Description of the integrated biodiversity assessment tool and the coded pilot tool

The BEAT methodology

This ETC/ICM version of the BEAT tool described here was developed for the European Environment Agency (EEA) for use in the upcoming assessment of Biodiversity in Europe's Seas. It represents a further development of similar assessment tools (references: HELCOM HOLAS, HARMONY, DEVOTES). Any references to "BEAT" hereafter refer to this specific version of the tool.

At the core of BEAT and other indicator-based assessment tools is the comparison of a representative status value for an indicator of ecosystem health with an agreed threshold value which defines the boundary between "Good" and "Not good" status.

For example, a biodiversity indicator should be some parameter which measures the condition of a component of ecosystem biodiversity (e.g. the spawning stock biomass of a fish species). In order to categorize the biodiversity status, the observed value of the indicator is compared with a target/threshold value. This value corresponds to the boundary between good and not-good biodiversity status.

Indicators are grouped within categories, representing different components of the ecosystem such as fish, birds and benthic communities. This grouping of indicators ensures that the status of different ecosystem components is taken into consideration in the overall biodiversity assessment.

The assessment process is described below. The assessment is made separately for each spatial assessment unit or geographical entity. In contrast with NEAT and more complex indicator-based assessment tools, no aggregation is made across spatial assessment units.

Step 1 – Normalisation of indicators

Before indicator values can be aggregated, they are normalised to a scale from 0 to 1, called an Ecological Quality Ratio (EQR), where 0 is the worst possible score and 1 is the best possible. In order to do this, it is also necessary to know the value of the indicator which represents the worst possible state for the ecosystem and also the indicator value which would be expected in a reference state i.e. a condition not perturbed by human activities.

On "threshold", "reference" and "bad" values: These three values are used to normalise the observed value of an indicator (the "Status" value) to a scale from 0 to 1 (Environmental Quality Ratio or "EQR" value, where).

Thus, four values are required to specify each indicator:

1. Status value – the observed (measured) value

2. Threshold value (boundary between "good" and "not-good")

3. Bad Value for the "worst" case

4. Reference Value corresponding to unperturbed case.

There are three fixed points on the scale. An observed indicator value equal to the Bad value results in an EQR of 0. An observed indicator value equal to the reference value gives an EQR of 1. Where the observed indicator value is equal to the good / not-good threshold value, the resulting EQR value is 0.6.

Where the observed indicator value lies below the threshold value, the EQR value is obtained by linear interpolation between the Bad value (EQR=0.0) and the threshold value (EQR=0.6). Where the observed indicator value lies above the threshold value, the EQR value is obtained by linear interpolation between the threshold value (EQR=0.6) and the Reference value (EQR=1.0)

This can be visualised as in the example shown in Figure 1. In this example, the "worst case" value of the indicator 2.0, the reference value of the indicator is 12.0 and the threshold value is 5.0.

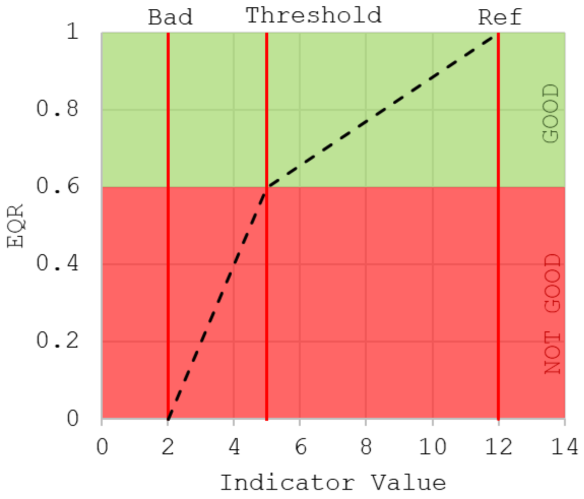


Figure 1 – Variation of EQR value with indicator value (shown by the black dashed line) for an example where boundary values (indicated by red lines) are: Bad Value = 2, Good/Not-good boundary Value = 5 and Reference Value = 12.

It should be noted that an indicator can show a positive or negative response. As seen in the previous example, an indicator can increase with improving biodiversity (e.g. population size of a species). It is also possible to include indicators whose value decreases with improving biodiversity (e.g. a species mortality rate). An example of the variation of EQR with indicator value for such an indicator is shown in Figure 2.

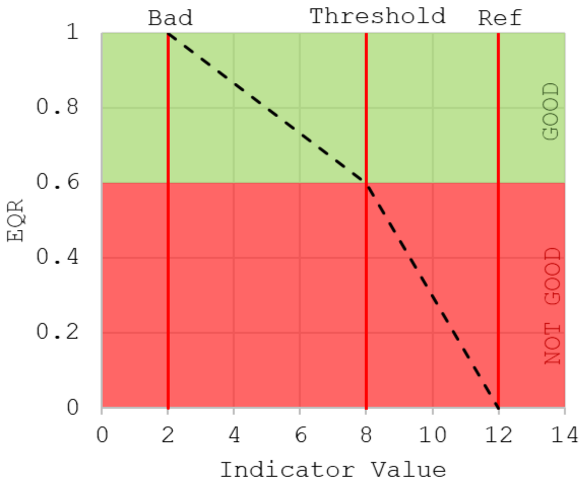
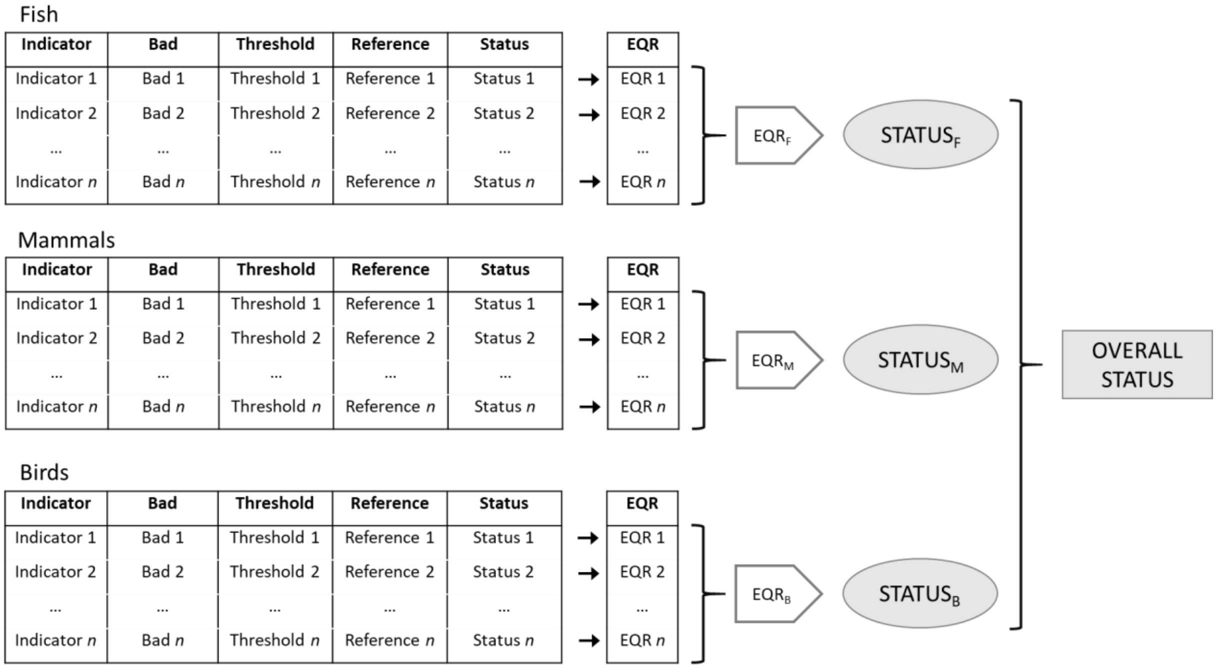


Figure 2 – Variation of EQR value for an indicator with negative response. That is increasing indicator value is associated with a deterioration in biodiversity status

However, the tool can only accommodate indicators whose values change monotonically: either Bad < Threshold < Reference or Bad > Threshold > Reference. This tool cannot make use of an indicator where there is an "optimum" range such that the biodiversity deteriorates both with increasing indicator value above the optimum range and decreasing indicator value below this range.

Step 2 – Aggregation of indicators

Following the normalisation of indicators, the EQR values for each category or Ecosystem component are calculated by taking the average of indicator EQR values within the category. The aggregation method is outlined in Figure 3. In this example we consider a case with only 3 ecosystem components (Fish, Mammals and Birds). The method remains the same where there are more indicator categories included in the assessment.



Fish

Indicator	Bad	Threshold	Reference	Status	EQR
Indicator 1	Bad 1	Threshold 1	Reference 1	Status 1	EQR 1
Indicator 2	Bad 2	Threshold 2	Reference 2	Status 2	EQR 2
...	...	...	...	...	...
Indicator *n*	Bad *n*	Threshold *n*	Reference *n*	Status *n*	EQR *n*

Mammals

Indicator	Bad	Threshold	Reference	Status	EQR
Indicator 1	Bad 1	Threshold 1	Reference 1	Status 1	EQR 1
Indicator 2	Bad 2	Threshold 2	Reference 2	Status 2	EQR 2
...	...	...	...	...	...
Indicator *n*	Bad *n*	Threshold *n*	Reference *n*	Status *n*	EQR *n*

Birds

Indicator	Bad	Threshold	Reference	Status	EQR
Indicator 1	Bad 1	Threshold 1	Reference 1	Status 1	EQR 1
Indicator 2	Bad 2	Threshold 2	Reference 2	Status 2	EQR 2
...	...	...	...	...	...
Indicator *n*	Bad *n*	Threshold *n*	Reference *n*	Status *n*	EQR *n*

Figure 3 – Outline of the BEAT methodology

Step 3 – Determination of Status within Category (Ecosystem Component)

For each Ecosystem component (Indicator category), its aggregated EQR values is used to assign a classification of the biodiversity status according to the table below:

EQR	Classification
0 ≤ EQR < 0.2	Bad
0.2 ≤ EQR < 0.4	Poor
0.4 ≤ EQR < 0.6	Moderate
0.6 ≤ EQR < 0.8	Good
0.8 ≤ EQR ≤ 1.0	High

Step 4 – Determination of Overall Status

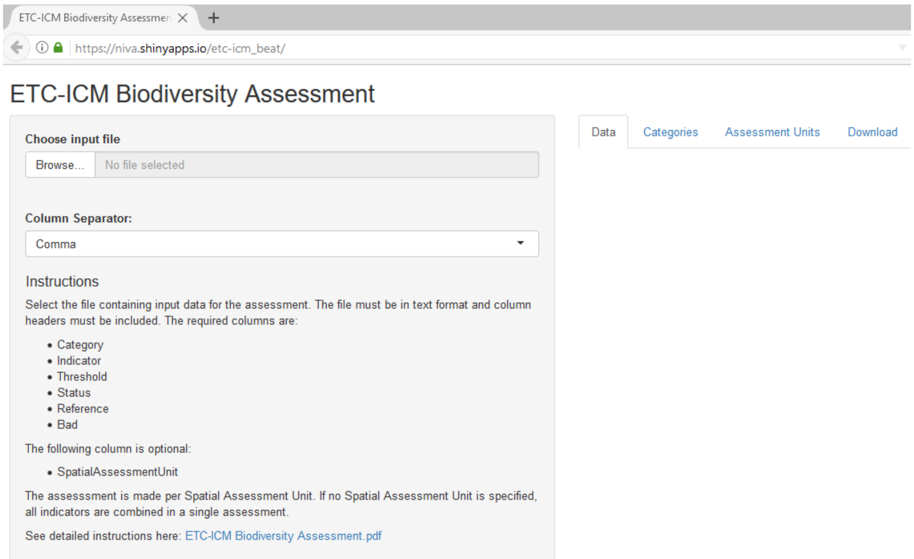
The final step in the assessment process is to determine the overall Biodiversity status. The overall status for a spatial assessment unit is given by the One-Out All-Out method (OOAO). That is, the ecosystem component having the worst biodiversity status determines the overall biodiversity status.

Web version of the BEAT tool – the BEAT Shiny App

The BEAT tool is written in R, a statistical programming language. For the purposes of testing, a web version of the BEAT tool was developed in Shiny. Shiny is a feature of R which allows R code to be implemented as a web application, known as a "Shiny App". See http://www.shinyapps.io/ for general information about Shiny. This allows a user to run and interact with the R code in a web browser without having to install an R compiler on their computer. In this way, anyone without relevant programming experience can make use of the tool.

A pilot version of the BEAT tool implemented in Shiny can be found at the following web address:

https://niva.shinyapps.io/etc-icm_beat/


ETC-ICM Biodiversity Assessmen
https://niva.shinyapps.io/etc-icm_beat/
Data
Categories
Assessment Units
Download
Browse...
No file selected

ETC-ICM Biodiversity Assessment

Choose input file

Column Separator: Comma

Instructions

Select the file containing input data for the assessment. The file must be in text format and column headers must be included. The required columns are:

- Category
- Indicator
- Threshold
- Status
- Reference
- Bad

The following column is optional:

- SpatialAssessmentUnit

The assesssment is made per Spatial Assessment Unit. If no Spatial Assessment Unit is specified, all indicators are combined in a single assessment.

See detailed instructions here: ETC-ICM Biodiversity Assessment.pdf

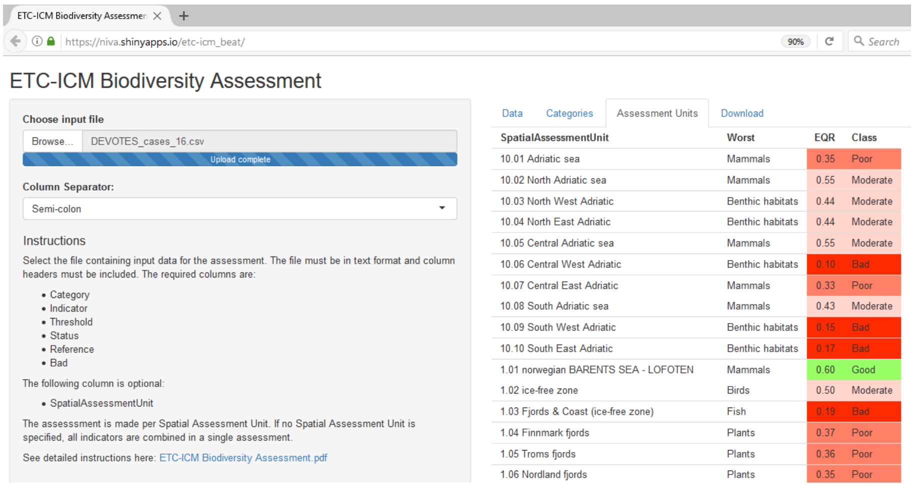
Figure 1 – Screen shot from implementation of BEAT as a Shiny App

Steps for performing an assessment using the Shiny web application:

1) Prepare a text file containing the input data for the assessment. For example, this can be done by tabulating the data in Microsoft Excel and exporting the table as a text file. The text file must contain the following columns:
    - *SpatialAssessmentUnit* – the geographical/spatial entity to which the indicator belongs.
    - *Category* – the ecosystem component
    - *Indicator* – the name of the indicator
    - *Threshold* – the indicator value defining the boundary between "good" and "not good" status
    - *Reference* – the indicator value which corresponds to "Reference conditions", i.e. an undisturbed state.
    - *Bad* -the indicator value corresponding to the worst possible state (e.g. 0 for a population)
    - *Status* – the current observed value of the indicator, representing the present state of biodiversity.
2) In a web browser, go to the address of the application https://niva.shinyapps.io/etc-icm_beat/
3) Browse to the input text file located on your computer and upload it to the application. The data contained in the file will appear in the web application.
4) Select the column separator which is used in your text file. If an incorrect separator is specified, the data uploaded will appear as only one column. Note this does not require data to be uploaded

again. Simply choose the correct separator and the data will then appear in the correct number of columns.

5) Click on the *Categories* and *Assessment Units* tabs to see results of the assessments, showing respectively, results for each category of indicator within each spatial assessment unit and overall results for each spatial assessment unit, as determined by the “worst” category within the assessment unit.



ETC-ICM Biodiversity Assessment

Choose input file

DEVOTES_cases_16.csv

Column Separator:

Semi-colon

Instructions

Select the file containing input data for the assessment. The file must be in text format and column headers must be included. The required columns are:

- Category
- Indicator
- Threshold
- Status
- Reference
- Bad

The following column is optional:

- SpatialAssessmentUnit

The assesssment is made per Spatial Assessment Unit. If no Spatial Assessment Unit is specified, all indicators are combined in a single assessment.

See detailed instructions here: ETC-ICM Biodiversity Assessment.pdf

SpatialAssessmentUnit	Worst	EQR	Class
10.01 Adriatic sea	Mammals	0.35	Poor
10.02 North Adriatic sea	Mammals	0.55	Moderate
10.03 North West Adriatic	Benthic habitats	0.44	Moderate
10.04 North East Adriatic	Benthic habitats	0.44	Moderate
10.05 Central Adriatic sea	Mammals	0.55	Moderate
10.06 Central West Adriatic	Benthic habitats	0.10	Bad
10.07 Central East Adriatic	Mammals	0.33	Poor
10.08 South Adriatic sea	Mammals	0.43	Moderate
10.09 South West Adriatic	Benthic habitats	0.15	Bad
10.10 South East Adriatic	Benthic habitats	0.17	Bad
1.01 norwegian BARENTS SEA - LOFOTEN	Mammals	0.60	Good
1.02 ice-free zone	Birds	0.50	Moderate
1.03 Fjords & Coast (ice-free zone)	Fish	0.19	Bad
1.04 Finnmark fjords	Plants	0.37	Poor
1.05 Troms fjords	Plants	0.36	Poor
1.06 Nordland fjords	Plants	0.35	Poor

Figure 2 – Screen shot showing an example of BEAT assessment results

Source Code for BEAT tool

At the core of the BEAT tool is a program written in R. The same code is used to perform the assessment whether by interacting with the "Shiny" web application or by running the R code directly.

The source code for the tool is publicly available at the GitHub code repository.

https://github.com/NIVA-Denmark/ETC-ICM_Biodiversity_Assessment

The code for the main assessment routine is shown here:

```
#==========================================================================
# function Assessment
Assessment<- function(assessmentdata,summarylevel=1){

  requiredcols <- c("Category","Indicator","Threshold","Status","Reference"
,"Bad")
  extracols <- c("SpatialAssessmentUnit")


  #Check column names in the imported data
  cnames<-names(assessmentdata)
  nimp = ncol(assessmentdata)
  nreq = length(requiredcols)
  nextra = length(extracols)

  ok <- rep(0, nreq)
  okextra <- rep(0, nextra)
  foundresponse=FALSE

  for (i in 1:nimp){
    for (j in 1:nreq){
      if(toupper(requiredcols[j])==toupper(cnames[i])){
        names(assessmentdata)[i] <- requiredcols[j]
        ok[j]=1
      }
    }
    for (j in 1:nextra){
      if(toupper(extracols[j])==toupper(cnames[i])){
        names(assessmentdata)[i] <- extracols[j]
        okextra[j]=1
      }
    }
  }

  n<-sum(ok, na.rm = TRUE)

  if(n<nreq){
    # The required columns were not found in the input data
    message("Error! Required column(s) were not found in the input data:")
    for (j in 1:nreq){
      if(ok[j]!=1){
        message(paste("    ",requiredcols[j]))
      }
    }
```

```r
    if(summarylevel==1){
      return(assessmentdata)
    }else{    return(NA)}
  }else{
    # The required columns are present - do the assessment
    for(j in 1:nextra){
      if(okextra[j]==0){
        if(extracols[j]=="SpatialAssessmentUnit"){
          assessmentdata[[extracols[j]]]<-"All"
        }else{
          assessmentdata[[extracols[j]]]<-1
        }
      }
    }

    # Change order of category factors
    cat1<-data.frame(unique(assessmentdata$Category))
    names(cat1)[1] <- 'Category'
    cat1$char<-as.character(cat1$Category)
    cat1$len<-nchar(cat1$char)
    cat1<-arrange(cat1,len)

    assessmentdata$Category <- factor(assessmentdata$Category, levels = cat1$char)

    # All combinations of categories and waterbodies
    # This is used to ensure that a NA is returned where the combinations are missing
    waterbodies<-unique(assessmentdata$SpatialAssessmentUnit)
    categories<-unique(assessmentdata$Category)
    categories<-expand.grid(waterbodies, categories)
    names(categories)[1] <- 'SpatialAssessmentUnit'
    names(categories)[2] <- 'Category'

    # Reorder assessment units

    df<-as.data.frame(unique(assessmentdata$SpatialAssessmentUnit))
    names(df)[1]<-"SpatialAssesmentUnit"
    df$SpatialAssesmentUnit<-as.character(df$SpatialAssesmentUnit)
    df$pos<-regexpr(" ",df$SpatialAssesmentUnit)
    df$n1<-as.numeric(substr(df$SpatialAssesmentUnit, 1, df$pos-4))
    df$n2<-as.numeric(substr(df$SpatialAssesmentUnit, df$pos-2, df$pos-1))
    df<-arrange(df,n1,n2)

    assessmentdata$SpatialAssessmentUnit<- factor(assessmentdata$SpatialAssessmentUnit, levels = df$SpatialAssesmentUnit)


    #"Category","Indicator","Threshold","Status","Reference","Bad"

    temp<-EQR(indData=assessmentdata,Obs="Status",Bad="Bad",ModGood="Threshold",High="Reference")
    assessmentdata$EQR<-temp$EQR
    QEdata<-summarise(group_by(assessmentdata,SpatialAssessmentUnit,Categor
y),
                      IndCount=n(),EQR=mean(EQR,na.rm = TRUE))

    QEspr<-spread(QEdata,Category,EQR)

    QEdata$CategoryClass<-EQRStatus(QEdata$EQR)
    QEdata<-left_join(categories,QEdata,c('SpatialAssessmentUnit','Category
'))
    QEdata<-arrange(QEdata,SpatialAssessmentUnit,Category)

    Overall<-summarise(group_by(QEdata,SpatialAssessmentUnit), EQR=min(EQR,
na.rm = TRUE))

    OverallQE<-inner_join(select(QEdata,-c(IndCount)), Overall,
                          c("EQR"="EQR","SpatialAssessmentUnit"="SpatialAss
essmentUnit"))
    OverallQE<-rename(OverallQE,Class=CategoryClass,Worst=Category)

    QEspr<-inner_join(QEspr, OverallQE, 'SpatialAssessmentUnit')


    for(j in 1:nextra){
      if(extracols[j]=='SpatialAssessmentUnit' & okextra[j]==0){
      }
    }
    Indicators<-assessmentdata #%>%
      #select(-c(Bad,Reference,Threshold,Status))

    #return(n)
    if(summarylevel==1){
      return(Indicators)
    }else if(summarylevel==2){
      return(QEspr)
    }else if(summarylevel==3){
      return(QEdata)
    }else if(summarylevel==4){
      return(OverallQE)
    }else{
      return(assessmentdata)
    }
  }
}
```