

DEVELOPMENT AND APPLICATION OF A MULTIFREQUENCY METHOD FOR FISH AND ZOOPLANKTON DISCRIMINATION AND BIOMASS ESTIMATION

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Abstract: Zooplankton, as any acoustic scattering object, can be discriminated from other organisms (i.e., fish) by using its acoustic properties and its frequency dependence. The ability to distinguish between scatter groups improves as the number and range of frequencies increase. In order to use multi-frequency acoustic data for marine organism discrimination and biomass estimation, it must be collected simultaneously with at least with three frequencies. This study aims to describe the development of an acoustic method that uses the 38,120 and 200 kHz frequencies for discriminating and quantifying the abundance and biomass of mesozooplankton, macrozooplankton and fish. Multifrequency hydroacoustic system consisting from three echo-sounders (Simrad EK60) with 38, 120 and 200 split beam transducers was used to collect all acoustic data.

Keywords: multi-frequency, acoustics, species identification, ground truth, zooplankton, fish.

INTRODUCTION

The recent commercial availability of scientific multifrequency acoustic systems offers a means to make improved abundance estimates. Inverse analysis of multifrequency acoustic data is effective for separation by size of fluid-filled organisms, if the frequency range encompasses the transition between Rayleigh scattering and geometric scattering [3,8]. For fluid-filled organisms, the Rayleigh-geometric transition occurs at approximately $ka = 1$, where k is the wavenumber and a is the spherical or cylindrical radius [2, 12]. The frequency range of 38-200 kHz spans the Rayleigh-geometric transition for radii of 1-6 mm, and is appropriate for the large zooplankters and small fishes that form the SSL. Researchers have successfully used this technique to estimate the abundance of differently-sized zooplankton and fishes [3,8]. Inverse analysis requires a model target strength (TS) frequency spectrum for each acoustic group [4].

The aim of this work is to provide an algorithm for automatically discriminating and quantifying fish and zooplankton using multifrequency acoustic measurements only, and independently of the net samples. A known scattering models are used to classify zooplankton and to separate these from fish. Acoustic data analyses and algorithm development are made using Matlab (MathWorksTM, Natick, Massachusetts, USA) software.

MULTIFREQUENCY ALGORITHM

Definitions, adaptation and implementation

The background for the proposed algorithm is the method designed and described in the publications of Holliday [5, 6] and Greenlaw and Johnson [4]. The original method was designed in particular for application to multi high frequency (up to several MHz) data to detect small zooplankton like copepods. The purpose here is to apply an expanded algorithm compared to the previous approach. The aim of the expansion is to design a classification tool that also allows classification of larger zooplankton organisms from the frequencies of the classical echosounders.

The fauna composition of sound scattering layer (SSL) in the Black Sea is represented mainly by three groups of marine organisms: crustaceans (copepods), gelatinous (ctenophores and jellyfish) and fish [1, 10, 11]. Therefore, in our algorithm the following models are integrated into the process: the truncated fluid sphere T.F.S. [7] for the copepods; regression equation [9] for the jellyfish; the gaseous sphere [2] for a swimbladder. The separation between fish and plankton in the frame of this inversion method is done by elimination, instead of adding a fish model (except the gaseous sphere as a simple swimbladder, but which is used mainly for fish larvae).

The input data for the multifrequency algorithm are the measured mean volume backscattering strengths (S_v) at the various frequencies for each integration cell, thus in this case at the three frequencies: 38, 120 and 200 kHz. Small integration cells are defined in order to come as close as possible to a situation where one type of organism dominates the acoustic reflection.

The basic hypotheses are:

- the mean volume backscattering index measured at one frequency for a given elementary volume, is the result of the linear combination of the individual contributions of the organisms present in the volume;
- multiple scattering between the organisms is negligible;
- the scatterers are uniformly randomly distributed throughout the sampled volume;
- there is a large number of scatterers in the volume.

In these conditions, the problem can be written:

$$\text{for } j = 1 \text{ to } n \quad s_v^j = \sum_i N_i * \sigma(\text{freq}^j, a_i)$$

where:

n - number of measured frequencies,

s_v^j - measurement made at the frequency j , it is the known value.

$\sigma(\text{freq}^j, a_i)$ - backscattering cross section of one organism presenting an equivalent radius of a_i , as it is obtained through the model at the frequency j . It is the result of a calculation, depending on the model used.

N_i - abundance of the organisms having an equivalent radius of a_i , it is the unknown for which the system is solved.

There is one such equation for each measured frequency, leading to an equations' system. To solve the system, Greenlaw [3] proposed use of the Non-Negative Least Square algorithm (NNLS). A matrix expression of the system can be written $S_v = N * \sigma$. Solving this system for N requires the solution to: $N = S_v \sigma^{-1}$. This is the inversion of the backscattering cross-sections matrix, so the values in this matrix must be uncorrelated. The least square algorithm minimises the difference between the measurements (S_v^{meas}) and calculated values from the resolution of the forward problem: after the resolution of the system, an N vector is obtained. From this vector, the knowledge of the model, the frequencies and the sizes of the organisms, s_v can be calculated, which will be noted (S_v^{calc}). The following parameter called the "residual error" (err) is minimized with a constraint of a non-negative solution.

$$\text{err} = \|S_v^{calc} - S_v^{meas}\| = \sqrt{\sum_j (S_v^{calc}^j - S_v^{meas}^j)^2}$$

To be able to solve the system it is necessary to input an a priori initial size vector on which the σ matrix will be calculated. It is chosen as a reasonable size range according to the type of organisms searched for, and to the non-linear part of the model curve in order to ensure inversion of the σ matrix. According to the expressions of the models, the "size" must be understood as an equivalent radius (ER), whatever its shape (cylinder, sphere, spheroid). After resolving the system, the biovolume for each size class is estimated from the size, the abundance (which is obtained in ind. m⁻³) and the shape corresponding to the model used. For example, in the case of N spheres of equivalent radius a , the biovolume for this size is $N * (4/3)\pi a^3$.

RESULTS

The acoustic data used for multifrequency processing are collected with an EK60 Simrad scientific echosounder with transducers mounted in a hull on RV ‘‘Akademik’’, IO-BAS, Varna in September-October 2008 in the West Shelf of the Black Sea operating with 3 frequencies 38, 120, and 200 kHz. The results from the multifrequency algorithm applied to acoustic data are shown on the examples in Figure 1 and Figure 2.

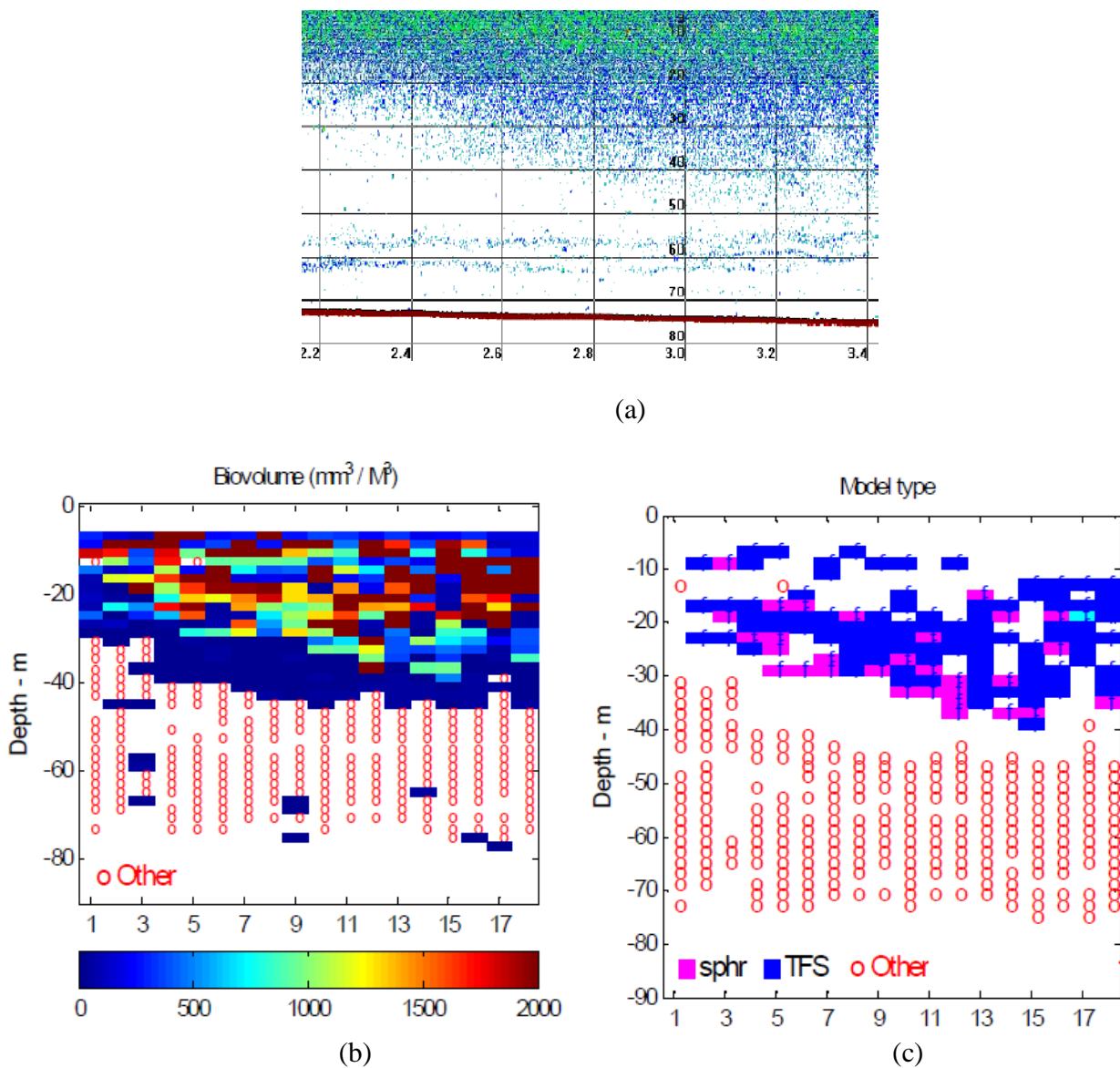


Figure 1. Echogram at 200 kHz (a) and multifrequency algorithm results (b,c).

In our completed algorithm, the residual error is calculated after solving the system with all the desired models. The value of the residual error is mainly correlated with the quality of the result in terms of biovolume, which is the more robust parameter among the different information extracted from the resolution of the system. Figure 2 shows the results obtained for one vertical profile. Above a certain threshold on the residual error, it must be considered that none of the models allows a good fit

between the measurements and the calculations, therefore the volume sampled is filled by organisms that are called “other” on figures 1 and 2, and that are expected to be fish. This threshold on the residual error to localise the “other” points, is a parameter that still has to be adjusted [6].

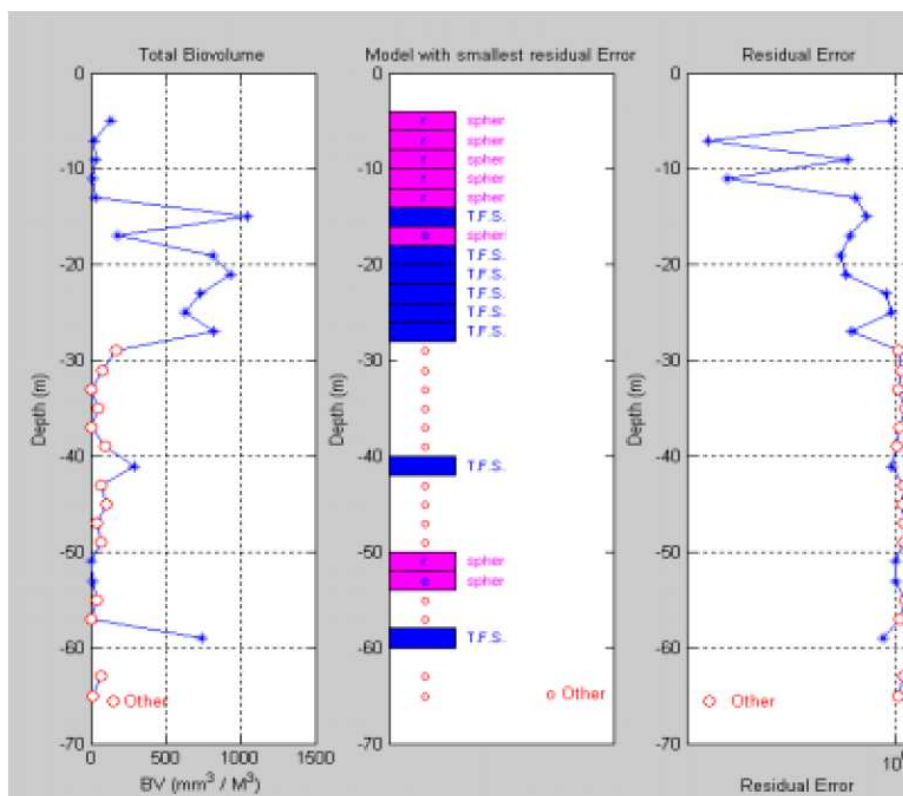


Figure 2. Estimated biovolume, shape and material type of organism and corresponding residual error for a vertical profile (results of the multifrequency algorithm). The residual error threshold has been set to 1 in this example: above this value, the organisms are classified "other".

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