75 76 In both SE	67 dominance of negative 68 level of ambiguity with 69 70 Table 5. Results of the 71 Fig. 2) and SD2 (set 72 feedback (wF) calcular 73 The value of maximum wF1 wF2 wF3 SD1 -1 -1 -0.99 SD2 -1 -1 -1 74 75	dominance of negative feed level of ambiguity with respect Table 5. 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Values alon feedback (wF) calculated at the system level th The value of maximum weighted feedback for e wF1 wF2 wF3 wF4 wF5 wF6 wF7 SD1 -1 -1 -0.99 -0.97 -0.94 -0.9 -0.83 SD2 -1 -1 -1 -0.99 -0.98 -0.95 -0.9 74	dominance of negative feedback cycles over positiv level of ambiguity with respect to the stability potentia Table 5. Results of the stability analysis for the sys Fig. 2) and SD2 (see Fig. 3). Values along eac feedback (wF) calculated at the system level that is in The value of maximum weighted feedback for each m $\frac{\text{wF1 wF2 wF3 wF4 wF5 wF6 wF7 wF8}}{\text{SD1 -1 -1 -0.99 -0.97 -0.94 -0.9 -0.83 -0.75}}$ SD2 -1 -1 -1 -0.99 -0.97 -0.98 -0.95 -0.9 -0.84 74	dominance of negative feedback cycles over positive one level of ambiguity with respect to the stability potential of the Table 5. Results of the stability analysis for the systems Fig. 2) and SD2 (see Fig. 3). Values along each row feedback (wF) calculated at the system level that is indicate The value of maximum weighted feedback for each model is $\frac{WF1  WF2  WF3  WF4  WF5  WF6  WF7  WF8  WF9}{SD1  -1  -1  -0.99  -0.97  -0.94  -0.9  -0.83  -0.75  -0.66}{SD2  -1  -1  -1  -0.99  -0.98  -0.95  -0.9  -0.84  -0.77}$	dominance of negative feedback cycles over positive ones, alor level of ambiguity with respect to the stability potential of the system Table 5. Results of the stability analysis for the systems represent Fig. 2) and SD2 (see Fig. 3). 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Values along each row correspond to we feedback (wF) calculated at the system level that is indicated by the ensuing m The value of maximum weighted feedback for each model is indicated by an as $\frac{WF1  WF2  WF3  WF4  WF5  WF6  WF7  WF8  WF9  WF10  WF11  WF12 \\ SD1  -1  -1  -0.99  -0.97  -0.94  -0.9  -0.83  -0.75  -0.66  -0.57  -0.5^{+}  - \\ SD2  -1  -1  -1  -0.99  -0.98  -0.95  -0.9  -0.84  -0.77  -0.69  -0.6  -0.51 \\ \hline 74 \\ \hline 75 \\ \hline 76 \\$	dominance of negative feedback cycles over positive ones, along with a moderate level of ambiguity with respect to the stability potential of the system. Table 5. Results of the stability analysis for the systems represented by SD1 (see Fig. 2) and SD2 (see Fig. 3). Values along each row correspond to weighted feedback (wF) calculated at the system level that is indicated by the ensuing number The value of maximum weighted feedback for each model is indicated by an asterisk $\frac{wF1 wF2 wF3 wF4 wF5 wF6 wF7 wF8 wF9 wF10 wF11 wF12 wF13}{SD1 -1 -1 -0.99 -0.97 -0.94 -0.9 -0.83 -0.75 -0.66 -0.57 -0.5* SD2 -1 -1 -1 -1 -0.99 -0.98 -0.95 -0.9 -0.84 -0.77 -0.69 -0.6 -0.51 -0.4274$

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1481	/89	Fig. 4. Positive feedback cycles from a) SD1 (see Fig. 2) and b) SD2 (see Fig. 3)
1482	407	The the readback cycles from a ODT (see Fig. 2) and b) OD2 (see Fig. 3).
1483	400	Each foodback avala links the basic resources of food and appear with one big and
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1485	401	and another stands around interpreter in any support filled simples represent positive
1486	491	one small functional group. Links ending in arrows and filled circles represent positive
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1488	492	and negative direct effects, respectively
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1500	109	Qualitatively specified feed web models often represent only a few dominant
1500	498	Qualitatively specified tood-web models often represent only a few dominant
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1502	499	species of marine benthic macroinvertebrates, while other community members may
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1505	500	be grouped into broad trophic categories (e.g., Carey et al., 2014; Reum et al., 2015).
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1507	501	This practice cannot explicitly account for key non-trophic interactions and tends to
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1500	502	ignore the rarest members of a community, in spite of evidence for their significant
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1511	503	contribution to ecosystem functioning (Lyons et al., 2005). This contribution can be
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1519<br/>1520504disproportionate to their abundance, as species with the most distinct combinations of1521<br/>1522505traits have been shown to be rarer than expected by chance (Mouillot et al., 2013).

The variables of the models developed here were built through a procedure that places emphasis on the species' functional role instead of their abundance; the latter is used only secondarily for the assignment of trait values to each group (Alexandridis et al., 2017). The wide functional scope of the traits that formed the basis for the grouping allowed the representation of not just trophic interactions, but the majority of the mechanisms that are expected to shape benthic communities in many parts of the world. Trait variation within the groups was found to be largely neutral, allowing a system representation that is free of functionally equivalent variability (Hérault, 2007). 

1543 515 **4.2** 

### 516 Signed digraphs

The evaluation of the functional grouping against its theoretical assumptions suggested that species abundances in the Rance estuary depend, at least to some extent, on species trait values (Alexandridis et al., 2017). The nature of this relationship was further elucidated through the investigation of associations of biological traits with environmental variables and with each other (see Supplementary Material). These results were combined with theoretical expectations and expert knowledge to define functional relationships between the groups and their basic resources. 

Each of the community assembly mechanisms that are represented by these relationships encompasses a variety of processes that could potentially be represented much more explicitly. The level at which each mechanism was actually represented was dictated by the available trait and environmental information. Hence, 

<sup>1578</sup> 529 biological traits were used as proxies for the role of functional groups in a set of
 <sup>1580</sup> 530 theoretically expected community assembly mechanisms that were illustrated through
 <sup>1582</sup> 531 a highly abstract representation of the system.

For instance, the biogeochemical aspects of sediment engineering were not explicitly represented, as the distinction between sediment stabilizers and destabilizers (Posey, 1987) was the best possible representation, given the available information at the species level. Still, this tenet of the mobility-mode hypothesis has been empirically upheld and shown to have cascading and long-lasting effects on benthic communities (Volkenborn et al., 2009). Similarly, the complex set of processes that comprise the phenomenon of resource competition was only represented through the use of each group's maximum size in the context of the concentration reduction hypothesis for space and food (Tilman, 1980). Space limitation due to adult-juvenile interactions and exploitative competition for food have been shown to play a central role in the successional dynamics of benthic communities, with the functional role of organisms largely defined by their size (Van Colen et al., 2008). The combined representation of food and space as limiting resources can significantly increase our understanding and predictability of marine benthic systems (Svensson and Marshall, 2015). 

The separation of benthic macroinvertebrates into algae/detritus feeders and predators/scavengers aimed to preserve the homogeneity of their resource base, so that theoretically expected community assembly mechanisms could be implemented. This choice might appear to ignore important differentiations in the feeding habits of these organisms, such as the distinction between suspension- and deposit-feeders. It has been, however, shown that feeding behaviour in the marine benthos is highly facultative and similar categorizations are not always valid (Snelgrove and Butman, 

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1994). Instead, the modification of networks of trophic interactions through expert
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knowledge is expected to increase their realism, while the use of allometric scaling
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should enhance their stability (Brose et al., 2006b).

Survival rates (Schratzberger and Larcombe, 2014) and colonization potential (Limberger and Wickham, 2011) have been separately involved in trade-offs with the competitive ability of benthic organisms. Our assumptions allow for both scenarios, while the deconstruction of competitive ability into two constituents, for the basic resources of food and space, could resolve inconsistencies in previous findings. 

The role of recruitment in the assembly of benthic communities may still be under-represented. Biological traits related to species' reproductive strategy were found to deviate the most from the theoretical assumptions that allowed the construction of the functional groups (Alexandridis et al., 2017). Relevant trait information is, however, consistently lacking (Tyler et al., 2012). A more accurate depiction of recruitment-related processes would allow the explicit representation of trade-offs that have been shown to play a significant role in the assembly of benthic communities (Lindquist and Hay, 1996; Marshall and Steinberg, 2014). 

The functional divergence between organisms that occupy the surface of the sediment (epifauna) and those that are buried in it (infauna) has been previously recognized in the study of marine benthos (Reiss et al., 2010). In the Rance estuary, the epifauna (SD1) features a lower functional diversity of algae/detritus feeders and a higher functional diversity of predators/scavengers, compared to the infauna (SD2). Additionally, a much higher number of groups ended up interacting with algae/detritus in SD2 compared to SD1. The complex diagenetic processes that affect the basic food resource within the sediment of the seafloor (Herman et al., 1999) could be responsible for the diversity of infaunal organisms that feed on it. On the other hand, 

the high structural complexity of the habitat occupied by epifaunal organisms may result in a higher diversity of predatory strategies. Trophic differences could be associated with a variety of biological traits, leading to observed patterns of functional diversity. The epifaunal system also appears to be more complex, with a higher proportion of possible interactions realized compared to the infaunal system. This is primarily caused by an under-representation of positive interactions in the latter system. The gualitatively antithetical role of biogenic habitat modification in the two systems (facilitating in SD1, mostly inhibiting in SD2) contributes partly to these differences. Its impact may extend to productivity patterns, as epifauna-dominated systems (seagrass/algae beds) seem in general to be more productive than infauna-dominated (estuaries) (Costanza et al., 1998). 

591 4.3

592 Feedback analysis

The results of the stability analysis suggest that the models developed in this work have a moderate to high potential for stability. This demonstrates the likelihood of the system to persist in time in spite of perturbations. These perturbations can take various forms, from local sediment re-suspension due to wave action, to system-wide reduction of secondary production during extremely cold winters (Desroy, 1998). Despite the impact of such pulse perturbations on spatial and temporal distribution patterns of benthic macroinvertebrates, the composition of their communities has been mostly stable in the Rance estuary since late 1970's. The agreement between observed stability levels and the predictions of feedback analysis can be considered as partial validation of the generated models. 

Populations of benthic macroinvertebrates in the Rance estuary are still expected to change in response to constant or press perturbations, but in a way that can be attributed to the structure of the qualitative models. For instance, the participation of the basic resource of food in positive feedback cycles in both SD1 and SD2 allows the formulation of predictions about the direction in which the other variables in these cycles would respond as a result of system-wide persistent changes in primary production. Within these cycles, which constitute a qualitative representation of Tilman's (1980) concentration reduction hypothesis, a decrease in the amount of available food is expected, in general, to lead to less smaller and more larger individuals, with a concomitant increase in the amount of available space. Similar patterns have been observed as a result of bathymetric decreases in nutrient input (Rex and Etter, 1998) and can have profound impacts on the functioning of ecological systems (Woodward et al., 2005). 

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618 Conclusions

Qualitative mathematical models have been successfully employed for the study of both soft- (Ortiz and Wolff, 2002) and hard-bottom (Marzloff et al., 2011) marine benthos. The properties of these models make them particularly well-suited for the integration of systems that comprise processes of disparate nature (Dambacher et al., 2007). Our approach primarily differs from previous work in the way organisms are represented and interactions are attributed between them. This is done through a 1800 624 systematic procedure that employs theoretical and expert knowledge from a wide range of sources. It can be applied, with adjustments of various degrees, for the 

1815
 627 mechanistic representation of many ecological systems for which empirical
 1816 1817
 628 information is limited.

Qualitative models sacrifice the element of precision, in order to produce a general and realistic representation of the causal relationships that shape a system (Levins, 1966). When there is uncertainty in the model components or interactions, alternative model configurations can be easily generated and assessed with respect to the functioning of the system (Dambacher et al., 2002). Qualitative modelling can, therefore, direct the initial steps of more quantitative approaches, before investment in model development has rendered structural changes too costly. We plan to use this property to inform the structure of dynamic and spatially explicit trait-based models of marine benthic communities in the Rance estuary (Alexandridis, 2017). 

Similar efforts in terrestrial environments were able to predict the responses of plant (Boulangeat et al., 2014) and animal communities (Scherer et al., 2016) to projected climatic and land use change. They faced issues that are shared by our study, such as the lack of information on important biological traits or the limited potential for validating model predictions with species data. Quite similar to our study, they addressed these issues by using surrogate traits or investigating the plausibility of their findings in view of specific system perturbations. The conclusion of our work should help bridge the gap between terrestrial and marine systems with regard to the formulation of reliable predictions of biodiversity responses to environmental change. 

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### SUPPLEMENTARY MATERIAL

### S.1 Environmental filtering

### S.1.1 Methods

Each station sampled in the spring of 1995 was associated with a particular sediment type (pure mud, mud, silty mud, sandy mud, muddy sand, fine/intermediate sand, intermediate/coarse sand, coarse sand, gravel), based on a sedimentary map established in 1994 (Bonnot-Courtois, 1997). The depth (or elevation) of each station was measured at low tide during the collection of samples. Each station was assigned a salinity regime, depending on which of three sectors of the Rance estuary it was situated in. The innermost part of the estuary, up to Pleudihen-sur-Rance, was subject to high salinity variation, ranging from 0.5 to 30. Beyond this point, downstream to Port-St-Hubert, salinity values ranged between 18 and 30. The rest of the estuary experienced more or less constant salinity levels, over the value of 30, similar to those of the open sea (Desroy, 1998).

Among the 14 biological traits for which the species of the system were assigned with values, we expect the trait of tolerance to tidal emersion and low salinity levels (T5) along with that of preferred substrate type (T6) to adequately represent the most important environmental limitations that are faced by benthic macroinvertebrates in the Rance estuary (Desroy, 1998). If this is indeed the case, these two biological traits, describing species preference for abiotic conditions, should show high degrees of covariation with the respective environmental variables. Other biological traits that might correlate with the two traits in question are also expected to show similar patterns of covariation.

RLQ analysis is a statistical technique that can relate the biological traits of organisms to the characteristics of the environment in which they live (Dolédec et al., 1996). L refers to a table of species abundance at a number of sites and it describes, among other things, the actual habitat utilization of different species. R refers to a table of environmental variables measured at the same sites as species abundance. Q refers to a table of biological traits for all the species of table L. RLQ analysis starts with the separate ordination of table L. It then uses the resulting sites and species weights in the separate ordinations of tables R and Q, respectively. The result is an ordination of the common structure of tables R and Q with a link expressed by table L.

Since environmental variables and biological traits include both qualitative and quantitative information, we opted for Hill and Smith analysis (Hill and Smith, 1976) for the separate ordinations of the 113 sites  $\times$  3 environmental variables (R) and the 240 species  $\times$  14 biological traits (Q) tables. Correspondence analysis (Legendre and Legendre, 1998) was

performed for the separate ordination of the 113 sites × 240 species abundance table (L). The application of correspondence analysis allows RLQ analysis to maximize the covariance between linear combinations of environmental variables and biological traits (Dolédec et al., 1996). This maximized covariance, projected on orthogonal axes of decreasing contribution to the total value, is called co-inertia.

The comparison of this eigenvalues decomposition (RLQ) with the eigenvalues decomposition from the separate ordinations of the environmental variables (R) and biological traits (Q) tables can show what part of the variance of the original data sets is represented in their common structure. The optimal correlation between sites and species scores from the separate ordination of the species abundance table (L) can be compared with the equivalent correlation from the RLQ analysis, in order to illustrate how well the original species abundance patterns are represented by the associations between environmental variables and biological traits. These associations can be best demonstrated by projecting environmental variables and biological traits side-by-side on the same dimensions of the common co-inertia space.

All analyses were performed using the statistical software R version 3.2.2 (R Core Team, 2015) with the package ade4 (Dray and Dufour, 2007).

### S.1.2 Results

The eigenvalues decomposition of the RLQ analysis shows that the proportion of the common structure between environmental variables and biological traits that is portrayed along the first axis (73%) is much larger than the proportion that is portrayed along the second one (17%). The first two axes combined represent 90% of the covariance between environmental variables and biological traits. The cumulated amount of variance that is preserved on the first two axes of the RLQ ordination, compared to the equivalent variance from the separate ordinations of the environmental variables (R) and biological traits (Q) tables, is just over 85% in both cases. The correlation values between sites and species scores along the first and second axes of the RLQ analysis are 76% and 60% of the respective correlation values from the separate ordination of the species abundance table (L).

The side-by-side projection of environmental variables (Fig. S1a) and biological traits (Fig. S1b) on the first two dimensions of the common co-inertia space reveals one conspicuous pattern: coarse sediment types are strongly associated with trait values that represent preference for gravel or rock (T6), no role in sediment engineering (T14), an

epifaunal position (T9) and the role of basibionts (T13). These trait values, along with the one that identifies epibiotic organisms (T13) and is associated with increasing water depth, are all characteristic of benthos that occupies the surface of the seabed, supported by structure of abiotic or biotic origin. Increasing water depth is further associated with a transition from organisms that tolerate tidal exposure to those that have to be submerged in high salinity levels (T5).



**Fig. S1** Projection of a) environmental variables and b) biological traits on the first two dimensions of the common co-inertia space of the RLQ analysis. In both graphs the horizontal axis represents the first dimension and the vertical the second. In the case of continuous and ordinal variables, the arrows indicate the direction of increasing values. In the case of nominal and binary variables, the tips of the arrows indicate the position of the centroids for the respective variable values (shown as variable.value). Plural in the variable names indicates the representation of multiple values that are close in nature and ordination. For details about the traits, see Table 2

### S.2 Functional trade-offs

### S.2.1 Methods

Our set of 14 biological traits allows the representation of functional trade-offs through specific combinations of trait values. In the case of a trade-off among benthic macroinvertebrates in their utilization efficiency for the two basic resources (food and space) (Tilman, 1980), we would expect trait values that confer a competitive advantage for each resource (greater size (T7) and lower minimum space requirement (T8)) to be negatively associated. A trade-off in the allocation of resources toward early survival versus colonization potential (Tilman, 1990) would result in the survival-enhancing brooded early development mode (T2) being negatively associated with both dispersal distance (T3) and maximum fecundity (T4). Finally, the stabilizers of the mobility-mode hypothesis (Posey, 1987) are expected to bind fine particles, thus leading to the creation of muddy sediments, while destabilizers are expected to disrupt the substrate, resulting in more heterogeneous sediment types. Since each group is assumed to create sediment conditions that are favourable to its own members and detrimental to those of the opposite group, sediment preferences (T6) among stabilizers and destabilizers should correspond to their respective effects on the substrate (T14).

Because values were assigned to the species independently for each biological trait, we can assess the ecological pertinence of each hypothesis, by inspecting the biological traits data set, looking for the respective trait associations. The multivariate ordination technique of Hill and Smith allowed the transformation of the 240 species  $\times$  14 biological traits table into a set of orthogonal variables that contain decreasing portions of the table's total variance (Hill and Smith, 1976). The eigenvalues decomposition, on which this technique is based, reveals the amount of variance that each of these variables represents. The projection of the initial trait variables on the first few axes of the transformed multivariate space can provide insights into the most important associations among biological traits.

All analyses were performed using the statistical software R version 3.2.2 (R Core Team, 2015) with the package ade4 (Dray and Dufour, 2007).

### S.2.2 Results

The eigenvalues decomposition of Hill and Smith for the biological traits data set shows that about twice as much variation can be found along each of the first two axes (15% and 14% of total variation) compared to each of the two axes that follow (8% and 7% of total

variation). The first four axes combined represent just over 43% of the total variation of biological traits among species of benthic macroinvertebrates.

The projection of biological traits on the first four dimensions of the transformed multivariate space reveals the most important biological trait associations. Along the first axis (Fig. S2a), maximum size (T7) is assumed to define a competitive hierarchy for food. Minimum space requirement (T8), in the same direction of the axis, is expected to define an inverse competitive hierarchy for space.

On the positive half of the first axis (Fig. S2a), high levels of maximum fecundity (T4) and dispersal distance (T3) are associated with planktonic early development mode (T2). The combination of these trait values is expected to lead to higher colonization potential among marine benthos. On the negative half of the same axis, low levels of maximum fecundity (T4) and dispersal distance (T3) are associated with brooded early development mode (T2) and high population growth rate (T11), thus forming a trait combination that is assumed to enhance early survival rates.

The second axis of the Hill and Smith ordination (Fig. S2a) mainly serves to distinguish organisms with an epifaunal position (T9) and requirement for hard substrates (T6). Trait differences among the rest of the organisms, which are mostly associated with soft bottoms (T6), are featured along the first (Fig. S2a) together with the third and fourth axes of the ordination (Fig. S2b). It appears that sessile organisms (T10) that prefer mud (T6), stabilize the sediment (T14) and create substrate for epibionts (T13) are distinguished from mobile (T10), destabilizing organisms (T14) that have a preference for coarser and mixed sediment types (T6).



**Fig. S2** Projection of biological traits on a) the first and second and b) the third and fourth dimensions of the transformed multivariate space of Hill and Smith analysis. In both graphs the horizontal axis represents the lower dimension and the vertical the higher. In the case of continuous and ordinal traits, the arrows indicate the direction of increasing values. In the case of nominal and binary traits, the tips of the arrows indicate the position of the centroids for the respective trait values (shown as trait.value). For details about the traits, see Table 2

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