

# BEQI2: Introduction

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## 1 Introduction

This tutorial provides a brief introduction to the **BEQI2**-package. This package should facilitate the analysis of benthos data. It estimates several quality indices as

- total abundance of species ( $N$ );
- species richness ( $S$ );
- Shannon index ( $H'$ );
- AZTI Marine Biotic Index (AMBI);
- of each indicator given above, an ecological quality ratio (EQR) is calculated using the indicator value, reference value and bad value;
- The BEQI2 index gives an EQR value, which is calculated as the average of the EQR values of species richness, Shannon and AMBI.

The package includes two additional optional features that enhance data preprocessing:

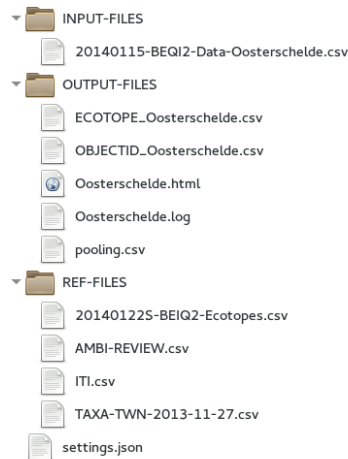


Figure 1: Default BEQI2-directory structure.

- genus to species conversion: taxa counts at the taxonomic genus level can optionally be converted to the species level. It is assumed that the unidentified taxa at the genus level can be proportionally distributed over the identified taxa at the species level in the same sample;
- pooling: small samples are combined to bigger samples with a standardized size to (a) meet the data requirements of the AMBI, (b) generate comparable species richness values and (c) give a higher benthos signal to noise ratio.

## 2 Quick-start

The workhorse function of the **BEQI2**-package is called **BEQI2**. This function performs a full BEQI2-analysis. It reads all its inputs from, and stores all its outputs to files. Storing these files in a structured way is therefore highly recommended. By default, the BEQI2-package uses the directory structure in Figure 1.

The default directory structure in Figure 1 can be created and populated with sample files by means of the **BEQI2dir** function. This will function will start after typing

```
BEQI2dir()
```

in the R-console. A directory selection dialogue will start to let you set an (existing!) working directory interactively. In non-interactive mode, the path to the working directory should be supplied as argument, *e.g.*:

```
BEQI2dir(path = "c:/myprojects/BEQI2/BEQI2_FILES")
```

Note that paths are separated by (forward) slashes. In both cases, the working directory needs to be empty to avoid overwriting existing data.

After running **BEQI2dir** three directories have been created:

- **INPUT-FILES**: a directory containing BEQI2-input files. These files contain the number of taxa that have been found in each sample. Consult Appendix B for more information.
- **OUTPUT-FILES**: all BEQI2 analysis results. This directory is empty after running **BEQI2dir**;
- **REF-FILES**: a directory containing BEQI2-reference files. These files contain information on waterbodies/ecotopes (Appendix E) and species sensitivities (AMBI (Appendix C), ITI (Appendix D)), and a recent copy of the Taxa Water management of the Netherlands (TWN) list. The latest version of this list can be downloaded from [sofus.ecosys.nl/taxabase.htm](http://sofus.ecosys.nl/taxabase.htm)

In addition, a file with the name ‘**settings.json**’ has been created. This file contains all settings specified by the user to run the BEQI2-tool. See Appendix A for more information.

The BEQI2-tool can be started by typing

```
BEQI2()
```

in the R-console. This will launch an interactive file selection dialogue. The user is asked to select the settings file (in this case 'settings.json').

Alternatively, one may also provide the name of the settings file directory as function argument:

```
BEQI2(filename = "c:/myprojects/BEQI2/BEQI2_FILES/settings.json")
```

After the BEQI2-run is completed, all results are available in the OUTPUT-FILE directory. In addition, your default web-browser will be launched showing the analysis report.

### 3 BEQI2 results

After running the tool, the following results are available in the OUTPUT-FILES directory (see also Figure 1):

- a report in HTML-format;
- output files aggregated to the ECOTOPE or OBJECTID (*e.g.*, water body) levels;
- log-file with informative, warning, and error messages;
- file with pooling information (optional).

## A BEQI2 Settings file

A BEQI2-run is entirely specified by the contents of a json-file (see `settings.json` in Figure 1). The format of this file is JavaScript Object Notation (JSON). This is a well structured, human-readable, open standard format ([www.json.org](http://www.json.org)). To improve readability, comments are allowed as an extension to the JSON-standard. Text after two (forward) slashes (//) are interpreted as comments and will be ignored. The figure below gives an example of a settings file. Each setting is explained by a comment. Most editors support editing JSON files, including the built-in editor of the Rgui for MS-Windows (see main menu: File | Open script...).

```
1 {
2   // ===== header information =====
3
4   // title of the analysis
5   "title": "BEQI-2 analysis Oosterschelde",
6
7   // person who performs this analysis
8   "user": "your name",
9
10  // date this file has been modified
11  "date": "2014-12-11",
12
13
14
15  // ===== input files =====
16
17  // working directory (optional)
18  // If commented out (i.e., adding // as prefix), the directory containing
19  // this JSON-file will be used as working directory.
20  // "working directory": "d:/projects/BEQI2",
21
22  // path of input file containing taxa counts (BEQI-format)
23  "BEQI-file": "INPUT-FILES/20140115-BEQI2-Data-Oosterschelde.csv",
24
25  // path containing the Taxa Watermanagement (the) Netherlands list
26  "TWN-file": "REF-FILES/TAXA-TWN-2013-11-27.csv",
27
28  // Infaunal trophic index (Gittenberger et al., 2013).
29  // optional: can be disabled by adding // before the following line:
30  "ITI-file": "REF-FILES/ITI.csv",
31
32  // Ecotopes reference file
33  "ER-file": "REF-FILES/BEQI2-Ecotopes-2014-04-11.csv",
34
35  // Optional species sensitivity (AMBI) file provided by the user.
36  // If not specified, a recent version (fall 2013) of the species
37  // sensitivities kindly provided by Dr. Angel Borja (AZTI- Tecnalia
38  // Marine Research Division, http://ambi.azti.es) will be used.
39  // In case a species sensitivity file is specified,
40  // it will update the data provided by Borja.
41  // Borja's sensitivities will be used as fallback for species that are
42  // missing in the user-supplied sensitivity file.
43  "AMBI-file": "REF-FILES/AMBI-NL+.csv",
44
45
46  // ===== analysis settings =====
47
48  // range of months to be analysed (e.g., 1: January, 12: December)
49  "months": [8, 12],
50
51  // should pooling be performed (true, false)
52  "pool": true,
53
54  // seed to initialize the pseudo random number generator (integer)
55  "random seed": 314,
56
57  // range of target area ([minimum, maximum])
58  "target area": [0.09, 0.11],
59
60  // Genus to species conversion per sample (true, false)
61  "Genus to species conversion": true,
62
63
64
65  // ===== output files =====
66  // In the section below all OUTPUT files are given
67
68  // path of HTML-document that should contain all results
69  "report-file": "OUTPUT-FILES/Oosterschelde.html",
70
71  // path of log-file for printing errors, warnings and messages
72  "log-file": "OUTPUT-FILES/Oosterschelde.log",
```

```
73
74 // pooling results
75 "pool-file": "OUTPUT-FILES/pooling.csv",
76
77 // output file
78 "output-file": "OUTPUT-FILES/Oosterschelde.csv"
79 }
```

---

## B BEQI2 input file

The format of the BEQI2 input file has been specified in the table below. The format is the so called comma-separated values format (CSV) with the following characteristics:

- decimal separator: period (.)
- column separator: comma (,)
- text values are preferably quoted

The following columns are compulsory: OBJECTID, ECOTOPE, SAMPLEID, TAXON, CHAR, SAMPDEV, AREA, DATE, and VALUE. Azoic samples must have a value of 0.

Item (header in data table)	Comments	Examples
Measuring object id (OBJECTID)	The WFD water body code is used here	NL91_veersmr
Ecotope code (ECOTOPE)	The ecotope code of the sample can be constituted freely, for example based on the intertidal/subtidal position, the salinity zone and the sediment composition.	MesohalineIntertidal
Sample-id (SAMPLEID)	Location code OR Transect station code OR Sample number Note1: the BEQI2 tool combines the sample code with the date to ensure a unique sample code. Note 2: replicas should have different sample codes, e.g. by adding an additional letter a, b,etc.	North Sea: e.g. NOORDWK2; Dollard: Transect-station code; Delta: 1304
Parameter (PAR)		COUNT
Taxon name (TAXON)	Standardized taxon code (see WoRMS-website) In NL: the TWN code	
Characteristic (CHAR)	Additional aspect of the taxon; e.g. Juvenile (JUVNL) or quality code (e.g REST). Note 1: different annual classes of specific taxa are combined for BEQI2 analysis.	
Compartment code (COMP)	Relevant compartment codes can be chosen freely.	BS = Bottom Sediment
Sampling device (SAMPDEV)	The code of the sampling device.	e.g., BOXCRR of VEENGB
Sampled area (AREA)	The sampling area is necessary for the data pooling process.	E.g. 0.015 m2.
Value processing code (WBEW)		NA = Not Applicable
Value determination code (WBEP)	Benthic sampling and analysis method code	e.g., A2.107 or Essink1991
Date (DATE)	ISO format: eejj-mm-dd is mandatory.	2001-03-05
Numerical value (VALUE)	Numerical value. Decimals are allowed. Note: the decimal sign must be a point (.)	20.5

## C AMBI-file

The species sensitivity file consists of two columns, and is stored in comma separated file format (csv). The first column contains the taxa, the second column the corresponding sensitivity classes. The table below gives an example of (part of) a species sensitivity file.

SUBMITTED.NAME	AMBI
Syllis fasciata	II
Myriochele olgae	III
Nassarius mendicus	IV
Hiatella rugosa	I
Pilumnus hirtellus	I
Tellina distorta	I
Polydora sp.	IV
Hippothoa divaricata arctica	I
Mitrella unifasciata	I
Granulina ovuliformis	I
Lumbrineris californiensis	II
Apherusa sp.	I
Odontaster penicillatus	I
Apionsoma misakianum	II
Crassilabrum crassilabrum	I
Podarke guanica	II
Monocorophium acherusicum	III
Hemipodus heteropapillatus	II
Achelia longipes	I
Paradoneis lyriformis	III
Sphaerosyllis tetralix	II
Mysta tchangsii	III
Monoculopsis longicornis	II
Tectura testudinalis	I
Autonoe megacheir	I

## D ITI-file

The Infaunal Trophic Index (ITI) file consists of two columns, and is stored in the comma separated file format (csv). The first column contains the taxa, the second column the corresponding sensitivity classes.

The table below gives an example of (part of) an ITI-file.

SUBMITTED.NAME	ITI
Kurtiella bidentata	II
Sagartia elegans	I
Harmothoe imbricata	III
Metridium senile	I
Scoloplos armiger	IV
Spirorbis tridentatus	I
Ensis siliqua	I
Neodexiospira brasiliensis	I
Brissopsis lyrifera	III
Cryptosula pallasiana	I
Petricolaria pholadiformis	I
Tellina tenuis	III
Microphthalmus similis	IV
Myriochele danielsseni	III
Alcyonium digitatum	I
Diadumene cincta	I
Pseudopotamilla reniformis	I
Callinectes sapidus	III
Polydora ciliata	III
Phoxichilidium femoratum	II
Macoma balthica	III
Hyas coarctatus	II
Harmothoe impar	III
Thyasira flexuosa	I
Arenicola defodiens	III
Magelona papillicornis	III
Arenicola marina	III
Halecium halecinum	I
Pseudopolydora pulchra	II
Paradoneis fulgens	III

The ITI classes have the following meaning:

ITI	description
I	Suspension feeders
II	Interface feeders
III	Surface deposit feeders
IV	Subsurface deposit feeders



## E Ecotope reference file

The Ecotope Reference file contains meta-information about each waterbody (OBJECTID) and ecotope. In this file, it is possible to use a correction factor (CORR) for the BEQI2\_EQR. At present, in the Dutch calculations a theoretical AMBI reference value of 0 has been used. Since this gives an underestimation of the BEQI2\_EQR of approx.  $-0.02$ , this correction factor of  $+0.02$  is applied. If however calculated AMBI reference values are used, this correction factor must be set at 0 in the Ecotope Reference file.

OBJECTID	ECOTOPE	RELAREA	SREF	SBAD	HREF	HBAD	AMBIREF	AMBIBAD	CORR	ITIREF	ITIBAD
nl89_westsde	BrakLitoraal	0.11	29	0	3.30	0	0	6	0.02	0	4.50
nl89_westsde	BrakSublitoraal	0.17	22	0	3.20	0	0	6	0.02	0	4.50
nl89_westsde	ZoutLitoraal	0.18	41	0	3.60	0	0	6	0.02	0	4.50
nl89_westsde	ZoutSublitoraal	0.54	31	0	3.80	0	0	6	0.02	0	4.50
nl89_oostsde	ZoutLitoraal	0.26	45	0	3.70	0	0	6	0.02	0	4.50
nl89_oostsde	ZoutSublitoraal	0.74	67	0	5.10	0	0	6	0.02	0	4.50
nl89_veersmr	ZoutSublitoraal	1.00	30	0	3.80	0	0	6	0.00	0	4.50
nl89_grevlemr	ZoutSublitoraal	1.00	44	0	4.20	0	0	6	0.00	0	4.50
NL94_11	ZoetSublitoraal	1.00	28	0	3.60	0	0	6	0.02	0	4.50
NL94_9	OligohalienSublitoraal	1.00	20	0	2.60	0	0	6	0.02	0	4.50
NL95_1A2A	ZoutSublitoraal	1.00	33	0	3.80	0	0	6	0.02	0	4.50
NL95_3A	ZoutSublitoraal	1.00	30	0	4.00	0	0	6	0.02	0	4.50
NL95_4A	ZoutSublitoraal	1.00	30	0	3.70	0	0	6	0.02	0	4.50
NL81_3	ZoutSublitoraal	1.00	30	0	3.70	0	0	6	0.02	0	4.50
NL81_2	BrakLitoraal	1.00	23	0	3.40	0	0	6	0.02	0	4.50
NL81_1	ZoutLitoraal	0.59	29	0	3.60	0	0	6	0.02	0	4.50
NL81_1	ZoutSublitoraal	0.41	23	0	3.50	0	0	6	0.02	0	4.50