

AMOEBA Plots

A MATLAB implementation for visualizing performance across multiple criteria

Iris Gray (Iris.Gray@noaa.gov) and Isaac Kaplan (Isaac.Kaplan@noaa.gov), NWFSC - NOAA

Based primarily on: *Collie, S.C. ; H. Gislason and M. Vinther, 2003. Using AMOEBAs to display multispecies, multifleet fisheries advice. ICES Journal of Marine Science, 60:709-720.*

Collie et al. were inspired by Ten Brink et al. (1991).

Purpose: To plot the performance of multiple options (e.g. fishery policy choices) in terms of multiple criteria (i.e. commercial harvest, fish biomass, or other ecosystem services).

This package contains the following files:

AMOEBAReadMe.pdf	- (this file)
vectarrow.m	- MATLAB code written by Rentian Xiong that draws our vectors.
BothAMOEBAS.m	- MATLAB code that produces AMOEBA plots for the variables and the sample entries.
VariablesAMOEBAS.m	- MATLAB code that produces an AMOEBA plot for only the variables.
SampEntriesAMOEBAS.m	- MATLAB code that produces an AMOEBA plot for only the sample entries.
ExampleData.mat	- Example data matrix, variables status quo vector, variables scenario vector, sample entries status quo vector, and sample entries scenario vector.

Requirements:

In order to run our code, one must have MATLAB's Statistics package.

Execution:

Perform the following steps:

1. Open BothAMOEBAS.m in MATLAB by double clicking the file name.

2. Type the following in MATLAB's command window:

```
load ExampleData
[decimalExp, variablesComparitiveArea, sampEntriesComparitiveArea] =
BothAMOEBA(Example_M, Example_V_Vstatq, Example_V_Vscen,
Example_V_SEstatq, Example_V_SEscen)
```

Note: Before pressing enter to run the code, make sure you are working out of the correct directory (the zip file in which the codes and data are stored). You should already be working out of this directory had you double clicked the file name (step 1), however, you may not be in the correct directory had your first step been simply starting up MATLAB.

This will generate two plots, one showing the fleets (variables) AMOEBA and one showing the species (sample entries) AMOEBA. Model outputs are described in 'Code Operations' under **Further Information**.

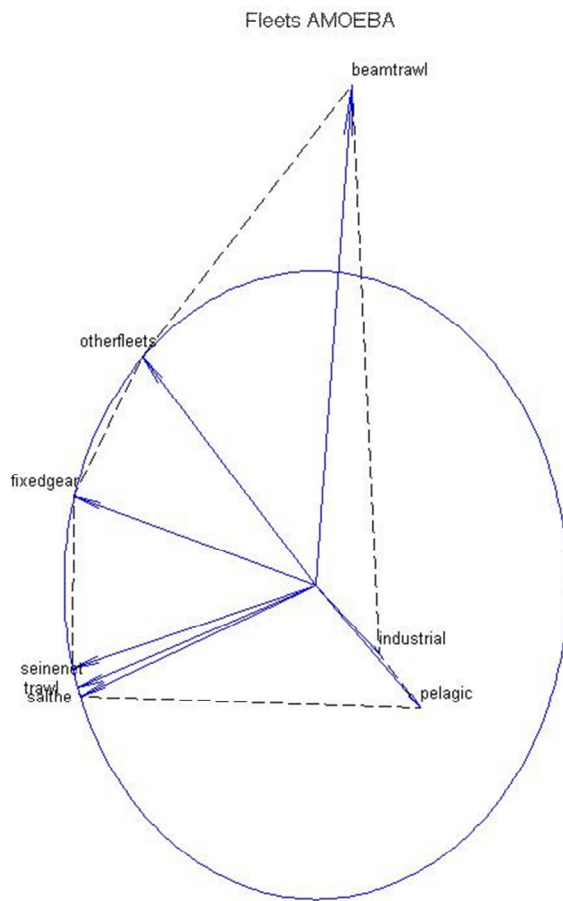


Figure 1. AMOEBA plot of our fleets. Relative to Status Quo (represented by circle), here we see increased catch of fleet 'beamtrawl', and decreased catch of fleets 'industrial' and 'pelagic'. The fleet AMOEBA encompasses 90.42% of its status quo area .

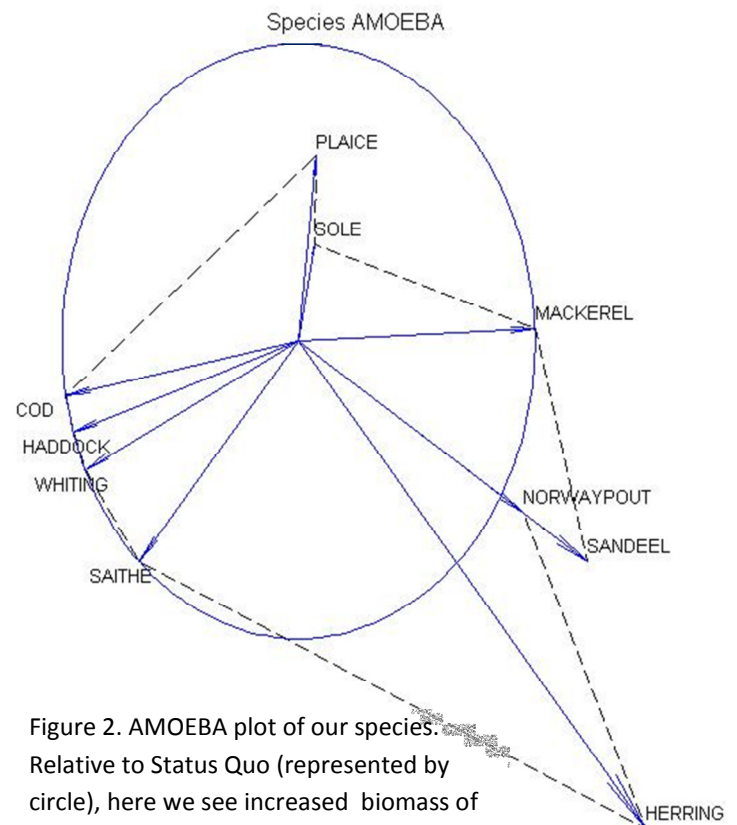


Figure 2. AMOEBA plot of our species. Relative to Status Quo (represented by circle), here we see increased biomass of species 'NORWAYPOUT', 'SANDEEL', and 'HERRING' (caught by fleets 'industrial' and 'pelagic') but decreased biomass of species 'PLAICE' and 'SOLE' (caught by 'beamtrawl'). The species AMOEBA encompasses 117.26% of its status quo area.

Further Information:

Code Operations:

The code uses the input matrix **M** to find the angles for the plotted vectors, for two separate plots. This matrix **M** is the first input described below. In the example, one plot is for fleets, and one for species. The other four input vectors are used to find the lengths of the plotted vectors. The vectors are plotted relative to status quo vectors, meaning that a vector with length = 1 performs as well as Status Quo.

- INPUTTING YOUR DATA (rather than the example data)

Create a new set of variables, such as `My_M`, `My_V_Vstatq`, `My_V_Vscen`, `My_V_SEstatq`, `My_V_SEscen`, as follows:

- Your input matrix `My_m` should be an n -by- p matrix, and must be entered such that $n \geq p$; In other words, the input matrix must have more rows than columns. Otherwise, problems arise with using `princomp.m` which is used to calculate the principal components.

The group categorized via the columns of your n -by- p input matrix will be associated with all items denoted by 'variables (V)'. In our example above, columns represent fleets. Renaming, or changing the number of names, can be done by going into the `VariablesAMOEBa.m` file and following the commented instructions just before the start of the code. Similarly, the group categorized by the rows of your n -by- p input matrix will be connected to all things 'sample entries (SE)'. In our example, rows represent species. Thus, renaming, adding, or removing sample entry names can be done similarly as described above for variables, only one will want to make those changes in `SampEntriesAMOEBa.m`.

An input matrix could be entered at the command line by typing:

```
My_M = [ 0.2 0.01 0 ;  
         0.1 0.1 0.01;  
         0.0 0.1 0.0 ;  
  
         0.0 0.1 0.1 ];
```

This matrix could have various meanings, but one option is for it to represent the annual fishing mortality caused by each fleet (column) on each species (row). In general, it should represent the interaction or correlation between 'variables' and 'sample entries'.

- If your scenario (i.e. policy choice) leads to harvest of 1 tons by fleet X, 2 tons by fleet Y, and 3 tons by fleet Z, but Status Quo leads to 1 tons by fleet X, 4 tons by fleet Y, and 0.5 tons by fleet Z, input this by typing:

```
My_V_Vstatq = [ 1 ; 2; 3 ]  
My_V_Vscen = [1 ; 4; 0.5 ]
```

- If your scenario (i.e. policy choice) leads to biomasses of 10 tons of species A, 20 tons of species B, and 30 tons of species C, and 35 tons of species D, but Status Quo leads to 15 tons of species A, 25 tons of species B, 35 tons of species C, and 36 tons of species D, you can enter this by typing:

```
My_V_SEstatq = [10 ; 20; 30; 35 ]
```

```
My_V_SEscen = [ 15; 25 ; 35; 36 ]
```

Yes, you need the semicolons, these force the data to be columns rather than rows.

Then to run, type: `[decimalExp, variablesComparitiveArea, sampEntriesComparitiveArea] = BothAMOEBA(My_M, My_V_Vstatq, My_V_Vscen, My_V_SEstatq, My_V_SEscen)`

- **OUTPUTS:**

- `decimalExp`, which tells the user what percentage of the variance within the matrix data is explained by the first two principal components.
- `variablesComparitiveArea`, which is the fraction of the status quo area encompassed by the variables AMOEBA. The status quo area is defined as the area said AMOEBA would span if all the vectors plotted were unit vectors (i.e., no change in effort, perpetuating a status quo scenario).
- Similarly, we have `sampEntriesComparitiveArea` which provides the fraction of its status quo area encompassed by the sample entries AMOEBA.

- **SAVED FIGURES:** The figures produced are immediately saved as `VariablesAMOEBA.pdf` and `SampEntriesAMOEBA.pdf`. The `VariablesAMOEBA` figure shows the user the effect of effort change for the fleets. The placement of the plotted vectors endpoints gives the user information about how each fleet was affected by the change in effort level, i.e., if the endpoint of the vector lies outside of the circle, then the scenario being evaluated increased that measure beyond the status quo level. The story is similar for the `SampEntriesAMOEBA` figure. When comparing the two figures, note that the direction in which the `SampEntriesAMOEBA` figures' plotted vectors (which represent species, in our example) point in the same direction as the fleet that collects them, shown in the `VariablesAMOEBA` figure.

FIGURE MODIFICATION:

- The figure(s) will often not pop up looking 100% percent aesthetically pleasing, as was shown above in Figures 1 and 2. Here are a few tips on how to remedy some issues:
 - ✦ The placement of the vector's labels will have the midpoint of the first letter start exactly at the endpoint of each vector. This placement may not be aesthetically pleasing. If the

user wishes to move some or all of them, go to the figure's 'Edit' tab and click 'Figure Properties', then the names of the vectors become text boxes that when clicked move freely within the figure space.

- ✦ Another issue is that the figure creates the size of the window tightly around the plot produced, which does not always make for a round reference circle. If the reference circle appears elliptical, simply stretch the figure window until it is as close to perfectly round as possible.
- ✦ After making these or any other changes, be sure to resave under either VariablesAMOEBA.pdf or SampEntriesAMOEBA.pdf.

Further description:

Fisheries managers, environmental scientists, and others in applied disciplines routinely are asked to present the performance of different options (e.g. fishery policy choices) as measured by multiple criteria (e.g. jobs, fish biomass, economic revenue, abundance of charismatic species, etc.). The AMOEBA plots of Collie et al. (2003) are one tool to visualize these types of tradeoffs. The MATLAB codes provided in this package create AMOEBA plots displaying the effect, relative to some status quo state, that some policy choice has on each fleet, on each species, or on each fleet–species combination, depending on the user's specific inquiry.

Using the work of Collie, Gislason, and Vinther (2003) as our inspiration, we created code that uses principal component analysis (PCA) to create a visual representation in the form of an AMOEBA, in which the most prominent patterns in the data are displayed with minimal loss of information. The visualized data are a two-way data matrix (for our purposes, a species-by-fleets parameter matrix), status quo vectors for species (biomass) and fleets (catch), and scenario vectors for species and fleets (also biomass and catch, in our example).

One of the most important benefits of creating AMOEBA's (as opposed to a "radar" or "spider web" plot of the type presented for instance in the Millenium Ecosystem Assessment) is the ability to analyze two-way data. This feature of the code's design ensures that the angles used to plot the species and fleet vectors are not arbitrarily chosen, but calculated explicitly from the two-way data matrix input by the user. Thus, the directions of the vectors themselves give information about the connections between species and fleets; i.e., the fleet (vectors) point in the same direction as the species (vectors) they catch.

Explanation of Sample Data and its Output:

We used fleet and species entries from Table 2 of Collie et al. (2003) as our two-way data matrix entries (matrix **M** described above). This matrix, which consisted of average fishing mortalities by fleet and species, was able to capture the connection between fleets and species as each species will have highest fishing mortalities via the fleets that capture them most often. Furthermore, data of this ilk would most likely already be available to the user provided that they are using this code to answer similar questions as those posed in Collie et al. (2003).

The values for all other input vectors, which determine vector length, are for demonstration only. We structured the scenario vectors by increasing the catch of fleet 'btr', and thus decreasing the biomass of species 'PLE' and 'SOL' compared to status quo levels (those species are caught by those fleets). Similarly, the catch of the fleets 'ind' and

'pel' were decreased and the biomass of 'HER', 'SAN', and 'NOP' were increased compared to status quo. This can be plainly seen in the figures generated by the example data seen below in Figures 1 and 2. Note that all other plotted vectors lie on the reference circle, since no change was made between status quo and scenario values. The percent of variability explained by the first two principal components for this model run is 65.13%.

References

Collie, S.C., Gislason, H. and Vinther, M. 2003. Using AMOEBA's to display multispecies, multifleet fisheries advice. *ICES Journal of Marine Science*, 60: 709-720.

Millennium Ecosystem Assessment. 2005. Available: <http://www.millenniumassessment.org/en/index.aspx>

Ten Brink, B. J. E., Hosper, S. H., and Colijn, F. 1991. A quantitative method for description and assessment of ecosystems: the AMOEBA approach. *Marine Pollution Bulletin*, 23: 265–270.