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Diversity beyond species richness along the salinit gradient of the Baltic Sea

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Diversity beyond species richness along the salinity gradient of the Baltic Sea

Ansatz zur Berechnung der Diversität entlang des Salzgradienten der Ostsee über Betrachtung des Artenreichtums hinaus

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1 Introduction

The Baltic Sea is located between central Europe and the Scandinavian Peninsula. The only connection the Baltic Sea has to an ocean is through the Kattegat and Skagerrak, which provides a link with the North Sea, and thereby, with the Atlantic Ocean. This is responsible for most of the Baltic Sea´s characteristics, and this small connection to fully saline waters also causes other specifics, such as the necessity of influx events of saline and oxygen rich water from the North Sea (Meier, 2007). First of all, most parts of the Baltic Sea are shallow and only a few areas show greater depths. The bathymetry of the Baltic Sea was formed through glacial erosion during the last ice ages. It is a rather young sea with a dynamic and continually evolving ecosystem. Equally, in the triangle between Sweden, Denmark and Germany, many both bigger and smaller islands diffuse the water inflows from the west; another factor that adds to various gradients along the waters of the Baltic. One main factor that diminishes from west to east is the salinity. Naturally, salinity is one central environmental factor that any marine animal must adapt to. Other abiotic factors that are relevant for the biodiversity of the Baltic Sea include bathymetry or the seabed substrate type (Gogina & Zettler, 2010). Further driving factors are oxygen content, temperature fluctuations, or the nutrient flow.

Benthic organisms and communities are no exception to these environmental rules. Differences in salinity is one factor that has a big impact on the diversity and community structure of benthic invertebrates (Ojaveer et al., 2010). Diversity has always been one of the major focuses of ecology and, over the years, and with progress in scientific knowledge, the concept of diversity has changed and become increasingly broad and today we distinguish between many different types (Bleich et al., 2011; Tuomisto & Ruokolainen, 2008).

In the past, indices such as Shannon- Wiener or Simpson- Yule, were used to describe communities and ecosystems, various other diversity indices account for species diversity, species richness and species eveness. In marine benthic ecosystems, functional diversity has traditionally been addressed by describing the taxonomic composition of assemblages (Bremner et al., 2003). Ecological experiments, observations and theoretical developments show that ecosystem function depends greatly on biodiversity in terms of the “functional characteristics” of organisms present in the ecosystem, and also on their distribution and abundance over space and time (Loreau et al., 2001). To investigate the functional characteristics of an ecosystem or a community, the assessment of behaviour displayed by

species that inhabit a certain area holds the descriptive power to characterise that ecosystem or community. The ability of ecosystems to function depends more on species specific traits than species richness (Loreau et al., 2001).

A new tool for such tasks has recently evolved. Biological traits analysis (BTA) is based on the habitat template theory, which states that species' characteristics evolve in response to habitat constraints (Southwood, 1977). BTA consolidates information on species functional and morphological features and is therefore able to illustrate the interdependency of abiotic criteria and species behaviour or traits. BTA is based on the assumption that phylogenetically unrelated organisms might have evolved with similar biological adaption, thus leading to functional similarity combined with taxonomic dissimilarity (Dolédec & Statzner, 1994). BTA stresses the fact of interdependency between species and habitat: special features of a species are exhibited in response to the environment or habitat. In other words, a species that displays their distinctive behaviour or traits, in turn regenerates the habitat they exist in. The functional structure of a community can be represented by a set of traits describing behavioural and morphological characteristics displayed by the observed species. The traits and their function both determine the functioning and stability of communities and ecosystems (Loreau et al., 2001).

BTA was largely developed in terrestrial and freshwater ecology (Olff et al., 1994; Townsend & Hildrew, 1994; Chevenet et al., 1994; Dolédec & Statzner, 1994), but is also a useful analytical approach in describing different aspects of function based on 'multiple' biological traits of aquatic invertebrates (e.g. mobility, feeding type, size, life span, and reproductive technique) (Bremner et al., 2003). In order to compile such a database of biological traits, a vast amount of information is needed. Even though this approach has been used for some years now, there is still less information on marine benthos than freshwater (Bremner et al., 2006), and even less for brackish waters.

Regardless of this, researchers have used BTA for various study purposes in recent years. It was used to assess the effects of disturbance on biological traits of invertebrates in freshwater ecosystems (Dolédec et al., 1999), to investigate fishing effects on benthic fauna (Bremner et al., 2003; Tillin et al., 2006), and to show functional diversity in different species assemblages (Bremner et al., 2003; Hewitt et al., 2008). The potential of BTA is even greater, however. Marchini et al. (2008) identified dominant traits in different transitional environments such as Mediterranean lagoons, and Neumann & Krönke, (2010) even used this tool to investigate the

effects of climate change. Recently, authors have increasingly used BTA to asses diversity along gradients (v. d. Linden et al. 2012; Darr et al., 2014) and it has simultaneously gained popularity as a management tool for conservation purposes (Bremner 2008; Frid et al., 2008). All of these developments are due to the fact that BTA holds a considerable advantage over traditional methods (Neumann & Krönke, 2010).

All of these examples demonstrate that BTA, in contrast to other conventional, taxonomical means, is able to assess functional diversity more expansively and serves as a framework for further analytical measures.

The aim of this study is to introduce and apply an advanced biological traits database, as newly compiled by the author, for the most dominant species in the German Baltic Sea. The database was created for the internal use of the working group, "Ecology of benthic organisms" at the IOW (Institut für Ostseeforschung Warnemünde). Additionally, this study will attempt to illustrate the differences in communities along a gradient under otherwise similar environmental conditions, and, if possible, identify functional differences that contribute to these community differences. In accordance, two hypotheses will be reviewed. Firstly, a reduction of abundance from higher to lower salinity is expected and secondly, a clear distinction between both key areas is expected to be shown.

2 Material and Methods

2.1 *Study area*

The study area is stretched throughout the majority of the German part of the Baltic Sea. All of the processed data is compiled in a large database which was provided by the Baltic Sea Research Institute (Institut für Ostseeforschung Warnemünde – IOW). The initially available part of the database is organized in a large Microsoft Excel file containing data from several monitoring, among other, programs of the Baltic Sea between 1999 and 2013. All of these programs were implemented by the IOW for IOW- internal projects, or in cooperation with BfN, BSH or DHI. For each sampling event presented in the database, four replicates were collected using a 0.1 m2 Van Veen grab. Three replicates were sieved through a 1 mm size mesh and preserved in a formaldehyde seawater solution for further biological analysis. The fourth replicate was frozen for granulometric analysis of the sediment. Overall, the unfiltered database comprises over 65,000 rows within the file giving information on the location of the sampling stations, such as their coordinates, in which program they were collected, and by

whom. Further abiotic parameters are also displayed in the database. These include median grain sizes of the substratum, the organic content of the substratum, the bottom near oxygen content in ml/l and salinity and depth of each sampling station. A vital part of this work is the biotic data, in addition to the species found at every location: the database gives information on each species abundance (in individuals per m^2) and their fresh weight, dry weight and ash free dry weight, which are all measured in mg per m^2.

The aim of the study was to compare diversity in species and their traits along the salinity gradient, and therefore, particular key areas needed to be established. First, all stations were filtered for those with a median grain size between 150 and 250 µm and a depth of between 10- 15 m. Unfortunately, these criteria did not leave enough stations to form a comparable set of data. So, in a second step, the database was filtered again for grain sizes ranging from 63 to 500 µm representing fine sand and medium sand according to the international scale (ISO 14688-1). In the same manner, the filter for depth was reset to stations of 10- 18 m deep. Initially four key areas were distinguished, representing from west to east the Kiel bay, Fehmarnbelt, Kadettrinne and Oderbank. Each of the key areas contained between 18 and 34 sampling stations. After reconsideration, the scale of median grain sizes was identified as being too wide, spreading from 63 to 500 µm designating fine to medium sand. The selected stations ran the risk of leaving misinterpretable results, by introducing the sediment gradient that could mask out the effect of salinity gradient that is in major focus in this case study. Different species with different traits might be analysed in a dataset with such a big variation. Species at the lower end of the selected range of median grain size are more likely to show special and distinct different behaviour than those at the upper end in more coarse sand. This potential source of error had to be eliminated as the goal of the study was to assess the change in diversity along the salinity gradient. Diversity changes always result from the complexity of interaction of abiotic and biotic factors. Therefore, analysing the change of diversity along a distinct single gradient is hard to perform. Nevertheless parameters can be chosen carefully and in a narrow scope to minimize their effect on diversity change. In a third step, stations were filtered again for grain sizes between 100 and 300 µm, the depth range remained as before with 10- 18 m. The now selected stations led to a new allocation of key areas. Due to their sediment structure, a lot of stations from the intermediate key areas, Fehmarnbelt and Kadettrinne, were excluded after repeated filtering of the database, leaving those areas with merely six or seven stations. This amount of sampling stations was considered too small for being representative for a certain area. Additionally those stations left spread over quite a vast

expanse. Due to this fact, these two key areas were excluded from the analysis so the remaining areas now were Kiel Bay as the westernmost and Oderbank as the easternmost. Later in the analysis the biomasses of single stations were supposed to be multiplied with the data from a biological traits analysis (BTA). To avoid bias of statistical analysis an equal amount of stations per key area is intrinsic. In the Kiel Bay 14 stations fitted the new narrow scaled criteria, the Oderbank contained several more stations. In order to create two comparable key areas, stations from the Oderbank were excluded until only 14 remained. Likewise, this selection was made due to certain thought; primarily stations with more than one sampling event were dismissed. This was motivated by the fact that some of the monitoring- programs always take samples from exact the same locations to assess the seasonal or annual change. For the purpose of this study it is rather reasonable to have each station at a different site as this ensures the inclusion of highest possible variability of the established key area, as spatial variability is usually considered being higher than temporal. After the identified stations were filtered and assembled, the program ArcGIS was used to create an overview map of the 28 stations in two areas (fig. 1).

2.2 *BTA- biological traits analysis*

In order to perform biological traits analysis an autecological database was compiled. All necessary information for the database is taken mainly from primary and secondary literature. Other sources for the BTA are web- sources, such as http://www.marinespecies.org, http://www.marlin.ac.uk/biotic/ or http://species-identification.org, and occasionally expert knowledge. Overall there are 196 represented species in the original BTA, all of them were chosen because they dominate the abundance and/or biomass of benthic macrofauna in the south- western Baltic Sea. The Database can be interpreted as a species by traits table. Thirteen traits were chosen, describing the morphology, behaviour and life strategy, habitat modification etc., each of them consists of several categories (table 2). The traits are divided further into categories in order to supply a tool to assess species with different trait- categories more accurate. This leads to 13 traits with 65 categories. An example: the trait size includes 3 different categories starting with small (0,5 – 5 mm), medium (5- 20 mm) and large (> 20 mm). Earlier version of the IOW BTA database used to sum the value of all categories for a trait to 1. If a species expressed behaviour that matched different categories, values between 0 and 1 were given in a way that all categories of a trait would sum up to 1, in order to prevent bias between different categories in further analysis. The potential problem here is that the

values are also supposed to express the species affinity for the certain category within the trait.

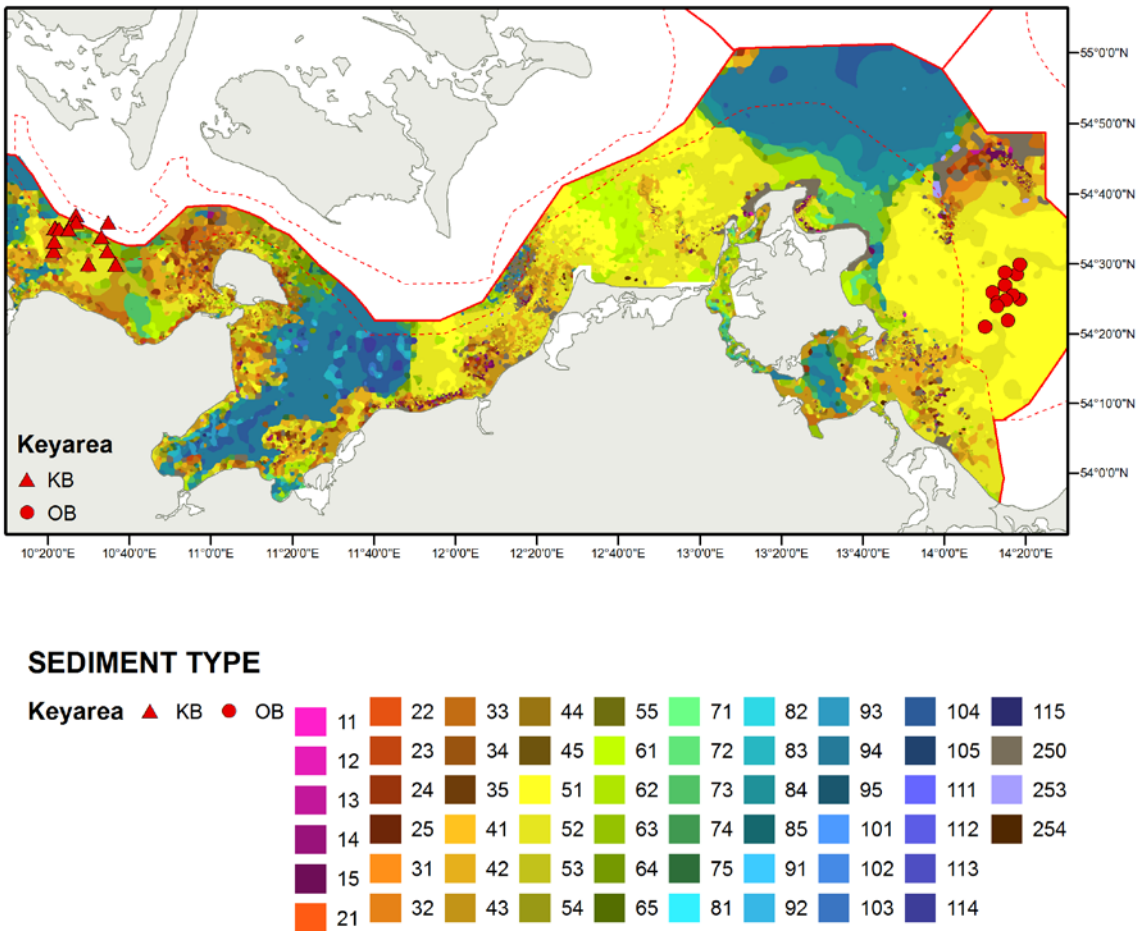


Fig 1. Map of the south- western Baltic Sea showing the position of the selected stations and the two areas Kiel bay (KB) and Oderbank (OB). Sediment legend (only for the areas in which the stations are): 31- 35 coarse sand, 41- 45 medium sand, 51- 55 fine sand, 61- 65 very fine sand. (Tauber, 2012)

If a species is more frequently found to live sedentary in a burrow but occasionally leaves the burrow to change its position and find shelter under stones this must be reflected in the BTA categories with corresponding values. In the case of our example, *Corophium volutator,* in the category 'permanent burrow' and 'temporary burrow' would get a 0,1 each and 'tube' a 0,8. This shows that the approach of valuing them between 0 and 1 might be misleading in this context especially as the BTA values later are supposed to be multiplied with biomasses. In order to eliminate this problem and create even more significant description of behavioural and functional variability between species, another rating was used. The scoring range of 0- 3 was adopted, with 0 showing no affinity and 3 showing high affinity for and magnitude of a category (Bremner et al., 2006). Using *Corophium volutator* again as an example, in this

ordination ‘permanent burrow’ and ‘temporary burrow’ would be given value 1, and ‘tube’ value 3. For all traits and categories “fuzzy coding” approach (Chevenet et al., 1994) was used. Additionally during the review of different literature contradictory information was often found. As an example: the Anthozoa *Actinia equina* in one work is said to be carnivorous. Therefore it was given the value 3. Other literature stated that occasionally *Actinia equina* is also found to filter feed and graze, therefore the values 1 were given for each of these categories. Overall far over a hundred books, essays, works, and journal- articles were assorted to collect information on the species. Some were found to provide information on the majority of taxa, those were: Hayward & Ryland, 1990.; Hartmann-Schröder, 1996.; Kirkegaard, 1992.; And Querios et al., 2013. If no information could be found for certain species, information on similar species, e. g. from the same genus, or information on higher taxa was used. Unfortunately in some cases it appeared rather futile to find information on the species traits that would incorporate possible differences between those traits depending on the habitat the species is found in. For example the invasive Polychaeta *Marenzelleria neglecta* was introduced from brackish North- American waters to the Baltic Sea via ballast water of ships. Now there is information on the North- American and European population in this case, for other taxa no information on the Baltic population could be found. Therefore information that was given on species living in North- America or South- East Asia was used to complete the database occasionally. Nevertheless, if found in literature information on features of the species living in the Baltic Sea or brackish water was utilised. Nevertheless the BTA database cannot be considered as a static finalized product, as newly published information on species and taxa is inexorably collected. The database might be viewed upon as dynamic. Traits were chosen to describe the species influence on the ecology of the habitat. “Traits can be selected based on the requirements and aims of individual studies, whether these to describe assemblage functioning, identify the presence and effect of anthropogenic impacts, or a combination of both” (Bremner et al., 2006). Further “one of the most exciting potential applications of BTA is as a monitoring tool over large geographical scales” (Bremner et al., 2006), which is the objective of this study. A list of all traits, categories and their labels is given in figure 2. The last of the traits in the list is the bioturbation index which is made up of the reworking mode and mobility class (Solan et al., 2004). Those 2 categories excluded, the BTA data file contained 9261 arrays of which 8519 were filled in with values. This leaves 92% of the BTA table filled with ascertained data. The remaining unfilled 8% of all arrays were filled with zeroes not to disturb further statistical and mathematical analysis (Chevenet et al., 1994).

2.3 *Statistical methods*

To examine the differences between the key areas, in the first explorative step for all of the stations the available abiotic parameters were compared. Namely these were: median grain size, oxygen- content of the near bottom water, depth and salinity. The best way to visualize these results was found to be in organising the information in boxplots, containing all stations of one key area in a plot. These Boxplots were created using the program IBM SPSS Statistics Version 20. Next step in the line was the classical assessment of diversity. Diversity is usually subdivided into different dimensions, commonly used are α-, β-, and γ- diversity. α- diversity is understood as the "diversity of a particular spatial unit as for example a single station. It is described by Species number or diversity- indices such as the Shannon- Wiener (H') or the Simpson- Yule index (1/D)" (Bleich et al., 2011) which are also used in this study. "γ- diversity describes the diversity of large entities such as landscapes" (Bleich et al., 2011). For this study most of the statistical analysis was implemented in order to assess β- diversity which is interpreted as "a measure of the change in species composition. The extent of species replacement or biotic change along environmental gradients is defined as 'species turnover', or the change in species composition from one community to another (Whittaker 1972). As the definition of β- diversity is pretty broad it is further subdivided into two measures according to (Tuomisto & Ruokolainen, 2008). One is the so called "regional diversity" which is interpreted as a measure of species turnover in an area, the other one is labelled "pairwise beta diversity" (Tuomisto & Ruokolainen, 2008) and defined as a measure of species turnover along an environmental gradient. Pairwise beta diversity is the main focus of this study.

The ES50 value, as well as the Shannon- Wiener and Simpson- Yule indices, were calculated using the program PRIMER 6 and later displayed in Boxplots using SPSS (IBM SPSS Statistics 20). Boxplots were chosen because of their ability to visualize mean values and variation in plots on the same axes. This makes them easy to interpret already on the first glance. After this classical approach was implemented to assess diversity within the key areas and compare them with each other, the next step on the way to evaluate and compare diversity beyond species richness had to be done. The idea of this work is to combine information on the different species traits, provided in the BTA, with the diversity change along the salinity gradient, so that single traits can be identified as being responsible for the fitness and functional performance of a community, and to judge whether such methods are reasonable and accurate. The concept behind this is to be able to estimate the emphasis of a certain trait

Trait	Category	Label	Trait	Category	Label
Size	0,5-5 mm	size.s	Movement-	None	mov.no
	5-20 mm	size.m	method	Swimm	mov.sw
	>20 mm	size.l		Crawl	mov.cra
Longevity	0-3 yr.	long.3		Burrow	mov.bur
	4-7 yr.	long.7		Jump	mov.ju
	7-11 yr.	long.11	Mobility	Sedentary	mot.sed
	>11 yr.	long.11+		Limited free movement	mot.lim
Reproductive-	Asexual reproduction	sex.asex		Freely motile in or on sediment	mot.fre
Mode	Indirect development (broadcast spawner)	sex.spa		Semi-pelagic	mot.spel
	Indirect development (egg layer-planctonic larvae)	sex.egg	Habitat-	None	hab.no
	Direct development (brood)	sex.bro	structuration	Form-settlement/attachment site	hab.settle
Body-	Soft	bd.so		Form-shelter	hab.shelt
design	Soft protected (tube/tunic cover)	bd.sopr		Action-sediment accretion	hab.acc
	Hard exoskeleton	bd.haex		Action-sediment removal	hab.rem
	Hard shell	bd.hash	Salinity-	freshwater	sal.f
Living-	Tube	liv.tube	preference	oligohaline (0.5-<5 psu)	sal.o
habitat	Permanent burrow	liv.perm		mesohaline (5-<18 psu)	sal.m
	Temporal burrow	liv.temp		polyhaline (18-<30 psu)	sal.p
	Crevice/hole/under stones	liv.crev		euhaline (30-<40 psu)	sal.e
	Epiphytic/epizoic	liv.epi	Hypoxia-	low (high or long tolerance ≥ 21 days)	hyp.low
	Free	liv.free	sensitivity	high (low or short tolerance0-2 days)	hyp.high
Living-	Surface	livp.sur	Sediment-	No transport	sed.no
location/	Interface	livp.int	transport	Diffusive mixing	sed.dif
position	Infauna: 0-5 cm	livp.5		Surface deposition	sed.surd
	Infauna: 5-10 cm	livp.10		Conveyer belt transp.	sed.con
	Infauna: >10 cm	livp.10+		Rev. conveyer belt transp.	sed.reco
Exposure-	Low (infauna or flat interface)	exp.l	Bioturbation-	Mobility	bio.mob
potential	Moderate (mound interface)	exp.m	index	Reworking	bio.rew
	High (erect interface)	exp.h			
Feeding-	Carnivore	fed.car			
strategy	Filter feeders	fed.fil			
	Interface feeders	fed.gra			
	Surface deposit feeders	fed.surd			
	Subsurface deposit feeders	fed.ssur			
	Carnivore/surface deposit feeders	fed.casu			
	Omnivore/carnivore	fed.omni			
	Commensalist	fed.com			

Table 2 Traits with categories and labels.

on the ecology of the whole community. All of this advisement rests on the hypothesis that species that are well adapted to a habitat show traits that are vital for a high fitness in this area. Equally species that seem to be well adapted or find their optimal environmental conditions in the area, are the ones that reach high biomasses. If the biomasses are multiplied with the values from the BTA (as explained earlier), this should leave a descriptive set of data which holds the power to distinguish traits with higher influence from the ones with lower

influence on the ecosystem functioning. In order to combine this information several steps of statistical analysis had to be performed. First all of the data had to be formatted in a manner that left it suitable for further statistical analysis. The BTA file was changed so that all traits and their categories were the head line of the table and the species labelled each row so that every given value for each category was displayed in the file. This ordination organised a species by traits table, the first of our two matrices. The second matrix contained the information from the sampling data- file organised in a station by species table. The first matrix is filled with affinity- values from the BTA file, the second matrix contains the biomasses in ash free dry weight (AFDW) of the sampled data. Also the matrices had to be concerted so that no species would be in one matrix but not the other. Further three categories had to be excluded from the BTA matrix for two different reasons. For one the category movement – jump was removed because no species in the sampled area showed affinity for this trait and the zero values would have caused trouble in further analysis, for the other the reworking and mobility indices were dismissed for reasons as explained above. Calculations were performed using "R Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL http://www.R-project.org." The program was found to be the right software to multiply both of our new matrices with each other.

This matrix was then used to perform a multi- dimensional scaling (MDS) analysis with the Program PRIMER 6. This method uses a dissimilarity matrix to show different dis- and similarities between the stations and display them. The values cannot be interpreted as absolute, but should naturally be interpreted like sample 1 is more similar to sample 3 than to sample 2.

After the implementation of the MDS, R studio was used again as it is not only useful in conducting basic actions, such as multiplying matrices. If R Studio is used with the right packages, a long set of other functions can be carried out with it. For all calculations in this study, the add- on package "ade 4" (**D**ata **a**nalysis functions to analyse **e**cological and **e**nvironmental data in the framework of **e**uclidian **e**xploratory methods) was used (Dray, & Dufour, 2007; Chessel et al., 2004; Dray et al., 2007). In order to assess differences in functional composition between traits and stations, FCA (fuzzy correspondence analysis) was performed for the different traits, as well as for the different stations. This method is the tool of choice for the analysis of a fuzzy data set. It represents results in various two- dimensional ordination plots. These plots can present different modalities of all analysed traits along the

gradient of the first two axes and are used to do the same for all single stations, or show the position of all stations and the centroid of their key areas in relation to the same axis. “FCA uses biomass- weighted biological traits to calculate their relative frequencies and ordinates them using their euclidean distances. Therefore FCA displays variability in each axes and the correlation ratios of every trait along the principal axes. This equally means that samples which are close along the plot coordinates have similar patterns of biomass across modalities” (Paganelli, 2012). “FCA is a parametric linear ordination method that uses eigenanalysis to investigate differences between samples, based on biological traits exhibited by species present in the assemblages, weighted by abundance or biomass” (Bremner et al., 2006). Both were performed using the multiplied matrix of species and traits in biomass, as biomass is considered the more descriptive in comparison to abundance (Darr et al., 2014).

The approach of both statistical means is fairly similar which leaves the urge for further explanation. Both tools hold strengths and weaknesses. MDS strengths are its simplicity, the fact that it is based on relevant sample information and the fact that it is generally applicable. Generally, the advantage of MDS is its ability to represent complex relations in low-dimensional space. MDS is recommended as one of the best ordination techniques (Everitt, 1978). Nevertheless FCA has various ways to visualize data. Therefore it holds the power to describe correlations deeper as the ordination can be implemented for traits and stations. Also factorial maps can be built, this study uses such an ordination to visualize possible differences between the areas. Nevertheless FCA also has some weaknesses. One of them is the fact that the distance preserving is poor. Having defined dissimilarity as distance in the p- dimensional species space, these distances are being projected onto a two dimensional ordination plane. This may distort some distances badly (Clarke & Warwick, 2001). Considering this, MDS is implemented in order to verify the results of the FCA.

3 Results

3.1 *Environmental characteristics*

The study focuses on the effects of salinity change on diversity and whether certain traits can be identified as profitable for higher or lower salinities. But in order to bind the information given by all statistical means into the context, first the key areas and their stations must be

compared. The following table gives an overview when the stations that were analysed in this work were sampled (table 3)

	KB	OB
2004	-	5
2005	4	2
2006	1	1
2007	2	-
2008	1	-
2009	1	1
2010	-	1
2011	-	4
2012	1	-
2013	4	-

Table 3 Number of sampled stations per key area/ year

The differences in sampling time are obvious and their possible influence on data will be discussed later in the text. As explained in material and methods, boxplots for all stations of a key area were created for the four abiotic parameters. The first two being displayed are the plots for depth and median grain size (fig. 4). Looking at the plot for grain size, first it can be stated that there is no huge difference between the median grain size of both key areas. The median for the Oderbank is just under 200 µm and all values range between 180 and 214 µm, whereas the median for the Kiel Bay is about 220 µm ranging from 129 to 301 µm. Based on this, both key areas can be considered quite similar concerning median grain sizes. Also the key area Oderbank can be considered the more homogenous habitat, as the range of values is quite narrow and no spikes could be identified. Equally the organic content of the sediment was found to be lower in the Oderbank with a percentage between 0,13% and 0,41 %. The organic content of the Kiel Bay varied from 0,3% up to 3,2 % and therefore is clearly higher. For Brevity a further boxplot for organic content wasn't compiled. If we look at the data describing the depth of all stations the key areas appear not quite as similar. On one hand the depth of the Kiel Bay varies between 15 and 18 m and even shows an outlier at 12,2 m, on the other hand depths in Oderbank alter between 10,2 and 15,3 m. The median for depth lies between 17 and 18 m for Kiel Bay and at about 11 m for Oderbank, accordingly the Oderbank is the shallower key area. Even if the key areas are not as homogenous for the criteria depth, their variation still is acceptable and leaves them to be interpretable and comparable with each other. The other two abiotic criteria organised in boxplots were the oxygen content in ml/l and salinity. The boxplots for both are displayed in figure 5. The boxplot for the oxygen content in

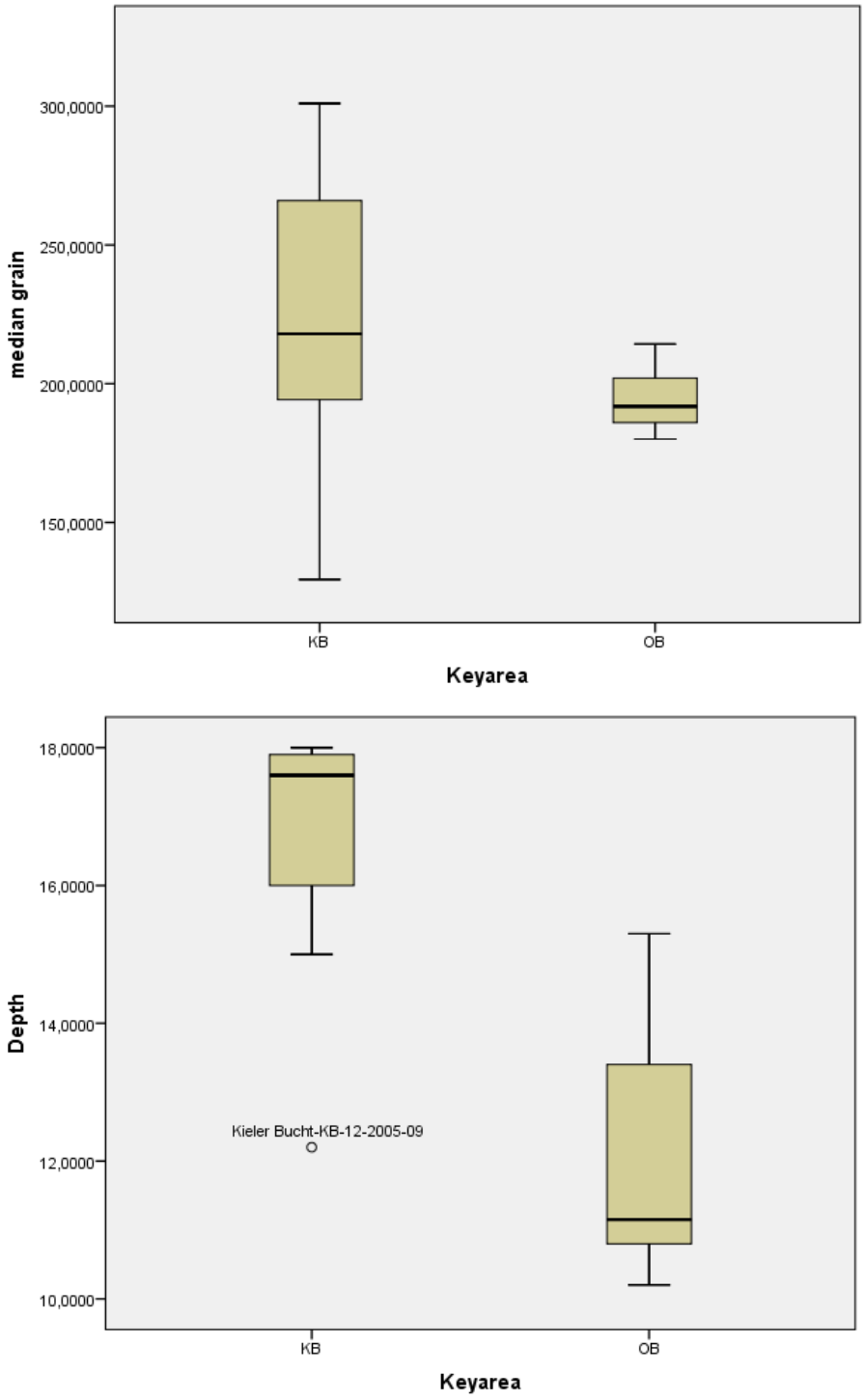


Fig. 4 Boxplots for median grain size and depth

Kiel Bay draws a rather homogenous picture. All values range between 4,7 and 7,4 ml/l and the median appears to be just over 6. The oxygen concenration in the Oderbank is slightly higher varying from 6,3 to 10,3 ml/l and showing a median of just over 8. It is known that

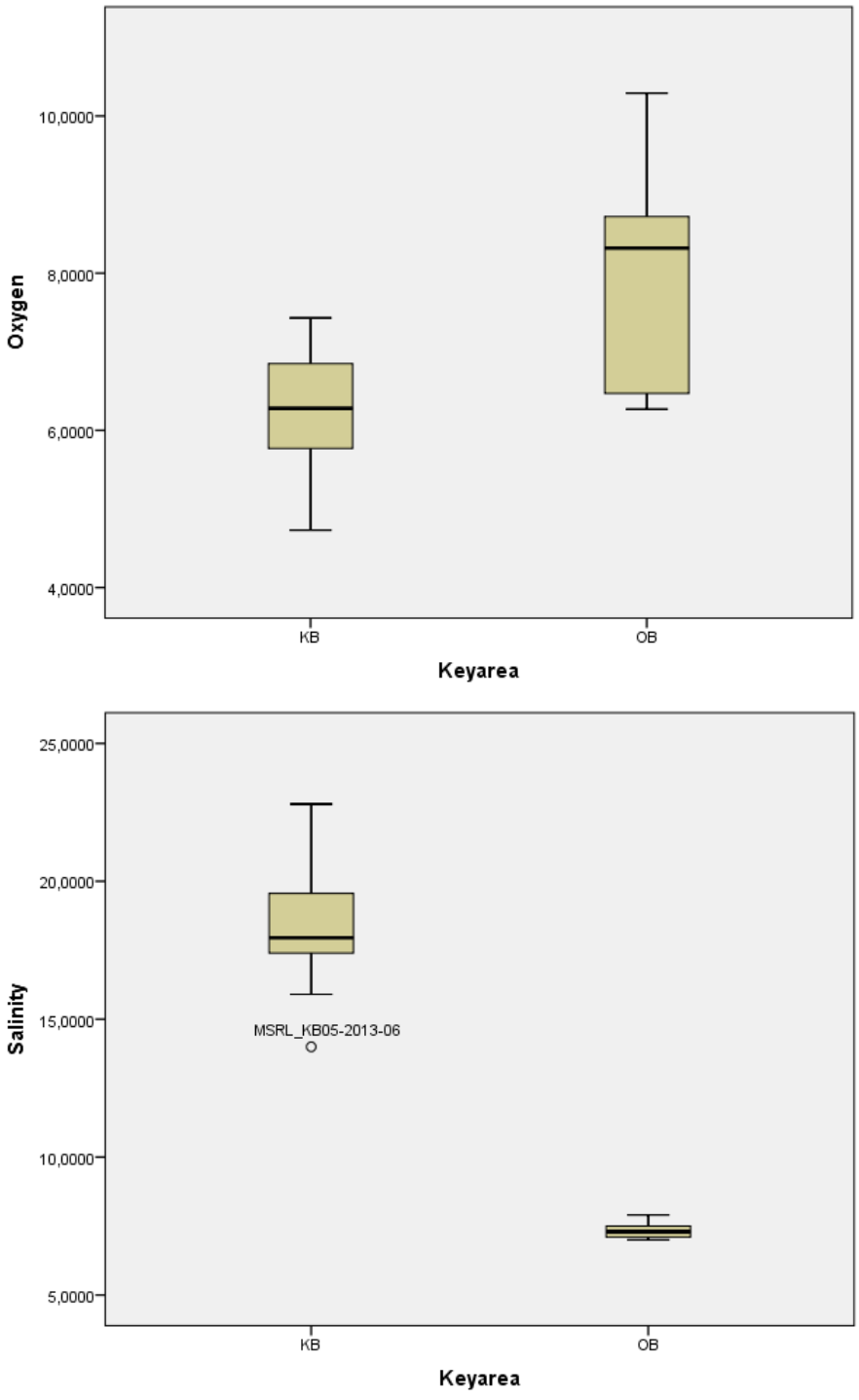


Fig. 5 Boxplots for oxygen content and salinity.

oxygen enters the Baltic Sea via water from the North Sea that also is more saline, ergo heavier and flows in on the sea floor due to events like big storms and other. In shallower areas such as the Oderbank more oxygen input also happens due to wind mixing and diffusion. Bearing oxygen rich water influxes in mind, actually the Kiel Bay key area should be the one with higher oxygen content, but regarding the information on depth from the

previous boxplots (fig. 4) the fact that stations in the Oderbank are shallower than the ones in Kiel Bay could be identified as the reason for the higher content in the Oderbank. Nevertheless in other literature authors speak of oxygen depletion at contents under 2 ml/l (Modig & Olafsson, 1998) as all stations exhibit higher contents than that, the assumption that the oxygen content doesn't affect diversity in our key areas can be kept hold of. The last of the four abiotic boxplots is for the salinity. As for the first 3 criteria homogeneity between the key areas was wanted now a clear difference between Kiel Bay and Oderbank must be found in order for this study to be significant. The salinity of the Kiel Bay differs between about 16 and 22,8 and even shows one outlier at 14. The median of all stations lies at about 18. The Oderbank otherwise, presents itself very homogenous. All values are between 7 and 7,9 which puts the median to approximately 7,5. The two median differ by over ten and even the lowest salinity content of the Kiel Bay is still discriminable higher than the highest value found in Oderbank. This saves our salinity gradient along the stations and is vital for the outcome of the whole work. Kruskal- Wallis tests were implemented for all abiotic criteria. In contrast to the previous statements the level of significance for all factors was under 0,05 ($p < 0,05$) which means that the null hypothesis must be refused, hence there are statistically significant differences in other parameters but salinity as well. Nevertheless the magnitude of these other parameters differences was limited as much as possible by very strict data filtering.

3.2 *General community description and taxonomic diversity*

All sampled species at all stations sum up to 145 species overall, of which 132 are found in Kiel Bay and 27 are found in Oderbank. The list given in table 6 provides an overview about which species were found and at how many of the sample stations per key area they were encountered. For a full list of species, with taxonomy matched with the internet based World Register of Marine Species (WoRMS- www.marinespecies.org) see the appendix. In Kiel Bay seven Species were found at all stations whereas merely 3 species were found at all stations in Oderbank. Namely the ones found at all sites in Kiel Bay were: Bivalves *Astarte borealis*, *Corbula gibba*, *Parvicardium pinnulatu*; Polychaetes, *Lagis koreni, Nephtys caceca, Scoloplos armiger* and Cumacea *Diastyles rathkei*. In Oderbank the Polychaeta: *Hediste diversicolor* and the Bivalves *Macoma balthica* and *Mya arenaria* could be found at all stations. The Polychaeta *Pygospio elegans* and Bivalve *Macoma balthica* were found at most stations in both keyareas, with frequencies over 80%. Equally interesting for the assessment of the benthic community, is each species percentage of total biomass in AFDW and total Abundance in Individuals per m^2, in comparison to the overall key area values. Looking at the

abundances for the Kiel Bay, one species clearly dominates the area. The sedentary Bivalve *Kurtiella bidentata* achieved 20,92% of the overall abundance and is followed by Bivalve *Abra alba* who is less than half abundant with a fraction of merely 8,66%. Focusing on biomasses it becomes clear that Bivalve species are dominant in this area. *Arctica islandica* holds the highest value with 69,92% of overall biomass. All three leading species are

Species	% Ind./m²	% AFDW mg/m²	Species	% Ind./m²	% AFDW mg/m²
Kurtiella bidentata	20,92%	0,17%	Arctica islandica	5,98%	69,92%
Abra alba	8,66%	0,91%	Astarte borealis	1,70%	18,04%
Lagis koreni	7,94%	0,86%	Astarte elliptica	0,38%	3,08%
Dipolydora quadrilobata	7,30%	0,03%	Nephtys caeca	1,05%	1,40%
Diastylis rathkei	6,10%	0,54%	Mya truncata	0,41%	1,01%
Arctica islandica	5,98%	69,92%	Abra alba	8,66%	0,91%
Pygospio elegans	5,66%	0,02%	Lagis koreni	7,94%	0,86%
Parvicardium pinnulatum	3,22%	0,10%	Macoma balthica	1,49%	0,62%
Scoloplos armiger	3,08%	0,14%	Diastylis rathkei	6,10%	0,54%
Corbula gibba	2,58%	0,05%	Asterias rubens	0,18%	0,34%
OB	% Ind./m	% AFDW	OB	% Ind./m	% AFDW
Peringia ulvae	35,21	7,15	Macoma balthica	2,80	39,43
Bathyporeia pilosa	18,55	3,13	Mya arenaria	12,32	17,35
Mya arenaria	12,32	17,35	Cerastoderma glaucum	7,50	15,74
Pygospio elegans	8,43	0,86	Marenzelleria neglecta	4,72	7,83
Cerastoderma glaucum	7,50	15,74	Peringia ulvae	35,21	7,15
Marenzelleria neglecta	4,72	7,83	Hediste diversicolor	2,96	6,61
Hediste diversicolor	2,96	6,61	Bathyporeia pilosa	18,55	3,13
Macoma balthica	2,80	39,43	Pygospio elegans	8,43	0,86
Mytilus edulis	2,30	0,64	Marenzelleria viridis	1,61	0,70
Marenzelleria viridis	1,61	0,70	Mytilus edulis	2,30	0,64

Table 6 Percentage of Abundance (Ind./m^2) and biomass (AFDW in mg/m^2) for both key areas.

Bivalves, the second and third are *Astarte borealis* and *Astarte elliptica*, all three together are forming over 90% of the areas biomass. The Oderbank shows a different picture. The most abundant species is the Gastropod *Peringia ulvae* with over 35% of overall abundance. The next most abundant species are the Athropod *Bathyporeia pilosa* and the Bivlave *Mya arenaria.* In this area the influence of Bivalves on biomass is high, just as in Kiel Bay. The leading three species are Bivalves and together they produce over 70% of the overall biomass. A full list of the ten Species dominating abundance and biomass for both key areas is given in table 6.

To assess the benthic biodiversity further, several diversity- indices were calculated and organised in boxplots for a better overview. The three indices calculated were the Shannon-Wiener (H') and Simpson- Yule (1- λ) index and the ES50 values for both areas. The Shannon- Wiener index declined from west to east. Whereas in the Kiel Bay the median for

Species	KB	OB	Gesamt	% KB	% OB	% Gesamt	Species	KB	OB2	Gesamt	% KB	% OB	% Gesamt
Abra alba	12		12	85,71%	0,00%	42,86%	Lineus ruber	5		5	35,71%	0,00%	17,86%
Actinia equina	1		1	7,14%	0,00%	3,57%	Macoma balthica	10	14	24	71,43%	100,00%	85,71%
Alitta succinea	1		1	7,14%	0,00%	3,57%	Macoma calcarea	9		9	64,29%	0,00%	32,14%
Ampharete acutifrons	2		2	14,29%	0,00%	7,14%	Malacobdella grossa	7		7	50,00%	0,00%	25,00%
Ampharete baltica	13		13	92,86%	0,00%	46,43%	Marenzelleria neglecta		13	13	0,00%	92,86%	46,43%
Amphibalanus improvisus		1	1	0,00%	7,14%	3,57%	Marenzelleria viridis		6	6	0,00%	42,86%	21,43%
Ancula gibbosa	1		1	7,14%	0,00%	3,57%	Megamphopus cornutus	1		1	7,14%	0,00%	3,57%
Arctica islandica	13		13	92,86%	0,00%	46,43%	Microdeutopus gryllotalpa	4		4	28,57%	0,00%	14,29%
Arenicola marina	8		8	57,14%	0,00%	28,57%	Molgula manhattensis	6		6	42,86%	0,00%	21,43%
Aricidea minuta	10		10	71,43%	0,00%	35,71%	Monocorophium insidiosum	1		1	7,14%	0,00%	3,57%
Aricidea suecica	11		11	78,57%	0,00%	39,29%	Musculus discors	2		2	14,29%	0,00%	7,14%
Astarte borealis	14		14	100,00%	0,00%	50,00%	Musculus niger	6		6	42,86%	0,00%	21,43%
Astarte elliptica	11		11	78,57%	0,00%	39,29%	Musculus subpictus	5		5	35,71%	0,00%	17,86%
Astarte montagui	6		6	42,86%	0,00%	21,43%	Mya arenaria	4	14	18	28,57%	100,00%	64,29%
Asterias rubens	8		8	57,14%	0,00%	28,57%	Mya truncata	9		9	64,29%	0,00%	32,14%
Balanus crenatus	1		1	7,14%	0,00%	3,57%	Mytilus edulis	12	10	22	85,71%	71,43%	78,57%
Bathyporeia pelagica		1	1	0,00%	7,14%	3,57%	Nais elinguis		1	1	0,00%	7,14%	3,57%
Bathyporeia pilosa	2	13	15	14,29%	92,86%	53,57%	Nemertea	13		13	92,86%	0,00%	46,43%
Bittium reticulatum	1		1	7,14%	0,00%	3,57%	Neomysis integer		1	1	0,00%	7,14%	3,57%
Buccinum undatum	1		1	7,14%	0,00%	3,57%	Nephtys caeca	14		14	100,00%	0,00%	50,00%
Bylgides sarsi	11		11	78,57%	0,00%	39,29%	Nephtys ciliata	5		5	35,71%	0,00%	17,86%
Callipallene brevirostris	2		2	14,29%	0,00%	7,14%	Nephtys hombergii	13		13	92,86%	0,00%	46,43%
Capitella capitata	7		7	50,00%	0,00%	25,00%	Nephtys pente	1		1	7,14%	0,00%	3,57%
Caprella septentrionalis	1		1	7,14%	0,00%	3,57%	Nereimyra punctata	9		9	64,29%	0,00%	32,14%
Caulleriella killariensis	1		1	7,14%	0,00%	3,57%	Oligochaeta		4	4	0,00%	28,57%	14,29%
Cerastoderma glaucum	1	13	14	7,14%	92,86%	50,00%	Onoba semicostata	1		1	7,14%	0,00%	3,57%
Chaetozone setosa	8		8	57,14%	0,00%	28,57%	Ophelia limacina	1		1	7,14%	0,00%	3,57%
Chironomidae	2		2	14,29%	0,00%	7,14%	Ophiura albida	9		9	64,29%	0,00%	32,14%
Ciona intestinalis	1		1	7,14%	0,00%	3,57%	Paraonis fulgens	3		3	21,43%	0,00%	10,71%
Corbula gibba	14		14	100,00%	0,00%	50,00%	Pariambus typicus	1		1	7,14%	0,00%	3,57%
Corophium volutator		2	2	0,00%	14,29%	7,14%	Parvicardium pinnulatum	14		14	100,00%	0,00%	50,00%
Crangon crangon		3	3	0,00%	21,43%	10,71%	Parvicardium scabrum	7		7	50,00%	0,00%	25,00%
Crassicorophium crassicorne	6		6	42,86%	0,00%	21,43%	Peringia ulvae	6	13	19	42,86%	92,86%	67,86%
Cyanophthalma obscura		2	2	0,00%	14,29%	7,14%	Phaxas pellucidus	6		6	42,86%	0,00%	21,43%
Dendrodoa grossularia	9		9	64,29%	0,00%	32,14%	Pherusa plumosa	4		4	28,57%	0,00%	14,29%
Diaphana minuta	3		3	21,43%	0,00%	10,71%	Philine aperta	4		4	28,57%	0,00%	14,29%
Diastylis rathkei	14		14	100,00%	0,00%	50,00%	Pholoe assimilis	11		11	78,57%	0,00%	39,29%
Dipolydora caulleryi	1		1	7,14%	0,00%	3,57%	Pholoe baltica	10		10	71,43%	0,00%	35,71%
Dipolydora quadrilobata	8		8	57,14%	0,00%	28,57%	Pholoe inornata	4		4	28,57%	0,00%	14,29%
Echinocyamus pusillus	5		5	35,71%	0,00%	17,86%	Phoronis sp.	8		8	57,14%	0,00%	28,57%
Ecrobia ventrosa		6	6	0,00%	42,86%	21,43%	Phoxocephalus holbolli	7		7	50,00%	0,00%	25,00%
Edwardsia danica	11		11	78,57%	0,00%	39,29%	Phtisica marina	2		2	14,29%	0,00%	7,14%
Enchytraeidae		5	5	0,00%	35,71%	17,86%	Phyllodoce groenlandica	1		1	7,14%	0,00%	3,57%
Ensis directus	1		1	7,14%	0,00%	3,57%	Phyllodoce maculata	1		1	7,14%	0,00%	3,57%
Eteone barbata	1		1	7,14%	0,00%	3,57%	Phyllodoce mucosa	9		9	64,29%	0,00%	32,14%
Eteone longa	9		9	64,29%	0,00%	32,14%	Pleurogonium rubicundum	1		1	7,14%	0,00%	3,57%
Euchone papillosa	2		2	14,29%	0,00%	7,14%	Polycirrus medusa	4		4	28,57%	0,00%	14,29%
Eudorellopsis deformis	5		5	35,71%	0,00%	17,86%	Polydora ciliata	3		3	21,43%	0,00%	10,71%
Eulalia bilineata	3		3	21,43%	0,00%	10,71%	Polydora cornuta	4		4	28,57%	0,00%	14,29%
Eumida sanguinea	1		1	7,14%	0,00%	3,57%	Protomedeia fasciata	2		2	14,29%	0,00%	7,14%
Exogone naidina	3		3	21,43%	0,00%	10,71%	Psammechinus miliaris	1		1	7,14%	0,00%	3,57%
Fabricia stellaris	1		1	7,14%	0,00%	3,57%	Pseudopolydora antennata	1		1	7,14%	0,00%	3,57%
Fabriciola baltica	3		3	21,43%	0,00%	10,71%	Pseudopolydora pulchra	1		1	7,14%	0,00%	3,57%
Facelina bostoniensis	2		2	14,29%	0,00%	7,14%	Pusillina inconspicua	2		2	14,29%	0,00%	7,14%
Flabelligera affinis	2		2	14,29%	0,00%	7,14%	Pygospio elegans	12	13	25	85,71%	92,86%	89,29%
Galathowenia oculata	2		2	14,29%	0,00%	7,14%	Retusa truncatula	9		9	64,29%	0,00%	32,14%
Gammarellus homari	2		2	14,29%	0,00%	7,14%	Rhodine loveni	1		1	7,14%	0,00%	3,57%
Gammarus salinus		4	4	0,00%	28,57%	14,29%	Scalibregma inflatum	2		2	14,29%	0,00%	7,14%
Gastrosaccus spinifer	9		9	64,29%	0,00%	32,14%	Scolelepis foliosa	2		2	14,29%	0,00%	7,14%
Halacaridae	2		2	14,29%	0,00%	7,14%	Scoloplos armiger	14		14	100,00%	0,00%	50,00%
Halcampa duodecimcirrata	2		2	14,29%	0,00%	7,14%	Sphaerodoropsis baltica	2		2	14,29%	0,00%	7,14%
Harmothoe imbricata	4		4	28,57%	0,00%	14,29%	Spio arndti	1		1	7,14%	0,00%	3,57%
Harmothoe impar	4		4	28,57%	0,00%	14,29%	Spio goniocephala	4		4	28,57%	0,00%	14,29%
Hediste diversicolor		14	14	0,00%	100,00%	50,00%	Spiophanes bombyx	2		2	14,29%	0,00%	7,14%
Heterochaeta costata		11	11	0,00%	78,57%	39,29%	Streblospio shrubsolii		10	10	0,00%	71,43%	35,71%
Heteromastus filiformis	11		11	78,57%	0,00%	39,29%	Terebellides stroemii	6		6	42,86%	0,00%	21,43%
Hiatella arctica	3		3	21,43%	0,00%	10,71%	Trochochaeta multisetosa	2		2	14,29%	0,00%	7,14%
Idotea balthica		1	1	0,00%	7,14%	3,57%	Tubificidae	5	4	9	35,71%	28,57%	32,14%
Kurtiella bidentata	13		13	92,86%	0,00%	46,43%	Tubificoides benedii	7	2	9	50,00%	14,29%	32,14%
Lagis koreni	14		14	100,00%	0,00%	50,00%	Tubulanus polymorphus	4		4	28,57%	0,00%	14,29%
Laonome kroeyeri	2		2	14,29%	0,00%	7,14%	Turbellaria	2	1	3	14,29%	7,14%	10,71%
Laonome kroyeri	4		4	28,57%	0,00%	14,29%	**Gesamtergebnis**	**667**	**182**	**849**			
Lepidonotus squamatus	1		1	7,14%	0,00%	3,57%							
Levinsenia gracilis	1		1	7,14%	0,00%	3,57%							

Table 7 Species list and occurrence at stations.

all stations was at about 3,7, in the east the median dropped down to about 2,4. Three stations in the Oderbank were displayed as divergent from the rest of stations. PB07-2006-04 reached the single highest value of about 3 and OB-8-2004-04 showed the lowest index at circa 1,7.

The Simpson- Yule index shows a similar picture. In the west the median of all stations is at about 0,85 with one sole low exception near 0,65. Along the decreasing gradient of salinity also the Simpson- Yule index decreases so that the median for the eastern key area lies around 0,71. The last determined value was the ES50. In Accordance with other biodiversity measures also the ES50 shows a decline from west to east. In Kiel Bay the median ES50 is up to just under 15, in opposite the median in Oderbank lies at 8. Additionally the box in the Oderbank is very dense and shows one higher and one lower station, the lower value is around 6 and the higher at around 10. All calculated indices imply the same loss of diversity from west to east. The boxplots are shown in figure 8. Kruskal- Wallis tests were performed for all of the indices and the significance for all was under 0.05 which means that there is a difference between them.

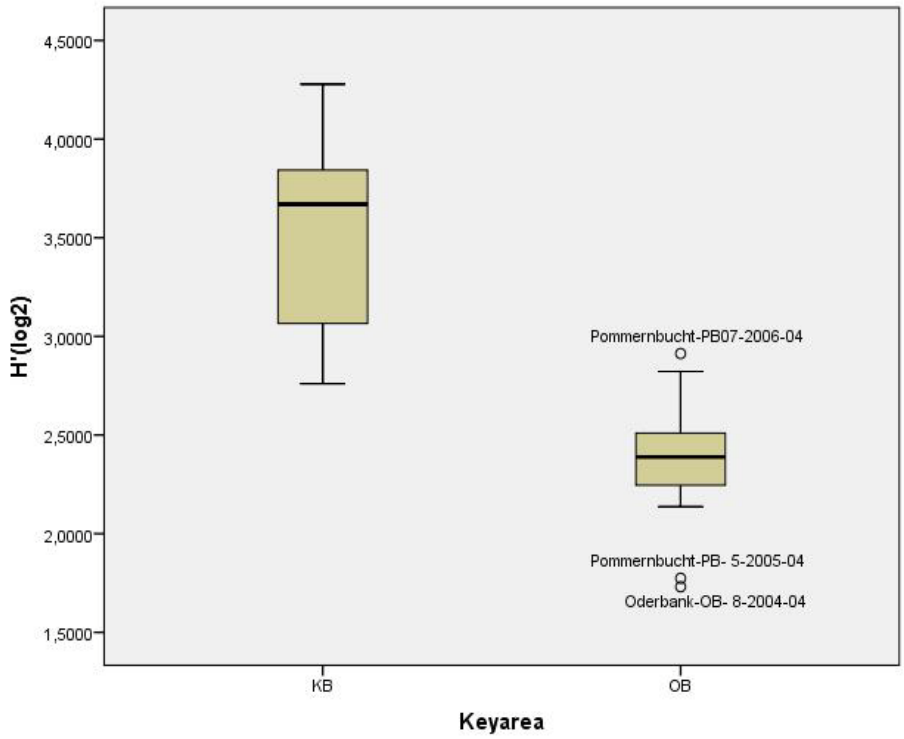


Fig. 8 Boxplots for Shannon- Wiener index (H'), Simpson- Yule index(1- Lambda) and ES50 value for both key areas

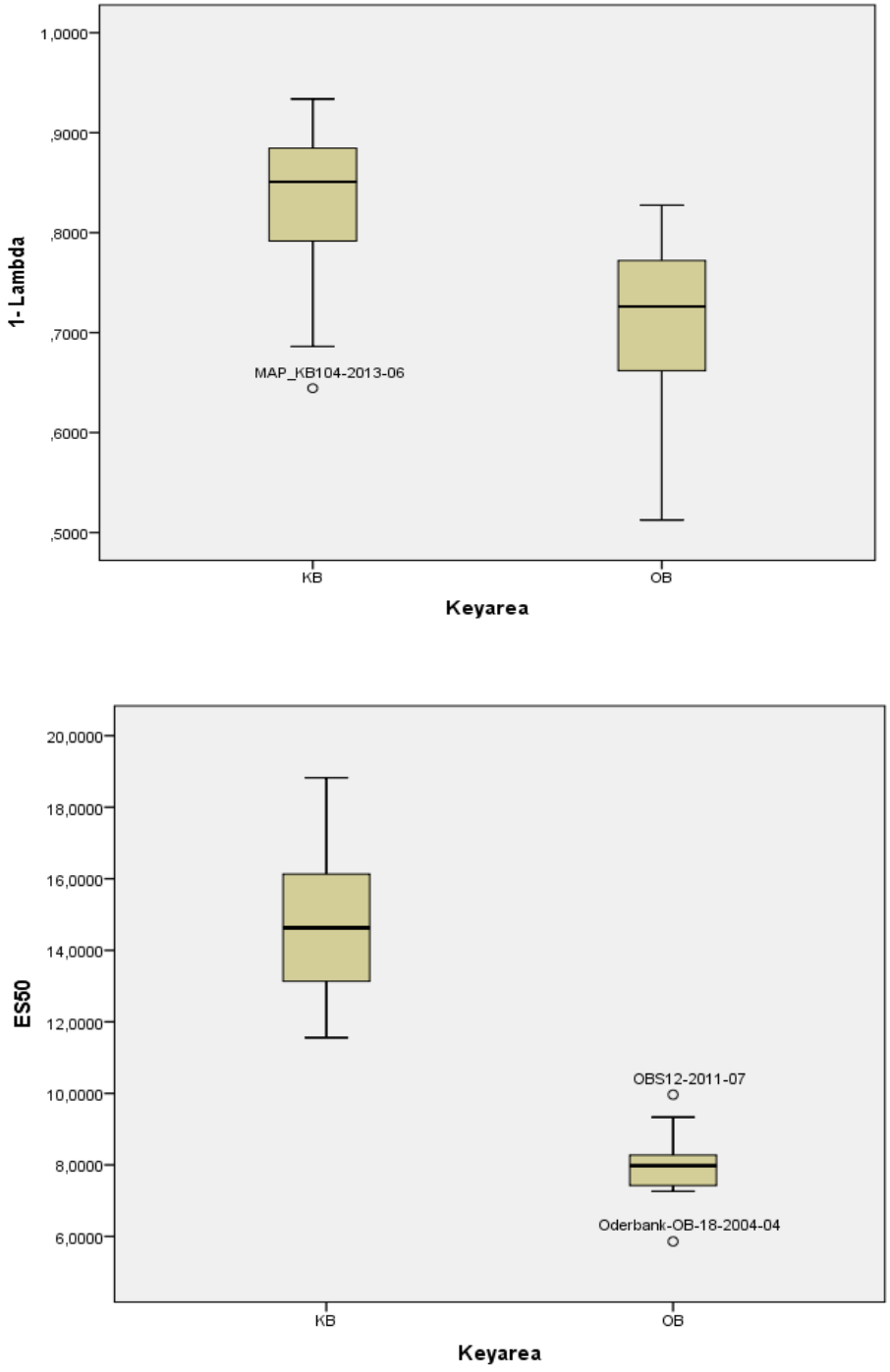


Fig. 8 Boxplots for Shannon- Wiener index (H'), Simpson- Yule index (1/Lambda) and ES50 value for both key areas

3.3 *Examination of functional patterns*

After the traits by stations table was calculated from the two matrices as explained in *Materials and methods*, a second species by traits table was organised in the same manner, the

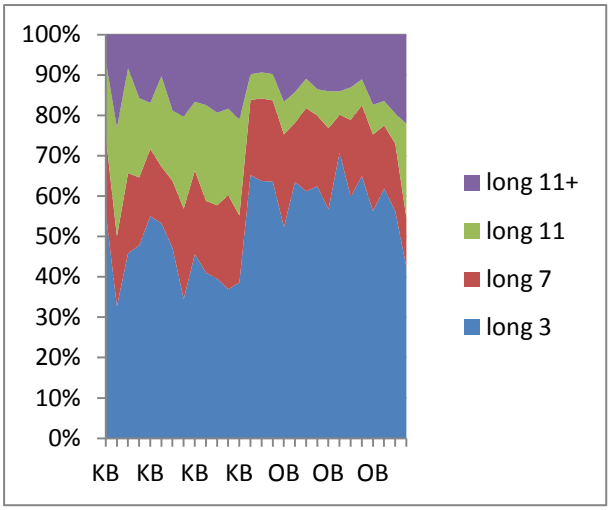


Fig. 9 Longevity plot

only difference being is that in this second table the multiplied values were not log-transformed. This effort was made in order to create plots that describe the composition of all categories of each single trait. A diagram showing the composition of traits was prepared for each trait. The idea behind is that the multiplied biomasses, organised in plots would give an overview over the different influences of single categories and also display differences in between both key areas. Nevertheless not all plots showed visible differences and only the ones that did are discussed in this point. All other plots are put together in the Appendix. Differences were identified for the traits longevity, motility, habitat structuration, sediment reworking and hypoxia. Starting with the trait longevity (fig. 9), a clear difference between the eastern and western researched area could be seen. In the Oderbank short- living species are dominant. On average 60% of species found, had a lifespan of not more than 3 years, at some stations peaks rose to nearly 70%. In comparison only about 40% of species in Kiel Bay showed such short lifespans.

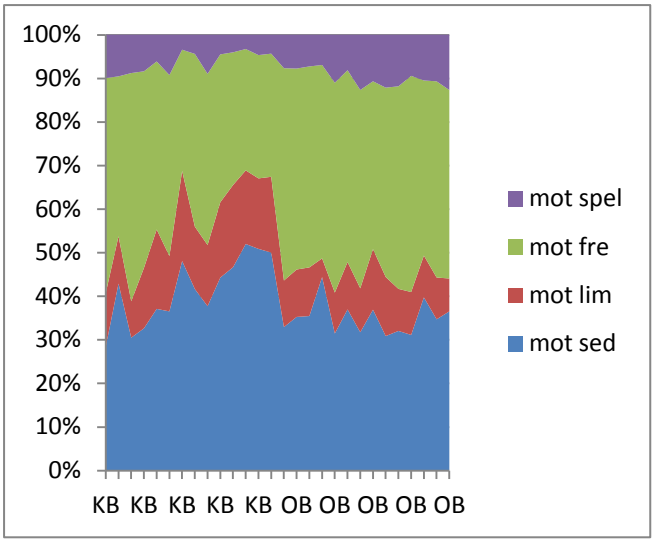
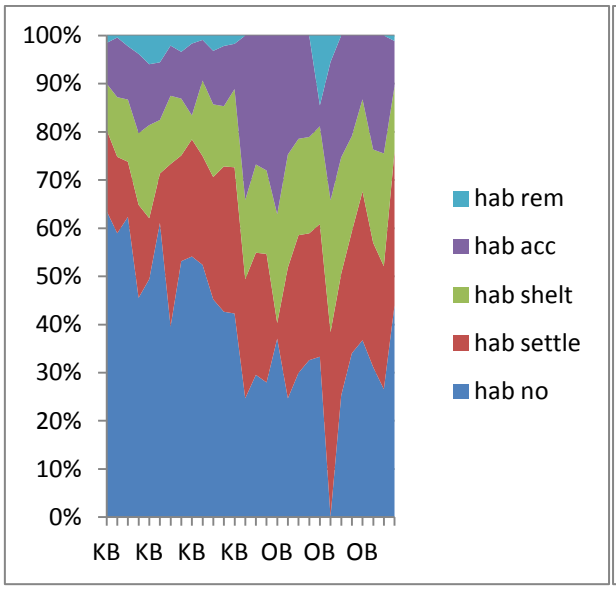


Fig. 10 Motility plot

Following this, the longer- living species were more dominant in Kiel Bay, approximately 40% of species match the categories 7- 11, and over 11 years. In the east merely 20- 25% showed such longevity. Discrepancy between the areas could also be seen in motility (fig. 10).

The biggest fraction of traits in the Oderbank is the category freely motile in/ on sediment, it contributes about 45% to the trait whereas in the Kiel Bay the influence alternates between 20 and 40%. In both areas the traits semi pelagic hold about the same percentage. The category that makes up for most of the loss in Kiel Bay, is limited free movement, reaching higher percentages than in Oderbank. Species that are sedentary are slightly more often found in Kiel Bay too.

Inequalities were also detected in the plot showing the composition of traits for habitat structuration (Fig. 11). The category no habitat structuration made up between 50 and 60% of the trait composition in Kiel Bay. In oppose the Oderbank percentage is at about 35 and even indicates absence of species playing no role in habitat structuration. Also the category form shelter was expressed slightly more in the Oderbank than in the western area. Another attribute that clearly separates both areas is the category action- sediment accretion. In Kiel Bay the value lies around 10% and is double as high for the eastern stations belonging to the Oderbank key area. The treatment of the data for sediment reworking also gave room for discussion and interpretation (Fig. 12). On the first glance the difference is imposed in the category no sediment reworking. In the Kiel Bay it makes about 35% of the overall composition



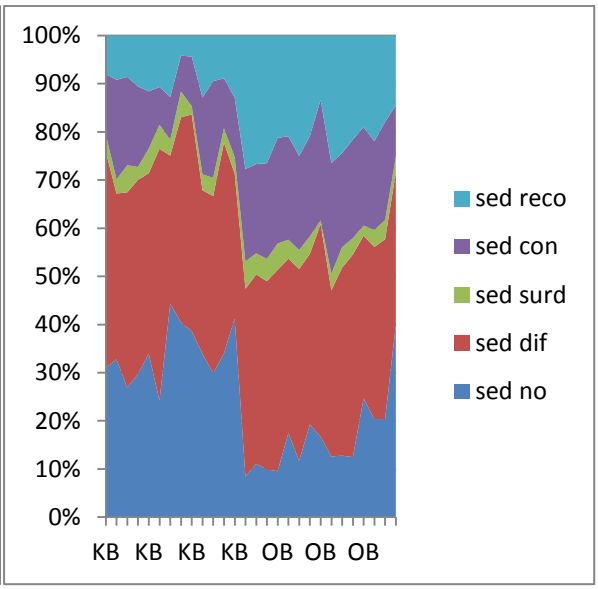


Fig. 11 Habitat structuration plot

Fig. 12 sediment reworking plot

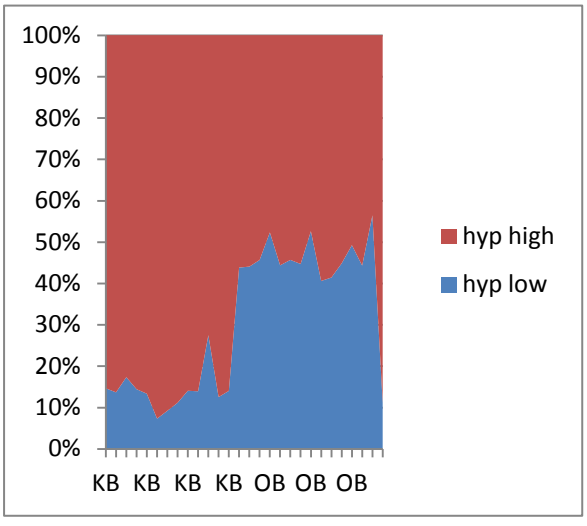


Fig. 13 Hypoxia sensitivity plot

and together with diffusive mixing accounts for the majority of the plot, meaning these traits are expressed by a lot of species. In Oderbank diffusive mixing is a on a similar level to that, the category no sediment reworking on the contrary only makes up about 15% of the whole plot. Another disparity can be seen if the two categories conveyor belt transport and reverse conveyor belt transport are compared. Together both

represent about 25% of the stations in the west, in the east both fractions are bigger. Together they describe about 40% of the diagram. The last trait showing differences is the one representing hypoxia sensitivity (fig. 13). A clear distinction between both key areas can be made. In Oderbank a bigger part of the plot shows a low hypoxia sensitivity than in Kiel Bay. According to this, more species in the eastern area are able to tolerate longer hypoxic periods, than in the western area. Later in the discussion the valuable information delivered by single trait plots based on the traits by station table is compared with other results of statistical analysis .

3.4 *Statistical tests using species by traits table*

The results of statistical means first presented in the following text are the MDS plots for the stations, which were generated using the program PRIMER 6. The MDS analysis was performed on data from the station by traits table that holds information on biomass to explore the (dis-) similarities of stations, in order to verify the results of the FCA. A 2 dimensional scatter (fig. 14) and a 3 dimensional scatter (fig. 15) were chosen to display the results of MDS analysis.

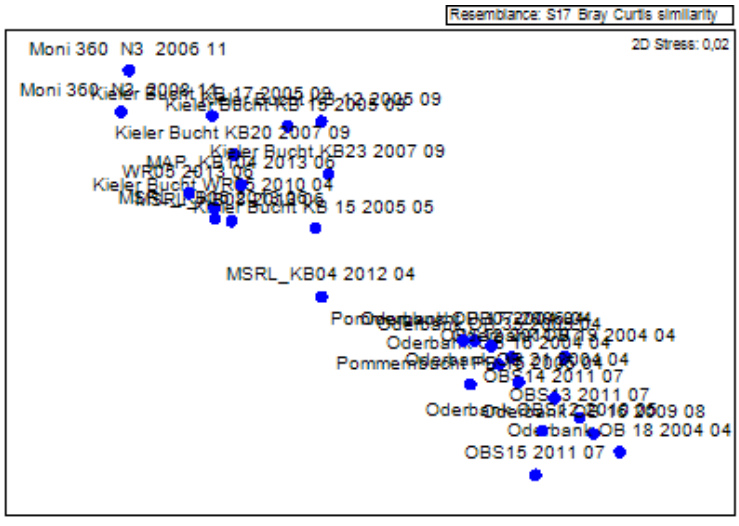


Fig. 14 2D MDS plot for station similarities

Both plots show satisfying stress levels. The stress level for the 2D scatter lies at 0,02. According to Clarke and Warwick, (2001) stress- levels under 0,05 “give an excellent representation with no prospect of misinterpretation”. This leaves both plots very well interpretable. If both plots are compared with each other, the stress level of the 3D scatter is

even lower than the 2D scatter one with a value of only 0,01, which means that the 3 dimensional ordination gives an even clearer view over the dissimilarities between the

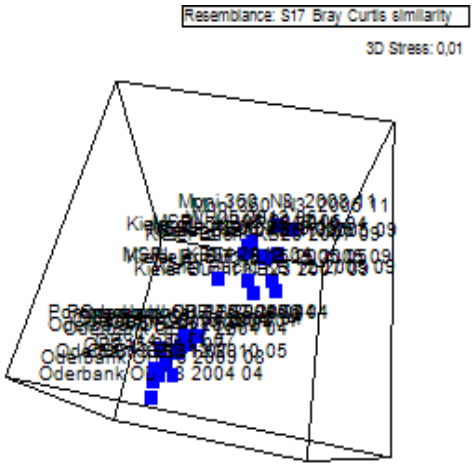


Fig. 15 3D MDS plot for station similarities

stations. Nevertheless both plots show two clusters, one representing the stations in Kiel Bay, the other the stations of the Oderbank which leaves the constructed key areas evidently distinguishable from each other. Comparing both clusters with each other, the Oderbank cluster appears to be slightly denser than the Kiel Bay cluster. The 2D scatter shows one station that is positioned right in the middle between the two area clusters. Station MSRL_KB04-2012-04 seems to be as similar (dissimilar) to the Oderbank cluster as to the Kiel Bay cluster. Looking at the 3D cluster, which concerning stress levels, is the more significant, the previous assumption cannot be confirmed. In the next step, Fuzzy Correspondence Analyses (FCA) were implemented and displayed in one table for all stations (fig. 16) and one for the traits (fig. 17). The station FCA showed a very clear difference between the stations of both key areas. All stations that belong to Kiel Bay are situated at the left of the first axes whereas all stations belonging to the Oderbank remain on the right side of the axes. This describes both key areas as definitely divergent along axes 1. Concerning the second axes, both key areas are slightly different. The Oderbank once again appears quite homogenous, the stations don't spread too much along the axes. Merely two stations (OBS 15 and PB 15) seem to be situated a bit further away from the rest of stations. The stations of Kiel Bay, situated at the left hand side of the plot, show a slightly different distribution along axes two. The Variation within the key area is wider than in the other key area. The separation of traits and categories on the factorial map based on the biomass can be seen in fig. 18 The

feeding type commensalist and soft protected body are the two traits located most left- handed in the plot, the next following with a quite a gap is longevity from 7- 11 years. On the right-

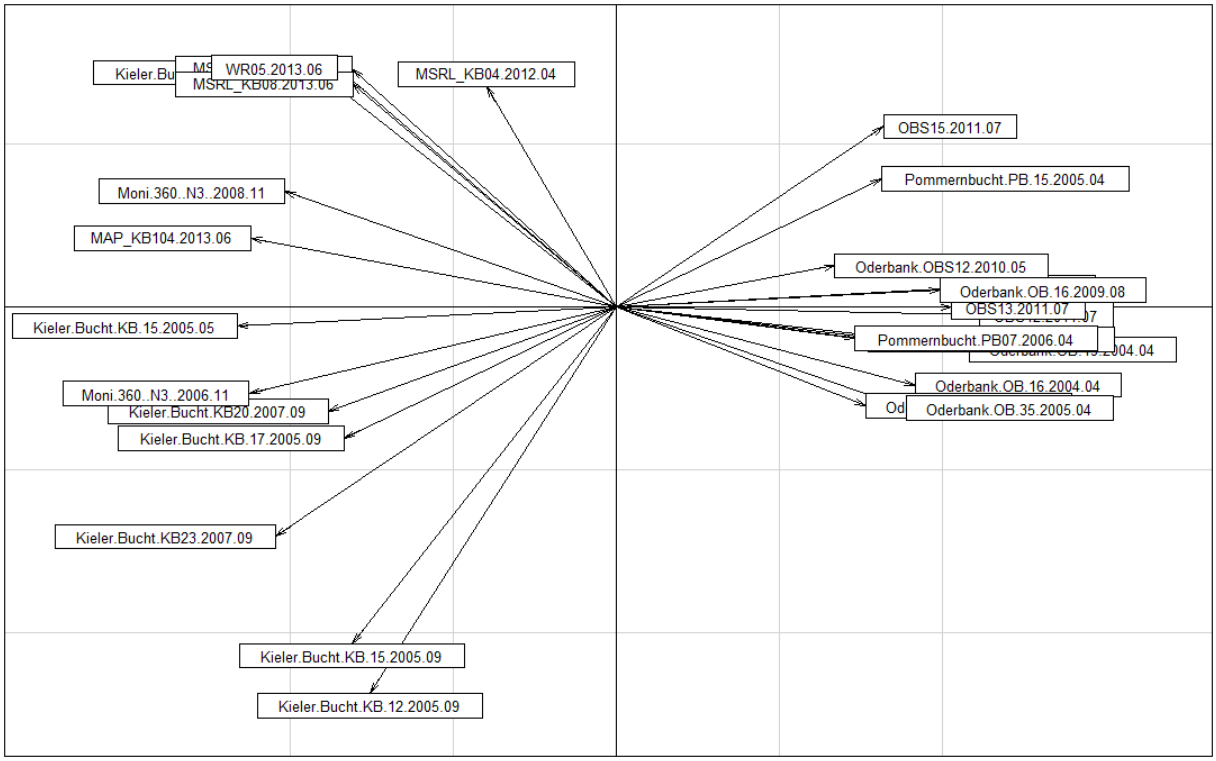


Fig. 16 FCA ordination plot showing the first two axes, based on log-transformed biomass data: station similarities

hand side only one far outlier can be seen, salinity preference freshwater, followed again with a bit of distance by hypoxia low.

The second axes also shows differentiation between the traits. The uppermost trait is movement no and it clearly is outstanding from the other traits. This trait describes species that are sedentary (can move somewhat). Outliers on the downside are feeding omnivore and body hard exoskeleton. Apart from the mentioned outliers, no real forming of clusters could be identified. Unfortunately the correlation of traits with the first two axes of the FCA was weak, only one trait exceeded a value over 0,1. This trait was found to be hypoxia, with a correlation value of 0,12. Hypoxia is followed by sediment transport which is not reaching the 0,1 but at least has a value of 0,075. Equally relatively high values can be seen for habitat structuration (0,072) and longevity (0,052). The correlation ratios for the second axes are expectedly even lower. None of the values reach 0,1 and solely 2 traits exceeded the 0,02. Namely these were body design and motility. For a full list of correlation values see table 18. The reason for the low correlation values is examined in the following ‘Discussion’- section. Nevertheless a rather large part of variation could be explained by the first two axes. Axes 1

described 49,46% of the data and axes 2 14,4%, together they add up to 63,87%. This leaves the FCA ordination plot useful for examining the underlying patterns of differences in trait composition. The plot showing FCA ordination of stations is presented in Figure 19. The two

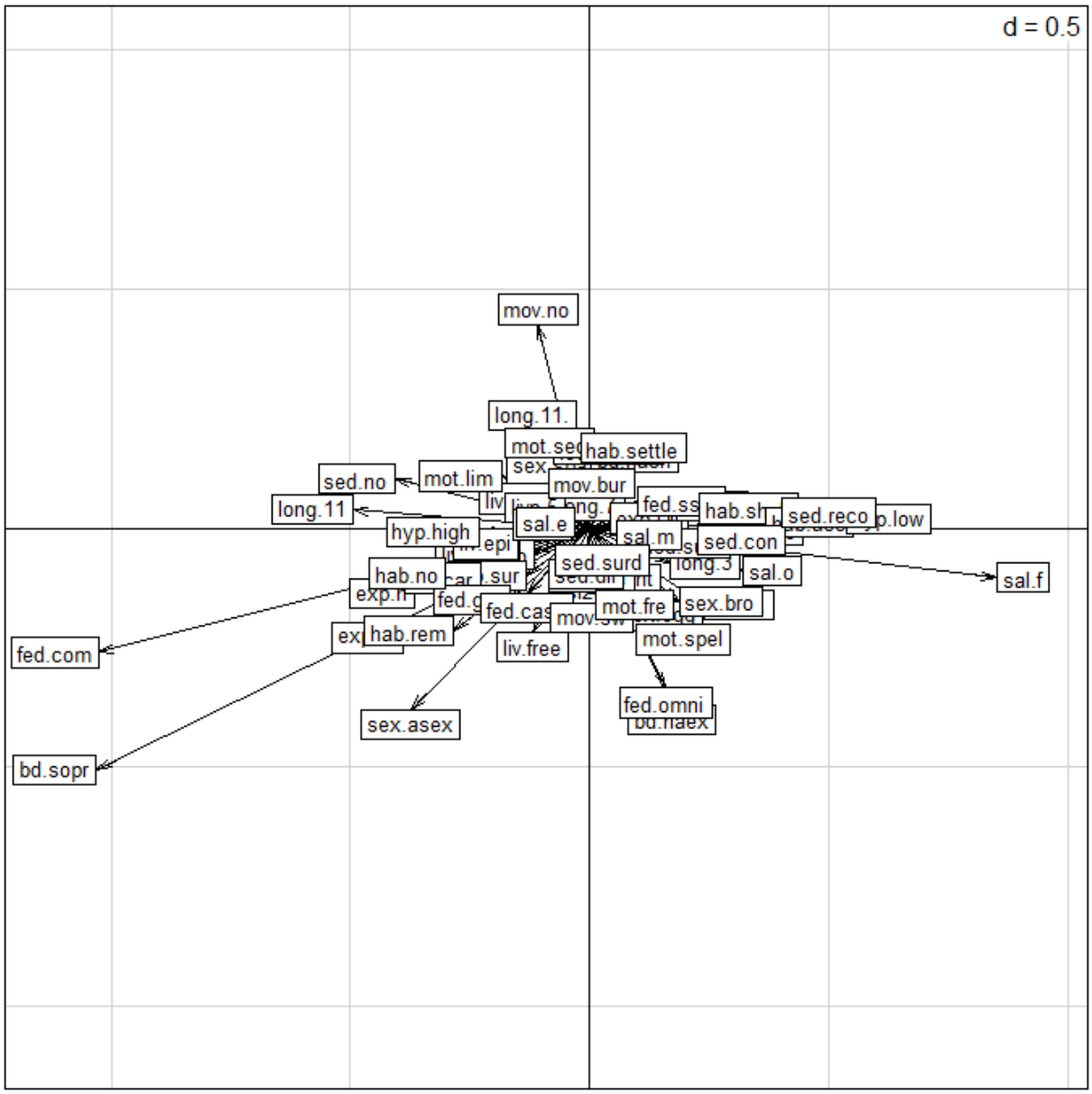


Fig. 17 FCA ordination plot showing the first two axes, based on log-transformed biomass data: trait distribution

key areas have distinct places on either sides of axes 1. Concerning axes 2 no real distinction can be seen between both key areas. As seen before in other considerations, again it becomes clear that the Oderbank is the more homogenous key area in comparison to the Kiel Bay. Another way to interpret which traits are responsible for the differences between the stations is an ordination of all trait categories along the first two axes of the FCA as implemented in figure 19. The label locations represent the centroids in each plot and the lines link the single stations with the centroids of the key areas they belong to. Looking at the plot it becomes

evident that feeding commensalist and body soft protected are more associated with the Kiel Bay than Oderbank. Equally the preference for the traits hypoxia low and salinity freshwater in the Oderbank can be seen in the plot. This way of showing the data offers a closer look into which traits are dominant in the areas.

Trait	RS1	RS2
Total inertia	49,46%	63,78%
Hypoxia	0,124	0
Sediment trans	0,075	0,005
Habitat Struc	0,072	0,009
Longevity	0,052	0,009
Body design	0,03	0,024
Living	0,023	0,013
Feeding	0,02	0,013
Sex	0,017	0,016
Exposure	0,016	0,004
Motility	0,014	0,02
Living pos	0,01	0,003
Size	0,007	0,007
Salinity	0,005	0
Movement	0	0,011

Table 18 Total inertia & correlation ratios

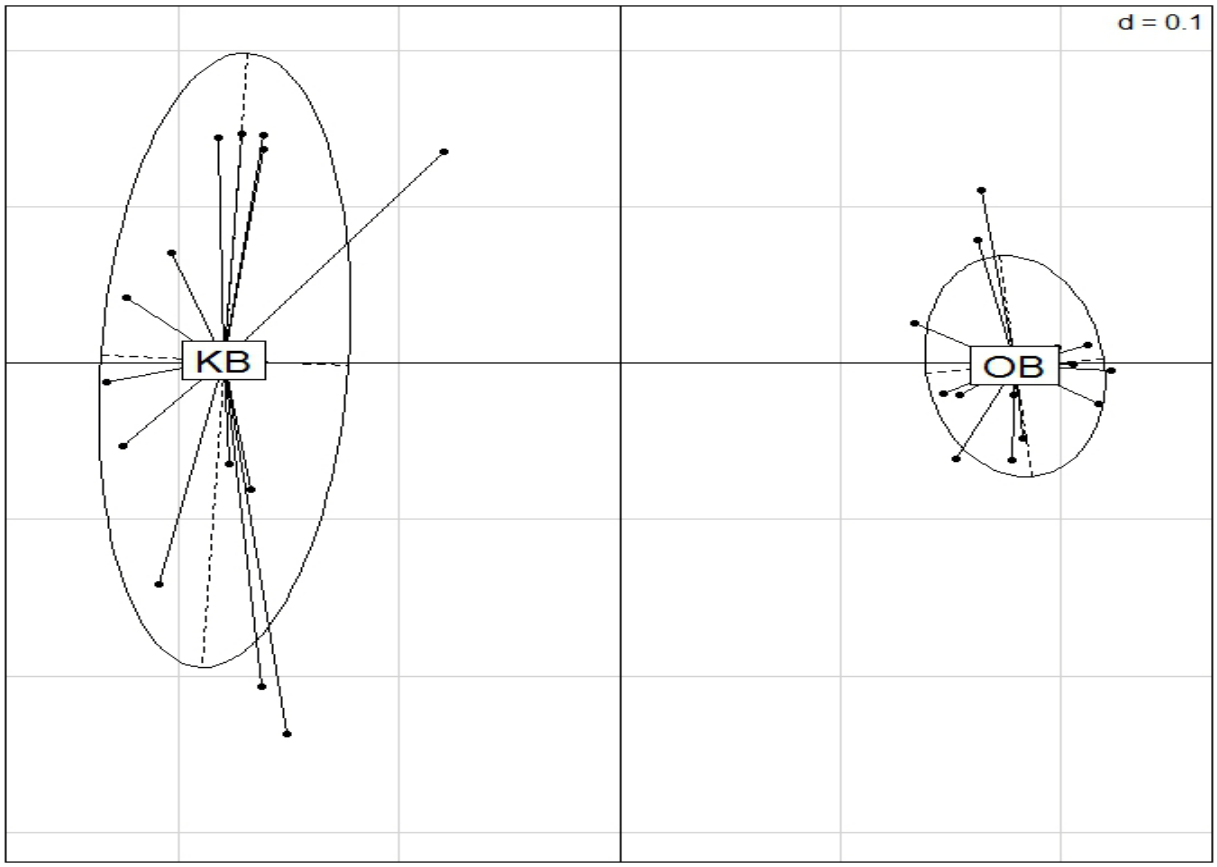


Fig. 19 Station Map

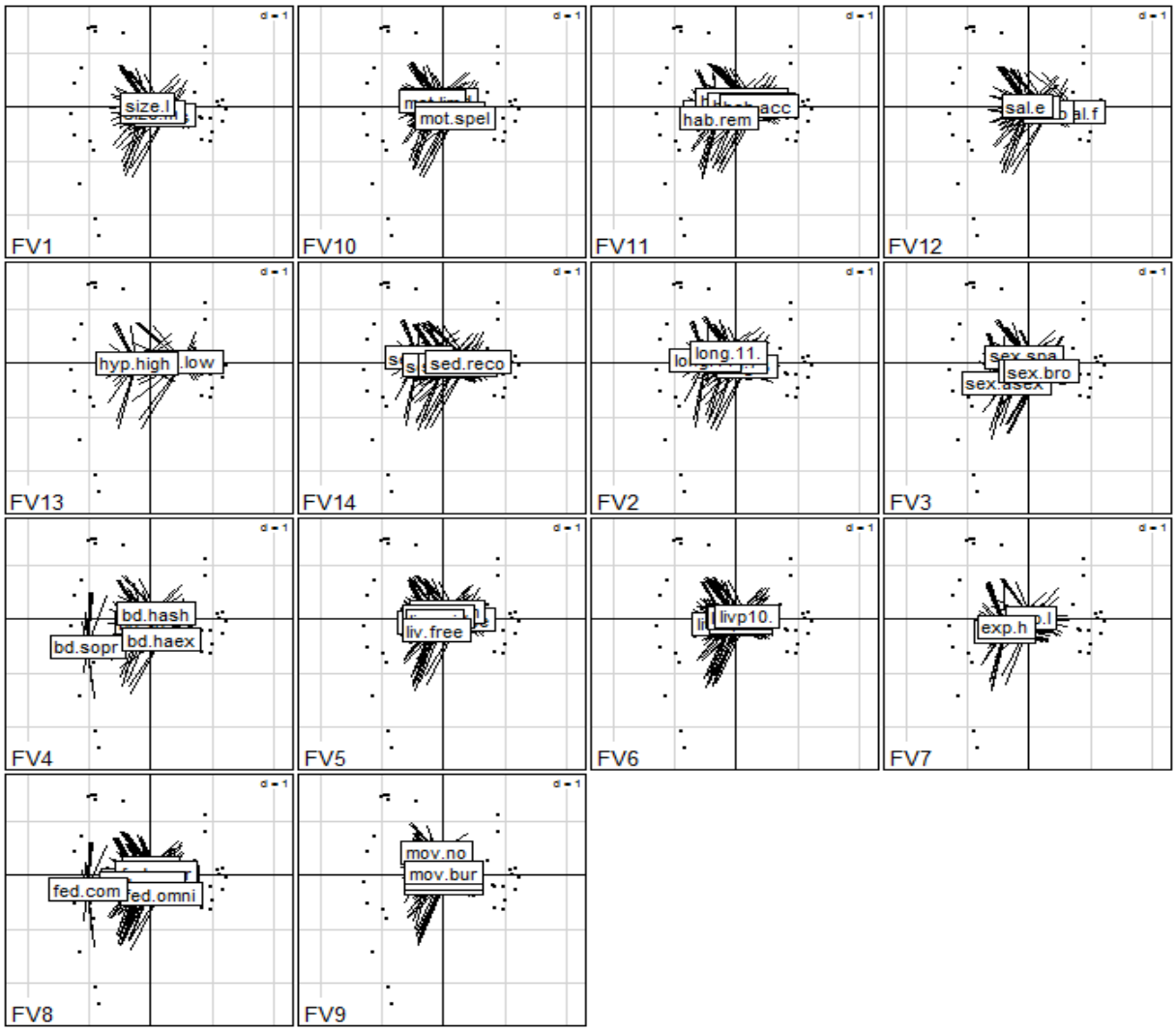


Fig. 19 Ordination of traits from the first two axes

4 Discussion & Conclusion

4.1 *General*

This study has shown a certain difference between the key areas. The central goal of this study was to show that this difference is combined with a shift of traits or living strategies along the salinity gradient. There is an approximate distance of 250km between the centres of both key areas. Environmental gradients, especially over larger scales such as this one, do not only alter in one way. In the Baltic Sea, for example, the oxygen rich, saline water enters through Kattegat and Skagerrak from the North Sea, and therefore the oxygen content of the water is only one of the gradients that need to be taken into consideration, too. Nevertheless, as already explained in previous parts, the variation of all abiotic criteria apart from salinity

was kept as low as possible and can be contemplated as not being massively influential for this work. Another problem that arises through this variation is that the selection of suitable stations might result in a small pack of data that possibly lacks descriptive power due to an unsufficient amount of data. Generally, statistical measures are more significant if implemented with a bigger set of data. When choosing the stations, the scope on all criteria at all times needed to be as narrow as possible. Next to the difficulties caused by this combination of environmental influences, troubles can also appear through the time shift amongst the interpreted data. As shown in table 3, the time that samples were taken at stations spreads over ten years. Keeping the problem of oxygen and salt influx in mind, this might also cause misleading conclusions. The influx of oxygen rich water with high salinity occurs occasionally in the manner of an influx event. So far these influxes are merely recognized afterwards and are not predictable. Therefore, the outcome of the study also depends on the time in which data was collected because of the possible North Sea water influx or the absence of those. Results of studies of this kind might indicate contradictory conclusions when implemented at different times with a different set of influxes in the previous years. Another abiotic criterion which needs to be taken into account is the sediment and appendent grain sizes. In the Oderbank, grain sizes varied by only around 34µm from 180 to 214µm, whereas in the Kiel Bay they varied by around 172µm from 129 to 301µm. Differences in sediment preference might cause different species to populate the lower or upper end of this variation. At least in this study, the median grain size of both key areas were found to be close enough to eliminate such problems, however, it cannot be assumed that there is no influence at all. Another reason to estimate the impact of this problem as small is that in both areas bivalves were the dominating species.

The calculation of indices came up with the expected results. There is an expansive amount of literature stating the loss of species diversity which goes hand in hand with a decline of Shannon- Wiener and Simpson- Yule indices along the decreasing salinity (Darr et al., 2014). Equally the decline of the ES50 value, which accounts for species richness, was expected before.

4.2 *Statistical measures*

Different analytical and statistical means were used to compare both key areas and to make a decision whether they are heterogeneous or not. The trait compilation diagrams (fig. 9- 13) already offered a first glance at the possible distinctive features. Next to traits like motility,

sediment reworking and habitat structuration the clearest difference between areas they showed were longevity and hypoxia. After the FCA was implemented this estimation could be confirmed. First of all the station FCA showed a clear distinction between the areas, the criterion dividing them can be interpreted as the difference in salinity. The FCA plot shows a shift of traits from long- living species with a soft- protected body and a trend to commensalism in the western key area of the Kiel Bay over to species with a higher hypoxia tolerance, freshwater resistance, and shorter longevity of up to three years, in the eastern Oderbank. So a part of the trait compilation diagrams can be verified with the outcome of the FCA. A shift from longer living to shorter living species with decreasing salinity is in accordance with findings of other authors such as (Tornroos, Bornsdorff, 2012). Also, a slight shift from bigger to smaller species from west to east, or high to low salinity, can be seen when looking at figure 18. In both key areas, bivalves made up the vast majority of biomass, considering this, the trend towards soft protected animals in the Kiel Bay seems interesting. This might be due to the inclusion of stations with finer sediment in the Kiel Bay. As hard shell bivalves are so dominant in both areas, this could show that next to the main body type also a soft protected body is of advantage in the more saline area as its expression in the plot shows the influence of this trait on biomass. Looking at the centre of the plot the traits euryhaline, mesohaline, surface- deposit feeding and longevity up to 7 years are the most common traits which could be interpreted in a way that animals expressing these traits can be expected to be ubiquitous in both habitats. Along the second axes no clusters or far outliers can be identified. The only far outlier is no movement at the top of the axes. Regarding the closest following traits, the existence of a functional unit can be discussed. The traits longevity 11+, sedentary, form settlement, limited free movement and burrow are all close to each other, even though they can't be identified as a separate group because other traits also appear inbetween. Nevertheless all of these traits account for species that are more or less bound to the sediment and stay close to their location, respectively don't move their position much. This could speak for a group of bivalves such as *Astarte sp*. or *Macoma balthica* and some Polychaetes as for example *Pygospio elegans* who were quite abundant in both areas. Equally, the traits no movement in combination with 'form settlement' must explain the high abundance of *Mytilus edulis* who builds settlement structures on the seafloor and is known to exhibit such behavior especially in the Oderbank/ Pommernbucht (Darr et al., 2014). Combining all of these traits, they can be interpreted as a group of sedentary species that stick to their position in the sediment. The other side of the axes shows a similar picture. The only two far outliers are 'omnivorous feeding' and a 'hard exoskeleton'. The next closest traits are

‘living free’, ‘freely motile on sediment’ and ‘semi pelagic’. Altogether this set of traits could describe animals that belong to the groups Amphipoda/ Isopoda, one possible animal found in our data base would be *Bathyporeia pilosa* who at least in Kiel Bay is very abundant. FCA is hard to interpret straightforward nevertheless the assumptions stated above are reasonable and in accordance with previously published studies.

The total inertia explained by two first FCA axes had a value of nearly 64% which is acceptable, nevertheless all correlation ratios for the traits remained really low. The reason for this most likely is the amount of trait categories. Overall 14 traits were described in 63 categories, this amount is the reason for the low correlation ratios. One way to eliminate this problem would be to split the traits into morphological and functional traits and perform two separate analysis, this should leave the correlations ratios at higher values.

4.3 *Outlook & Conclusion*

V. d. Linden (2012) published a first case study from the river Mondego in Portugal. Next to the classical diversity index, the Shannon- Wiener index, he also calculated functional diversity (Rao’s quadratic entropy or RQE) and calculated the ratio by dividing functional diversity (FD) with the Shannon- Wiener index which serves as a tool for the assessment of functional redundancy. Due to a lack of time, RQE wasn’t calculated in this study. Nevertheless, v. d. Linden identified ‘salinity preference’ as the main trait characterising the communities. Just as in this study, the Shannon- Wiener index decreased with decreasing salinity. Another outcome of his study was to highlight the significance of the trait ‘salinity preference’ for estuarine/ transitional waters. This study shows similar results and also displays the relevance of this trait. As an outlook to the next step of this study, the calculation of RQE and FD/H’ should be performed to describe function of the ecosystem in more detail.

Conclusively, the study did show heterogeneity between both key areas. Also possibly favourable traits for each area could be found. The outcome of this study does depend on many different factors though. There is a high variability of a lot of gradients that have an influence on the descriptive fashion. Still, using BTA files and sampled data together in a combined FCA holds the potential to identify major impacts on the trait composition of a community. And it definitely provides a tool to look deeper into community diversity than simply calculating diversity indices.

5 Acknowledgements

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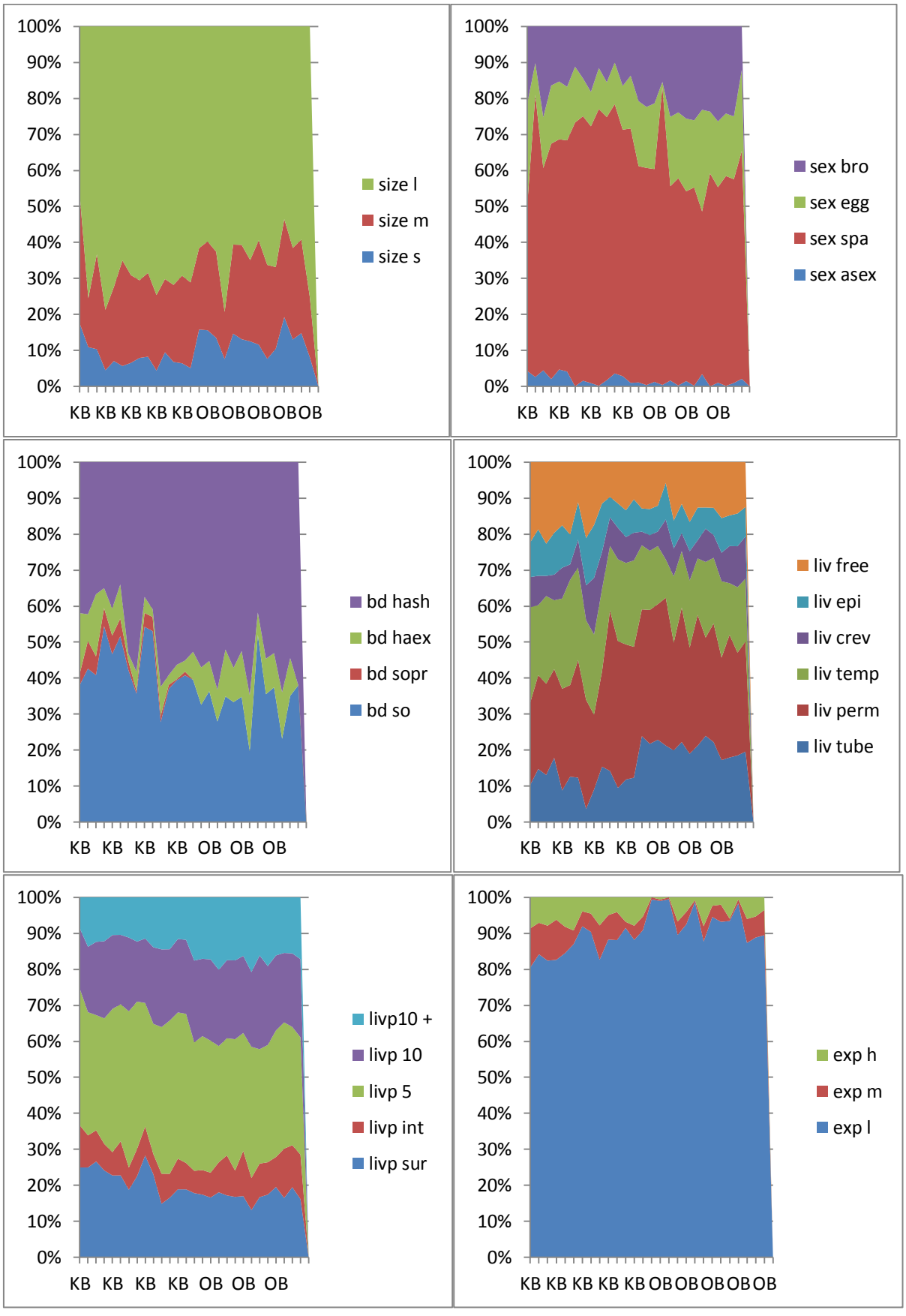
7 Appendix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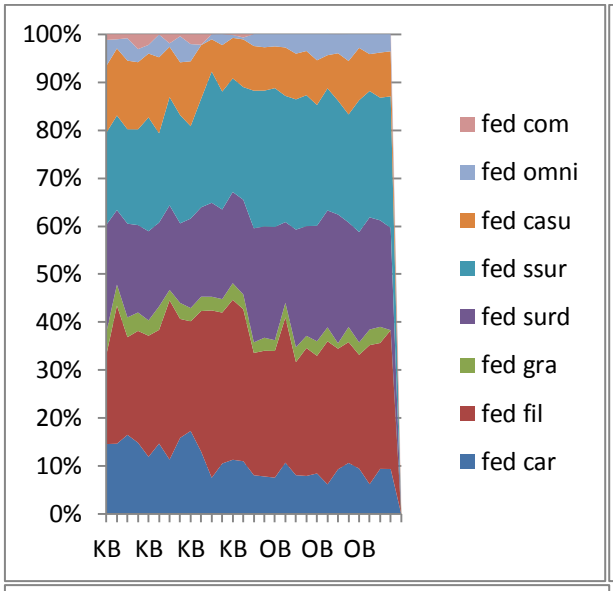

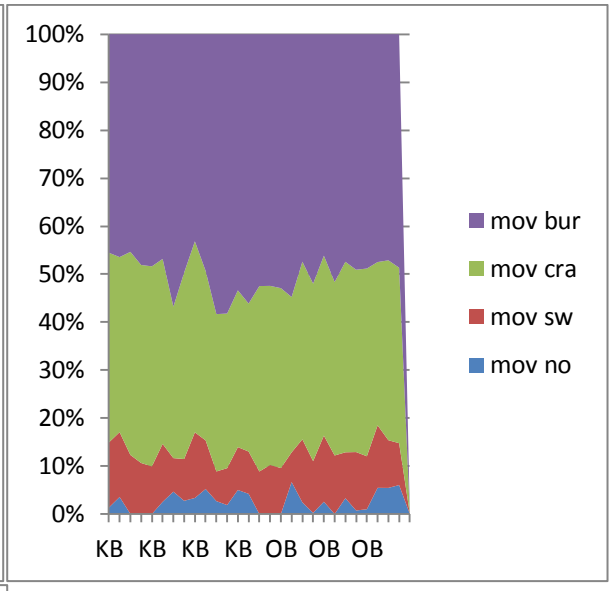

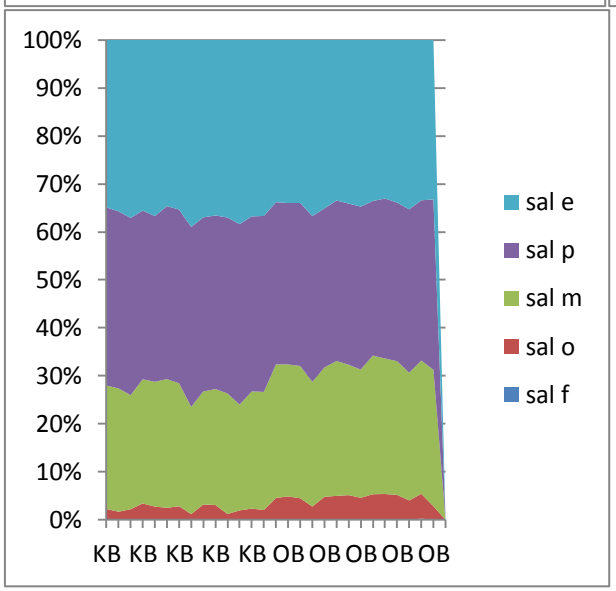

Artlist Kiel Bay

ScientificName	Phylum	Class	Order	Family
Abra alba	Mollusca	Bivalvia	Veneroida	Semelidae
Actinia equina	Cnidaria	Anthozoa	Actiniaria	Actiniidae
Alcyonidium diaphanum	Bryozoa	Gymnolaemata	Ctenostomatida	Alcyonidiidae
Alcyonidium polyoum	Bryozoa	Gymnolaemata	Ctenostomatida	Alcyonidiidae
Alitta succinea	Annelida	Polychaeta	Phyllodocida	Nereididae
Ampharete acutifrons	Annelida	Polychaeta	Terebellida	Ampharetidae
Ampharete baltica	Annelida	Polychaeta	Terebellida	Ampharetidae
Ampithoe rubricata	Arthropoda	Malacostraca	Amphipoda	Ampithoidae
Ancula gibbosa	Mollusca	Gastropoda	Nudibranchia	Goniodorididae
Apherusa bispinosa	Arthropoda	Malacostraca	Amphipoda	Calliopiidae
Aporrhais pespelecani	Mollusca	Gastropoda	Littorinimorpha	Aporrhaidae
Arctica islandica	Mollusca	Bivalvia	Veneroida	Arcticidae
Arenicola marina	Annelida	Polychaeta		Arenicolidae
Aricidea minuta	Annelida	Polychaeta		Paraonidae
Aricidea suecica	Annelida	Polychaeta		Paraonidae
Astarte borealis	Mollusca	Bivalvia	Carditoida	Astartidae

Astarte elliptica	Mollusca	Bivalvia	Carditoida	Astartidae
Astarte montagui	Mollusca	Bivalvia	Carditoida	Astartidae
Asterias rubens	Echinodermata	Asteroidea	Forcipulatida	Asteriidae
Balanus crenatus	Arthropoda	Maxillopoda	Sessilia	Balanidae
Bathyporeia pilosa				
Bittium reticulatum	Mollusca	Gastropoda	Caenogastropoda*	Cerithiidae
Bowerbankia gracilis	Bryozoa	Gymnolaemata	Ctenostomatida	Vesiculariidae
Bowerbankia imbricata	Bryozoa	Gymnolaemata	Ctenostomatida	Vesiculariidae
Buccinum undatum	Mollusca	Gastropoda	Neogastropoda	Buccinidae
Bylgides sarsi	Annelida	Polychaeta	Phyllodocida	Polynoidae
Cadlina laevis	Mollusca	Gastropoda	Nudibranchia	Cadlinidae
Callipallene brevirostris	Arthropoda	Pycnogonida	Pantopoda	Callipallenidae
Callopora lineata	Bryozoa	Gymnolaemata	Cheilostomatida	Calloporidae
Capitella capitata	Annelida	Polychaeta		Capitellidae
Caprella linearis	Arthropoda	Malacostraca	Amphipoda	Caprellidae
Caprella septentrionalis	Arthropoda	Malacostraca	Amphipoda	Caprellidae
Carcinus maenas	Arthropoda	Malacostraca	Decapoda	Portunidae
Caulleriella killariensis	Annelida	Polychaeta	Terebellida	Cirratulidae
Celleporella hyalina	Bryozoa	Gymnolaemata	Cheilostomatida	Hippothoidae
Cerastoderma glaucum	Mollusca	Bivalvia	Veneroida	Cardiidae
Chaetozone setosa	Annelida	Polychaeta	Terebellida	Cirratulidae
Chalinula limbata	Porifera	Demospongiae	Haplosclerida	Chalinidae
Cheirocratus sundevalli	Arthropoda	Malacostraca	Amphipoda	Cheirocratidae
Chironomidae	Arthropoda	Insecta	Diptera	Chironomidae
Ciona intestinalis	Chordata	Ascidiacea	Phlebobranchia	Cionidae
Corbula gibba	Mollusca	Bivalvia	Myoida	Corbulidae
Crangon crangon	Arthropoda	Malacostraca	Decapoda	Crangonidae
Crassicorophium crassicorne	Arthropoda	Malacostraca	Amphipoda	Corophiidae
Cribrilina punctata	Bryozoa	Gymnolaemata	Cheilostomatida	Cribrilinidae
Dendrodoa grossularia	Chordata	Ascidiacea	Stolidobranchia	Styelidae
Dexamine spinosa	Arthropoda	Malacostraca	Amphipoda	Dexaminidae
Diaphana minuta	Mollusca	Gastropoda	Cephalaspidea	Diaphanidae
Diastylis rathkei	Arthropoda	Malacostraca	Cumacea	Diastylidae
Dipolydora caulleryi	Annelida	Polychaeta	Spionida	Spionidae
Dipolydora quadrilobata	Annelida	Polychaeta	Spionida	Spionidae
Echinocyamus pusillus	Echinodermata	Echinoidea	Clypeasteroida	Echinocyamidae
Edwardsia danica	Cnidaria	Anthozoa	Actiniaria	Edwardsiidae
Einhornia crustulenta	Bryozoa	Gymnolaemata	Cheilostomatida	Electridae
Electra pilosa	Bryozoa	Gymnolaemata	Cheilostomatida	Electridae
Ensis directus	Mollusca	Bivalvia	Euheterodonta*	Pharidae
Escharella immersa	Bryozoa	Gymnolaemata	Cheilostomatida	Romancheinidae
Eteone barbata	Annelida	Polychaeta	Phyllodocida	Phyllodocidae
Eteone longa	Annelida	Polychaeta	Phyllodocida	Phyllodocidae
Euchone papillosa	Annelida	Polychaeta	Sabellida	Sabellidae
Eucratea loricata	Bryozoa	Gymnolaemata	Cheilostomatida	Eucrateidae
Eudorellopsis deformis	Arthropoda	Malacostraca	Cumacea	Leuconidae
Eulalia bilineata	Annelida	Polychaeta	Phyllodocida	Phyllodocidae
Eumida sanguinea	Annelida	Polychaeta	Phyllodocida	Phyllodocidae
Exogone naidina	Annelida	Polychaeta	Phyllodocida	Syllidae
Fabricia stellaris	Annelida	Polychaeta	Sabellida	Fabriciidae
Fabriciola baltica	Annelida	Polychaeta	Sabellida	Fabriciidae
Facelina bostoniensis	Mollusca	Gastropoda	Nudibranchia	Facelinidae
Farrella repens	Bryozoa	Gymnolaemata	Ctenostomatida	Farrellidae
Flabelligera affinis	Annelida	Polychaeta	Terebellida	Flabelligeridae

Flustra foliacea	Bryozoa	Gymnolaemata	Cheilostomatida	Flustridae
Galathowenia oculata	Annelida	Polychaeta	Sabellida	Oweniidae
Gammarellus homari	Arthropoda	Malacostraca	Amphipoda	Gammarellidae
Gastrosaccus spinifer	Arthropoda	Malacostraca	Mysida	Mysidae
Halacaridae	Arthropoda	Arachnida	Trombidiformes	Halacaridae
Halcampa duodecimcirrata	Cnidaria	Anthozoa	Actiniaria	Halcampidae
Halichondria panicea	Porifera	Demospongiae	Halichondrida	Halichondriidae
Haliclona oculata	Porifera	Demospongiae	Haplosclerida	Chalinidae
Halisarca dujardini	Porifera	Demospongiae	Chondrosida	Halisarcidae
Halisarca dujardinii	Porifera	Demospongiae	Chondrosida	Halisarcidae
Halitholus yoldiaarcticae	Cnidaria	Hydrozoa	Anthoathecata	Pandeidae
Harmothoe imbricata	Annelida	Polychaeta	Phyllodocida	Polynoidae
Harmothoe impar	Annelida	Polychaeta	Phyllodocida	Polynoidae
Hartlaubella gelatinosa	Cnidaria	Hydrozoa	Leptothecata	Campanulariidae
Heteromastus filiformis	Annelida	Polychaeta		Capitellidae
Hiatella arctica	Mollusca	Bivalvia	Euheterodonta*	Hiatellidae
Idotea balthica	Arthropoda	Malacostraca	Isopoda	Idoteidae
Kurtiella bidentata	Mollusca	Bivalvia	Veneroida	Montacutidae
Lacuna pallidula	Mollusca	Gastropoda	Littorinimorpha	Littorinidae
Lacuna parva	Mollusca	Gastropoda	Littorinimorpha	Littorinidae
Lacuna vincta	Mollusca	Gastropoda	Littorinimorpha	Littorinidae
Laeospira corallinae	Annelida	Polychaeta	Sabellida	Serpulidae
Lagis koreni	Annelida	Polychaeta	Terebellida	Pectinariidae
Laonome kroeyeri	Annelida	Polychaeta	Sabellida	Sabellidae
Lepidochitona cinerea	Mollusca	Polyplacophora	Chitonida	Lepidochitonidae
Lepidonotus squamatus	Annelida	Polychaeta	Phyllodocida	Polynoidae
Leucosolenia sp.	Porifera	Calcarea	Leucosolenida	Leucosoleniidae
Levinsenia gracilis	Annelida	Polychaeta		Paraonidae
Lineus ruber	Nemertea	Anopla		Lineidae
Littorina littorea	Mollusca	Gastropoda	Littorinimorpha	Littorinidae
Macoma balthica	Mollusca	Bivalvia	Veneroida	Tellinidae
Macoma calcarea	Mollusca	Bivalvia	Veneroida	Tellinidae
Malacobdella grossa	Nemertea	Enopla	Monostilifera	Malacobdellidae
Megamphopus cornutus	Arthropoda	Malacostraca	Amphipoda	Photidae
Metridium senile	Cnidaria	Anthozoa	Actiniaria	Metridiidae
Microdeutopus gryllotalpa	Arthropoda	Malacostraca	Amphipoda	Aoridae
Molgula manhattensis	Chordata	Ascidiacea	Stolidobranchia	Molgulidae
Monocorophium insidiosum	Arthropoda	Malacostraca	Amphipoda	Corophiidae
Musculus discors	Mollusca	Bivalvia	Mytiloida	Mytilidae
Musculus niger	Mollusca	Bivalvia	Mytiloida	Mytilidae
Musculus subpictus	Mollusca	Bivalvia	Mytiloida	Mytilidae
Mya arenaria	Mollusca	Bivalvia	Myoida	Myidae
Mya truncata	Mollusca	Bivalvia	Myoida	Myidae
Mytilus edulis	Mollusca	Bivalvia	Mytiloida	Mytilidae
Nemertea	Nemertea			
Neoamphitrite figulus	Annelida	Polychaeta	Terebellida	Terebellidae
Nephtys caeca	Annelida	Polychaeta	Phyllodocida	Nephtyidae
Nephtys ciliata	Annelida	Polychaeta	Phyllodocida	Nephtyidae
Nephtys hombergii	Annelida	Polychaeta	Phyllodocida	Nephtyidae
Nephtys pente	Annelida	Polychaeta	Phyllodocida	Nephtyidae
Neptunea antiqua	Mollusca	Gastropoda	Neogastropoda	Buccinidae
Nereimyra punctata	Annelida	Polychaeta	Phyllodocida	Hesionidae
Nicolea zostericola	Annelida	Polychaeta	Terebellida	Terebellidae
Nymphon brevirostre	Arthropoda	Pycnogonida	Pantopoda	Nymphonidae

Odostomia scalaris				
Onchidoris muricata	Mollusca	Gastropoda	Nudibranchia	Onchidoridae
Onoba semicostata	Mollusca	Gastropoda	Littorinimorpha	Rissoidae
Opercularella lacerata	Cnidaria	Hydrozoa	Leptothecata	Campanulinidae
Ophelia limacina	Annelida	Polychaeta		Opheliidae
Ophiura albida	Echinodermata	Ophiuroidea	Ophiurida	Ophiuridae
Palaemon adspersus	Arthropoda	Malacostraca	Decapoda	Palaemonidae
Palaemon elegans				
Paraonis fulgens	Annelida	Polychaeta		Paraonidae
Pariambus typicus	Arthropoda	Malacostraca	Amphipoda	Caprellidae
Parvicardium pinnulatum	Mollusca	Bivalvia	Veneroida	Cardiidae
Parvicardium scabrum	Mollusca	Bivalvia	Veneroida	Cardiidae
Peringia ulvae	Mollusca	Gastropoda	Littorinimorpha	Hydrobiidae
Phaxas pellucidus	Mollusca	Bivalvia	Euheterodonta*	Pharidae
Pherusa plumosa	Annelida	Polychaeta	Terebellida	Flabelligeridae
Philine aperta				
Pholoe assimilis	Annelida	Polychaeta	Phyllodocida	Pholoidae
Pholoe baltica	Annelida	Polychaeta	Phyllodocida	Pholoidae
Pholoe inornata	Annelida	Polychaeta	Phyllodocida	Pholoidae
Phoronis sp.	Phoronida			
Phoxocephalus holbolli	Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae
Phtisica marina	Arthropoda	Malacostraca	Amphipoda	Caprellidae
Phyllodoce groenlandica	Annelida	Polychaeta	Phyllodocida	Phyllodocidae
Phyllodoce maculata	Annelida	Polychaeta	Phyllodocida	Phyllodocidae
Phyllodoce mucosa	Annelida	Polychaeta	Phyllodocida	Phyllodocidae
Platynereis dumerilii	Annelida	Polychaeta	Phyllodocida	Nereididae
Pleurogonium rubicundum	Arthropoda	Malacostraca	Isopoda	Paramunnidae
Polycirrus medusa	Annelida	Polychaeta	Terebellida	Terebellidae
Polydora ciliata	Annelida	Polychaeta	Spionida	Spionidae
Polydora cornuta	Annelida	Polychaeta	Spionida	Spionidae
Praunus inermis	Arthropoda	Malacostraca	Mysida	Mysidae
Protomedeia fasciata	Arthropoda	Malacostraca	Amphipoda	Corophiidae
Psammechinus miliaris	Echinodermata	Echinoidea	Camarodonta	Parechinidae
Pseudopolydora antennata	Annelida	Polychaeta	Spionida	Spionidae
Pseudopolydora pulchra	Annelida	Polychaeta	Spionida	Spionidae
Pusillina inconspicua	Mollusca	Gastropoda	Littorinimorpha	Rissoidae
Pygospio elegans	Annelida	Polychaeta	Spionida	Spionidae
Retusa truncatula	Mollusca	Gastropoda	Cephalaspidea	Retusidae
Rhodine loveni	Annelida	Polychaeta		Maldanidae
Rissoa membranacea	Mollusca	Gastropoda	Littorinimorpha	Rissoidae
Sagartia sp.	Cnidaria	Anthozoa	Actiniaria	Sagartiidae
Sarsia tubulosa	Cnidaria	Hydrozoa	Anthoathecata	Corynidae
Scalibregma inflatum	Annelida	Polychaeta		Scalibregmatidae
Scolelepis foliosa	Annelida	Polychaeta	Spionida	Spionidae
Scoloplos armiger	Annelida	Polychaeta		Orbiniidae
Sertularia cupressina	Cnidaria	Hydrozoa	Leptothecata	Sertulariidae
Sphaerodoropsis baltica	Annelida	Polychaeta	Phyllodocida	Sphaerodoridae
Spio arndti	Annelida	Polychaeta	Spionida	Spionidae
Spio goniocephala	Annelida	Polychaeta	Spionida	Spionidae
Spiophanes bombyx	Annelida	Polychaeta	Spionida	Spionidae
Spisula subtruncata	Mollusca	Bivalvia	Veneroida	Mactridae
Styela coriacea	Chordata	Ascidiacea	Stolidobranchia	Styelidae
Terebellides stroemii	Annelida	Polychaeta	Terebellida	Trichobranchidae
Trochochaeta multisetosa	Annelida	Polychaeta	Spionida	Trochochaetidae

Tubificidae	Annelida	Clitellata	Haplotaxida	Tubificidae
Tubificoides benedii	Annelida	Clitellata	Haplotaxida	Tubificidae
Tubulanus polymorphus	Nemertea	Palaeonemertea		Tubulanidae
Turbellaria	Platyhelminthes	Turbellaria		
Urticina felina	Cnidaria	Anthozoa	Actiniaria	Actiniidae
Walkeria uva	Bryozoa	Gymnolaemata	Ctenostomatida	Walkeriidae

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Amphibalanus improvisus	Arthropoda	Maxillopoda	Sessilia	Balanidae
Bathyporeia pelagica	Arthropoda	Malacostraca	Amphipoda	Bathyporeiidae
Bathyporeia pilosa	Arthropoda	Malacostraca	Amphipoda	Bathyporeiidae
Calliopaea bellula	Mollusca	Gastropoda	Sacoglossa	Limapontiidae
Cerastoderma glaucum	Mollusca	Bivalvia	Veneroida	Cardiidae
Corophium volutator	Arthropoda	Malacostraca	Amphipoda	Corophiidae
Crangon crangon	Arthropoda	Malacostraca	Decapoda	Crangonidae
Cyanophthalma obscura	Nemertea	Enopla	Monostilifera	Tetrastemmatidae
Ecrobia ventrosa	Mollusca	Gastropoda	Littorinimorpha	Hydrobiidae
Einhornia crustulenta	Bryozoa	Gymnolaemata	Cheilostomatida	Electridae
Enchytraeidae	Annelida	Clitellata	Enchytraeida	Enchytraeidae
Gammarus oceanicus	Arthropoda	Malacostraca	Amphipoda	Gammaridae
Gammarus salinus	Arthropoda	Malacostraca	Amphipoda	Gammaridae
Gammarus zaddachi	Arthropoda	Malacostraca	Amphipoda	Gammaridae
Hartlaubella gelatinosa	Cnidaria	Hydrozoa	Leptothecata	Campanulariidae
Hediste diversicolor	Annelida	Polychaeta	Phyllodocida	Nereididae
Heterochaeta costata	Annelida	Clitellata	Haplotaxida	Tubificidae
Idotea balthica	Arthropoda	Malacostraca	Isopoda	Idoteidae
Jaera albifrons	Arthropoda	Malacostraca	Isopoda	Janiridae
Macoma balthica	Mollusca	Bivalvia	Veneroida	Tellinidae
Marenzelleria neglecta	Annelida	Polychaeta	Spionida	Spionidae
Marenzelleria viridis	Annelida	Polychaeta	Spionida	Spionidae
Mya arenaria	Mollusca	Bivalvia	Myoida	Myidae
Mysis mixta	Arthropoda	Malacostraca	Mysida	Mysidae
Mytilus edulis	Mollusca	Bivalvia	Mytiloida	Mytilidae
Nais elinguis	Annelida	Clitellata	Haplotaxida	Tubificidae
Neomysis integer	Arthropoda	Malacostraca	Mysida	Mysidae
Oligochaeta	Annelida	Clitellata		
Peringia ulvae	Mollusca	Gastropoda	Littorinimorpha	Hydrobiidae
Praunus flexuosus	Arthropoda	Malacostraca	Mysida	Mysidae
Pygospio elegans	Annelida	Polychaeta	Spionida	Spionidae
ScientificName	Phylum	Class	Order	Family
Streblospio shrubsolii	Annelida	Polychaeta	Spionida	Spionidae
Tubificidae	Annelida	Clitellata	Haplotaxida	Tubificidae
Tubificoides benedii	Annelida	Clitellata	Haplotaxida	Tubificidae
Turbellaria	Platyhelminthes	Turbellaria		

***unassigned**

EIDESSTATTLICHE ERKLÄRUNG

Ich erkläre an Eides statt, dass ich die vorliegende Arbeit selbstständig verfasst, andere als die angegebenen Quellen/Hilfsmittel nicht benutzt und die den benutzten Quellen wörtlich und inhaltlich entnommenen Stellen als solche kenntlich gemacht habe.

Rostock, am …… ……..

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I declare that I have authored this thesis independently, that I have not used other than the declared sources / resources and that I have explicitly marked all material which has been quoted either literally or by content from the used sources.

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