

Automatic Detection of Hadal Macro Biological using Machine Learning Method

JUNPENG DENG¹, ZHENLING MA², RUILONG LUO³ AND QINGSONG YANG⁴

¹Shanghai Ocean University and jpdeng@shou.edu.cn

²Shanghai Ocean University and zlma@shou.edu.cn

³Shanghai Ocean University and rlluo@shou.edu.cn

⁴Shanghai Ocean University and qsyang@shou.edu.cn

With the development of science and technology, human being began to explore many unknown areas, such as hadal area. The existence of living organisms in the hadal, and the physiological characteristics of these organisms is one of the directions of human concern. However, due to its unique geographical features, it is difficult to capture the species and the number of species in the hadal. To solve this problem, researchers have developed the ability to work in the hadal of the lander and submersibles, they can shoot the images of the hadal of biological information. But due to the large amount of video data, the probability of the emergence of life is very small, the researchers search for a part of the biological in a large number of videos is very time-consuming. Therefore, in view of the above problems, this work proposed an automatic method for hadal macro biological detection.

For this work, the hypothesis is that in the deep ocean, the modification of background is slight, thus the matrix or the set of background frames is a low rank one. If the biological appeared in the video, it can be considered as sparse part in the frame. Therefore, the detection of hadal macro biological can be described as sparse and low rank matrix decomposition problem.

PCA is arguably the most widely used statistical tool for data analysis and dimensionality reduction today. However, in general, training data may contain undesirable artifacts due to occlusion, illumination, image noise. Thus SLRMD was proposed that can be used to construct low-dimensional linear-subspace representations from this noisy data. The cost function of SLRMD can be written as:

$$\min_{\mathbf{A}, \mathbf{E}} \|\mathbf{A}\|_* + \lambda \|\mathbf{E}\|_1, s.t. \mathbf{D} = \mathbf{A} + \mathbf{E} \quad (1)$$

Here $\|\mathbf{A}\|_*$ is nuclear norm which equals to $\text{trace}(\sqrt{\mathbf{A}^* \mathbf{A}})$, and $\mathbf{A}^*$ is conjugate transpose of $\mathbf{A}$. To solve this constrained optimization problem, many algorithms have been proposed, including the accelerated proximal gradient method, the augmented Lagrange multiplier (ALM) method, and the alternating direction method (ADM). In this work, matrix $\mathbf{E}$ represents the macro biological.