

Fully-automated identification of fish species based on otolith contour: using short-time Fourier transform and discriminant analysis (STFT-DA)

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ABSTRACT

Background. Fish species may be identified based on their unique otolith shape or contour. Several pattern recognition methods have been proposed to classify fish species through morphological features of the otolith contours. However, there has been no fully-automated species identification model with the accuracy higher than 80%. The purpose of the current study is to develop a fully-automated model, based on the otolith contours, to identify the fish species with the high classification accuracy.

Methods. Images of the right sagittal otoliths of 14 fish species from three families namely Sciaenidae, Ariidae, and Engraulidae were used to develop the proposed identification model. Short-time Fourier transform (STFT) was used, for the first time in the area of otolith shape analysis, to extract important features of the otolith contours. Discriminant Analysis (DA), as a classification technique, was used to train and test the model based on the extracted features.

Results. Performance of the model was demonstrated using species from three families separately, as well as all species combined. Overall classification accuracy of the model was greater than 90% for all cases. In addition, effects of STFT variables on the performance of the identification model were explored in this study.

Conclusions. Short-time Fourier transform could determine important features of the otolith outlines. The fully-automated model proposed in this study (STFT-DA) could predict species of an unknown specimen with acceptable identification accuracy. The model codes can be accessed at <http://mybiodiversityontologies.um.edu.my/Otolith/> and <https://peerj.com/preprints/1517/>. The current model has flexibility to be used for more species and families in future studies.

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INTRODUCTION

Automated taxon identification (ATI) systems which rely on pattern recognition and machine learning techniques have been developed in different areas of biology (*Arbuckle et al., 2001; Chun et al., 2007; Cope et al., 2012; Culverhouse et al., 1996;*