Trait-based products of EMODnet benthic biology

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# Abstract

# Aim of this analysis.

Through their activity, benthic animals play an important role in marine ecosystem functioning. More specifically, they mix the sediment by their movement and feeding, a process called “bioturbation”. They also create water movements, enhancing the exchange of dissolved constituents such as oxygen, and dissolved inorganic nutrients, a process called “bio-irrigation”.

Both these activities have a large impact on the biogeochemical cycles in the environment, and they are commonly parameterised as single parameters in biogeochemical models.

Biologists have tried to categorise the bioturbation or bio-irrigation activity based on the identity of the organims. They do not derive the rate parameters as used in the biogeochemical models but rather derive a potential of the organisms to perform these tasks.

Here we use Benthic abundance data from EMODnet to estimate the bioturbation potential and the bioirrigation potential index.

To derive these potentials we need information on:

* The weights of the species and their total biomass
* The species mobility and sediment reworking mode

# Reading the data

## Species taxonomic tree

The names of all species encountered in the dataset were checked against the WORMS database, and their taxonomic tree added (this was done via , menu item *tools/Match taxa*). These data are read first. The dimensions of the data set and the first two entries are printed.

##   
## dimension and first part of the data set :

## [1] 7650 8

## id phy clas ord fam  
## 1 7500 Hemichordata Enteropneusta [unassigned] Enteropneusta   
## 2 1 Cnidaria Hydrozoa Leptothecata Sertulariidae  
## gen tx txa  
## 1 [unassigned] [unassigned] Enteropneusta [unassigned] Enteropneusta  
## 2 Abietinaria Abietinaria Abietinaria

## the MWTL data

The MWTL data is the only data set that contains both species *biomass* and *densities* (the other data sets comprise only densities or just presence/absence). This data is used to estimate mean individual weights of the various species. The file *occ.csv* has been prepared by Olivier Beauchard as part of the EMODNET product on trait types. It contains average density and biomass per taxon and station. Averaging was over time. Some taxa lumping has been done in the preparation of the file, as well as taxonomic checks against WORMS.

Biomass is in *g AFDW/m2*, density in *number/m2*

##   
## dimension and first part of the data set :

## [1] 394 5

## X tax mw gmw n  
## 1 1 Abludomelita obtusata 0.0003002036 0.0003002011 12  
## 2 2 Abra alba 0.0028563437 0.0004744354 425

### Expanding the weight dataset

Next we estimate mean weights on species level, on genus level, on the family level, and on the level of order and bind all in one data.frame(*mws*).

The total number of weight values thus obtained is 873, of which 394 are estimated at species level, 280 at genus level, 156 at family level, and and 43 at level or order.

## FeedingTypes

Feedingtypes are known from a subset of the species. The following types are distinguished:

* “CaSc” = carnivore/scavenger
* “De” = depositfeeder
* “He” = herbivore
* “Om” = omnivore
* “Pa” = parasite
* “Su” = suspension feeder
* “SuDe” = suspension/deposit feeder

##   
## dimension and first part of the data set :

## n.acc Trophy  
## 1 Abludomelita obtusata De  
## 2 Abra alba SuDe

##   
## CaSc De He Om Pa Su SuDe   
## 78 100 20 56 3 79 37

### Feeding types on higher taxonomic levels

We now assign feeding types to the genera and families, for which we take the most commonly encountered feedingtype at the lower level.

## taxon ft level n  
## 1 Abludomelita obtusata De species 1  
## 2 Abra alba SuDe species 1

The total number of feeding types thus obtained is 857, of which 373 are known at species level, 270 at genus level, 167 at family level and 47 at order level.

## life history traits

Life history traits are also assigned on genus and family level, where we take the most commonly encountered trait at the lower level.

##   
## dimension and first part of the data set :

## [1] 273 21

## phy cla ord fam gen  
## 1 Annelida Polychaeta Sabellida Serpulidae Spirobranchus  
## 2 Annelida Polychaeta Sabellida Sabellariidae Sabellaria  
## taxon Motility Body.size Burrowing.depth Morphology  
## 1 Spirobranchus triqueter Tubicolous 1-3cm 0cm Cylindrical  
## 2 Sabellaria spinulosa Tubicolous 3-10cm 0cm Cylindrical  
## Mobility Mixing.type Mixing.rate Mi Mi2 Ri Morphology.2  
## 1 Very low Surface mixing Very low 1 1 2 1  
## 2 Very low Surface mixing Very low 1 1 1 1  
## Morphology.2.1 Body.size.2 Burrowing.depth.2 Mixing.rate.2  
## 1 1 2 1 2  
## 2 1 3 1 3

The total number of traits thus obtained is 523, of which 273 are estimated at species level, 131 at genus level, 89 at family level and 30 at order level.

We tabulate the number of occurrences of each trait in the resulting data.frame.

## motility:

##   
## Attached Crawler Crawler-Swimmer Tubicolous   
## 15 288 132 88

## Body size:

##   
## <1cm >20cm 1-3cm 10-20cm 3-10cm   
## 101 36 106 55 225

## Burrowing depth:

##   
## >30cm 0-5cm 0cm 10-15cm 15-30cm 5-10cm   
## 28 216 78 61 83 57

## Morphology:

##   
## Articulated Bivalved Cylindrical Flat Globular Stellar   
## 118 108 232 1 38 26

## Mobility:

##   
## High Intermediate Low Very low   
## 40 246 153 84

## Mixing type:

##   
## D/U conveying Diffusion Downward conveying   
## 34 123 23   
## Regeneration Surface mixing Upward conveying   
## 10 301 32

## Mixing rate:

##   
## High Intermediate Low Very high Very low   
## 34 62 143 44 240

## Mi:

##   
## 1 2 3 4   
## 84 153 246 40

## Ri:

##   
## 1 2 3 4 5   
## 28 275 86 124 10

## The density data

Density data are read.

##   
## dimension and first part of the data set :

## [1] 1128549 6

## data sta x y tx dens  
## 1 HELCOM HELCOM1 8.267167 56.72267 Abra alba 139.8601  
## 2 HELCOM HELCOM1 8.267167 56.72267 Abra nitida 139.8601

##   
## total number of data points per provider :

##   
## HELCOM MACROBEL MAREANO MWTL NSBS ODAM PMP PORT   
## 10399 12701 21591 8475 14622 94544 333 6796   
## REBENT RSMP SHARK SMHI   
## 24516 875244 56268 3060

Some data providers did not record density, but just presence/absence; these data are removed.

The total number of species in this data set is 5433

# A look at the data

Species densities are summed per station to give the total densities

## total number of stations per provider :

##   
## HELCOM MACROBEL MAREANO MWTL NSBS ODAM PMP REBENT   
## 914 768 370 103 235 3057 23 216   
## RSMP SHARK SMHI   
## 23915 6925 587

The total number of stations in this data set is 37113

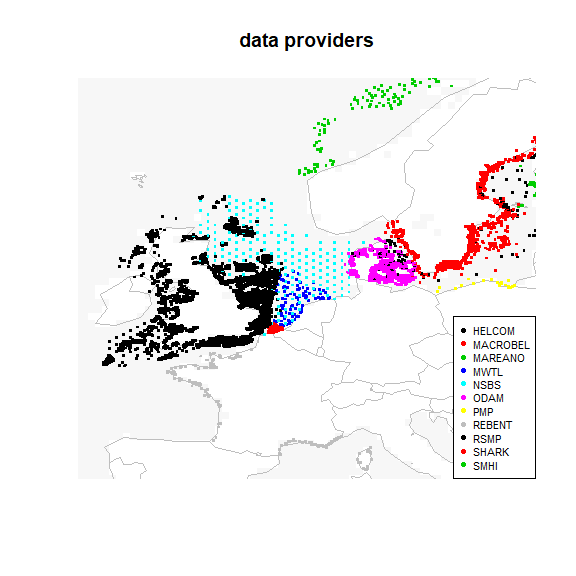
The positions of the stations are plotted, colored according to the data provider

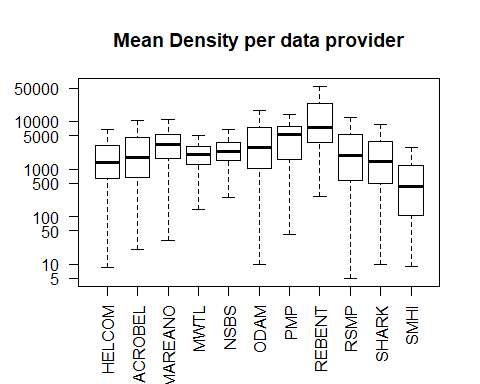
## Loading required package: rworldmap

## Loading required package: sp

## ### Welcome to rworldmap ###

## For a short introduction type : vignette('rworldmap')





# Adding individual weights and traits to density data

Weights and trait information is not available for all species, even after determining this information on genus and familiy level. We create data sets that remove the species that do not have all information. We then calculate total density on this reduced data set and see what fraction of total density we obtain.

First the required taxonomic information is added to the density list:

## integer(0)

To merge density data with the other data sets, a function is created.

## Merging density and weights

The fraction of data for which individual weight could be estimated = 0.8758442.

The type of organisms for which the information is lacking belong to the phyla:

##   
## Cnidaria Mollusca Chordata Annelida   
## 34134 26415 10237 10028   
## Echinodermata Bryozoa Arthropoda Sipuncula   
## 9953 9538 9340 7669   
## Porifera Nemertea Cephalorhyncha Platyhelminthes   
## 5996 2787 2546 2437   
## Rhodophyta Ciliophora Entoprocta Foraminifera   
## 1568 1394 1347 483   
## Hemichordata Chaetognatha Brachiopoda   
## 347 182 136 134   
## Gastrotricha Phoronida Tardigrada Chlorophyta   
## 101 95 46 38   
## Nematomorpha Ochrophyta Xenacoelomorpha Tracheophyta   
## 25 25 14 8   
## Nematoda Acanthocephala Myzozoa   
## 6 4 1

Many of these phyla are small organisms (Tardigrada, Foraminifera,…), so the biomass that is not taken into account is probably limited.

## Merging density and traits

The fraction of data for which traits could be estimated = 0.8451735 The unclassified organisms belong to:

##   
## Bryozoa Mollusca Cnidaria Arthropoda   
## 66661 30504 25460 11490   
## Chordata Sipuncula Annelida Echinodermata   
## 8566 7000 6579 5512   
## Porifera Cephalorhyncha Ciliophora Nemertea   
## 3262 2505 1394 708   
## Foraminifera Rhodophyta Platyhelminthes Hemichordata   
## 342 341 177 123   
## Brachiopoda Chaetognatha Chlorophyta Ochrophyta   
## 107 85 38 24   
## Nematoda Tracheophyta Myzozoa   
## 5 2 1

## Merging density and feeding types

The fraction of data for which feeding types could be estimated = 0.8743257 The unclassified organisms belong to:

##   
## Bryozoa Cnidaria Mollusca Chordata   
## 66661 25460 11121 8566   
## Sipuncula Annelida Porifera Arthropoda   
## 7000 6579 3262 3086   
## Cephalorhyncha Ciliophora Echinodermata Nemertea   
## 2505 1394 1123 708   
## Foraminifera Rhodophyta Platyhelminthes Hemichordata   
## 342 341 177 123   
## Brachiopoda Chaetognatha Chlorophyta Ochrophyta   
## 107 85 38 24   
## Nematoda Tracheophyta Myzozoa   
## 5 2 1

## Data for estimating bioturbation potential

## [1] 880265 23

## [1] 1103726 14

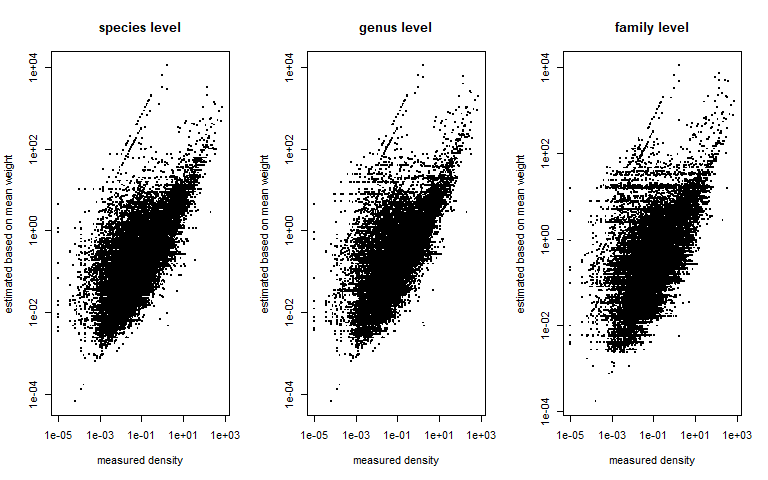
The fraction of data that has all information to estimate bioturbation potential = 0.7975394

## Check on the representativeness of the reduced data set

For the mwtl data we now compare the measured biomass with the biomass that we estimate, based on the mean weights. Note that in the MWTLdata, the density is called “ind” (from number of individuals)

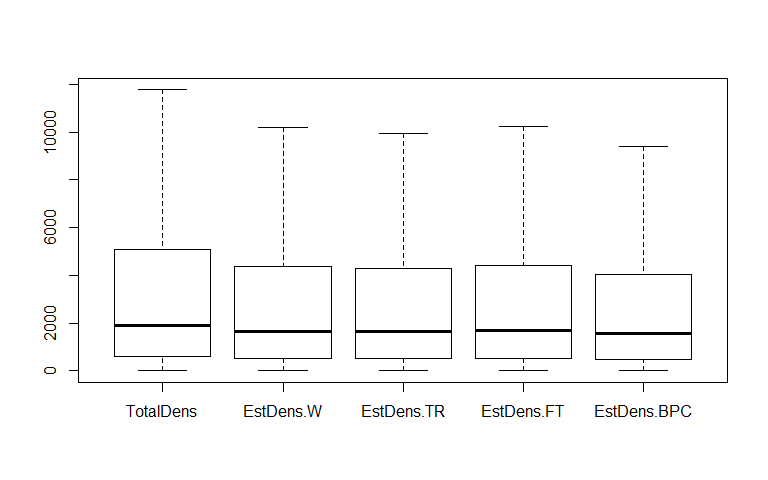
## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## -274.205 -0.001 0.011 1.743 0.128 11264.787

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## -264.275 -0.001 0.010 2.966 0.171 11264.787



## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## -323.832 -0.001 0.028 4.318 0.357 11264.787

We also check the error we would make in the density data if we would estimate them on the merged data sets.



## fraction of density based on species for which weight is known:

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.001316 0.830189 0.929717 0.883898 0.996558 1.000000

## fraction of density based on species for which traits are known:

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.001121 0.813509 0.936709 0.878555 0.999525 1.000000

## fraction of density based on species for which feeding type is known:

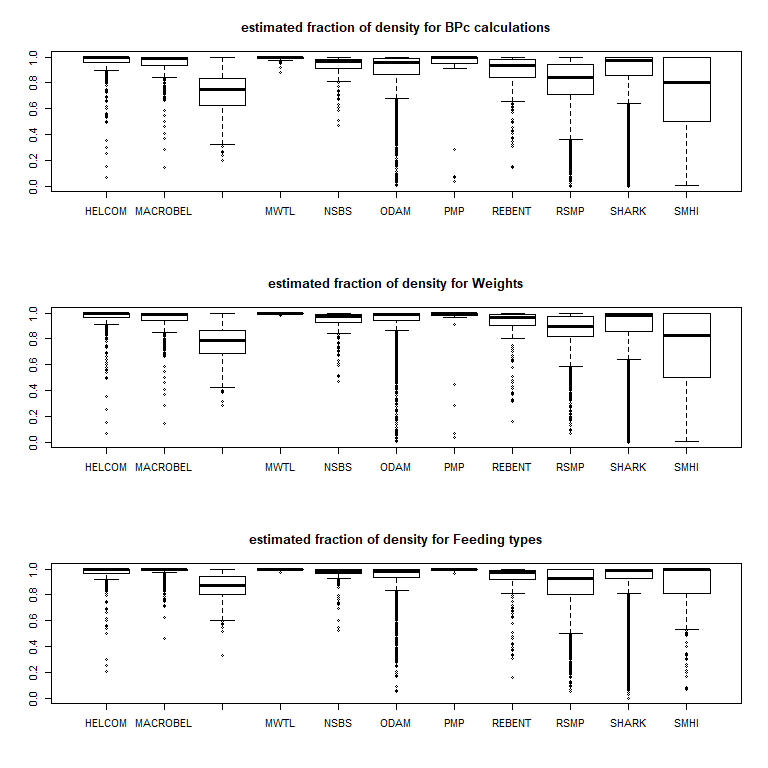
## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.001316 0.840909 0.957272 0.896053 1.000000 1.000000

## fraction of density based on species for which all is known:

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.001121 0.741935 0.888889 0.832443 0.984615 1.000000

The estimated density if we only use species for which have all data required for BPc estimation is thus on average 0.8324433 of the true value.

As we want to estimate bioturbation potential, we now split this number for the different data providers to see for which data sets we make the largest errors.



The mean recovered fraction of density for the various data providers is :

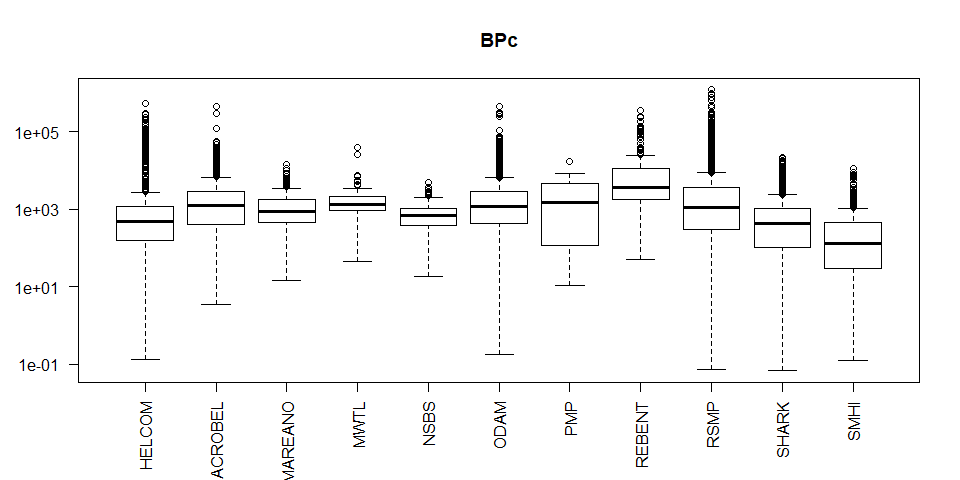
|  |  |  |  |
| --- | --- | --- | --- |
|  | BPC | W | FT |
| HELCOM | 0.9609198 | 0.9672662 | 0.9702654 |
| MACROBEL | 0.9500470 | 0.9520774 | 0.9826944 |
| MAREANO | 0.7202315 | 0.7688202 | 0.8585159 |
| MWTL | 0.9907961 | 0.9992683 | 0.9992434 |
| NSBS | 0.9297956 | 0.9352938 | 0.9611760 |
| ODAM | 0.8868025 | 0.9363271 | 0.9308547 |
| PMP | 0.8376353 | 0.8564493 | 0.9974889 |
| REBENT | 0.8687459 | 0.9011789 | 0.9079913 |
| RSMP | 0.8114143 | 0.8821951 | 0.8777615 |
| SHARK | 0.8589040 | 0.8606155 | 0.9233342 |
| SMHI | 0.7239096 | 0.7388481 | 0.8860511 |

# Estimating BPc, the bioturbation potential

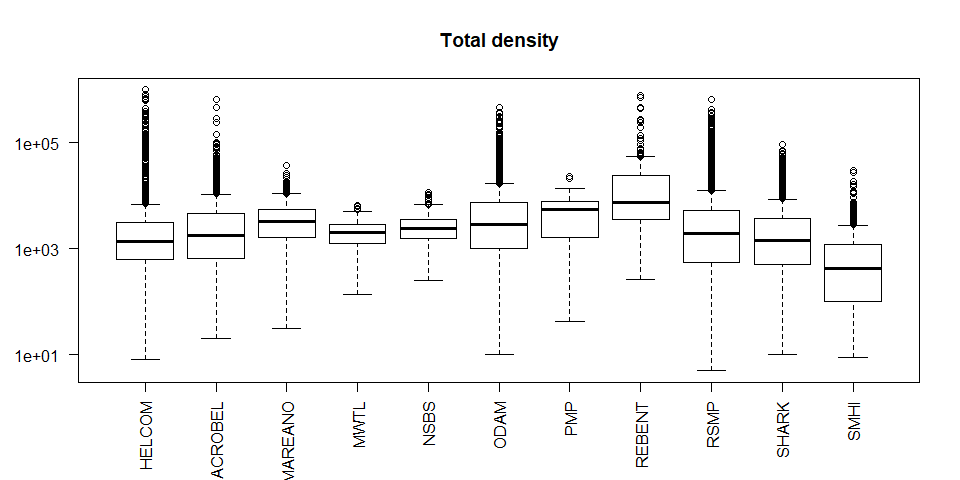
The bioturbation potential is now estimated on the reduced data set. First the contribution of each species to BPc is estimated, based on the indivual weight, the abundancy, and their mobility and reworking mode.

Then the BPcs of all species per station are added.

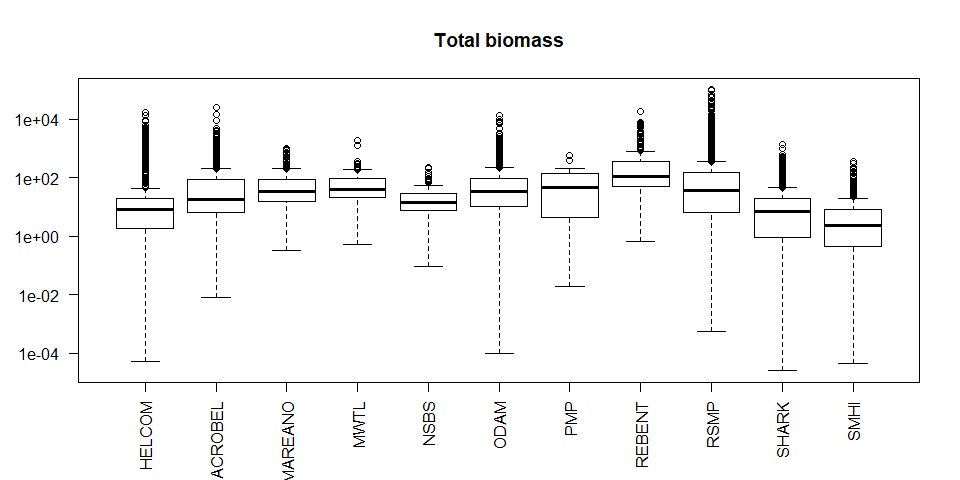
# Characteristics per data provider



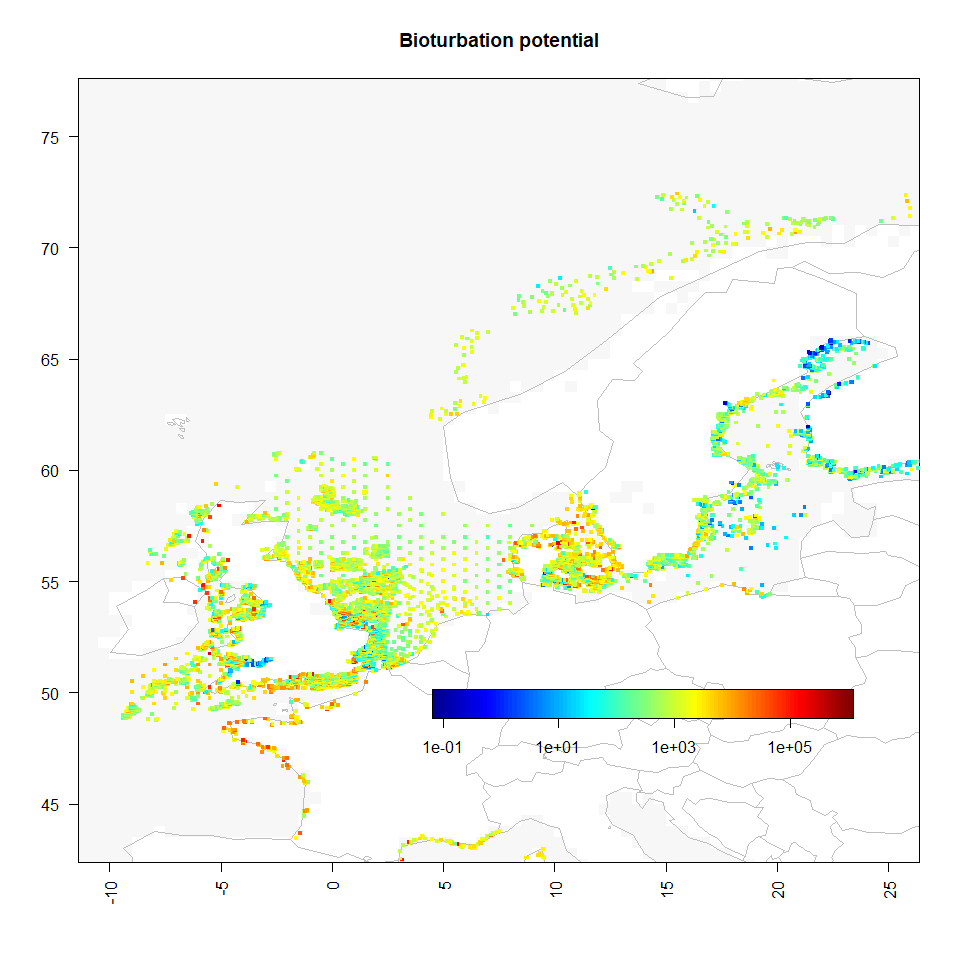
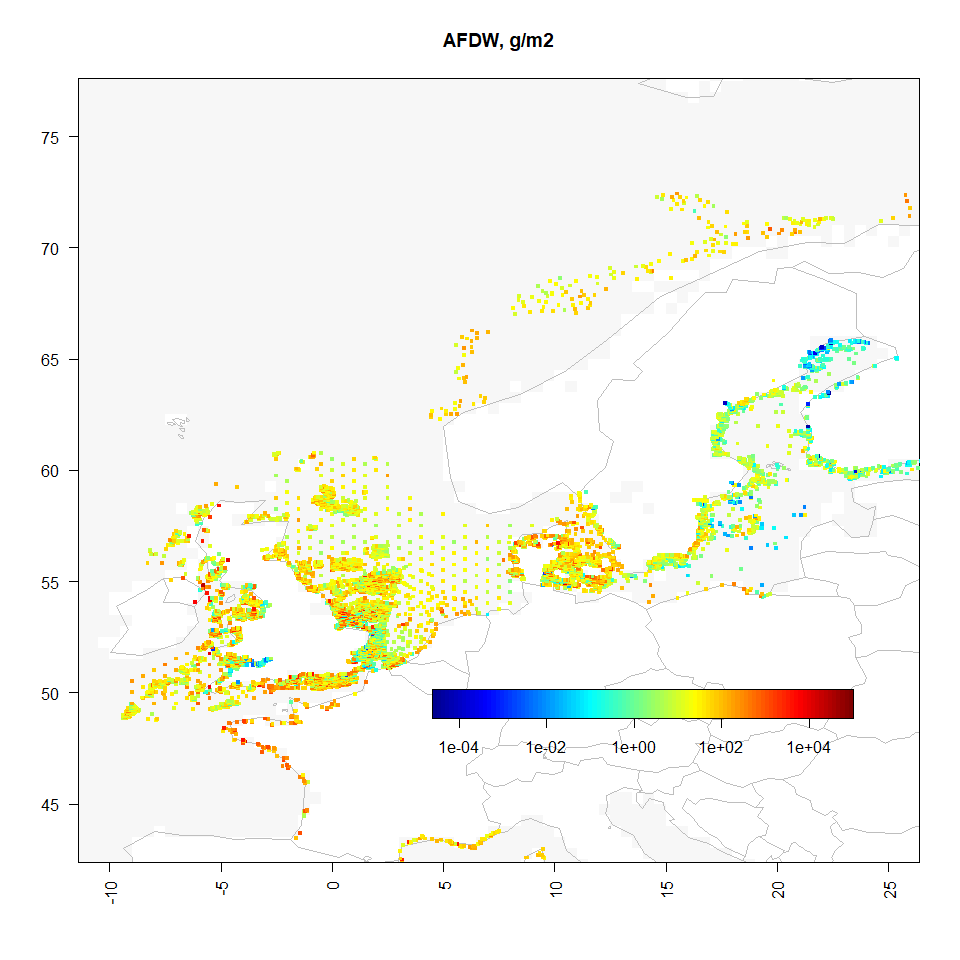
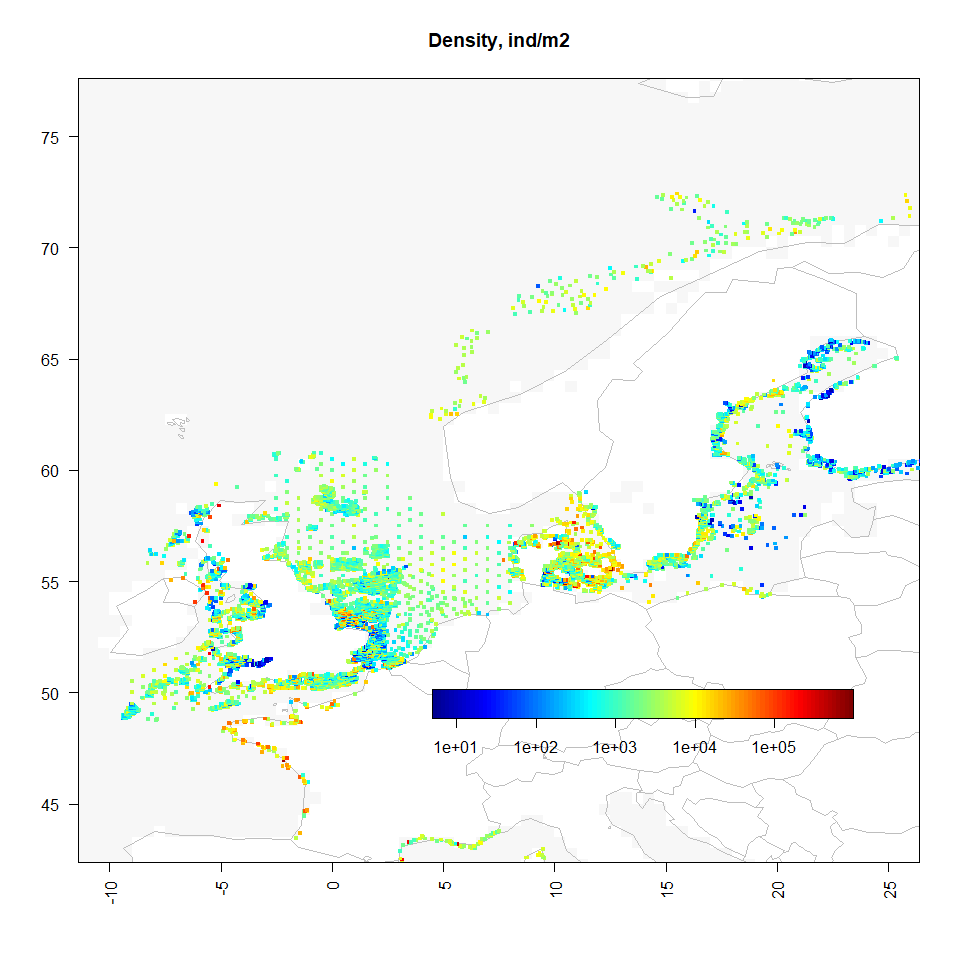
TotalDensity was already calculated



The total biomass per station:



A function is created to generate image plots

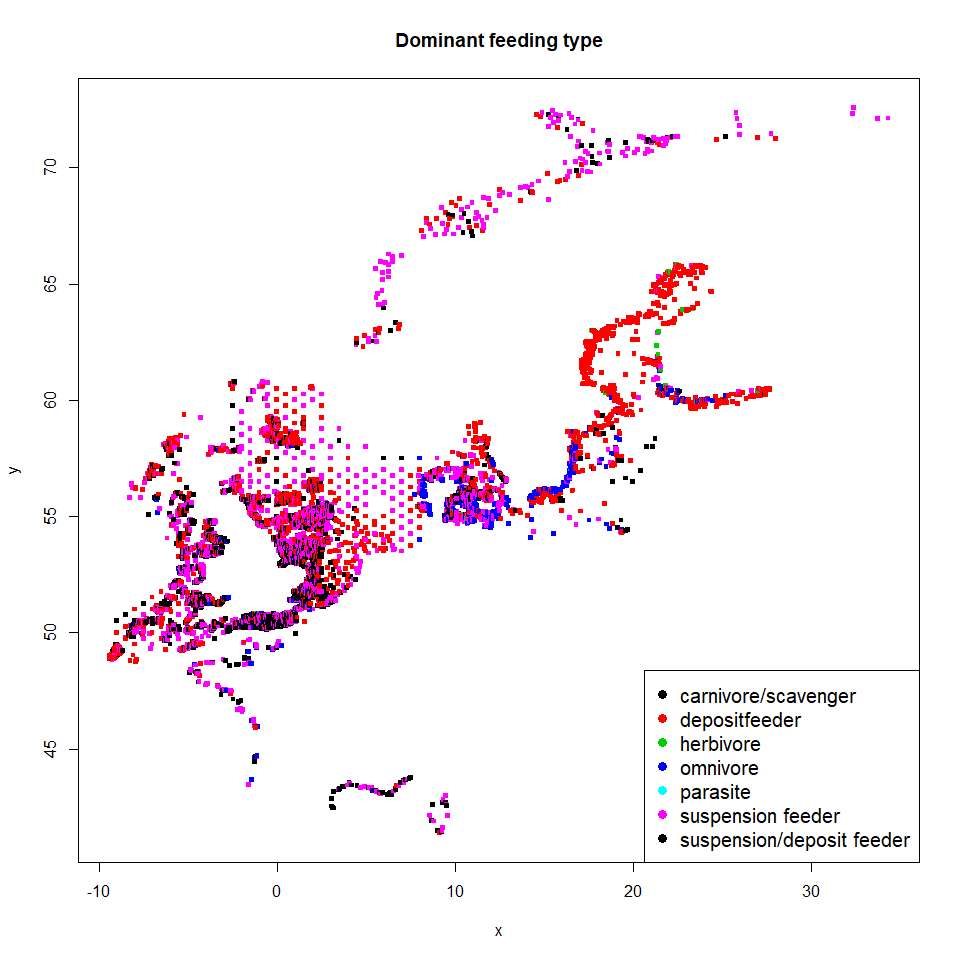


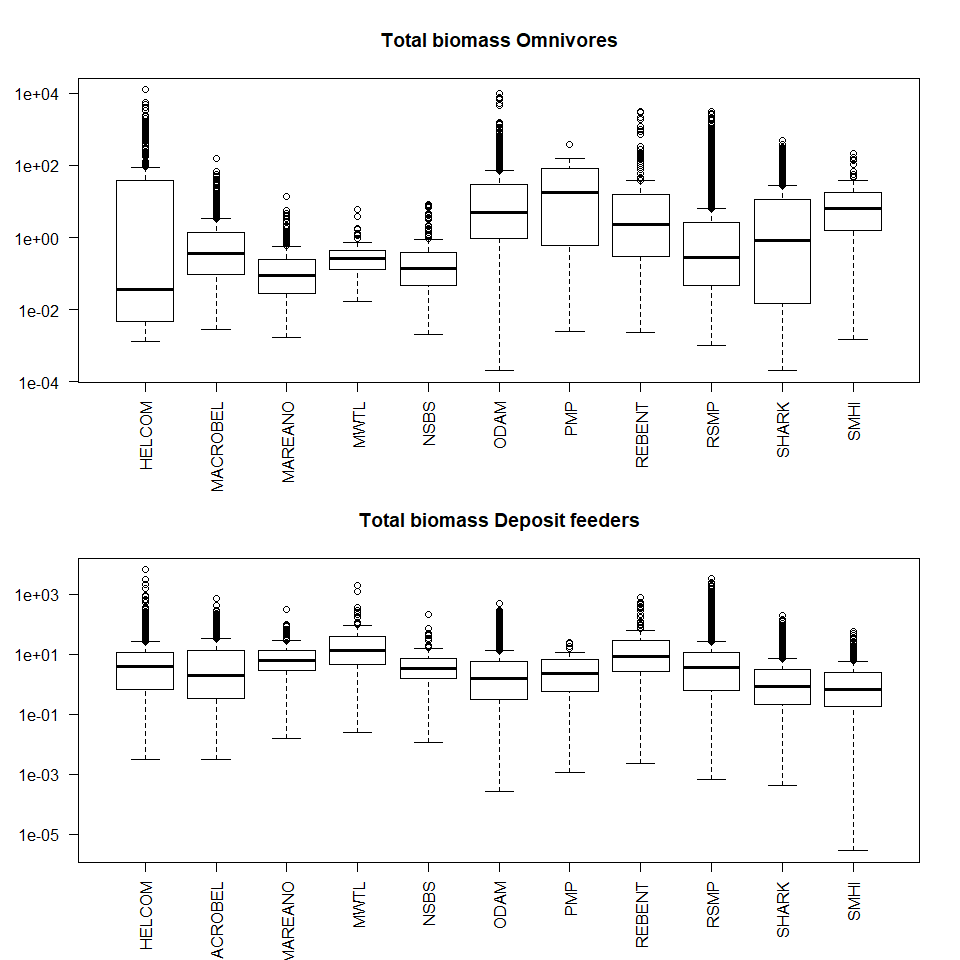
## Biomass per feeding type

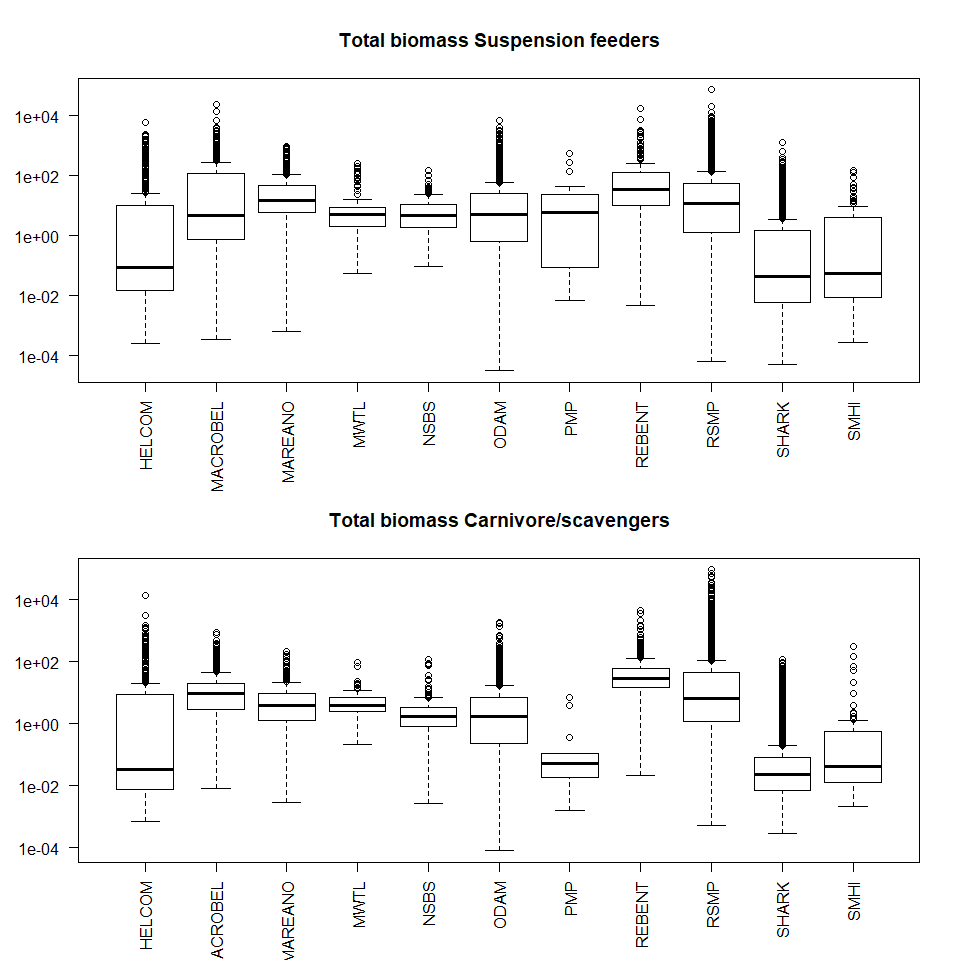
## sta data x y AFDW CaSc De  
## 1 HELCOM1 HELCOM 8.267167 56.72267 1448.25300 17.149599 42.126847  
## 2 HELCOM10 HELCOM 9.238333 56.65717 2397.50931 1.317834 222.075764  
## 3 HELCOM100 HELCOM 11.485833 56.20500 103.42123 16.583690 19.015784  
## 4 HELCOM101 HELCOM 11.500000 57.83333 16.53744 4.145739 1.867202  
## 5 HELCOM102 HELCOM 11.516667 57.75000 14.20329 2.931471 2.878464  
## 6 HELCOM103 HELCOM 11.525000 57.54998 149.55492 57.640406 23.736603  
## He Om Pa Su SuDe AFDW\_FT  
## 1 0.07849892 514.74474652 NA 788.696816 81.543487 1444.34000  
## 2 NA 123.90006780 NA 2045.790024 4.425617 2397.50931  
## 3 0.09126297 NA NA 24.847185 32.864295 93.40222  
## 4 0.05977934 0.06218908 NA 4.780328 5.622207 16.53744  
## 5 0.08151728 0.09328362 NA 4.373339 3.845220 14.20329  
## 6 0.14673111 2.01267472 NA 34.686426 31.332081 149.55492

The stations where none of the feeding types are known are removed, and the most dominant feeding type selected.

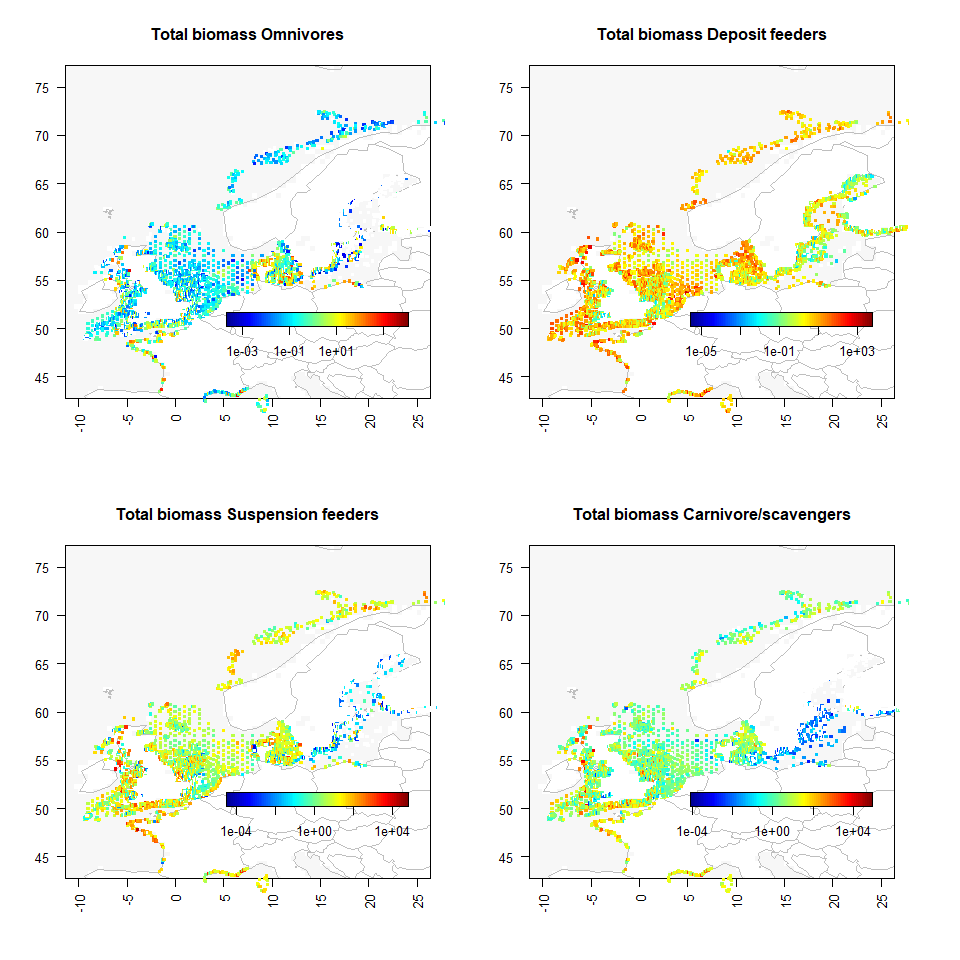
## ISNAS  
## 0 1 2 3 4 5 6 7   
## 1077 5117 13905 6480 4270 3601 2360 48



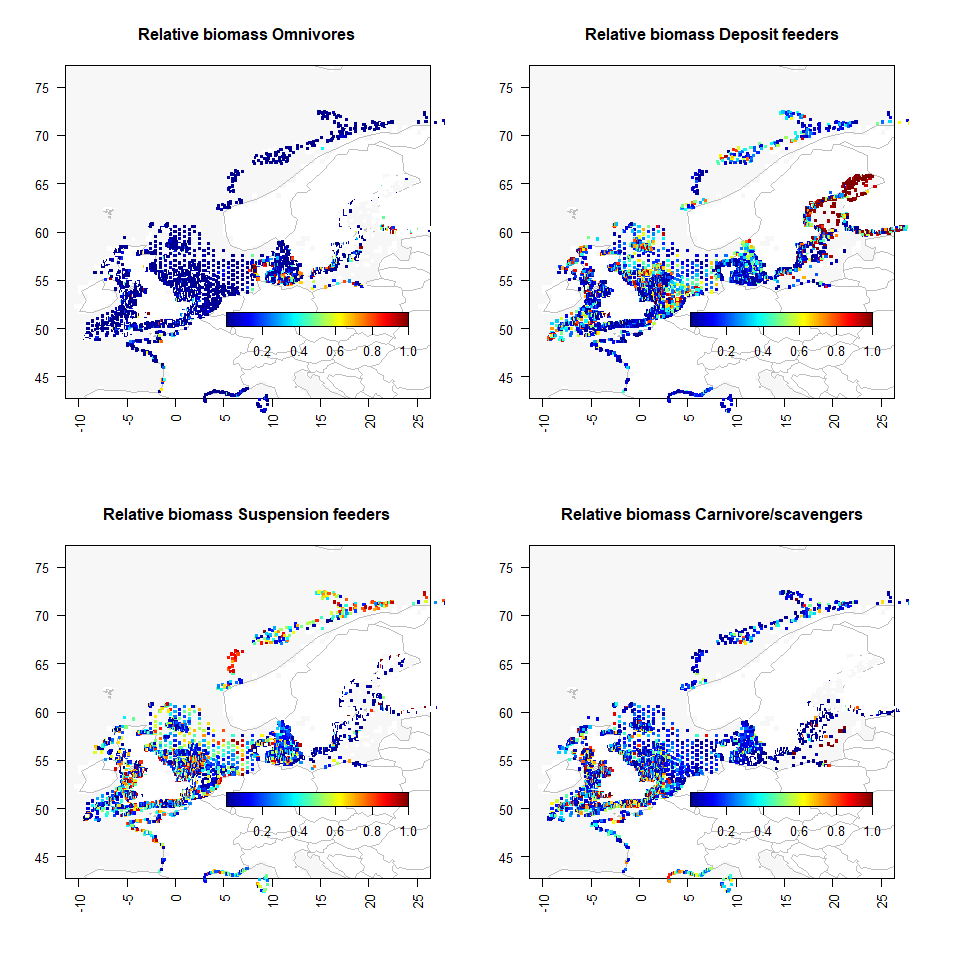




The total biomasses of feeding types



The relative biomasses of feeding types



# Writing the results