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Meiofauna Images Generation Using StyleGAN2: A Case Study of Copepoda

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Abstract :

In this work, we propose two StyleGAN2 hierarchical transfer learning approaches in order to generate images of animals belonging to the Copepoda group. Copepods are one of the most represented groups of the aquatic environment, yet only few publicly available images are available. These animals, like other groups of meiofauna, are formidable bio-indicators of environmental changes or pollution of an habitat. The used Copepoda dataset is composed of animals belonging to four orders namely Calanoida, Cyclopoida, Harpacticoida and Siphonostomatoida. Our approaches consists in first training with the available data of all the orders or with the most represented order images before training again with the images of the specimens we wish to synthesise. We evaluate the results using the FID and KID metrics. The synthetic images are promising, showing typical morphological features of Copepods, and could be used by future taxonomists. Generated images could represent a new research object for the creation of meiofauna classifiers, models that require a large number of images for training.

Keywords : Machine Learning, Generative Adversarial Net-works, StyleGAN2, Meiofauna

I. INTRODUCTION

Molly F. Mare first defined the word “Meio Benthos” in 1942 to describe an assemblage of benthic metazoans distinguishable from macrobenthos by their small size (the word *meio* coming from the ancient Greek $\mu\epsilon\iota\omicron\nu$ meaning “smaller”). The size scale, ranging from $20\mu m$ to about $1mm$, is defined experimentally, following the standard size of sieves used by biologists to sort marine sediments and specimens. The words meiobenthos and meiofauna are used in ambiguous ways in the literature, in this article we also use them synonymously. Zeppilli et al. [1] have shown that meiofauna species play a key role in the benthic food web, both as producers and consumers. Meiofauna species react more quickly than macrofauna to the different forms of stress to which they are exposed, making them excellent bio-indicators of ecological changes [2], pollution of an environment [3] or even global warming [1]: trawling, industrial and agricultural dumping, plastic pollution, heavy metal and hydrocarbon pollution, nuclear waste discharge, munitions waste, marine mineral exploitation, ocean acidification and deoxygenation, etc. Moreover, some species survive in extreme environments and therefore have considerable economic potential, for example in the fields of agriculture, chemical synthesis, detergents and pharmaceuticals [4]. With 11,290 accepted marine species [5], the Copepoda group is the second

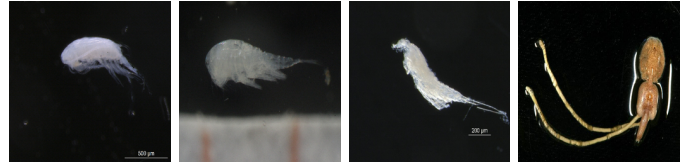


Fig. 1: Examples of Copepoda images. From left to right, the animal belongs to the order: Calanoida, Cyclopoida, Harpacticoida and Siphonostomatoida, respectively.

most abundant in the meiofauna. It is also one of the most important group in planktonic life in this range size. Copepods includes benthic and pelagic animals, their size varies between $250\mu m$ and $3cm$. Like the other groups of the meiofauna, the number of unknown species is very large and the estimation varies widely: the lowest estimate, between 30,125 and 50,125 species, is given in 2012 by Appeltans et al. [6], Humes et al. [7] in 1994 estimated this number at 75,000, and finally, Seifried et al. [8] gave a much higher estimate in 2003 of 450,000 species of copepods still unknown. Figure 1 shows some examples of copepods images.

However, the taxonomic identification of the meiofauna is difficult. This work relies on the use of taxonomic keys and involves the expertise of taxonomists specializing in the species studied, requiring several weeks of work for a sample of a few hundred individuals. This tedious work is made more difficult by the lack of manpower, making the development of artificial intelligence tools a major challenge for the study of the meiofauna. This development is hindered by the lack of data. Motivated by recent improvements in high-definition Generative Adversarial Networks (GANs) trained with small datasets, we investigate in this work the use of artificial neural networks for the generation of synthetic copepods data. First introduced in 2014, GANs [9] have demonstrated to be remarkable tools in various areas of data generation, such as image generation, image-to-image or text-to-image translation, data augmentation, denoising, etc. GANs consist of two competing artificial neural networks. The first, called a generator, creates false data that must deceive the second, called a discriminator. The latter is trained to distinguish real data from the generated data. Following the first proposed

architecture, many new models have emerged, increasing the quality and resolution of the generated images. Recently, two GANs have greatly improved the quality of synthetic images; BigGANs [10] and StyleGANs [11] are capable of generating high resolution images, typically of 512x512 pixels or even 1024x1024 pixels. The main disadvantage of BigGANs is the large size of its network requiring a very large number of images for training. Recent enhancements of the second version of the StyleGAN, namely StyleGAN2 [12], in the case of limited dataset led us to choose this network as a base for our work. For its training, we propose two hierarchical approaches.

The model, its enhancements and the proposed methods are explained in further details in Section II. The training data and the evaluation metrics are described in Sections III and IV, respectively. Finally, we discuss the results of our proposed methods in Section V.

II. PROPOSED METHOD

Introduced in 2014, DCGAN [13] is one of the most popular convolutional architecture, this network is less costly in term of calculation and less complex to train than the other presented networks. The particularity of StyleGAN is the introduction of style vectors: instead of feeding a gaussian noise vector directly to the generator, a dense network called mapping network transforms it first into an intermediate latent space vector. The resulting latent vector is then transformed via affine transformations into a style vector \mathbf{A} . The latter is then fed into each block of the generator. Over the last two years, various improvements have made StyleGAN capable of generating high-definition images while having a limited number of images in the dataset. Firstly, a second version of StyleGAN, StyleGAN2, improves on its predecessor, enhancing its performances and avoiding the appearance of artefacts. StyleGAN2 generator blocks are described in the Figure 2, the style vector \mathbf{A} is the output of the mapping network, in our case a two-Layer Perceptron. Stochastic variations in the image are provided by the parallel injection of a noise vector \mathbf{B} . The modulation scales the input features weights by the style:

$$w'_{ijkl} = s_i \cdot w_{ijkl} \quad (1)$$

where w and w' are the original and modulated weights, k and l are the spatial indices, j is the output feature map indice and s_i is the style corresponding to the i input feature map. Following this operation, the output activations have a standard deviation of:

$$\sigma_j = \sqrt{\sum_{i,k,l} w'_{ijkl}{}^2} \quad (2)$$

The authors of StyleGAN2 perform a demodulation operation:

$$w''_{ijkl} = \frac{w'_{ijkl}}{\sqrt{\sum_{i,k,l} w'_{ijkl}{}^2 + \epsilon}} \quad (3)$$

where ϵ is a small constant that prevents numerical issues.

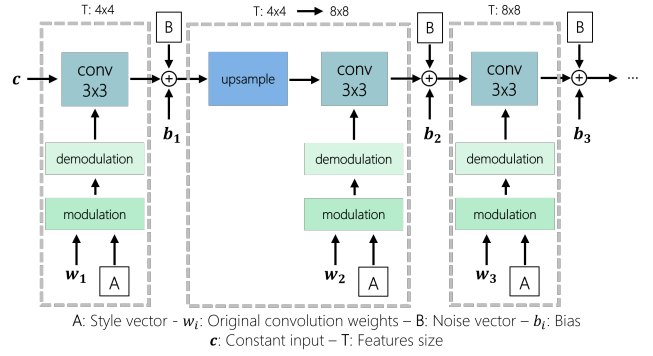


Fig. 2: Description of the StyleGAN2 first generator blocks [12]. The following blocks build up until the size of the output image is reached.

Finally, we propose to use ADA (Adaptive Discriminator Augmentation) [14] and LeCam regularization [15] (given as (4)).

$$R_{LC} = \mathbb{E}_{x \sim \tau} [\|D(x) - \alpha_F\|^2] + \mathbb{E}_{z \sim p_z} [\|D(G(z)) - \alpha_R\|^2] \quad (4)$$

where τ is the training image set, p_z is the prior distribution, G and D are the generator and the discriminator, respectively, and finally, α_F and α_R are two exponential moving averages. The two methods demonstrated to stabilize the training in the case of limited datasets, our experiments on the Calanoida dataset will corroborate with those results.

We define two training protocols to obtain synthetic images generation models according to the desired taxonomic rank. Our first proposed method aims to benefit from the knowledge acquired on another specimen than the one studied. It consists in training first the network using a dataset of another specimen of the same taxonomic rank and then on the dataset of the animal under study. This way, the images of the animal to be synthesised are not used initially, and therefore the common characteristics of the specimen of the same taxonomic rank are learned, then the images of the animal are used to specify the characteristics of the animal. This method is referred to as ‘‘Sideways approach’’. We propose a second approach, allowing the network to memorize common features of specimens of a higher taxonomic rank, and finally fine tune the model to the desired lower taxonomic rank. This hierarchical manner is referred to as ‘‘Downward approach’’.

III. TRAINING DATA

The data used this study are from the BOLD (The Barcode of Life Data System) dataset [16]. The images were sorted to keep only the examples of a size greater than 256 x 256 pixels and representing the whole animal. The images were then resized to 256 x 256 pixels. The images shown in Figure 1 come from this dataset. Copepods are identified by their taxonomic order. The dataset is composed of 1969 Copepoda

including 902 Calanoida, 766 Cyclopoida, 150 Harpacticoida and 151 Siphonostomatoida.

IV. EVALUATION METRICS

To assess the quality of the generated images, we use the FID (Fréchet Inception Distance) [17] and the KID (Kernel Inception Distance) [18]. The FID measures the difference between the statistical distributions of the features, generated using a pre-trained Inception model, of the synthetic and real images. In particular, in the case of FID-50k, the features of the real dataset are compared using the Fréchet distance to the features of 50,000 generated images. However, Keras et al. [14] have shown that the FID is not an ideal metric in the case of limited datasets. In this case the KID, an unbiased measure, is more suitable to account for the quality of the generated images. The KID is calculated with the Maximum Mean Discrepancy (MMD) of the features, generated in the same way as the FID, of the generated and real images. Better quality generated images show lower FID and KID values.

V. RESULTS AND DISCUSSION

In order to validate our hypotheses regarding the advantages of the StyleGAN2 (and its enhancements), we also trained and evaluated a DCGAN model with the same Calanoida dataset. We report the quantitative results of the DCGAN and StyleGAN2 models in the Table I, respectively. DCGAN struggles to generate images realistic enough to be identified as real ones: we only find in the generated images the global shape of the animal but without any details. StyleGAN2, however, reaches better results. Having validated the choice of the StyleGAN2 over the DCGAN, we experiment the ADA and LeCam regularization that both improve StyleGAN2 performances (Table I).

TABLE I: Quantitative results of the different models trained with the Calanoida dataset.

Model	Fid50k ↓
DCGAN [13]	239.240
StyleGAN2 [12]	137.426
StyleGAN2 + ADA [14]	44.774
StyleGAN2 + ADA + R_{LC} [15]	39.341

In Table II, we report the quality metrics (FID and KID) of the three analysed training methods: from scratch, sideways and downward Approaches. Unsurprisingly, the more data we have, the better the quality of the images generated; thus the models trained on the Calanoida dataset show the best results. We observe for each specimen that downward transfer learning from the copepods allows the model to generate improved quality data. Transfer learning significantly enhance the results of orders with fewer samples. This hierarchical transfer learning approach, by first training to the more general taxonomic rank (here copepods) and then fine tuning the model to the more specific taxonomic rank, appears to be the most effective method. It is interesting to note the differences in image quality perception of the two metrics used; we note

for example that when the models trained on Cyclopoida and Harpacticoida have respectively close KIDs, their respective FIDs are far apart. This difference is, according to us, due to the differences in size and diversity of the two datasets. Indeed the Harpacticoida dataset is much smaller (150 images) than the Cyclopoida one (766 images) and collects much less diversified images (posture, size of individuals, type of microscope used). Of course, these performance measures do not necessarily quantify the full spectrum of characteristics of each specimen. Their ability to account for differences between orders is yet to be established, especially when these orders have very similar characteristics requiring the judgment of a taxonomic expert. For instance, we cannot know if the images generated are animals that could be identified to the order level, or chimeras. We already showed our images to taxonomists that recognized copepods in the synthetic images but the assessment of taxonomic experts on the quality of the images, on lower taxonomic level, seems necessary.

Some examples of images generated by our models (trained on the full set of copepods images and then fine tuned with the images at the desired taxonomic order) are shown in Figure 3.



Fig. 3: Copepoda images generated using the downward approach. First, second, third and fourth rows are Calanoida, Cyclopoida, Harpacticoida and Siphonostomatoida, respectively.

In Figure 4, we give other generated examples with more visible details. They show some complex features such as rulers (used as size references by taxonomists), light reflections (Figure 4d) or even eggs (Figure 4a). The diversity of the generated images (posture of the animal, type of background, eggs present in the image, etc), depends of course on the quality of the starting dataset. Orders with fewer samples may be less representative of the range of existing families. Finally, some images present errors like “phantom” legs or two rulers. The numbers on these rulers remain difficult to read, notably because of the definition of the images.

TABLE II: Comparison of the performances of the training methods used (from scratch, sideways and downward). For each order we train with its dataset, a model without transfer learning with the weights initialized randomly, a model pre-trained with the Calanoida data and a model pre-trained with the Copepoda data (aggregated dataset).

Order	From Scratch		Sideways Approach		Downward Approach	
	Fid50k ↓	Kid50k ↓ ($\times 10^2$)	Fid50k ↓	Kid50k ↓ ($\times 10^2$)	Fid50k ↓	Kid50k ↓ ($\times 10^2$)
Calanoida	39.341	1.204	X	X	36.529	0.931
Cyclopoida	60.401	2.327	50.504	1.545	47.017	1.215
Harpacticoida	119.298	2.323	114.288	2.070	108.533	1.503
Siphonostomatoida	111.865	1.611	107.610	1.549	96.995	0.990

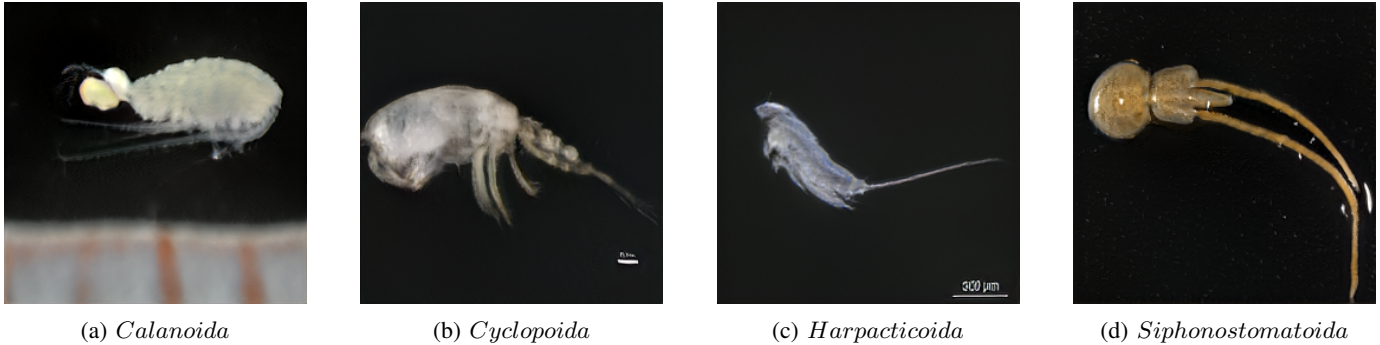


Fig. 4: Examples of synthetic Copepoda images generated using the downward approach.

VI. CONCLUSION AND FUTURE WORK

We propose two hierarchical transfer learning methods towards the generation of synthetic images of Copepods using a StyleGAN2 network. This approach can be used on other specimens of the meiofauna in order to generate synthetic data for specimens where few data are available. We achieve very promising results, generating animal images that were identified as copepods by taxonomists. This synthetic data could be a new tool to train future taxonomists or could be used to train classifier networks. However, it is still difficult to assess the quality of these images in a very precise way with the metrics available in the literature. A proper experiment with taxonomists is ongoing to validate the relevance of our methods for lower taxonomic levels. Further improvements are to be explored, such as adding high-level information at the beginning of the network.

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