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Using Color Thresholding and Contouring to Understand Coral Reef Biodiversity

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Using Color Thresholding and Contouring to Understand Coral Reef Biodiversity

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Using Color Thresholding and Contouring to Understand Coral Reef Biodiversity

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ABSTRACT

This paper presents research outcomes of understanding coral reef biodiversity through the usage of various computer vision applications and techniques. It aims to help further analyze and understand the coral reef biodiversity through the usage of color thresholding and contouring onto images of the ARMS plates to extract groups of microorganisms based on color. The results are comparable to the manual markup tool developed to do the same tasks and shows that the manual process can be sped up using computer vision. The paper presents an automated way to extract groups of microorganisms based on color without the use of manual work.

Keywords— computer vision, OpenCV, color thresholding, segmentation, contouring, machine learning, coral reefs, biodiversity

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I. INTRODUCTION

A. The importance of coral reefs

With global carbon emissions stemming from industrial activities and the burning of fossil fuels continuing to rise, the Global Carbon Project estimated that the total carbon emissions from all human activities for 2019 to cap off at about 43.1 billion tons [1]. As we experience higher temperatures, melting glaciers, and rising sea levels, the planet's oceans continuously act as a buffer by absorbing the carbon dioxide. Between 1994 and 2007, the oceans absorbed 34 gigatons of carbon dioxide, which helped Earth from warming up faster than it possibly could [2]. But beneath the ocean surface, the carbon dioxide leads to ocean acidification, which plays a role in dissolving the calcium carbonate that makes up the coral skeletons of the coral reefs [2]. Coral reefs directly help support over 500 million people worldwide by providing various ecosystem services, such as subsistence food, protection from flooding and sustaining the fishing and tourism industries [4]. Besides helping sustain life both on land and underwater, they serve as key indicators of global ecosystem health and a warning sign of what may happen to other less sensitive systems [4]. They have begun to show signs of wear and tear, with estimations that a fifth of all corals have died within the past three years [3]. If the current carbon emission rates continue to rise as they do now, the coral reefs in all 29 reef-containing UNESCO World Heritage sites may cease to exist by the end of this century [3]. Coral reefs have shown themselves to be very susceptible to local impacts, such as sedimentation and resource exploitation, but can be affected greatly by global impacts and mass coral bleaching events

due to the increase in global ocean surface temperature caused by anthropogenic greenhouse gas emissions [4].

Fig. 1. Coral reef in the Gulf of Aqaba, Red Sea. (Photo: Guilhem Banc-Prandi)

B. Autonomous Reef Monitoring Structures (ARMS)

With the goal to understand more about the current state of coral reefs and be able to sample the biodiversity, the Coral Reef Division (CRED) of the National Oceanic Atmospheric Administration (NOAA) developed the Autonomous Reef Monitoring Structure (ARMS), which helps provide standardized samples of coral reef life by mimicking the complex habitats of coral reefs. ARMS structures, made up of eight gray Type-1 PVC plates, are long-term collecting devices that mimic to some extent the structural complexity of coral reefs [14]. They provide a way to monitor the diversity of

each coral reef site over time and show the growth and decline in richness in the communities in and around the coral reefs. Once the ARMS are retrieved from the ocean floor and are completely taken apart by researchers, each plate of each ARMS is photographed and the species are identified, recorded, and sampled for DNA processing [8]. Currently, the Heller Research Group has in hand approximately 13,000 images courtesy of Dr. Russell Brainard, which have been collected from the 17 sites across the Pacific Ocean that were recovered between 2013 and 2015 [9]. These 13,000 images collectively would require an impossibly immense amount of manual reviewing and labelling from experts in various domains.

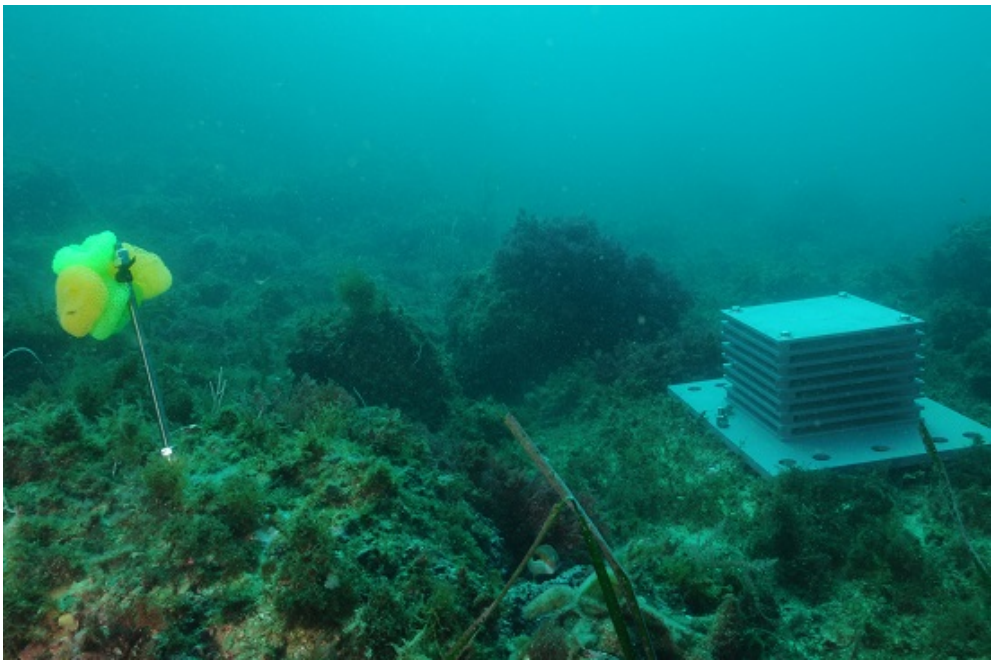

Fig. 2. *Pristine ARMS and ASU* (Photo: F. Zuberer)

C. Related works

In an effort to further understand and detect bio-geographical, spatial, and environmental effects on coral reefs, David et. al. [10] investigated and analyzed photos of the ARMS structures to assess the relevance of photo analysis as a fast and efficient screening tool for biodiversity monitoring of coral reefs. Their research was mainly focused on determining whether they could identify animal and algae groups on the ARMS plates and they concluded that photo analyses of the images of the ARMS plates can be used as a fast-screening tool to detect community composition of the structures in the various locations these structures are placed in. This shows that there is value in applying machine learning and computer vision techniques on images of the ARMS structures to further understand the current state of coral reefs.

As the amount of visual data, such as videos and images, accumulates, computer vision is being widely used to identify and process objects to help lessen the manual work that would be required [15]. There exist many image processing techniques in computer vision that can be utilized to analyze the images. Vojjila tested various techniques such as k-means clustering and fuzzy c-means clustering, then used a neural network to further understand the clustering results [11]. Additionally, Bhodia made use of histogram equalization and canny edge detection to show how computer vision can be used to help create training data [9] by modifying the image to focus on what needs to be analyzed.

Fig. 3. Sample image of an ARMS plate

Bhodia also cropped the images of the ARMS plates to maintain only the plate [9]. But as seen in Fig. 3, by cropping the image, I run the potential of losing data on the edges of the plate. Therefore, for this paper, I decided to keep the images as is to lessen the possibility of losing critical information that may help us fully understand the biodiversity of coral reefs in regard to color.

D. Existing markup tool

As the current focus is color, the training data will mainly center around patches of microorganisms that are similar in color. A markup tool was developed by Dr. Philip Heller that provides the ability to manually mark up the images with bounding boxes. Each bounding box represents a location in an image of a patch of microorganisms that is of the color in question. The markup tool saves the contents of each bounding box as a separate image and saves the coordinates of the location to a CSV file for future reference. Unfortunately, with such a large database of images, it requires quite a bit of manual work in order to complete the task. Therefore, the appeal of using computer vision over a manual markup tool is to remove the manual aspect of analyzing images.

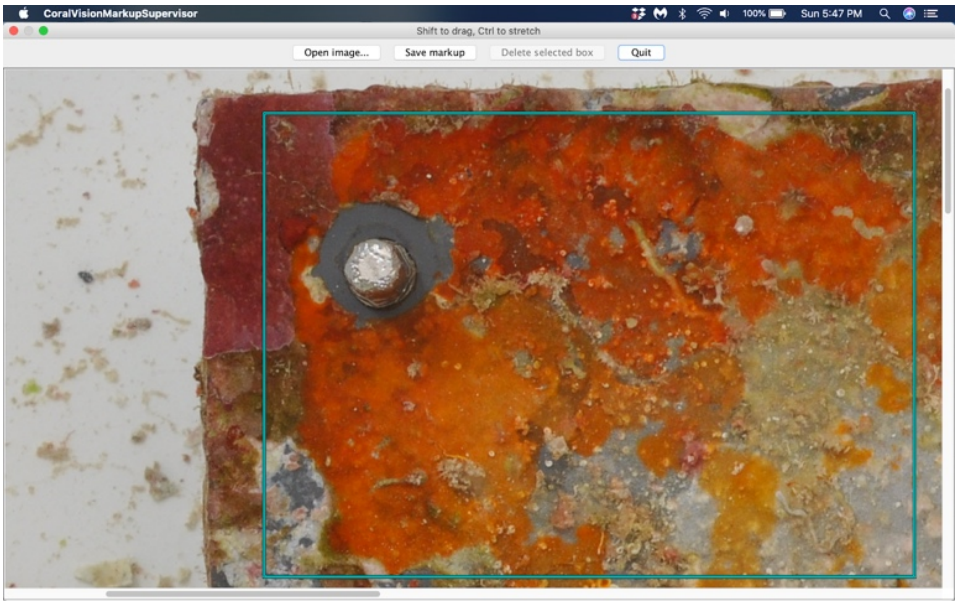

Fig. 4. Markup tool developed by Dr. Philip Heller. The image has been expanded to show the upper-left corner of the plate, and a bounding box (turquoise) has been drawn.

An image processing technique that can be used to help focus on colors is thresholding. Thresholding is typically used on grayscale images to create binary images, but in recent years, multilevel thresholding or color thresholding has been used widely on images in the RGB and HSV color space [12].

E. RGB color space

The images in the data set used for this paper are all represented using the RGB color space format when viewed on a computer. The RGB color space focuses on three specific components - red, green, blue - which are mixed to create a specific color.

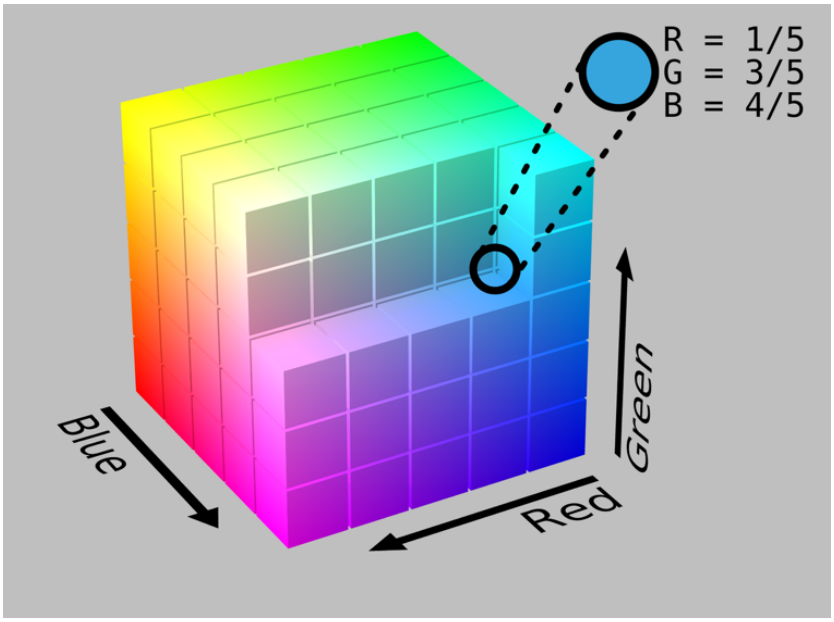

Fig. 5. The RGB color space visualized as a cube (Photo: Michael Horvath)

Each component (red, green, and blue) ranges between 0 to 255. For example, an RGB triplet of (255, 0, 0) results in solid red. The RGB color space can be visualized as a cube as illustrated in Fig. 5.

F. HSV color space

To take into consideration that the markup tool developed by Dr. Heller requires the human eye to identify groups of microorganisms based on colors, I decided to compare the RGB color space against the HSV color space. The HSV color space is closer to how humans perceive color and helps map the RGB color space into dimensions that are more intuitive to humans. It has three components: hue, saturation, and value. As explained by Jacci Howard Bear, "this color space describes colors (hue or tint) in terms of their shade (saturation or amount or gray) and their brightness value [17]." Hue is the color portion of the model, while saturation describes the amount of gray in a particular color. The saturation "when set to 100%, gets you the purest color possible whereas 0% would yield grayscale." Additionally, "value works in conjunction with saturation and describes the brightness or intensity of a color [17]." A value of 0 for a hue would lead to black, whereas a value of 100 is the brightest and reveals the most color. It is important to note that the three dimensions of the HSV color space are interdependent. If the value dimension of a color is set to 0%, the amount of hue and saturation does not matter as the color will be black. If the saturation of a color is set to 0%, the hue does not matter as there is no color used [19].

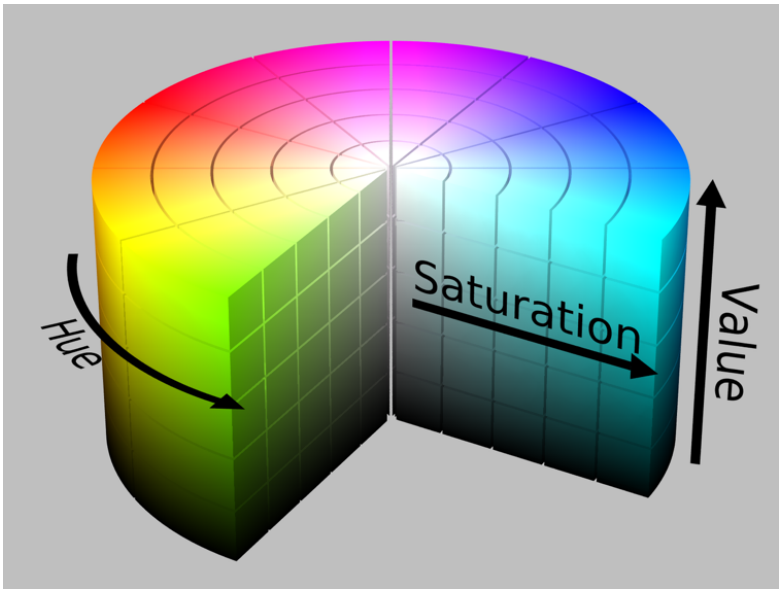

Fig. 6. The HSV color space visualized as a cylinder (Photo: Michael Horvath)

G. Why HSV color space over RGB color space

As the HSV color space more closely aligns with how humans perceive color when compared to the RGB color space, the HSV color space was chosen as the color space to go forth with for this paper. In an article by Rehan Guha, he explains that “color is a perception based on electromagnetic waves" with natural properties including its intensity, its frequency, and its wavelength [18]. The human eye is only able to respond, “or resonate to three main light frequencies (red, green, blue)” and with this response being non-linear, the eye’s retina is able to distinguish a given color or frequency by the “combined response of the three-color components.” While the RGB color space does indeed replicate how the human retina views color, it does not replicate how humans interpret color. In place of the RGB color space, the HSV color space mimics how humans perceive color as “it separates luma, or the image intensity, from chroma of the color information. The luma varies greatly

in the scene based on the amount of light falling on the object as it gives the luminosity. Chroma, on the other hand, correlates better with the object's intrinsic properties, and for properly white-balanced images is more-or-less invariant [18].”

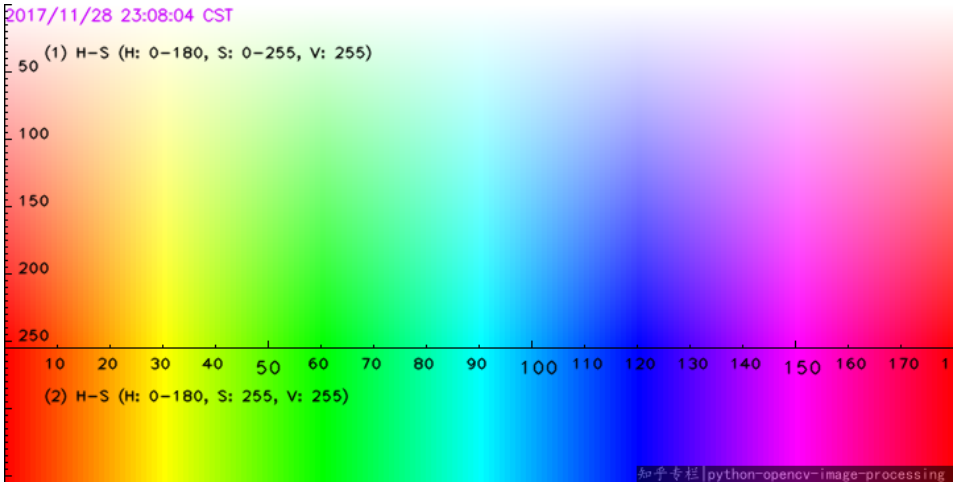

Fig. 7. HSV color space range [1]

H. HSV color space ranges

Geared with a focus on color specifically for this paper and desire to be able to extract each color separately from an image of an ARMS plate, the HSV color space range illustrated in Fig. 7 was utilized to determine the ranges in terms of hue, saturation, and value for 7 clearly distinguishable colors. These values are summarized in Table 1.

[1] The HSV color space range iamge is taken from the following SO Answer https://stackoverflow.com/questions/10948589/choosing-the-correct-upper-and-lower-hsv-boundaries-for-color-detection-withcv/48367205#48367205

TABLE I. HSV COLOR SPACE RANGES

Color	***Hue***		***Saturation***		***Value***	
	Low	*High*	*Low*	*High*	*Low*	*High*
Red	0	8	65	255	95	255
Orange	8	18	120	255	50	255
Yellow	18	27	50	255	20	255
Green	27	100	50	255	10	255
Blue	100	130	50	255	50	255
Purple	130	150	20	255	20	255
Pink	150	180	50	255	50	255

I. Color thresholding

In regard to color thresholding, the technique can be utilized with either the RGB color space or the HSV color space. When thresholding is applied on color images, a separate threshold is designated for each of the RGB components of the image and then combined with an AND operation [12]. Kulkarni et al. utilized multilevel thresholding on natural images and was successful in separating the object from the background based on the RGB color information that is obtained through the specification of the range of intensities for each color channel. Based on the color information, objects that lie outside the selection range will be rejected and the algorithm itself should be capable of extracting pixels of a specific color and reject all other pixels [12].

J. Contouring

After applying color thresholding on an image, contour-based segmentation can be used as a process to separate the required information from the image for further processing [13]. With the ability to place emphasis on specific areas of the images based on colors using multilevel thresholding, contour-based segmentation could be used to further separate the required information from the ARMS images through contouring or bounding boxes. Contour-based segmentation allows the creation of contours around the area of interest in an image as it subdivides the image into constituent regions based on what the user wants - in our case, regions of the images where the organisms correspond to the color that is chosen. In a paper by Hemalatha et al, they used an active contour-based segmentation image processing technique that makes use of energy constraints and forces in the image in order to segment the region of interest from the rest of the image by defining a boundary or curvature for the regions of the target objects [12]. The image processing technique of segmentation was used successfully on brain CT images, MRI images, cardiac images, as well as on images of the skin and septum slides [12][13].

This paper explores the use of color thresholding and contour-based segmentation (concepts in computer vision) using OpenCV alongside the applications/techniques from the two aforementioned papers to help facilitate the analysis of the data collected through ARMS. The desired result of this paper is to have a means to segment and identify patches of microorganisms that are similar in color, such that the obtained results are comparable to the results of manual analysis using the previously mentioned markup tool.

II. METHODS

Fig. 8. Sample image of an ARMS plate

A. Color thresholding application

Prior to applying color thresholding to the images of the ARMS structure, detection of gray pixels was done followed by the removal of such pixels. The removal of the gray

pixels may possibly be a useful first approximate estimation of biodiversity on each plate. The results of this can be seen in Fig. 9.

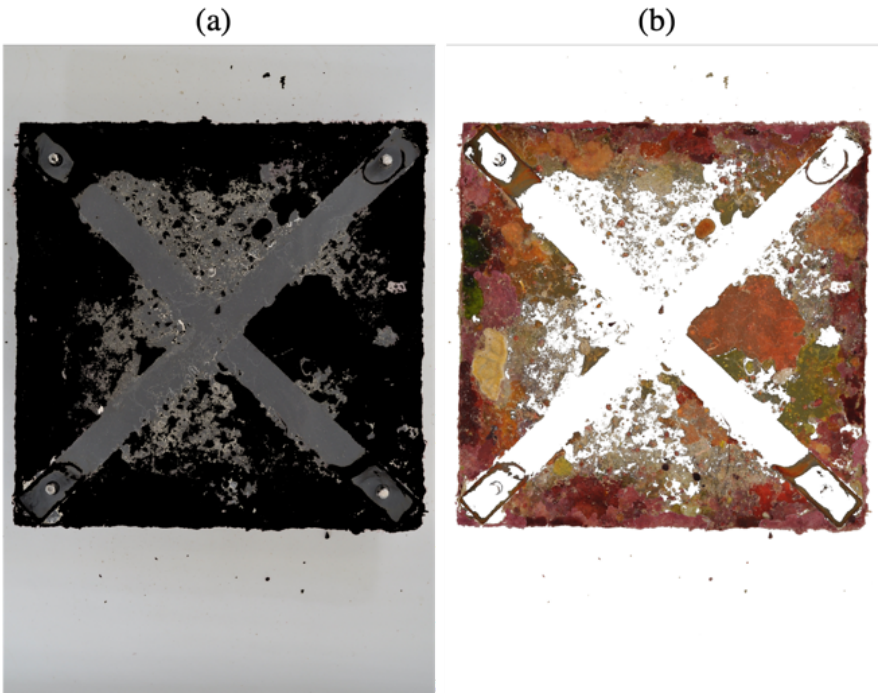

Fig. 9. Image of ARMS plate after the removal of gray pixels. a, only the gray pixels are shown. b, the original image with all gray pixels removed

With a set list of colors identified to focus on for this paper, any image being analyzed needed to be converted from the RGB color space to the HSV color space before any calculations and modifications could be done to them. The OpenCV function cvtColor was used to convert each image to the HSV color space with the COLOR_BGR2HSV parameter.

After the color space conversion was applied to an image, the pixels of the image were iterated through to keep count of the total number of pixels of each color – the counts were then used to determine the most and least dominant colors. Table II depicts the colors from

most to least dominant for Fig. 8 with orange being the most dominant and pink being the least dominant.

TABLE II. PIXEL COUNT PERCENTAGE FOR FIGURE 8

Color	***Percentage in Figure***
Orange	10.179%
Red	9.509%
Yellow	4.882%
Pink	1.589%
Green	0.337%
Purple	0.013%

With a list of the colors arranged by most dominant to least dominant, the next task was to create a range for each color that would be used to help identify whether a pixel of an image was of that color. This range is called a mask and is created using the values in Table I. A mask was created using OpenCV's inRange function, where the image was passed in along with the lower HSV range and upper HSV range of a color. For example, the color orange has (8, 120, 50) as its lower HSV range and (18, 255, 255) as its upper HSV range.

When a mask is applied to an image, it results in a binary image (a black and white image) with the pixels of the color in question converted to white pixels, while all other colored pixels converted to black pixels. Fig. 10a illustrates an example of a binary image. Subsequently, by applying OpenCV's bitwise_and function with the mask, the white pixels of the binary image are reverted to the original orange pixels of Fig. 8. Fig. 10b depicts when the bitwise_and function is applied to an image with a mask.

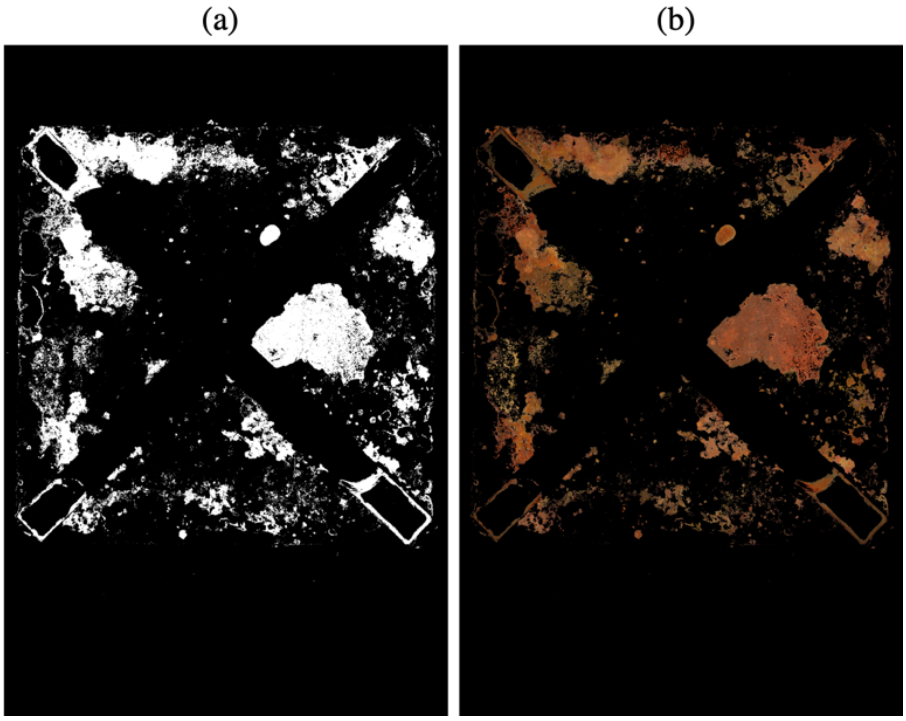

Fig. 10a-b. Binary images based on Figure 1. a, the original image with a mask applied. b, the original image with a mask applied along with the original orange pixels of image

In order to facilitate the extraction of each color separately and sequentially, each color was replaced with white pixels after all modifications were completed for it. After the mask was applied to an image, if a pixel of the binary image generated was white, the pixel (in the same location of the original image) would be replaced with a white pixel. Fig. 11 depicts all orange pixels replaced by white pixels such that for the next color (red), I no longer need to worry about orange pixels.

Fig. 11. Image depicts orange pixels replaced with white pixels

B. Contouring application

With color thresholding mimicking the human eye identifying colors, contouring was applied to the images to mimic the manual process of creating bounding boxes around groups of microorganisms that are of the same color.

Contours are curves that connect points that belong to an area in the image that are of the same color. They are useful for detecting objects and grouping similar areas in an image for further analysis. In the case of this project, contouring helps identify microorganisms of the same color.

To identify and contour the microorganisms, OpenCV's findContours function was used. It takes three arguments - the source image, the contour retrieval mode, and the contour approximation method. RETR_TREE was used as the contour retrieval mode since I wanted to retrieve all the contours in the image and CHAIN_APPROX_SIMPLE was used as the contour approximation method in order to just obtain the points of the contour.

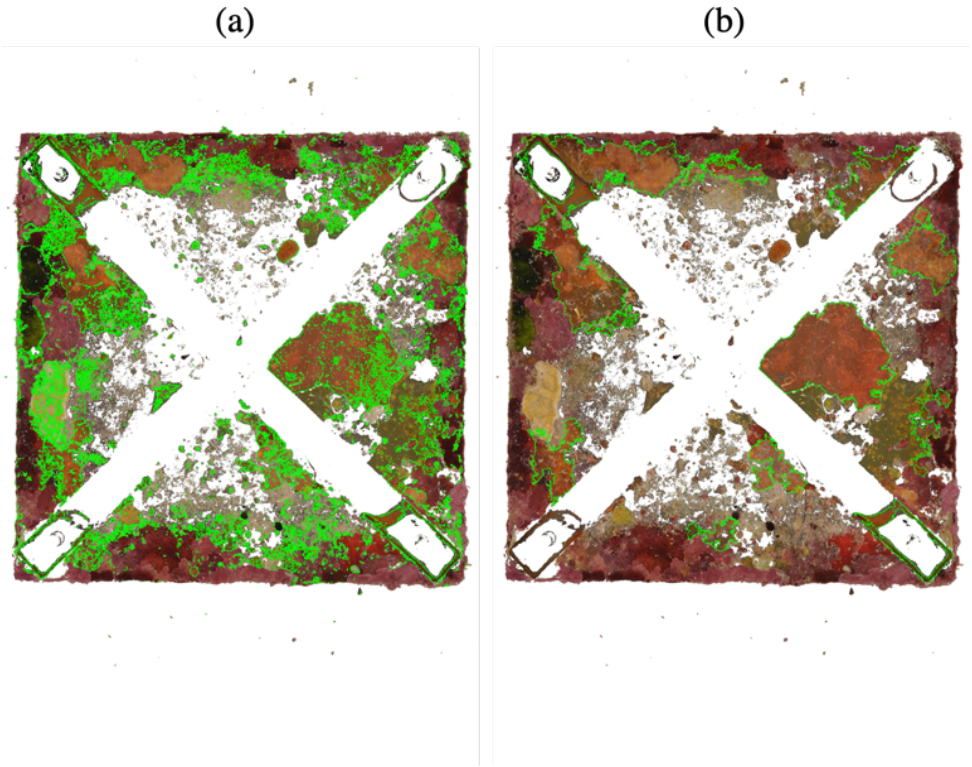

Fig. 12a-b. Basic contour - all contours and selected contours

With all of the contours identified in the image, the array of contours was iterated through and based on the specified size criteria, the contour was drawn onto the image as seen in Fig 12. Fig. 12a depicts all contours being drawn, whereas Fig. 12b depicts only contours that were greater than the specified size criteria, which was set to 25,000 pixels. Though the contouring depicted in Fig. 12 more closely outlines the groups of microorganisms based on color, it does not mimic the markup tool that Dr. Heller developed. Therefore, for the project, I also created rectangular contours (bounding boxes) around the groups of microorganisms. Fig. 13 illustrates groups of microorganisms that are orange with an area greater than 25,000 pixels.

Fig. 13. Rectangular contours or bounding boxes

III. RESULTS

A. Color thresholding results

After color thresholding was applied to the images, it resulted with various versions of images of the ARMS plates that could be used for further analysis by marine biology experts.

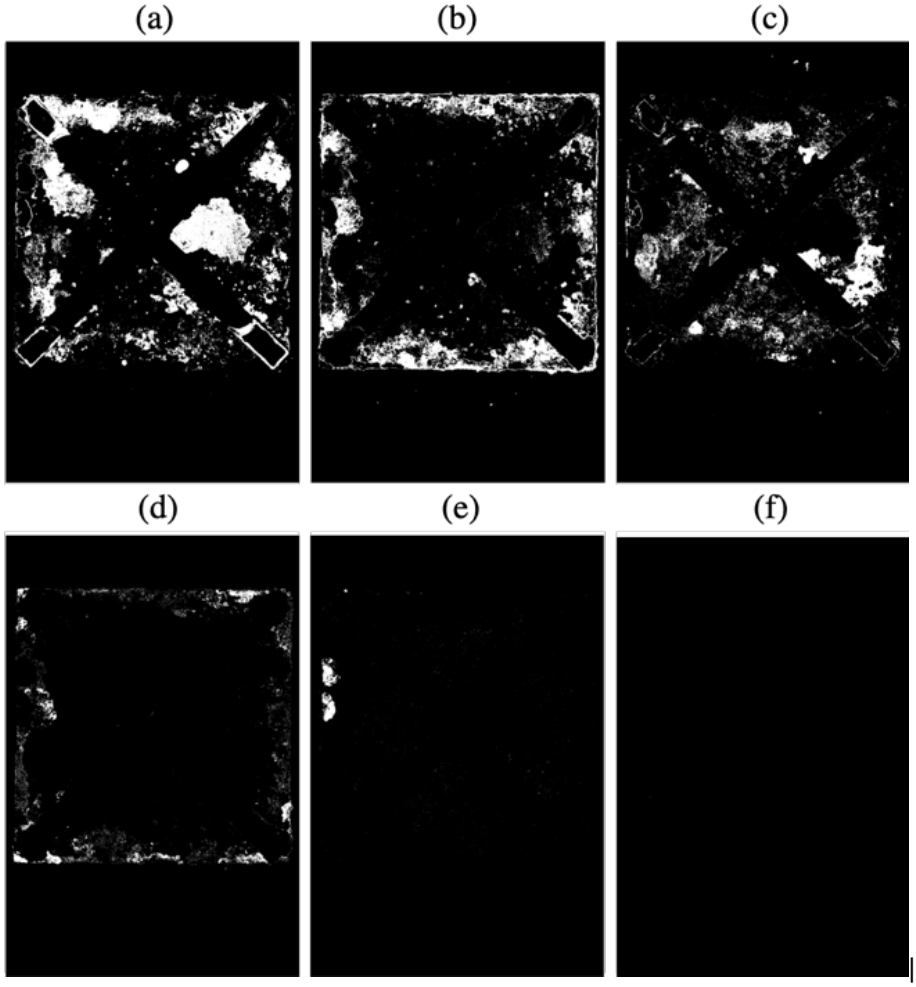

Fig. 14. Mask for each color (from most dominant to least dominant)

As can be seen in Fig. 14, by creating a binary image, each color is separated from the other colors allowing for a more focused image. Additionally, it gives us a visual

representation of which color is more abundant in an image and a swift way to see if anything stands out in an image at a quick glance.

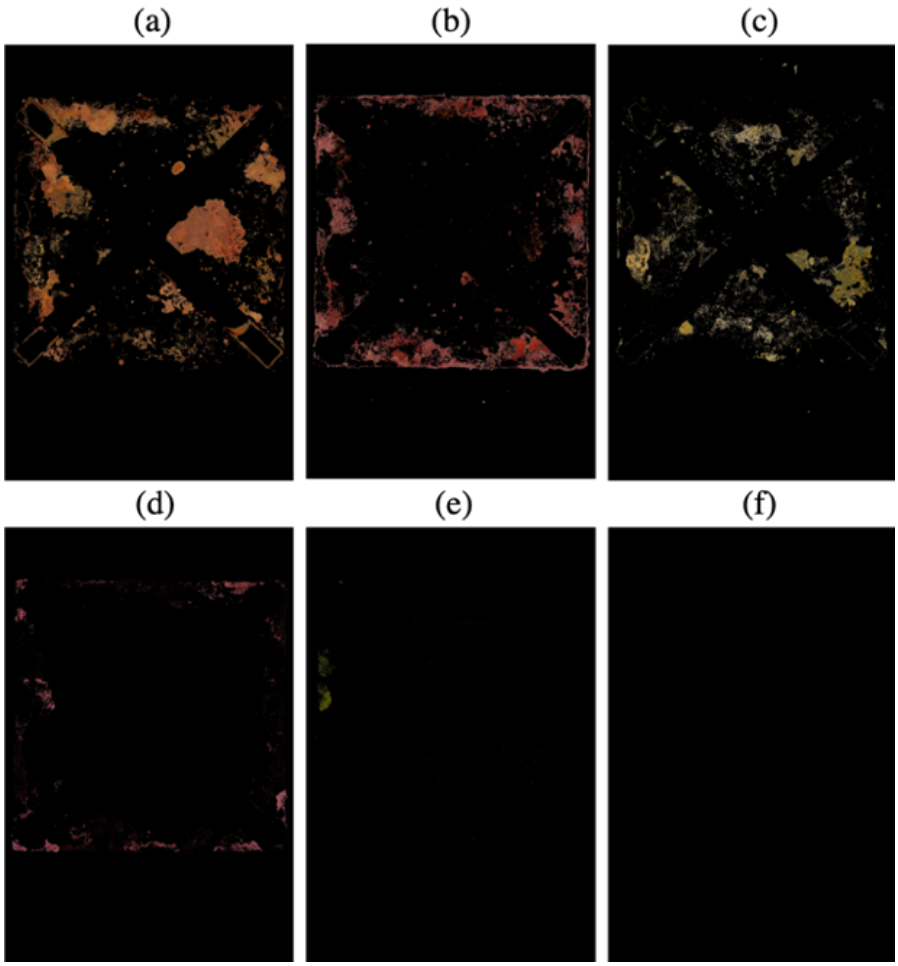

Fig. 15. Image for each color extracted separately

But in order to make the binary images more informational, applying OpenCV's bitwise_and function with the mask allowed the creation of the images in Fig 15. As illustrated in Fig. 15, the images are now presented with the color in question such that it would provide marine biology experts in each color domain a more visual image to analyze. For example, a marine biologist with knowledge in orange organisms could look at

Fig. 15a and be able to identify organisms without worrying about other colored organisms. Unfortunately, it is possible that some organisms on the ARMS plate may be multi-colored and color thresholding could possibly be a drawback since these multi-colored organisms are no longer considered as one.

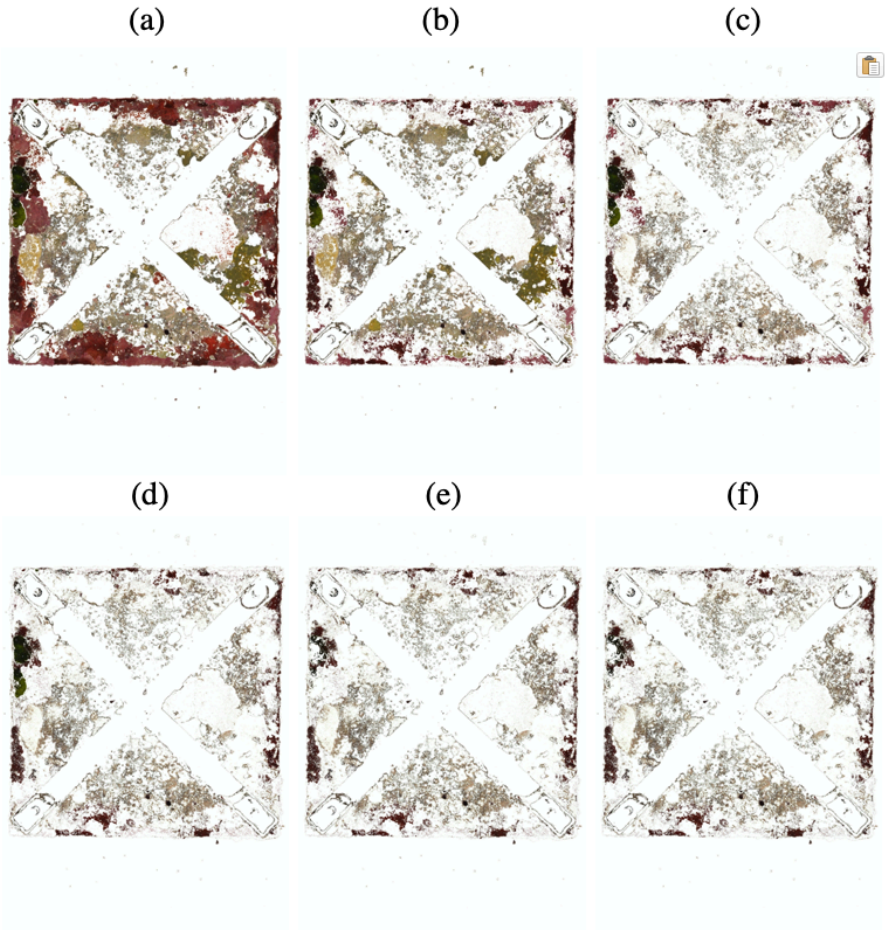

Fig. 16. Progression of each color being removed

Another approach that was done using color thresholding was to remove each color – one at a time – from the most dominant to least dominant. Fig. 16 illustrates the gradual extraction of each color from the ARMS plate. The results in Fig. 16 show that there are

very few organisms left on the plate and if any are left, they can be further analyzed without the interference of any other colors that may otherwise be a distraction.

B. Contouring results

With the ability to extract each color separately using color thresholding, I wanted to mimic the markup tool developed by Dr. Philip Heller. I utilized OpenCV functions to contour the organisms similar to how a person would do so manually using the markup tool. Fig. 17 illustrates how all organisms of a color are contoured in a neon green color. As can be seen, the more abundant a color is on the plate, the more contours that will exist on the image. Fig. 17(a) illustrates contours for orange organisms while Fig. 17(d) illustrates contours for pink organisms.

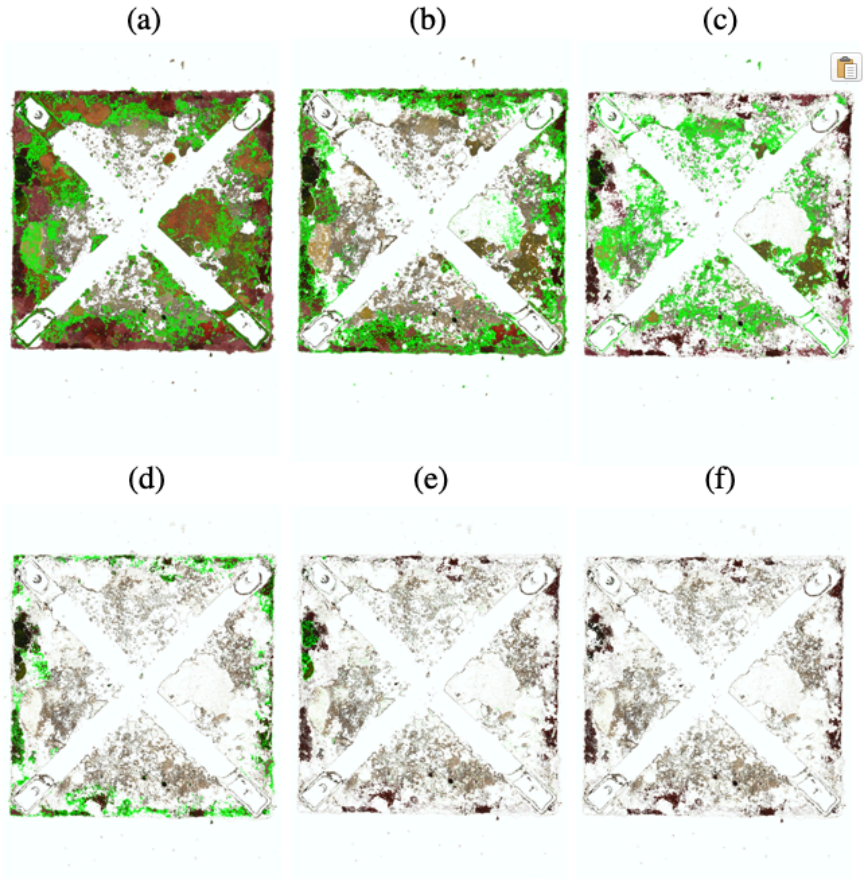

Fig. 17. Contouring of each color separately

C. Comparison of automated process and markup tool

In order to compare the contouring output from my code with contouring generated using Dr. Philip Heller's markup tool, I made use of an existing project that was developed by a fellow student - Minhan Cao. Minhan's application allowed the regeneration of the bounding boxes using the data created by the markup tool. Fig. 18 illustrates the regeneration of the bounding boxes that I manually marked using the markup tool while Fig. 19 illustrates the bounding boxes that my code generated using both computer vision techniques of color thresholding and contouring.

In an ideal situation, both manual and automatic contouring would result in the same bounding boxes, but as seen when comparing the two figures, there are some differences. When creating manual bounding boxes using the markup tool, I marked any areas of orange pixels that seemed distinguishable from other groups of orange pixels – disregarding the possibility that I may be bounding a larger organism into two possible smaller organisms. On the other hand, the contouring done automatically tended to create bounding boxes that were larger in size when compared to the manually created bounding boxes. This anomaly may require additional expertise to determine whether or not which grouping of organisms is correct.

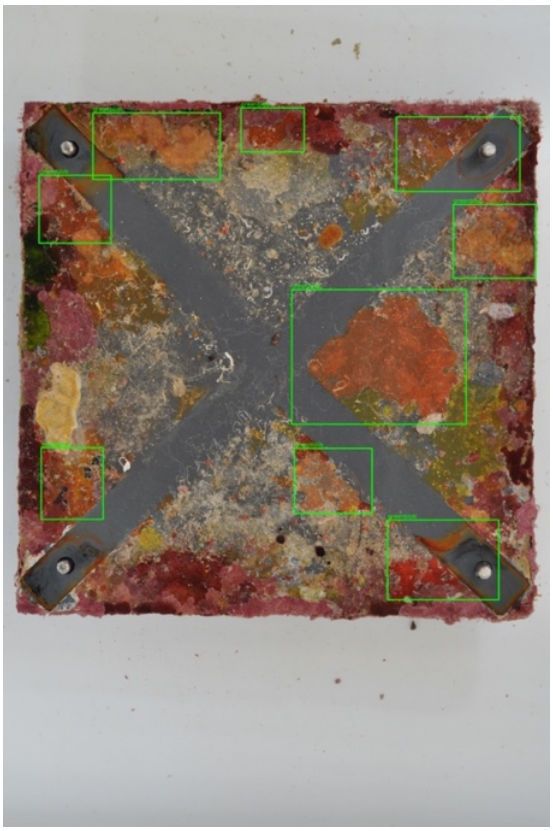

Fig. 18. Results of manual markup tool

Fig. 19. Results of automating the process of creating bounding boxes

All of the code written for this project can be found at the following link: https://github.com/vuongtrans/coralvision-sjsumasters.

IV. CONCLUSION

This work explored the possibility of automating the process of extracting organisms separately based on color. It was intended that each color – once extracted - can then be further analyzed by marine biology experts. Two main computer vision techniques were utilized in this work – color thresholding and contouring. Color thresholding provided the ability to create a set of data images that focused solely on each color separately, while contouring resulted in an additional set of data images that drew bounding boxes around organisms in the image. The results led to the conclusion that it is indeed possible to automate the process of manually reviewing each image in the data set containing the images of the ARMS plates. This automated process can prove useful when considering the amount of manhours that would be required to manually mark up all the images in the data set.

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