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Towards automated scyphistoma census in underwater imagery: A useful research and monitoring tool

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ABSTRACT

Manual annotation and counting of entities in underwater photographs is common in many branches of marine biology. With a marked increase of jellyfish populations worldwide, understanding the dynamics of the polyp (scyphistoma) stage of their life-cycle is becoming increasingly important. In-situ studies of polyp population dynamics are scarce due to small size of the polyps and tedious manual work required to annotate and count large numbers of items in underwater photographs. We devised an experiment which shows a large variance between human annotators, as well as in annotations made by the same annotator. We have tackled this problem, which is present in many areas of marine biology, by developing a method for automated detection and counting. Our polyp counter (PoCo) uses a two-stage approach with a fast detector (Aggregated Channel Features) and a precise classifier consisting of a pre-trained Convolutional Neural Network and a Support Vector Machine. PoCo was tested on a year-long image dataset and performed with accuracy comparable to human annotators but with 70-fold reduction in time. The algorithm can be used in many marine biology applications, vastly reducing the amount of manual labor and enabling processing of much larger datasets. The source code is freely available on GitHub.

1. Introduction

Jellyfish represent an important component of marine biota characterized by a large numerical variability (Boero et al. 2008) and sometimes appear in huge masses (blooms). These mass events attract public attention since they prevailingly occur in coastal and shelf seas and frequently interfere with human enterprises (Lucas et al. 2014). An increase in frequency and intensity of jellyfish blooms has been reported in areas worldwide (Brotz et al. 2012; Purcell 2012; Kogovsek et al. 2018). In these locations jellyfish are affecting tourism, clogging intakes of power-plants and desalination facilities and are also causing harm to fisheries and aquacultures (Richardson et al. 2009; Purcell 2012; Gershwin 2013). On the other hand, the high demand for jellyfish in some Asian food markets has opened new possibilities to fishermen in many parts of the world (Brotz and Pauly 2016). Recent research shows that the role of jellyfish in the ecosystem is far from negligible. They are voracious predators of plankton including fish eggs and larvae, they deplete food for other plankton feeders (Graham et al. 2014) and might be crucial in transporting organic carbon into deeper parts of the water column (Lebrato et al. 2013). When decomposing in large numbers, jellyfish cause significant bacterial community shifts (Tinta et al. 2010, 2012) and influence the nitrogen cycle (Tinta et al. 2016).

Seventy percent the reported mass occurrences of gelatinous taxa are attributable to scyphozoans (Lucas and Dawson 2014). Among the key traits that facilitate production of large number of individuals is a bipartite life history – the life cycle of most Scyphozoa alternates between a free-swimming medusa and an attached polyp. Sexually-reproducing pelagic medusa generates planulae which, after settling, develop into polyps, which in turn asexually produce free-swimming ephyrae (juvenile medusae). While most medusae reach sizes in the order of tens of centimeters, the polyps are much smaller (few millimeters) and are much harder to find and monitor. Consequently most scientific research focused on the medusa phase. Understanding the polyp population dynamics is vital for explaining the mechanisms and dynamics of jellyfish blooms since polyps have the potential to produce large numbers of recruits to the medusa population (Lucas and Dawson 2014). Despite the importance of the perennial polyp phase, the in-situ population studies are scarce (Willcox et al. 2008; Purcell et al. 2009;

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Makabe et al. 2014; Hočevar et al. 2018; Fox et al. 2016). Our knowledge is largely derived from laboratory experiments (Lucas et al. 2012) and the reason likely lies in the substantial and tedious work required for obtaining sufficient amounts of representative data (Olariaga et al. 2014).

Recent research shows that coastal (Malej et al. 2012; Makabe et al. 2014; Hočevar et al. 2018) and offshore (Janßen et al. 2013; Vodopivec et al. 2017) man-made structures could have a significant impact on jellyfish populations in many areas. The polyps preferably attach to downward facing hard substrate (Schiariti et al. 2014) and such structures are scarce, which results in polyp populations clustering on relatively small regions. Understading the causes of jellyfish blooms and properly evaluate the influence of marine man-made constructions on jellyfish population dynamics, requires numerous field studies, based on quantifying polyp abundance over a period of several months/seasons. The change at each temporal unit is estimated by counting the number of polyps in a wild population, which can be done using underwater photographs. Each image may contain over a thousand polyps (Hočevar et al. 2018), which demands a significant focus, accuracy and time from the expert. Therefore, a method that could speed up the annotation process and reduce the amount of manual work would significantly improve the feasibility of large scale in-situ experiments.

With a rapid development of digital imaging techniques manual counting issues are becoming common in various branches of biology. The capacity to analyze images has not advanced at the same pace as the ability to collect them (Durden et al. 2016a; Beijbom et al. 2015). Monotonous operations like manual tagging and counting lead to reduction of the annotator's concentration. Furthermore, the manual work is subjected to the annotator's bias and their prior experience with the annotation domain (Schoening et al. 2017). The obtained counts of target entities allow researchers to estimate their population and infer individual characteristics, yet the amount of manual work often precludes large-scale studies. Therefore, automatic counting solutions based on image-processing techniques are often sought, both in order to alleviate the manual work-load and to reduce inter- and intra-operator variance.

In most cases, automatic counting is used on in-vitro samples since it allows a high degree of control over the image background (Friedland et al. 2005). Typically the samples are further stained with contrasting agent to increase the foreground-background separation (Di Mauro et al. 2011). This significantly simplifies the problem and allows application of basic image processing techniques. Several approaches are in fact implemented as macros or plugins within available image-processing suites, such as ImageJ software (Rasband 2012). On the other hand, jellyfish polyps are typically observed in highly diverse environments that surpass the capabilities of basic image processing (Durden et al. 2016b). Over the last five years, significant advances have been made in the field of computer vision, particularly in object detection and recognition, as demonstrated on established large-scale benchmarks (Everingham et al. 2010; Russakovsky et al. 2015). The state-of-the-art detection approaches are based either on fast hand-crafted features (Dollár et al. 2009), or, with increasing prevalence, on deep learning (LeCun et al. 2015; He et al. 2017). For example, Girshick et al. (2014) and Girshick (2015) decompose images into regions of interest using an object-agnostic region proposal algorithm, and classify them using features extracted from a pre-trained convolutional neural network (CNN) (Krizhevsky et al. 2012). Ren et al. (2015) and He et al. (2017) extended this approach with end-to-end learning, in which the region proposal algorithm is also trained inside the CNN framework. We leverage these modern computer vision approaches to enable semi-automatic polyp population census. In particular, we train a fast detector from Dollár et al. (2010) to generate potential regions of interest, and classify them using the approach akin to R-CNN Girshick et al. (2014). As such, our approach addresses the polyp appearance variations and is robust to the challenging background environment.

We make the following two contributions. Our primary contribution is a two-stage detection algorithm for automatic polyp count estimation (PoCo). The PoCo approach combines state-of-the art computer vision and machine learning methods, tailored to the specific domain of polyp counting. PoCo is evaluated on a set of human-annotated images (Section 3.2). To provide accurate ground truth for our algorithm evaluation, these images have been annotated by several annotators. Our second contribution is a quantitative evaluation of human annotator variation in counting from typical polyp images (Section 3.1). PoCo was applied to a one-year population dynamics analysis of moon jellyfish polyps from Hočevar et al. (2018). Based on our in-depth analysis of the annotation problem from perspective of count variance and PoCo failure cases, image acquisition guidelines are outlined to facilitate future use in population studies (Section 4.1). To the best of our knowledge, this is the first work that holistically addresses the problem of automated polyp count estimation and quantitatively exposes the problem of human annotation errors in this task.

2. Methods

The purpose of this research is development and evaluation of a computer-vision based automated polyp counting approach. For evaluation purposes we acquired a large annotated dataset of 3894 polyps from 7 sample images using manual annotation. This dataset has two purposes: evaluation of the algorithm and evaluation of human annotation quality.

2.1. Image acquisition

Underwater polyp images were obtained by scuba divers during a 3-year survey in the Port of Koper (northern Adriatic) where polyps were found attached to under-surfaces of oysters growing on port pillars (Malej et al. 2012). The entire under-surfaces of five selected shells were photographed once per month at depth ranging from 2 m to 6 m and were taken with two cameras of different quality (Nikon D2X with Nikkor AF-D micro 60 mm f/2.8 lens and Pentax Optio WG-1 compact camera). The images varied in resolution from 1180×863 to 4288×2848 pixels. The distance varied as well, since no distance rig was used. Nikon D2X shots were made using two external lights (Subtronic Pro270 flash and Nikon SB-800 AF Speedlight flash in Sealux CX-800 housing, both mounted to Sealux CT25 flash arms), while the Pentax Optio WG-1 shots were taken with a built-in flash only. An approximate metric calibration was performed for each shell at the start of the monitoring campaign. A photograph of each shell with a ruler placed next to it was taken to estimate the shell surface area, which was subsequently used to obtain the polyp densities from the obtained polyp counts. Further details about in situ study and the results of manual counts are given in Hočevar et al. (2018).

The acquired underwater images significantly vary in the jellyfish polyps appearance (Fig. 1). This accentuates subjectivity and is expected to lead to a wide inter-annotator variation. These factors negatively affect the consistency of annotations, and consequently increase the uncertainty of the obtained results (Durden et al. 2016b).

2.2. PoCo: An automated polyp counter

In our automated polyp counter, we adopt a two-stage detection paradigm found in modern computer-vision based object detection approaches (Girshick et al. 2014; Girshick 2015; Ren et al. 2015; He et al. 2017). In the first stage, the image is processed using an algorithm that produces a large number of regions that potentially contain objects of interest. In the second stage, each proposed region is encoded as a feature vector by a pre-trained convolutional neural network (CNN), and classified as an object of interest or discarded as background.

An overview of the PoCo algorithm is illustrated in Fig. 2. As we are interested in a single class of objects (i.e., polyps), we avoid a generic region proposal algorithm in the first stage and use a fast Aggregate