CLASSIFICATION OF CRUSTACEAN IMAGES USING MACHINE AND DEEP LEARNING, WITH EMPHASIS ON THE SUPERORDER PERACARIDA (MALACOSTRACA: CRUSTACEA)

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ABSTRACT

This study investigates the use of Artificial Intelligence for classifying specimens of the Superorder Peracarida, evaluating the effectiveness of different models for identifying this group. Given the scarcity of research on crustaceans, a systematic review was conducted on the use of AI in plankton classification. Two experiments were conducted: the first compared Deep Neural Networks (DNN), Convolutional Neural Networks (CNN), and a neural network similar to Support Vector Machines (SVM) for classifying images of nine crustacean orders, with CNN achieving the highest accuracy (82.8%) due to its ability to extract complex visual patterns. In the second experiment, CNN was applied exclusively to the classification of Peracarida images, achieving an accuracy of 63.69%, highlighting the difficulty in distinguishing between orders due to high morphological similarity. The results indicate that while CNN proved to be the most effective model for general crustacean classification, identifying Peracarida remains a challenge. This pioneering study contributes to the advancement of image recognition techniques applied to marine taxonomy.

KEYWORDS: Image recognition, Neural Networks, Computational Biology, Amphipoda, Cumacea.

CLASSIFICAÇÃO DE IMAGENS DE CRUSTÁCEOS USANDO APRENDIZADO DE MÁQUINA E APRENDIZADO PROFUNDO, COM ÊNFASE NA SUPERORDEM PERACARIDA (MALACOSTRACA: CRUSTACEA)

RESUMO

Este estudo investiga o uso de Inteligência Artificial na classificação de espécimes da Superordem Peracarida, avaliando a eficácia de diferentes modelos para a identificação desse grupo. Dada a escassez de pesquisas sobre crustáceos, foi realizada uma revisão sistemática sobre o uso de IA na classificação de plâncton. Dois experimentos foram conduzidos: o primeiro comparou Redes Neurais Profundas (DNN), Redes Neurais Convolucionais (CNN) e uma rede neural similar a Máquinas de Vetores de Suporte (SVM) para a classificação de imagens de nove ordens de crustáceos, com a CNN apresentando a maior acurácia (82,8%) devido à sua capacidade de extrair padrões visuais complexos. No segundo experimento, a CNN foi aplicada exclusivamente à Superordem Peracarida, alcançando uma acurácia de 63,69%, evidenciando a dificuldade de distinção entre as ordens devido à alta similaridade morfológica. Os resultados indicam que, apesar da CNN ser o modelo mais eficaz para classificação geral de crustáceos, a identificação de Peracarida ainda representa um desafio. Este estudo pioneiro contribui para o aprimoramento das técnicas de reconhecimento de imagem aplicadas à taxonomia marinha.

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1 INTRODUCTION

The Subphylum Crustacea is a taxonomically diverse group, both morphologically and ecologically, with marine, estuarine, freshwater, and even terrestrial representatives (Dunn et al., 2014). Crustaceans are characterized by having two pairs of antennae, which are articulated uniramous or biramous appendages, a body with six segments, and nauplius larvae (Martin & Davis, 2001).

The Superorder Peracarida Calman, 1904, within the Class Malacostraca, is known for its representatives with a cephalon fused with one or two thoracic segments, an abdomen with six segments, and a telson (the last segment of the body) (Brusca; Moore; Shuster, 2018). The orders of peracarids include: Amphipoda, Bochusacea, Cumacea, Ingolfiellida, Isopoda, Lophogastrida, Mictacea, Mysida, Stygiomysida, Tanaidacea, and Thermosbaenacea (Arai, 2024). The size of these organisms varies depending on their habitat. For example, cumaceans can measure between 1 and 30 millimeters, requiring specific methods for collection and taxonomic identification, which involves classification into smaller taxa down to the species level, the most specific level in Biological Taxonomy.

The orders Amphipoda, Cumacea, Isopoda, Mysida, and Tanaidacea, shown in Figure 1, were chosen for the second experiment because they are the groups with the largest number of currently described species (WoRMS, 2025).

Scientific studies on Peracarida commonly highlight the difficulty of studying this group, either due to the amount of research available on the subject or the challenging methodology for preserving specimens after collection (Brito & Serejo, 2020).

Figure 1: Main orders of the Superorder Peracarida. Source: WoRMS - World Registry of Marine Species

Caption: A. Order Amphipoda; B. Order Cumacea; C. Order Mysida; D. Order Isopoda; E. Order Tanaidacea.

Artificial Intelligence is already widely used in the field of Marine Biology, both for data analysis and for identifying patterns in images (Song *et. al.*, 2023). However, there is a theoretical gap regarding the use of Artificial Intelligence applied to crustacean taxonomy (see section 2).

Some examples used by large corporations are based on image classification, such as: authorizing employees to access a service or system through facial recognition (Taigman et al., 2014); medical diagnostics for metastatic cancers with the help of image classification (Jiao et al., 2020); security monitoring systems that identify objects in real-time images (Ren et al., 2017); and monitoring environmental damage such as deforestation, pollution, and wildfires (Ronneberger; Fischer; Brox, 2015). All of these applications share a common goal: to perform classification quickly and accurately in order to extract relevant information and make decisions or gain insights.

To classify images, Artificial Intelligence is associated with neural networks in the context of pattern recognition and subsequent image classification. Neural networks aim to replicate the functioning of the human brain to process information and make decisions. They consist of three main types of layers: the input layer, hidden layers, and the output layer (Figure 2). These layers are responsible for processing and transforming input data to achieve the desired results (Nielsen, 2015).

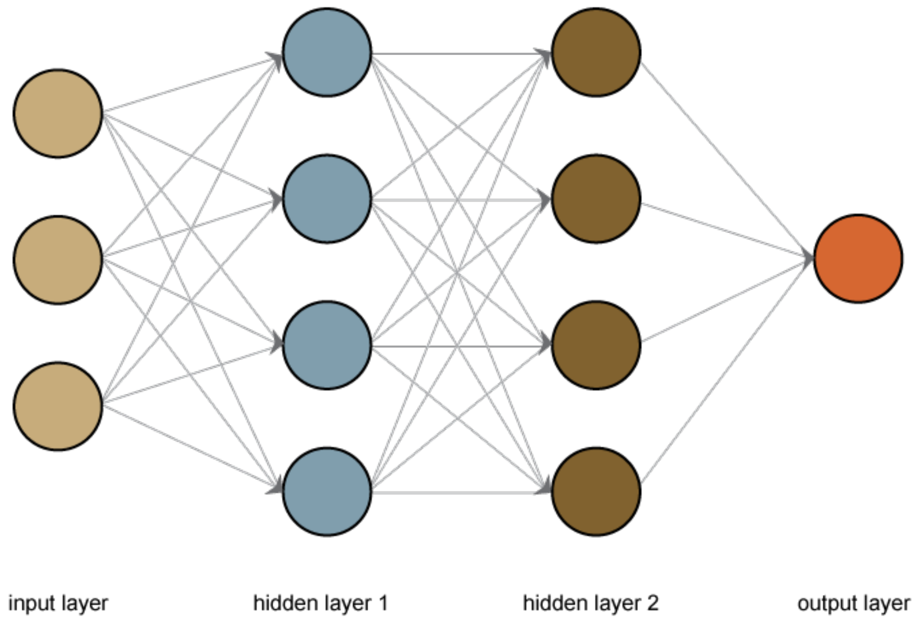

Figure 2. Schematic of neural network layers. Source: (Megaputer, 2019).

The input layer is the first layer of the neural network and receives the input data, which can be image pixels, attributes from a dataset, or any other information being used for classification or prediction. Each node corresponds to a feature of the input data. The hidden layers are so named because the values of their nodes are not directly observable, unlike the input and output values. The hidden layers perform calculations to transform the input data into a form that can be used to make predictions or classifications.

In a convolutional neural network (CNN) computer vision is commonly used, and therefore the hidden layers consist of fully connected pooling layers. In these layers, filters are applied to extract relevant features from the input images, reducing the dimensionality of the extracted features and making processing more efficient. Fully connected layers then combine the features extracted from the previous layers to make the final classification.

The output layer is the last layer of the neural network and provides the network’s final results, usually representing the nodes corresponding to the classes or categories the network is trying to predict or classify. Through the training process, the weights of the connections between units in each layer are adjusted to optimize the network's performance in the specific task, such as image classification of the Peracarida group.

An experiment that enables the classification of Peracarida images could contribute to the increase of openly accessible images on the internet, as many researchers take photos of the organisms they collect. These photos could be used in the training and prediction script developed in the experiments. Making these images available as open data could not only support research on the group but also expand the general community’s knowledge of the Superorder Peracarida.

Given this, the following research question was formulated: **What is the ideal neural network model for classifying images of the Superorder Peracarida?** Thus, the overall objective of this work is to measure the effectiveness of Peracarida image classification.

To deepen knowledge in the field of Artificial Intelligence applied to crustacean image classification, a Systematic Literature Review was conducted. Subsequently, applied research was developed using the experimental method for the procedures. This work is pioneering in the study of image classification for crustaceans of the Superorder Peracarida.

2 LITERATURE REVIEW

Ignacio Heredia (2017) conducted a study aimed at classifying images of marine planktonic organisms, using an image classification algorithm previously developed for plant classification (Heredia, 2017).

The algorithm designed for planktonic organism classification adapted a code originally developed to address large-scale flora monitoring issues for a more specific problem: marine zooplankton. The accuracy results for each class grouping (each group with 5 classes) ranged from 99.77% to 85.79%, with images of fish, mollusks, crustaceans, debris, fibers, and other artifacts collected along with the organisms. The neural network used was ResNet-50, a residual neural network with 50 different layers, a type of architecture found in convolutional neural networks (CNNs). Among the 50 convolutional layers, pooling layers and fully connected layers are included. The architecture features residual blocks that are repeated several times to form the network structure.

The use of Artificial Intelligence had already been advocated by Sadaiappan et al. in a 2021 study on copepods, where operational taxonomic units (OTUs) of bacteria dominant in species of the genera Calanus and Pleuromamma were identified. The Gradient Boosting Classifier (GBC) performed better than the Random Forest Classifier (RFC). The RFC model achieved an overall accuracy of 0.923 with a precision ratio of 1.68, while the GBC model yielded a prediction accuracy of 0.967 with a precision ratio of 1.76. Prediction accuracy of key OTUs in Calanus spp. and Pleuromamma spp. was 1.00 for both models (Sadaiappan et al., 2021). Unlike Céspedes Sisniega's research, this study did not use neural networks but rather machine learning algorithms.

2.1 Systematic Literature Review

The systematic review was conducted between December 2022 and January 2023, with results gathered on January 27, 2023. Following the guidelines of Wohlin et al., (2020) and Nakagawa (2017), the review followed these steps: identifying the need for the review, specifying a research question, developing and evaluating a review protocol, conducting the review based on the protocol, and analyzing the results.

During the planning phase, the research question, source selection, and study selection were considered. During the execution, studies were selected, evaluated, and reviewed, along with the extraction of information. The analysis of results could be qualitative, quantitative, or mixed.

Various techniques, such as bibliometric analysis, were applied at this stage. In this paper, bibliometric analysis was used to quantitatively visualize the information extracted from the systematic literature review, with the goal of informing future research projects.

To develop the research question, the following parameters were set for planning the systematic review: Population, deep learning image analysis algorithms; Intervention, neural network models used to train and analyze images; Comparison, comparing the accuracy levels of the models used in the articles; Outcome, identifying neural network models with the highest accuracy levels in image analysis. The research question formulated was: **Which neural network model is most effective in training and analyzing images of planktonic organisms?**

2.1.1 Source Selection Criteria

Two bibliographic databases were selected to initiate the systematic review. The IEEE database is widely recognized in the technology field and includes over 300 journals. Scopus is a database frequently used to search for articles in natural sciences, chosen for this systematic review due to its considerable data volume.

2.1.2 Language of the Studies

The search terms were defined in English to expand the results, as it is the predominant language in most scientific publications.

2.1.3 Source Identification, Methods, and Search Strings

To obtain the necessary results, a search string was developed for use in the IEEE and Scopus databases via manual web searches. Since the primary focus of the research is "Artificial Intelligence" and specifically "Image Recognition," these were the first two terms chosen for the search string. However, the combination of these two words resulted in overly broad results, requiring a focus on the biological study subject, crustaceans from the order Cumacea.

Table 1. Comparative analysis of results obtained from IEEE and Scopus databases.

Search String	Databases	Total Results	Contextual Results
("Full Text & Metadata":cumacea) AND ("Full Text Only":artificial intelligence) AND ("Full Text Only":image recognition)	*IEEE*	1	1
ALL (cumacea) AND TITLE-ABS-KEY (artificial AND intelligence) AND TITLE-ABS-KEY (image AND recognition)	*Scopus*	0	0
("Full Text & Metadata":crustacea) AND ("Full Text Only":artificial intelligence) AND ("Full Text Only": image recognition)	*IEEE*	1	0

ALL (crustacea) AND TITLE-ABS-KEY (artificial AND intelligence) AND TITLE-ABS-KEY (image AND recognition)	*Scopus*	2	1
("Full Text & Metadata":plankton) AND ("Full Text Only":artificial intelligence) AND ("Full Text Only": image recognition)	*IEEE*	72	10
ALL (plankton) AND TITLE-ABS-KEY (artificial AND intelligence) AND TITLE-ABS-KEY (image AND recognition)	*Scopus*	24	10

Source: Compiled by the Author (2023)

The choice of the “AND” operator to be used between the three search terms and the spelling of the words in English were factors selected to obtain a broader range of results. The first word related to the biological group was searched with the most comprehensive index to ensure that more results could be found. The other two words related to the topic of Artificial Intelligence were searched with a filter restricted to the title, abstract, and/or keywords of the article to ensure that the results obtained were closer to the expected population of articles.

Initially, the first keyword in the search sequence contained the word “Cumacea” in an attempt to obtain more specific articles about a particular taxonomic order of crustaceans, in order to direct the systematic literature review toward the image analysis of a specific group. However, few results were obtained, so the second test was conducted with the word “Crustacea” in an attempt to obtain broader results on the group of interest.

Finally, the last test was conducted with the word “Plankton”, which resulted in more articles, as it encompasses several groups, including the order Cumacea, the group of interest that justifies the development of this systematic literature review. Using this keyword, it was possible to obtain results from articles on phytoplankton (microscopic algae) image recognition, which may also be relevant since the neural networks used in some studies are the same for both types of organisms, whether algae or animals (Céspedes Sisniega, 2018). Using the keyword "Plankton," 72 results were obtained from the IEEE database and 24 from the Scopus database, with 8 and 10 results within the research context, respectively. For the systematic review, articles from both the IEEE and Scopus databases were considered to ensure a comprehensive analysis of the results.

2.1.4 Selection Criteria for Retrieved Articles

To ensure the relevance and quality of the studies included in the systematic review, the following selection criteria were adopted: (i) only peer-reviewed articles published in scientific journals or conference proceedings; (ii) studies available in open access to ensure research reproducibility; (iii) publications written exclusively in English, due to the predominance of this language in scientific literature; (iv) articles whose title, abstract, and/or keywords were directly related to the research context; and (v) experimental or empirical studies, excluding systematic literature reviews. These criteria ensured the inclusion of studies aligned with the objective of this work, which is the deep learning approach applied to plankton or small crustaceans.

The articles that did not meet these criteria and were therefore not included in the analysis are listed in the appendix of this paper.

2.1.5 Qualitative Results of the Systematic Literature Review

The chosen search sequence used the following keywords: "Plankton," "Artificial Intelligence," and "Image Recognition." A comparative analysis of the usability of the platforms and the availability of articles was conducted, as shown in Table 2.

Table 2. Comparative analysis of results obtained from IEEE and Scopus databases

Bibliographic Database	Contextual Results	Open Access	Usability of Search Platform	Other Languages Besides English
IEEE	8	7	User-friendly interface, simplified search, automated export to .csv and in .zip format.	1
Scopus	10	6	User-friendly interface, simplified search, automated export to .csv, BibTex, RIS, HTML, RefWorks and in .zip.	1

Source: Compiled by the Author (2023)

For the primary selection of the studies obtained from the IEEE and Scopus databases, a qualitative selection approach was adopted, where the criteria in Table 3 were used for the evaluation.

Criterias	Weight
Is there a clear statement of the research objectives?	1
Does the research analyze images of planktonic organisms?	2
Is the documentation of research methods adequate?	1
Is the most suitable neural network model for the research documented?	2
Are the results clearly reported?	1
Does the article cite references with similar objectives?	1
Do the results add value to the field of research?	1
Does the research specifically address the identification of cumaceans through image recognition?	1

Table 3. Criteria for qualitative evaluation of retrieved articles

Source: Compiled by the Author (2023)

To determine which articles would be discussed, the title, abstract, and obtained results were analyzed, following this order to exclude articles that are not aligned with the research theme (Dybå; Dingsøyr; Hanssen, 2007). The number of articles within the research context is reflected in the second column of Table 2, i.e., studies on the identification of planktonic organisms through training and image recognition were considered.

Based on the evaluation criteria and the assigned weights, the selected articles received the scores according to Table 4.

Tabela 4. Pontuação dos artigos analisados

Autores	Pontuação	Breve descrição

Source: Compiled by the Author (2023)

Sixteen papers obtained through a review of the Scopus and IEEE databases were analyzed. All are being discussed in this section. Among the 16 articles, three did not analyze images of planktonic organisms, and two others were not published in English and were therefore excluded from the review.

These scores reflect the overall quality and suitability of each article to the research objectives. Luo et al. (2004), Bi et al. (2015), Leow et al. (2015), Bergum et al. (2020), Apostol et al. (2016), Li et al. (2022), and Yang et al. (2021) received the highest scores of 9 points, indicating that they comprehensively addressed the research objectives, analyzed planktonic organisms, adequately documented research methods, clearly reported results, cited relevant references, added value to the research field, and specifically addressed the identification of planktonic organisms through image recognition.

On the other hand, Lai et al. (2016), Li et al. (2020), Sun et al. (2022), and Setiawan et al. (2021) received scores of 7 points. Although these articles met several evaluation criteria, they may have presented limitations in certain aspects, such as not analyzing planktonic organisms (Sun et al., 2022) or not having an appropriate neural network model (Lai et al., 2016) (Li et al., 2020). Setiawan et al. (2021) presented an innovative method, but its accuracy of 73.33% may indicate limitations in its use for large-scale automated monitoring.

It is important to note that these scores are relative and based on the specified evaluation criteria and the weights assigned to each question. They serve as a quantitative measure to compare the selected papers and identify their strengths and weaknesses concerning the research objectives.

The article published by Luo et al. in 2004 aimed to develop a new strategy for image selection using Support Vector Machine (SVM) for training and data reduction. In addition to SVM being effective for smaller datasets, a comparison was made with the Cascade Correlation neural network, which is more efficient for both large and small datasets (Luo, 2004). Ten years later, the article published by Bi et al. in 2015 also used SVM for planktonic organism analysis, contributing to a better understanding of this type of neural network in plankton identification (BI et al., 2015).

The publication by Leow et al. in 2015 focused on a specific group of organisms, copepods, which have a wide distribution (Leow et al, 2015). In this work, only one artificial neural network, which the authors called DNN (Deep Neural Network), however, analyzing the information contained in the article, such as the network architecture (“feed-forward”) with two layers (input and dense) with sigmoid activation function (ten nodes in each) and one output layer (eight nodes) with softmax activation function, the network was trained with scaled conjugate gradient backpropagation using 143 epochs, that is, in reality a multi layer neural network (MLP) or dense neural network (DNN) was used.

Following this line of automated identification, Apostol et al. (2016) presented the RaDSS system, an SVM-based system for classifying radiolarian species in microphotographs. It details the extraction of image features and the model training for automated identification, speeding up the classification of these organisms. Meanwhile, Bergum; Saad; Stahl (2020) focused on in situ plankton segmentation using Mask R-CNN, improving ecological analysis accuracy by outperforming traditional segmentation methods.

In the field of automated identification of harmful organisms, Setiawan et al. (2021) proposed an expert system assisted by ontology for identifying harmful algal blooms. The system used certainty factors and a knowledge base based on morphological characteristics, achieving an accuracy of 73.33%. This method proved to be a useful alternative for rapid identification and early monitoring of these organisms.

The development of systems for capturing and monitoring in situ plankton was addressed in different studies. Li et al. (2022) described the creation of an underwater imaging system attached to a buoy, combining optimized lighting, onboard image processing, and deep learning for automated analysis. Tests showed that the system improves the accuracy and efficiency of long-term plankton monitoring.

The quality of images obtained for identification was also a research topic. Yang et al. (2021) presented methods for focus evaluation in in situ plankton images obtained with dark field illumination. Two algorithms were proposed: one based on edge gradient statistics and another on CNNs, balancing computational efficiency and accuracy. Lai et al. (2016), in turn, explored the chemistry of lenses used to capture plankton images, contributing to improving image quality. Sun et al. (2022) proposed a new image processing method aimed at improving the visual quality of environments where planktonic organisms are found, which can help obtain more precise images for analysis.

Among the analyzed articles, the main objectives observed were: the identification of planktonic organisms through image analysis, the automation of the image training process, and the improvement of the quality of the images analyzed. The number of referenced papers that share the same research focus suggests that this field is undergoing an increasing number of studies, presenting an excellent opportunity to study the methodologies already employed and develop new methods for training and image processing, including collaboration with researchers who are already studying the topic. None of the articles analyzed images of cumaceans, which presents an opportunity to develop the first study focused exclusively on this order in the literature, integrating Taxonomy and Artificial Intelligence applied to this group. Therefore, the theoretical gap was identified, which confers the pioneering nature of this research.

3 METHODOLOGY

Applied research emphasizes the development of practical solutions. In this sense, it aligns with the objective of measuring the effectiveness of Peracarida image classification, as it involves evaluating the accuracy and performance of machine learning models. The chosen procedural method was experimental, which is widely used in science to investigate phenomena, test hypotheses, and obtain reliable and replicable results. In the specific case of Peracarida crustacean classification, the experimental method was chosen due to its ability to provide precise and systematic data, allowing for objective analysis.

Based on the applications of Artificial Intelligence in Biological Sciences, two experiments were proposed: one to train and validate images from the "Crustacea, ZooScan Image Database" and another to train and validate images from a specific database for the superorder Peracarida. The goal of the first experiment is to compare the DNN models and SVM algorithms obtained from the Systematic Literature Review, as well as the CNN models, which is efficient for image classification (KRIZHEVSKY, SUTSKEVER, and HINTON, 2012). The objective of the second experiment, based on the first, is to use the CNN model to train a new image database of Peracarida crustaceans with images collected from the internet using a web crawler, as well as original images and those provided by expert researchers on the orders Amphipoda, Cumacea, Isopoda, Mysida, and Tanaidacea. Since two experiments were conducted, the first will be referred to as Microcrustacean Classification, and the second as Peracarida Classification.

3.1 Materials

Below is a list of the tools used to develop the image training scripts.

3.1.1 Programming language, frameworks, and libraries for machine learning and image processing:

- Python: A language with clean syntax, accompanied by various native and third-party libraries.
- TensorFlow: An open-source framework used to develop and train neural network models.
- Keras: A high-level library for building and training neural networks, which uses TensorFlow as the backend.
- OpenCV: A library used for image preprocessing, adjusting properties such as height, width, and channels.
- Scikit-learn: A machine learning library in Python that provides tools for model training and evaluation, including accuracy metrics.

3.1.2 Definitions, Components and Techniques:

- Adam: Optimizer used to compile neural network models.
- Categorical Cross Entropy: Loss function used to measure the difference between predicted probabilities and the actual classes of images.
- Flatten Layer: Flattening layer that transforms the image into a one-dimensional vector.
- Dense Layer: Dense layer that maps the image features to classification.
- Convolutional Neural Network (CNN): A neural network model specialized in image processing.
- Deep Neural Network (DNN): An artificial neural network model with multiple layers of interconnected neurons.
- Support Vector Machine (SVM): A supervised learning algorithm used for classification and regression.
- Train Test Split: A function from scikit-learn used to split images into training and validation sets.
- Dropout: A layer that randomly deactivates some neurons during training to prevent overfitting and improve model regularization.
- MaxPooling2D: A pooling layer used to reduce the dimensionality of feature maps.

3.1.3 Evaluation Metrics and Visual Representation:

- **Accuracy**: A metric used to evaluate the performance of the models.
- **Precision**: A metric that measures the proportion of correctly classified positive examples relative to the total number of examples classified as positive.

- **Recall**: A metric that measures the proportion of correctly classified positive examples relative to the total number of examples that should have been classified as positive.
- **F1-score**: A metric that provides a combined measure of precision and recall, taking into account both false positives and false negatives.
- **Confusion Matrix**: A visual representation of the model's performance in terms of correctly and incorrectly classified images for each class.

3.2 Methods

3.2.1 Crustacean Classification

3.2.1.1 Dataset

The dataset originally extracted from Kaggle[1] included 24 classes, representing genera, families, and orders of crustaceans. To meet the objective of this study, which was to train images of crustaceans, including the order Cumacea, all genera and families present in the dataset were grouped into their respective orders, resulting in nine classes: Calanoida, Calyptopsis, Cladocera, Cumacea, Cyclopoida, Decapoda, Harpacticoida, Mysida, and Ostracoda. The images were obtained from a ZooScan, which is a device used to scan biological samples that utilizes a camera to capture high-resolution images and subsequently produce three-dimensional images of these samples.

For the order Cumacea, original photos taken by the author of the article using a stereomicroscope were used, as well as images obtained from various databases, such as Wikispecies[2], BioDiversity4All[3], Smithsonian Museum[4], Aphotomarine[5], Alchetron[6] e Pinterest[7]. However, only 87 images of Cumacea were found, highlighting the difficulty of finding image databases for the order Cumacea, as well as for crustaceans in general. On the other hand, the other orders have considerable numbers of images for training, such as Calanoida with 10,352 images, Calyptopsis with 1,505 images, Cladocera with 162 images, Cyclopoida with 493 images, Decapoda with 51 images, Harpacticoida with 917 images, Mysida with 179 images, and Ostracoda with 6,241 images.

In this study, the classes in the training and validation directories are also categorized by taxonomic order, reflecting their biological naming hierarchy.

[1] https://www.kaggle.com/datasets/iandutoit/crustacea-zooscan-image-database
[2] https://species.wikimedia.org/wiki/Cumacea
[3] https://www.biodiversity4all.org/observations?place_id=any&subview=map&taxon_id=144115
[4] https://collections.nmnh.si.edu/search/iz/
[5] https://www.aphotomarine.com/cumacea.html
[6] https://alchetron.com/Cumacea
[7] https://br.pinterest.com/

3.2.1.2 Image Training Script

The crustacean image classification experiment used three distinct techniques: DNN (Deep Neural Network), CNN (Convolutional Neural Network), and a Neural Network with an architecture inspired by SVM (Support Vector Machine). The choice of these models was based on their demonstrated effectiveness in related works, where they showed promising results in similar tasks. DNNs are effective at learning complex representations, CNNs excel in computer vision tasks, and SVMs are robust in scenarios with smaller datasets. The training was conducted using TensorFlow and Keras, widely used tools for neural networks.

The SVM model is a supervised learning algorithm used for classification and regression. For this experiment, the algorithm inspired the development of a neural network with a flatten layer, which transforms the image into a one-dimensional vector, and a dense layer, responsible for mapping the image features to the classification (Demir and Erturk, 2009). The SVM is compiled using the categorical cross-entropy loss function, which measures the difference between predicted probabilities and the true classes of the images, along with accuracy metrics from scikit-learn to evaluate the model's performance.

The DNN model is an artificial neural network that consists of several interconnected layers of neurons (Ahmed, Dey and Sarma, 2011). In this experiment, the DNN model has three dense layers. Additionally, two dropout layers are incorporated, which randomly deactivate some neurons during training to prevent overfitting and improve model regularization. Like the SVM, the DNN model is compiled with the categorical cross-entropy loss function and precision metrics.

The CNN model is a type of neural network specialized in image processing and is therefore more complex, featuring two convolutional layers to extract image features, two pooling layers to reduce data dimensionality, two dense layers for final classification, and a dropout layer for regularization (Nielsen, 2015) (Nunes & Dantas, 2021) (Silva, Peixoto & Santos, 2023). As with the previous models, the CNN is compiled with the categorical cross-entropy loss function and precision metrics.

3.2.2 Classification of the Superorder Peracarida

3.2.2.1 Dataset

To develop an experiment that specifically classifies images of peracarids, a second experiment was conducted to create a new dataset. The images were obtained by implementing a web crawler to capture images from the site images.google.com, as well as images provided by researchers specializing in Peracarida, with a maximum size of 250 x 250 pixels. The references for the images include the following sources in alphabetical order:

Alchetron, Aphotomarine, BioDiversity4All, Canadian Museum of Nature[8], Flickr[9], iNaturalist[10], iStock[11], Idtools[12], International Barcode of Life[13], Magnolia Press[14], Monterey Bay Aquarium, Pinterest, World Register of Marine Species[15], Smithsonian Museum, WikiSpecies, Wikipedia, Wikitionary, and other free image databases. After this procedure, we obtained 5 classes and a total of 895 images distributed as follows: Amphipoda with 187 images; Cumacea with 308 images; Isopoda with 217 images; Mysida with 86 images; Tanaidacea with 98 images.

3.2.2.2 Image Training Script

Based on the results obtained from the first experiment, the most efficient neural network model was chosen for the training and validation of the Peracarida dataset, using the to_categorical function provided by TensorFlow.Keras.utils. The model configuration was performed using manually selected hyperparameters: batch size = 16, input shape = (150, 150, 3), random state = 42, alpha = 1e-5, epoch = 10. The optimizer chosen was Adam, with a learning rate of 0.0001. For compilation, sparse categorical cross entropy was used as the loss function, and accuracy was used to evaluate each training epoch. Validation was performed in a similar procedure to calculate accuracy and loss using the training and validation groups.

The dataset did not have a standard for the images, as they were obtained from various different sources where the only filter and requirement was that there be only one individual with the whole body in the photo. The lack of standardization may have hindered the results of the model used. The image dataset is not provided in this article, as some of the photos represent new species for science that have not yet been published.

3.2.3 Image processing

For both experiments, two image folders were used for model training: one for training and another for validation. The OpenCV library was used to preprocess the images by adjusting properties such as height, width, and channels of each image. The second experiment differed from the first by using the *train_test_split* function from the Python library *scikit-learn*, which separates the images based on a predefined value—in this case, 80% for training and 20% for validation in a random manner. The first experiment had an overall approximate ratio of 90% for training and 10% for validation.

The choice of data proportions for training and validation depends on factors such as the amount of data and the model's objective. In the first experiment (90%/10%), 90% was used for training to maximize the amount of data available for the model, while 10% was sufficient for a

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8 https://nature.ca/en/our-science/collections/online-collection-data/
9 https://www.flickr.com/search/?text=cumacea
10 https://www.inaturalist.org/observations
11 https://www.istockphoto.com/br
12 https://idtools.org/
13 https://ibol.org/
14 https://mapress.com/
15 https://www.marinespecies.org/index.php

reasonable evaluation. In the second experiment (80%/20%), the 80/20 proportion was chosen to ensure a more rigorous validation, providing a more accurate assessment of the model's performance. The difference in proportions reflects the intention to balance training and validation, with the choice being influenced by the context and the amount of available data.

3.2.4 Architecture of Neural Network Models

Below are the architectures of the DNN, CNN, and SVM neural networks used in the first experiment to compare and understand which neural network is best suited for use in the second experiment.

3.2.4.1 DNN, CNN and SVM Architecture for Crustacean Classification

3.2.4.1.1 DNN Architecture

The architecture of the DNN neural network model is as follows:

- **Flatten Layer:** This layer takes the input in tensor format and transforms it into a one-dimensional vector. In this model, the input is an image with the shape (224, 224, 3).
- **Dense Layer with ReLU Activation:** This layer has 128 units and uses the ReLU (Rectified Linear Unit) activation function, which introduces non-linearity into the model. The dense layer is responsible for mapping the features extracted by the flatten layer to more abstract representations.
- **Dense Layer with Softmax Activation:** This layer is the output layer of the model and is responsible for mapping the outputs from the previous layer to the target classes using the softmax activation function. The number of units in this layer is equal to the number of classes in the problem (num_classes).

This architecture follows a common pattern in neural network models for image classification. The flatten layer transforms the image into a feature vector, the dense layers add non-linearity, and perform the final classification. The ReLU activation function is widely used to introduce non-linearity, while the softmax activation function is used to obtain classification probabilities for each class.

The DNN model is compiled with the Adam optimizer, the categorical_crossentropy loss function (for multi-class classification problems), and the accuracy evaluation metric. It is then trained using the training data (train_generator) according to a specific number of epochs.

3.2.4.1.2 CNN Architecture

- **Convolutional Layer (Conv2D) with 32 Filters and Kernel Size 3x3:** This layer receives input with the shape (224, 224, 3), representing a color image of 224x224 pixels with 3 channels (RGB). It applies 32 convolutional filters of size 3x3 to each channel of the image, producing feature maps.

- **Max Pooling Layer (MaxPooling2D) with Pool Size 2x2:** This layer reduces the dimensionality of the feature maps by half, retaining the most relevant features. This helps to decrease the number of parameters and computations required in the model.
- **Another Convolutional Layer (Conv2D) with 64 Filters and Kernel Size 3x3:** This layer applies an additional 64 convolutional filters of size 3x3 to the feature maps obtained from the previous layer, generating more complex feature maps.
- **Another Max Pooling Layer (MaxPooling2D) with Pool Size 2x2:** This layer performs dimensionality reduction again, maintaining the most important features.
- **Flatten Layer:** This layer transforms the outputs from the previous layer into a one-dimensional vector, preparing the data for input into a dense neural network.
- **Dense Layer (Dense) with 128 Units and ReLU Activation:** This densely connected layer maps the features extracted from the previous layer to more abstract representations. It uses the ReLU activation function to introduce non-linearity into the model.
- **Dense Layer (Dense) with a Number of Units Equal to the Number of Classes (num_classes) and Softmax Activation:** This is the output layer of the model, producing classification probabilities for each class. The softmax activation function is used to ensure that the probabilities sum to 1 and can be interpreted as a probability distribution.

The architecture of the CNN model follows the common pattern of convolutional layers followed by max pooling layers to extract relevant features from the image. Next, dense layers are used for the final classification. The ReLU activation function is applied in both the convolutional and dense layers to introduce non-linearity. The softmax activation function is used in the output layer to obtain the classification probabilities.

The model is compiled with the Adam optimizer, the categorical_crossentropy loss function (for multi-class classification problems), and the accuracy metric for evaluation. Then, the model is trained using the training data for a specified number of epochs.

3.2.4.1.3 SVM based Architecture

The described architecture, consisting of a flattening layer (Flatten) followed by a dense layer (Dense) with softmax activation, was based on the **SVM (Support Vector Machine)** machine learning model, which is a linear classifier. The SVM model aims to find a hyperplane that best separates the different classes in a feature space, and similarly, the flattening layer transforms the input (image) into a one-dimensional vector, representing a set of features extracted from the image. The dense layer then performs the final classification based on these features, much like the SVM would classify by separating the classes in the feature space.

The choice of a flattening layer followed by a dense layer reflects the idea of mapping the extracted features from the input to a final decision, similar to the SVM model that performs classification based on a linear feature space. The softmax activation in the dense layer is used to provide a probability for each class, similar to how the SVM generates a prediction for the class closest to the hyperplane. Although this architecture does not include convolutional layers, the principle of mapping features for classification is similar to the SVM's linear separation process, making this architecture a simplified yet effective adaptation of the SVM's concept of linear separation. The use of the Adam optimizer, the **categorical_crossentropy** loss function, and the **accuracy** metric are common choices in neural networks for multi-class classification tasks, complementing the model's training and evaluation process.

3.2.4.2 Neural Network Architecture for Peracarida Classification

For the second experiment, focused on peracarida, the neural network with the best performance was chosen, that is, the one that achieved the highest accuracy during the first experiment. The architecture used was also the same; however, an evaluation of the layers was necessary, as the objective of the second experiment is more specific and will receive images from various sources, unlike the first scenario, which only worked with photographs taken by a Zooscan.

4 EXPERIMENTS, RESULTS AND DISCUSSION

To evaluate the performance of the models, confusion matrices were generated using the Scikit-learn[16] library. The confusion matrices provided a visual representation of the model's performance in terms of correctly and incorrectly classified images for each class. This analysis helped identify which classes were more challenging for the models to distinguish and determine areas for improvement in the training process. To further assess the models' performance, various metrics were calculated, including precision, recall, and F1 score. The precision metric measures the overall performance of the model in terms of correctly classified images, while the recall metric measures the proportion of true positive classifications among all positive classifications.

The recall metric, also known as sensitivity or true positive rate, measures the proportion of true positive classifications among all actual positive instances. Finally, the F1 score is the harmonic mean of precision and recall and provides a measure of the model's overall accuracy, taking both false positives and false negatives into account. These metrics were calculated for each model and each class to provide a comprehensive evaluation of the model's performance.

4.1 Evaluation of Results and Comparison Between Neural Networks on Crustacean Image Classification

The main differences between the DNN, CNN, and SVM architectures are:

- **DNN Architecture:** Does not use convolutional layers, only dense layers for feature extraction and classification. The ReLU activation function is used in the dense layers.
- **CNN Architecture:** Utilizes convolutional layers to extract relevant features from the image. Additionally, it has max pooling layers to reduce the dimensionality of the feature maps. The ReLU activation function is applied in both convolutional and dense layers.
- **SVM based Architecture:** Does not use convolutional layers, only dense layers for feature extraction and classification. It uses the softmax activation function in the output layer to

[16] https://scikit-learn.org/stable/index.html

obtain classification probabilities. It is a linear classifier that seeks to find a hyperplane that best separates the classes.

These architectural differences influence the performance and generalization capability of each model. The convolutional layers in the CNN architecture allow for the automatic extraction of relevant features from images, while the dense layers perform the final classification based on these features. Therefore, the CNN architecture is more suitable for computer vision tasks where the spatial features of images are important.

Table 3. Comparison of the Three Neural Networks: DNN, CNN, and SVM based Architecture

Neural Network Features	DNN Architecture	CNN Architecture	SVM based Architecture
Flatten Layer	Transforms the input into a 1D vector	Transforms the 2D vector from the previous layer into a 1D vector	Transforms the input into a 1D vector
Dense Layer	128 units, ReLU activation	128 units, ReLU activation	Softmax activation, number of units = num_classes
Output Layer	Softmax activation, num_classes units	Softmax activation, num_classes units	Softmax activation, num_classes units
Activation Function	ReLU, Softmax	ReLU, Softwax	Softmax
Use of Convolutional Layers	No	Yes	No

Source: Author (2023)

The results obtained from the developed script show that the CNN neural network model had the best overall accuracy in the training procedure, with 82.8%, followed by SVM inspired with 72.8%, and DNN with 71.7% (Figure 3).

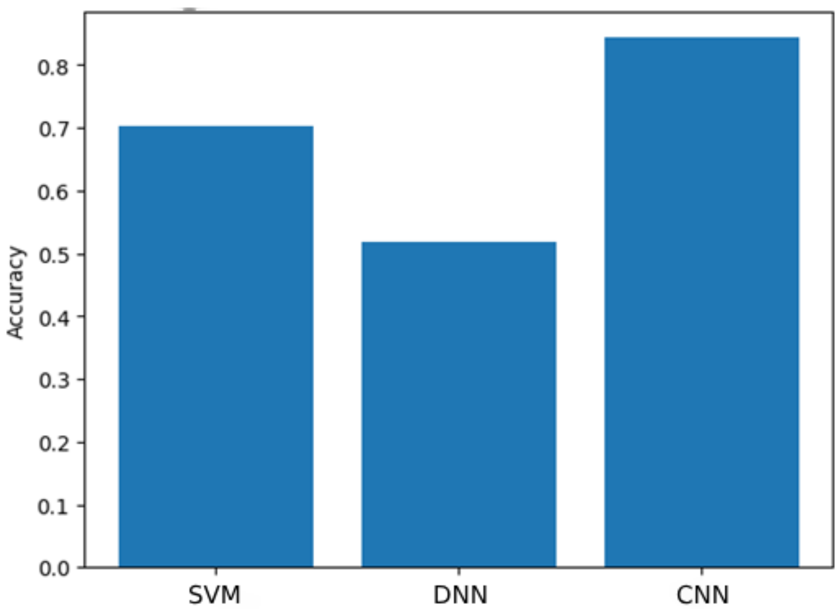

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Figure 3. Comparison of accuracy values by neural network. Source: Author (2023)

The CNN also had the highest accuracy for the orders Calyptopsis, Cyclopoida, Harpacticoida, and Mysida, while SVM had the highest accuracy for the order Ostracoda. DNN had the highest accuracy for the order Calanoida. The Cumacea order had the same accuracy rate for the SVM and CNN models (Figure 4). The Cladocera and Decapoda orders did not achieve a significant accuracy rate in any of the neural network models and were omitted from Figure 4.

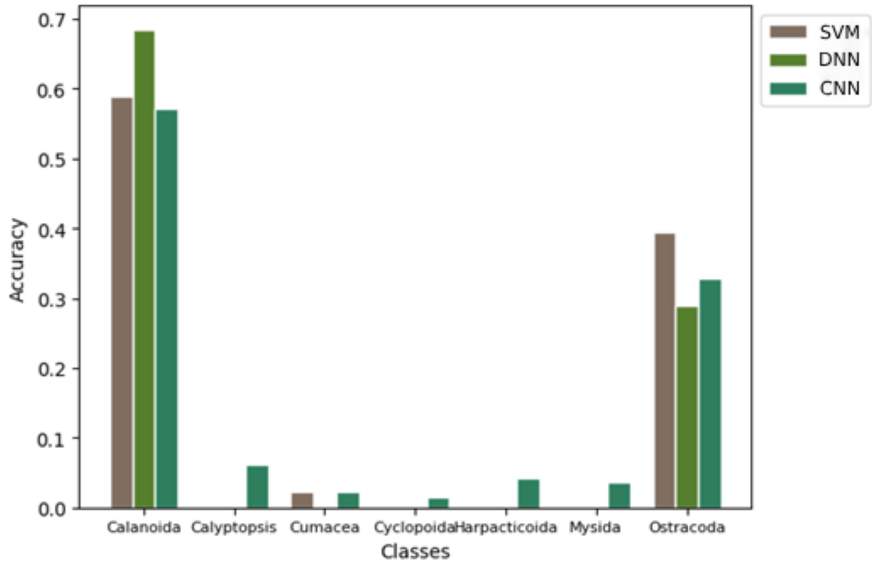

Figure 4. Comparison of accuracy values by classes and neural networks. Source: Author (2023)

The imbalance in the number of images per class can significantly impact the model's results, as the more images a class contains, the more examples the model will have to learn the specific characteristics of that class. This may lead to superior performance for classes with more images, as observed by Deng (2009). Furthermore, it is important to highlight that class imbalance can also affect the model's performance, with classes containing fewer data yielding less accurate results. To mitigate these effects, strategies such as manual oversampling in the minority classes were adopted; however, due to the images being collected with a specific microscope, a significant number of additional samples could not be obtained. Nonetheless, other factors also influence the model's performance, such as the quality and diversity of the images in each class, the complexity of the classification task, and the choice of model and hyperparameters. The discussion about the imbalance and its implications was included in the work to contextualize the results and justify the potential limitations.

These results suggest that the CNN algorithm is the most suitable for the classification task used in this study. However, it is important to note that other evaluation metrics, in addition to accuracy, can be used to compare algorithm performance, such as precision, recall, and F1-score. Precision is the proportion of examples correctly classified as positive relative to the total number of examples classified as positive. Recall is the proportion of examples correctly classified as positive relative to the total number of examples that should have been classified as positive. The F1-score is a harmonic mean of precision and recall and is used to evaluate the overall accuracy of the model.

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Table 4 shows that some classes (such as Calanoida and Ostracoda) perform reasonably well, with Precision, Recall, and F1-score values above 0.3, while other classes (such as Calyptopsis, Cladocera, and Cyclopoida) perform very poorly, with Precision, Recall, and F1-score values close to zero.

Table 4. Confusion Matrix Results

Class	Precision	Recall	F1
Calanoida	0.590	0.572	0.580
Calyptopsis	0.000	0.062	0.010
Cladocera	0.000	0.000	0.000
Cumacea	0.022	0.022	0.012
Cyclopoida	0.000	0.016	0.000
Decapoda	0.000	0.000	0.000
Harpacticoida	0.000	0.042	0.000
Mysida	0.000	0.037	0.000
Ostracoda	0.395	0.329	0.362

Source: Author (2023)

In Table 4, we can observe that the Calanoida order has a precision of 0.590, indicating that 59% of the examples classified as Calanoida were correct. The recall for this class is 0.572, meaning that 57.2% of the examples were correctly identified. The F1-score is 0.580, providing a combined measure of class performance. However, other classes such as Calyptopsis, Cladocera, Cyclopoida, Decapoda, Harpacticoida, and Mysida have very low or zero precision, recall, and F1-score values, indicating poor model performance for these classes. On the other hand, the Ostracoda class has a precision of 0.395, recall of 0.329, and F1-score of 0.362, indicating moderate performance for this class.

These results are important for evaluating the model's ability to correctly classify the different classes and identifying classes with better and worse performance.

4.2 Evaluation of Peracarida Image Classification Results

4.3 *4.2.1 Adaptations in the CNN Neural Network Architecture from the First Experiment*

For the second experiment, the same CNN architecture was used with the addition of a layer. The main difference between the two CNN architectures is the presence of a dropout layer in the second architecture (architecture 2). This dropout layer randomly discards 50% of the activations from the previous layer during training, which helps prevent overfitting by reducing the reliance on specific neurons.

This difference can influence the results of each architecture. In the first experiment, which dealt with crustaceans in general, there is no dropout layer, which could make the model more susceptible to overfitting. Overfitting occurs when the model fits the training data too well but fails to generalize to new data. Therefore, this architecture may have a higher tendency to overfit the training data.

In contrast, the architecture used for the experiment with the superorder Peracarida includes the dropout layer, which helps combat overfitting. The randomness in discarding activations during training makes the model more robust and less dependent on specific neurons. This can result in a model that generalizes better to unseen data, reducing the likelihood of overfitting and improving the model's generalization ability.

Thus, the inclusion of the dropout layer in the second architecture can provide additional regularization to the model, making it more robust and improving its generalization capacity compared to the first architecture.

4.4 4.2.2 Results After CNN Architecture Adaptations for Peracarida

According to Figures 5 and 6, the model's behavior is similar to overfitting, where good performance is achieved with the training data, but the results with the validation data are not as strong. Specifically, up until epoch 5, these characteristics were not observed, but after that, the difference between the training and testing lines in both graphs increased.

Below are the generated graphs, as well as the confusion matrix in Figure 7.

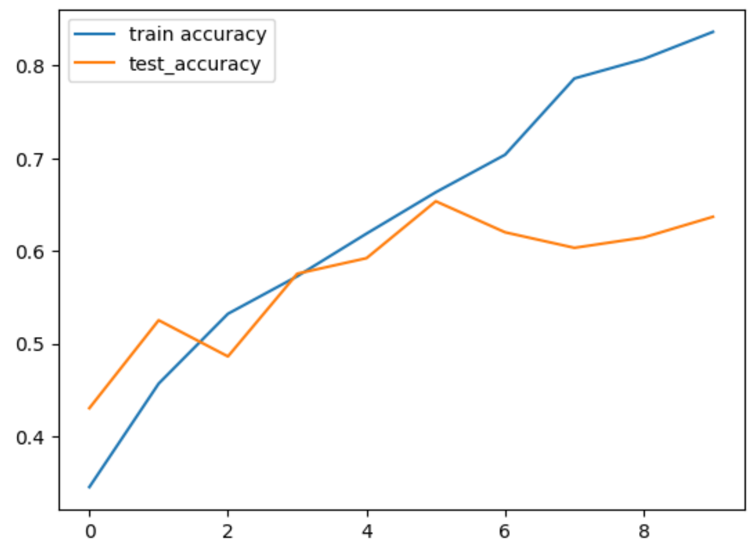


Figure 5. Training and validation accuracy. Source: Prepared by the author (2023)

The model behaves appropriately with a monotonically increasing evolution until epoch 5-6. Using a higher number of epochs, due to the size of the image dataset, may cause overfitting, which can be addressed by adding more instances to the dataset, thus increasing its complexity and preventing overfitting. The use of dropout can also prevent overfitting, as it discards some neural network pathways that may contribute to over-specialization in training rather than generalization. Another strategy is early stopping, which involves preferring to achieve lower accuracy for training and testing, rather than allowing the model to continue and excessively specialize in the training data, which would lead to overfitting.

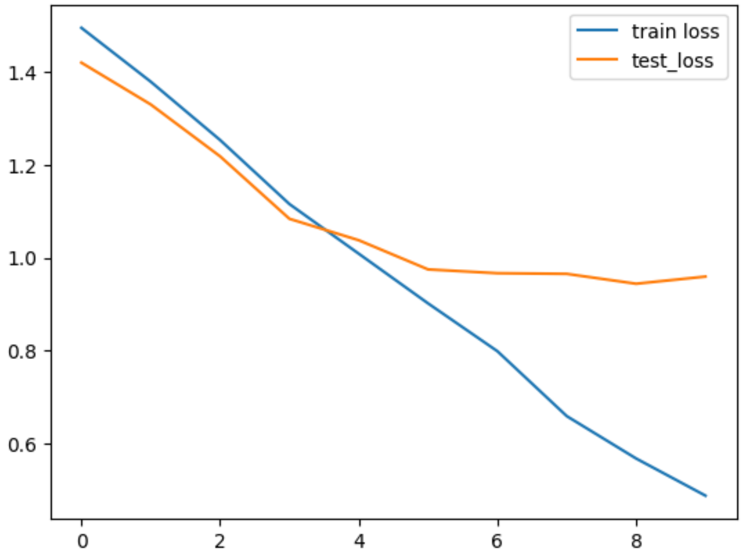
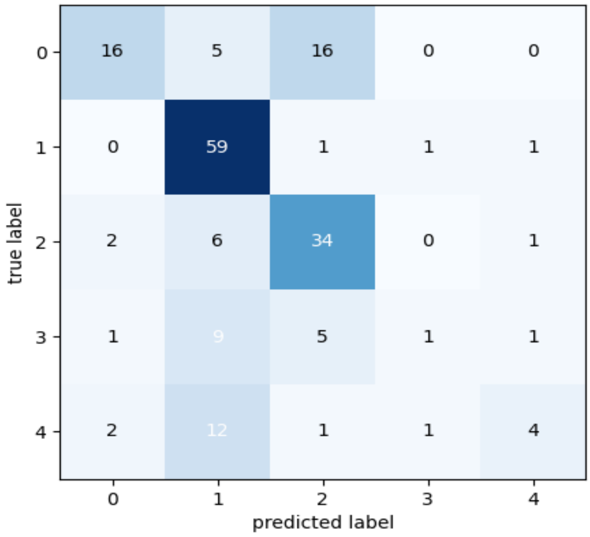


Figure 6. Loss function for training and validation. Source: Compiled by the author (2023)

The model behaves similarly to the accuracy in the error analysis through the loss function, as it shows a decreasing trend until epoch 4-5. In this case, using a higher number of epochs, due to the size of the image dataset, could lead to overfitting. This behavior can be seen in the graph in Figure 6 through the difference between the training and testing curves. A lower error is observed in the training curve with each epoch, potentially reaching zero if an additional 4 epochs were added. Meanwhile, the error curve for the test data stabilizes at epoch 5. Minimization factors for this issue have already been explained in the previous paragraph.



4.5 **Figure 7. Confusion matrix. Source: Prepared by the author (2023)**

Classes 0, 1, and 2, that is, Amphipoda, Cumacea, and Isopoda, respectively, were considered adequate, with a note for the Amphipoda class, which had a high number of predictions as class 2, representing almost 50% false positives. The high number of false positives for the order Amphipoda may be associated with the great similarity in the proportional size of the segments in relation to the body. On the other hand, classes 3 and 4, Mysida and Tanaidacea, respectively, did not have a sufficient number of samples.

Other metrics were calculated in this experiment, using only the test data. Precision, Recall, F1, and support values were calculated for each class, as well as the macro and weighted averages for all classes.

Table 5. Metrics by class.

Label	Precision	Recall	F1	Support
Amphipoda	0.76	0.43	0.55	37
Cumacea	0.65	0.95	0.77	62
Isopoda	0.60	0.79	0.68	43
Mysida	0.33	0.06	0.10	17
Tanaidacea	0.57	0.20	0.30	20
accuracy			0.64	179
macro average	0.58	0.49	0.48	179
weighted average	0.62	0.64	0.59	179

Source: The author (2023)

Table 5 shows that some classes achieved better results than others. For example, the order **Amphipoda** had high precision (0.65) and recall (0.95), indicating good performance in correctly classifying positive examples. On the other hand, the order **Mysida** had low precision (0.33) and recall (0.06), indicating poor performance in identifying positive examples. This is due to the number of images in the dataset, as amphipods had 187 images, while mysids had only 86, making it the order with the fewest available images for training and validation.

The table also presents the macro average precision and the weighted average precision for all classes, which were 0.58 and 0.62, respectively.

Table 6 provides the overall metrics of the experiment, where the model's overall accuracy was 0.6369, indicating that it correctly classified approximately 63.69% of the examples. The weighted average precision was 0.6209, showing the weighted average of the precisions for all classes. The weighted average recall was 0.6369, reflecting the weighted average recall for all classes. The weighted average F1-score was 0.5871, representing the weighted average F1-score for all classes. Cohen's Kappa coefficient was 0.4937, indicating a moderate level of agreement beyond chance.

Table 6. General metrics for the experiment

Metrics	Value
General accuracy	0.6369
Precision (weighted avg)	0.6209
Recall (weighted avg)	0.6369
F1 (weighted avg)	0.5871
Cohen Kappa	0.4937
Sensitivity	0.7619
Specitivity	1.0000

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Source: The author (2023)

The model's sensitivity was 0.7619, representing the proportion of correctly classified positive examples, and its specificity was 1.0000, representing the proportion of correctly classified negative examples.

To apply the second experiment in a distributed system, a Minimum Viable Product (MVP) called **Peracarida Classifier** was developed. This system receives an image from a user and predicts the order to which that image belongs. Three containers were deployed for each service: one with the script from the second experiment responsible for making the image prediction, another with the application's frontend developed in Next.JS, and the last one with the backend using RabbitMQ to handle communication between the sending and receiving of requests among the system's services.

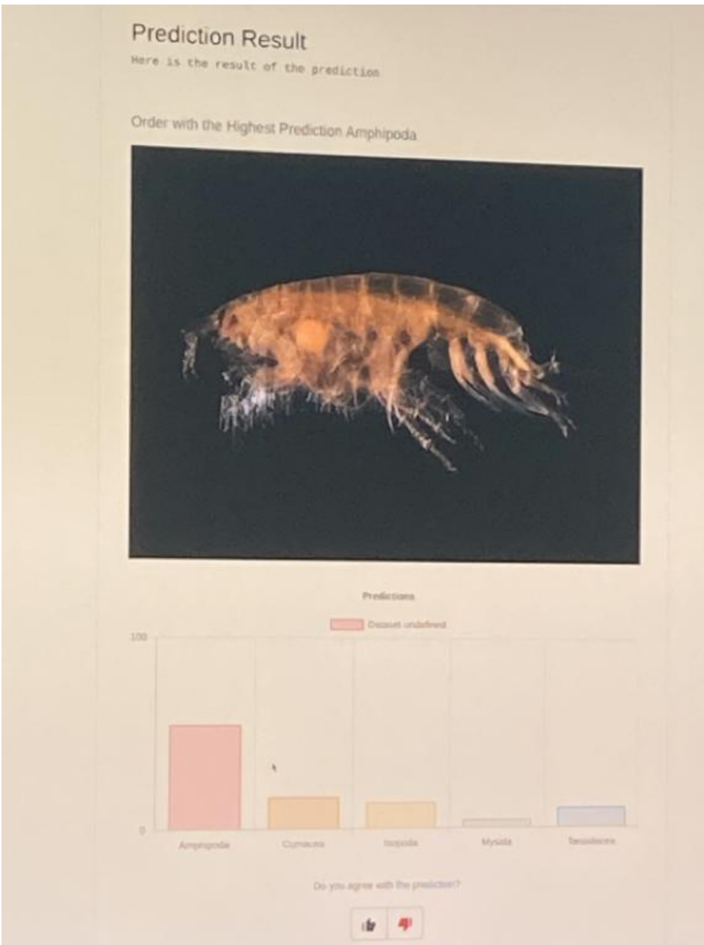

Figure 8. Prediction result screen. Source: Prepared by the author (2023)

The result is displayed to the user with a graph showing the percentage likelihood of the image belonging to each of the trained orders. In the example shown in Figure 8, the user uploaded an image of an amphipod, and the prediction was made correctly, showing a high percentage for the order **Amphipoda**.

5 FINAL CONSIDERATIONS

Based on the evaluation of the first experiment on general crustacean classification, the results contributed to understanding that CNN is the best model for classifying images of these organisms. In addition, it helps to lay the foundation for future studies, as this was the first experiment aimed at classifying images of the previously mentioned crustacean orders.

Several strategies can be employed to improve the overall performance of neural network models, such as using data augmentation techniques to increase the number of examples in the classes, applying dropout, early stopping, cross-validation, and even active learning. The lack of a good computer with a GPU to run the experiment may limit hyperparameter tuning and the use of more complex models. Other evaluation metrics, such as Precision, Recall, and F1-score, should also be considered in addition to accuracy to assess the overall performance of the models.

Regarding the classification of Peracarida images, we suggest that future studies with the same objective conduct a more detailed review of the dataset, aiming to ensure that the training and validation folders have the same proportion of images and that the images exhibit varied characteristics (background color, microscopic setup, color and frontal lighting, etc.), improving the quantity and normalizing the distribution in a straightforward approach. We believe that by following these recommendations, it will be possible to improve the performance of the experimental script and, consequently, enhance the classification of microscopic crustaceans using machine learning and deep learning methods. Overall, this study contributes to the development of Artificial Intelligence applied to biological taxonomy, specifically for the classification of microcrustacean images.

The results obtained here can be used as a starting point for the development of an application that allows users to upload images and obtain prediction results regarding the order to which the image belongs. For this purpose, an MVP has already been developed (see Figure 8) and could be replicated or further improved in future work. The experiments can also serve as precursors to studies that provide a better understanding of the diversity and importance of these organisms in maintaining the marine ecosystem through Artificial Intelligence.

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