Benthos Package Handout

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## Introduction

The benthos-package provides functions for analysing benthic data sets.

The functions have been designed to integrate seamlessly with those of the dplyr-package, which implements a grammar of data manipulation to make data analysis more efficient and clear.

The benthos-package is also designed to use the forward-pipe operator (%>%), which can be used for chaining multiple data operations together,leading to cleaner and more readable code.

The benthos-package follows the same philosophy as the dplyr package: in stead of providing complicated functions that can do many tasks it provides a set of ‘small functions that each do one thing well’ (Wickham & Francois, 2017; ‘Introduction to dplyr vignette’). As a consequence, you will not find functions in this package which perform a complete analysis; rather, it provides basic building blocks that you can use to build your own functions and applications.

## Features and Functions

The benthos-package can be summed with four main components:

**Abundance Analysis** -Determine relative counts of taxa in a dataset, such as using abundance or species richness functions.

**Marine Biodiversity Indices** -Access to indices for analysis such as Shannon’s index or entropy,Hill’s diversity number, AZTI Marine Biotic Index, Infaunal Trophic Index, and many more.

**Supplementary functions for indices** -Accompanying functions for clean data comparisons between the indices, such as get\_iti or is\_azoic.

**Data Preparation** -Various functions for packaging data for final presentation, such as genus-to-species conversion or data pooling.

## Installation

Use the following line of code to get started:

install.packages("benthos")  
library(benthos)

## Example

The abundance is the total number of individuals per taxon in a sampling unit. It can be computed by means of the abundance-function:

abundance(taxon=\_\_\_,count=\_\_\_)

Species richness is the number of different species in a (pooled) sample. It can be computed by means of:

species\_richness(taxon=\_\_\_,count=\_\_\_)

Multiple measures of biodiversity for a specified grouping of the data can be computed for all sampling units by means of:

group\_by(HABITAT, YEAR, POOLRUN, POOLID) %>%   
summarise(  
N = total\_abundance(count =\_\_\_),  
S = species\_richness(taxon =\_\_\_, count =\_\_\_),  
D = margalef(taxon =\_\_\_, count =\_\_\_),  
SN = rygg(taxon =\_\_\_, count =\_\_\_),  
SNa = rygg(taxon =\_\_\_, count =\_\_\_, adjusted = TRUE),  
H = shannon(taxon =\_\_\_, count =\_\_\_))

Example tibble:

A tibble: 569 x 10  
 Groups: HABITAT, YEAR, POOLRUN [60]  
 HABITAT YEAR POOLRUN POOLID N S D SN SNa H  
 <chr> <chr> <int> <int> <dbl> <int> <dbl> <dbl> <dbl> <dbl>  
 1 Polyhaline-Intertidal 2010 1 1 519 24 3.68 1.73 1.60 2.41  
 2 Polyhaline-Intertidal 2010 1 2 616 41 6.23 2.00 1.85 3.64  
 3 Polyhaline-Intertidal 2010 1 3 370 21 3.38 1.71 1.57 2.67  
 4 Polyhaline-Intertidal 2010 1 4 283 27 4.61 1.90 1.74 3.58  
 5 Polyhaline-Intertidal 2010 1 5 515 31 4.80 1.87 1.73 2.79  
 6 Polyhaline-Intertidal 2010 1 6 368 28 4.57 1.88 1.72 3.45  
 7 Polyhaline-Intertidal 2010 1 7 595 28 4.23 1.80 1.67 3.16  
 8 Polyhaline-Intertidal 2010 2 1 500 25 3.86 1.76 1.63 2.66  
 9 Polyhaline-Intertidal 2010 2 2 413 25 3.98 1.79 1.65 3.33  
10 Polyhaline-Intertidal 2010 2 3 394 29 4.69 1.88 1.73 3.83  
 … with 559 more rows

## Other Information

**Reference Manual:** <https://cran.r-project.org/web/packages/benthos/benthos.pdf>

**Vignette:** <https://cran.r-project.org/web/packages/benthos/vignettes/benthos.html>

**Additional Help:** <https://rdrr.io/cran/benthos/>