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Deep Learning Approaches for Image-Based Classification of Honey Bee (*Apis mellifera*) Lineages

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Abstract: Honey bees (*Apis mellifera*) play a vital role in maintaining ecosystem balance and supporting the sustainability of agricultural production. Accurate classification of these insects at the species and subspecies levels is essential for biodiversity monitoring, understanding local adaptation, and developing effective conservation strategies. In recent years, deep learning algorithms have emerged as powerful tools for automatic classification based on visual data. This review presents a comprehensive synthesis of studies utilizing deep learning-particularly convolutional neural networks (CNNs), transfer learning approaches, and hybrid models-for the image-based identification of honey bee lineages. The reviewed methods are evaluated in terms of their performance in image analysis and morphological differentiation. While the results demonstrate the high accuracy and rapid classification potential of deep learning models, current limitations such as dataset size, labeling challenges, and environmental variability are also discussed. By examining these strengths and constraints, this review aims to provide an in-depth perspective on the applicability of deep learning in honey bee research and outlines promising directions for future studies in this rapidly advancing field.

Keywords: Honey bee, deep learning, automatic classification, image processing, lineage classification, biodiversity

1. Introduction

Honey bees (*Apis mellifera*) play a fundamental role not only as critical pollinators within ecosystem services but also in enhancing agricultural productivity. However, recent colony losses have heightened the need for more effective and systematic approaches to the conservation and breeding of bee populations (Panziera et al., 2022). Accurate identification and classification of honey bee genotypes or subspecies are essential for monitoring natural selection, assessing local adaptation, and tracking disease tolerance (da Silva et al., 2015). In this context, classification methods based on the morphological characteristics of honey bees have long been employed (Zhang et al., 2025). Nevertheless, such methods are often time-consuming, observer-dependent, and have low repeatability.

With advances in image processing techniques, data derived from digital microscopy or macro-scale photographs of honey bees have introduced new potential for developing automated classification systems (Karthiga et al., 2021). In particular, deep learning algorithms have emerged as powerful tools due to their capacity to autonomously learn complex and high-dimensional visual patterns (De Nart et al., 2022; Rodrigues et al., 2022). Architectures such as Convolutional Neural Networks (CNNs) can accurately classify honey bees by recognizing visual cues such as wing venation, body morphology, or pattern variations (De Nart et al., 2022; Garcia et al., 2022; Rodrigues et al., 2022). These automated systems not only reduce the workload for researchers but also provide more objective and reproducible results. Moreover, they enable the analysis of large datasets and can be integrated with field-derived visual records.

This review aims to provide a comprehensive examination of the potential of deep learning methods for classifying honey bees at the species, subspecies, or genotype level based on visual data. The review begins by outlining the basic principles and architectures of artificial neural networks (ANNs), followed by a detailed explanation of the structural components of CNNs. Subsequently, approaches based on these architectures that have been applied to honey bee image classification are presented alongside relevant examples from the literature, with a comparative evaluation in terms of accuracy, data requirements, and limitations. Finally, key challenges such as class imbalance, model interpretability, and environmental variability in image-based classification are discussed, and recommendations for future studies are provided.

2. Fundamentals of Deep Learning

The concept of artificial intelligence (AI) first gained theoretical grounding in 1935 when Alan Turing proposed the idea of "machines that can learn." Over the years, this idea evolved into practical applications through advancements in algorithm development (Grzybowski et al., 2024). One of the major outcomes of this evolution is machine learning, which is defined as a set of algorithms that mimic human learning processes by learning from data and improving their accuracy over time. Deep learning, introduced by Rina Dechter in 1986, is regarded as a subfield of machine learning. Inspired by the structure of the human brain, deep learning is a powerful approach that uses multi-layered ANNs to automatically extract patterns from data (Luo et al., 2022).

Although machine learning and deep learning are often used interchangeably, they differ significantly in methodology. Traditional machine learning models typically require feature engineering, where domain-specific features are manually extracted. In contrast, deep learning models can perform this process automatically, without explicit programming. Especially deep neural networks have the ability to uncover meaningful patterns from large datasets, enabling them to make highly accurate predictions (Khanikar et al., 2022). This capability makes deep learning particularly advantageous for analyzing large and complex datasets.

Today, one of the most impactful areas where deep learning is applied is computer vision. Architectures such as CNNs are specifically designed to capture and learn spatial relationships in images (Traore et al., 2018). These models excel at tasks such as image classification, object detection, and segmentation by recognizing visual patterns in data. In biological imaging, deep learning has also proven effective in applications ranging from cell identification to leaf disease detection and animal species classification. Within this context, deep learning offers an effective and scalable solution for classifying morphologically diverse organisms such as honey bees.

3. Artificial Neural Networks

Artificial neural networks are inspired by the principles of the nervous system in advanced biological organisms. In biological systems, the fundamental unit of the nervous system is the neuron, which consists of three main parts: dendrites, the soma (cell body), and the axon. Neurons are interconnected through dendrites and axons, and these connection points are called synapses. Dendrites collect signals from presynaptic neurons or the environment and transmit them to the soma. These signals are processed in the soma, and if they exceed a certain threshold, an action potential is generated and propagated along the axon (da Silva et al., 2016). Upon reaching the end of the axon, this signal triggers the release of chemical messengers known as neurotransmitters into the synaptic cleft, transmitting the signal to the next neuron. This sequence of electrical and chemical reactions forms the basis of learning and response mechanisms in organisms (Hodgkin and Huxley, 1952).

Inspired by this biological framework, the artificial neuron-the basic unit of an ANN-was first introduced in 1943 by neurophysiologist Warren McCulloch and mathematician Walter Pitts. Artificial neurons are mathematical functions modeled after biological neurons and serve as the fundamental building blocks of ANNs (Kubat, 2021).

An artificial neuron is defined by input signals (I_1, I_2, ..., In) and corresponding weights (W_1, W_2, ..., Wn), which may have positive or negative values. Each input signal is multiplied by its respective weight, and the total input is calculated as the sum of these products ($\sum IiWi$). This sum is compared to a threshold value, and the result is passed through an activation function to produce an output, which is then transmitted to the next neuron. In this system, weights are adjustable parameters that are updated during the learning process and determine the influence of each input. The strength of the effect on the postsynaptic neuron is represented by the magnitude of each IiWi product.

Multilayer ANNs, which are widely used across many fields including animal husbandry, consist of multiple computational layers. These typically include three main components: an input layer, one or more hidden layers, and an output layer. The learning process begins with initializing weights

(Wij) and biases (bj) for the connections in the network. Neurons process a large number of training samples and produce predictions, which are then compared to actual outputs to compute the error (loss value). To minimize this loss, the backpropagation algorithm is used. Backpropagation calculates the contribution of each parameter to the error by propagating it backward and adjusts the weights accordingly.

This process is repeated until the network reaches the desired level of accuracy. Through this iterative refinement, ANNs are capable of learning and making predictions with high accuracy, even in large datasets with complex relationships (Krogh, 2008).

4. Convolutional Neural Networks

Convolutional Neural Networks are a specialized architecture of artificial neural networks designed specifically for deep learning tasks involving visual data, such as image recognition, object detection, and biomedical image analysis. Unlike traditional ANNs, CNNs are highly effective at capturing spatial and local correlations within data. This ability makes them a powerful tool for analyzing and classifying morphological differences among biological species (Zhao et al., 2024).

The core principle behind CNNs lies in their use of a series of specialized layers that automatically extract meaningful features from input images. When trained on large-scale image datasets, this architecture can learn subtle patterns and relationships that are often imperceptible to the human eye, thereby achieving high levels of classification accuracy (Grzybowski et al., 2024).

4.1. Common CNN architectures

4.1.1. LeCun Network (LeNet)

LeCun Network is one of the earliest CNN architectures in the field of deep learning, developed by Yann LeCun and colleagues in 1998. Originally designed for the recognition of handwritten digits, this architecture features a simple structure comprising a limited number of convolutional and pooling layers. The LeNet architecture consists of sequential layers that progressively reduce the spatial dimensions of the data, followed by fully connected layers for classification. Although relatively shallow in depth and rarely used directly in modern applications, LeNet remains foundational in the evolution of CNN architectures (Zhao et al., 2024).

4.1.2. Alex Krizhevsky Network (AlexNet)

AlexNet marked a turning point in the rise of deep learning within the field of computer vision by winning the ImageNet Large Scale Visual Recognition Challenge (ILSVRC) in 2012. It was the first architecture to popularize the use of the ReLU (Rectified Linear Unit) activation function and employed the dropout technique to reduce overfitting. The architecture consists of five convolutional layers and three fully connected layers, and was trained using two separate processing pipelines to enable data parallelism. Compared to LeNet, AlexNet is significantly more advanced in terms of depth and filter sizes, achieving high accuracy on large datasets and paving the way for deeper and more complex CNN architectures (Rafiq et al., 2023).

4.1.3. Visual Geometry Group Network (VGGNet)

VGGNet was developed in 2014 by the Visual Geometry Group at the University of Oxford and is notable for its use of sequential 3×3 convolution filters to increase network depth (Tasyurek and Arslan, 2023). The VGG architecture simplified and modularized the network by employing the same filter size across all layers. Versions such as VGG-16 and VGG-19, which contain 16 and 19 layers respectively, are widely used-especially in transfer learning applications. While its deep structure enables the network to learn complex patterns effectively, the high number of parameters results in relatively high computational costs (Alzubaidi et al., 2021).

4.1.4. Google LeNet Architecture (GoogLeNet)

Google LeNet Architecture, also known as Inception-v1, won first place in the 2014 ILSVRC competition and introduced a groundbreaking architectural concept known as network-in-network design. Instead of using a single convolutional layer, this architecture employs Inception modules, which apply filters of various sizes in parallel. This approach enables the network to be enriched both in width and depth while maintaining a manageable number of parameters. Subsequent versions, including Inception-v2, v3, and v4, introduced further optimization techniques and increased architectural depth (Barber and Oueslati, 2024).

4.1.5. Residual Network (ResNet)

Residual network was developed by Microsoft Research in 2015 to address the issue of performance degradation in deep networks, which often occurs as network depth increases (Khan et al., 2019). The architecture introduced the concept of residual connections (also known as skip connections), which allow the input of a layer to be directly added to its output after a few layers. This mechanism facilitates the flow of gradients during backpropagation, thereby enabling the successful training of much deeper networks. Variants such as ResNet-50 and ResNet-101 are widely used today, particularly in transfer learning tasks, and are known for their high accuracy and robustness (Wu et al., 2019).

4.2. Core components of convolutional neural networks

A typical CNN model is composed of convolutional, activation, pooling, and fully connected layers. These layers progressively abstract the input image and extract the most salient features to perform classification (Gu et al., 2018).

4.2.1. Convolution layer

The convolution layer enables the model to extract local features from input data (e.g., an image of a honey bee) using small matrices called kernels or filters. These kernels, typically of size 3×3 or 5×5, are slid across the input image to generate feature maps. The convolution operation can be mathematically represented as shown in Equation 1 (Gu et al., 2018).

$$Y(i,j)=\sum_{m}\sum_{n}X(i-m,j-n)W(m,n) \quad (1)$$

In this equation, *X(i, j)* represents the input image, *W(m, n)* denotes the convolution filter (kernel), and *Y(i, j)* refers to the resulting feature map.

This operation enables the model to extract edges, textures, and salient structures from the input image, thereby providing powerful features that help distinguish between different honey bee lineages.

4.2.2. Activation function

The feature maps obtained from the convolution operation are initially the result of a linear transformation. To enable the model to learn non-linear representations, an activation function is applied. One of the most commonly used activation functions in CNNs is the Rectified Linear Unit (ReLU) (Puig-Arnavat and Bruno, 2015), which is mathematically defined in Equation 2.

$$f(x)=\max(0,x) \quad (2)$$

In this equation, *x* denotes the input value, while *f(x)* represents the corresponding output of the activation function.

The ReLU function accelerates and enhances the learning process by mapping all negative values to zero. Alternatively, other activation functions such as Leaky ReLU and ELU (Exponential Linear Unit) can also be employed depending on the task and network architecture (Nair and Hinton, 2010).

4.2.3. Pooling layer

The pooling layer reduces the spatial dimensions of the feature maps produced by the convolutional layer, thereby decreasing the number of parameters and overall computational cost. The most commonly used pooling operation is Max Pooling, which summarizes information by selecting the maximum value within a defined window (Estrach et al., 2014), as shown in Equation 3.

$$P(i,j)=\max_{(m,n)\in f}X(i+m,j+n) \quad (3)$$

In this equation, *X(i+m, j+n)* denotes the input values within the local region *f*, and *P(i, j)* represents the pooled output, which corresponds to the maximum value in that region.

Pooling contributes to spatial invariance, enabling the model to become more robust to changes in scale and orientation-such as those found in honey bee images.

4.2.4. Fully connected layer

In the final stage of a CNN, the low-dimensional representation obtained from the pooling layer is flattened and passed to the fully connected layers. At this point, the network functions similarly to a traditional artificial neural network, computing class probabilities-such as those corresponding to specific honey bee species-using activation functions like Softmax or Sigmoid.

The fully connected layer performs the classification based on the features learned throughout the preceding layers. For multi-class classification tasks, the Softmax function is commonly used and is defined in Equation 4 (Scabini and Bruno, 2023).

$$z_i=\sum_{j}w_{ij}x_j+b_i \quad (4)$$

In this equation, *xj* denotes the input features, *wij* represents the weight connecting input *j* to neuron *i*, *bi* is the bias term, and *zi* is the resulting linear combination before the activation function is applied.

The Softmax function normalizes the predicted values into probabilities, ensuring that the total sum across all classes is equal to 1.

5. Image-Based Classification of Honey Bees

The CNN architectures and processing components discussed in the previous sections form the foundational elements of the recent advances in honey bee image classification. By integrating convolutional operations, pooling strategies, and activation mechanisms, these deep learning models can efficiently learn the subtle morphological patterns that distinguish honey bee subspecies, wing venation structures, and even health-related abnormalities. The following studies demonstrate how these components have been effectively applied to image-based honey bee classification tasks.

The classification of honey bee species has long attracted scientific interest due to the complex nature of both morphological and molecular data. In particular, the limitations of traditional classification methods in handling multivariate and implicit relationships have led to the emergence of next-generation artificial intelligence-based approaches in this field (Crisci et al., 2012). In this context, deep learning-based image processing methods offer a powerful alternative for the automated classification of honey bees in terms of species, subspecies, and even health status.

Recent studies have demonstrated the effectiveness of CNN architectures, especially for the classification of images based on wing morphology. For instance, De Nart et al. (2022) aimed to differentiate honey bee subspecies by recognizing wing images using AI-based techniques. A dataset consisting of 9,887 wing images from seven subspecies and one hybrid was analyzed using ResNet-50, MobileNet V2, Inception Net V3, and Inception ResNet V2. As a result, individual wing classification accuracies exceeded 0.92, and all models were reported to outperform traditional morphometric evaluation methods. These findings confirm that CNN-based architectures can surpass conventional classification methods in terms of accuracy and consistency, especially when trained on large, balanced, and high-resolution datasets.

Similarly, Rodrigues et al. (2022) developed a software tool named DeepWings©, which performs geometric morphometric classification of honey bee wings by automatically detecting 19 landmarks on digital wing images. To achieve this, they applied a combination of machine learning techniques: (i) using a CNN to detect the wings, (ii) applying a U-Net model for landmark segmentation, and (iii) employing a Support Vector Machine (SVM) for classification. The subspecies classifier achieved an average accuracy of 86.6% across 26 subspecies, and 95.8% accuracy for a subset of five major subspecies. The final implementation of the system demonstrated excellent processing speed, requiring only 14 seconds to analyze 10 images. However, despite its promising performance, DeepWings© shows reduced classification power for certain subspecies with high intra-population variability-emphasizing the need for further refinement using molecularly validated training sets.

The accuracy and overall performance of this software were also validated in an independent test study conducted by Garcia et al. (2022). The researchers evaluated the tool using 14,816 wing images from five different subspecies (*A. mellifera carnica*, *A. mellifera caucasia*, *A. mellifera iberiensis*, *A. mellifera ligustica*, and *A. mellifera mellifera*). Their results showed that 92.6% of the *A. mellifera iberiensis* colonies were matched to the correct subspecies with a high average probability of 0.919. In contrast, only 41.1% of the *A. m. mellifera* colonies were matched to their correct subspecies, although those that were matched exhibited a very high probability of 0.994. When compared to molecular data, the correlation between wing-based and molecular marker-based classification for 1.214 colonies was found to be significant but weak ($r= 0.31$; $p<0.0001$). This indicates that wing-based classification alone may not always reflect true genetic identity, especially in hybrid zones or genetically admixed populations.

A different approach was proposed by Rebelo et al. (2021). The researchers developed a system that analyzes the vein patterns of the forewings of bees, and supported this method with image segmentation techniques. They reported achieving a species-level accuracy of 96% and a genus-level accuracy of 99% on a large dataset comprising 48 species and 23 genera. These levels of accuracy represent highly remarkable outcomes within the scope of morphometric classification approaches, and point to the generalizability of deep learning models even beyond the *A. mellifera* species complex.

In addition, a study by Karthiga et al. (2021) proposed a CNN model capable of classifying not only honey bee species but also their health status.

The study employed a convolutional neural network composed of two-dimensional layers to perform species and health condition analysis on a large dataset. To address class imbalance and better represent minority classes, Synthetic Minority Over-sampling Technique (SMOTE) was applied for data augmentation. The model was trained on more than 5.000 honey bee images, achieving 86% accuracy in subspecies classification and 84% accuracy in health status prediction. This result underscores the potential of CNN models to move beyond taxonomic classification and contribute to colony health monitoring-an increasingly vital area in apicultural research.

Such applications demonstrate that deep learning can be utilized not only for species identification but also for broader analytical purposes, such as assessing colony health and detecting morphological deviations linked to environmental stressors. These findings emphasize the transformative potential of CNN architectures, when combined with curated datasets, to deliver fast, scalable, and accurate classifications in honey bee research. Nevertheless, a consistent limitation across these studies is the scarcity of large-scale, geographically diverse, and molecularly confirmed image datasets-a gap that future research must address to enhance model robustness and generalizability.

6. Conclusions

This review has highlighted the current potential and applications of deep learning techniques in the image-based classification of honey bees. Studies in the literature have reported high classification accuracies-ranging from 86% to 99%-mostly based on honey bee wing images. Notably, the application of pretrained CNN architectures such as ResNet and Inception through transfer learning has yielded successful outcomes, even in cases where data availability is limited.

However, despite these promising findings, research in this field remains relatively limited and often constrained to specific datasets. For instance, most of the image data used to date are derived from forewing structures, while approaches based on body segmentation, behavioral visual data, or three-dimensional imaging are not yet widespread. Moreover, existing studies tend to focus predominantly on European subspecies (e.g., *A. mellifera carnica*, *A. mellifera ligustica*, *A. mellifera mellifera*), with a notable lack of image-based classification applications involving local variants from regions such as Anatolia, the Middle East, or Africa.

Another limiting factor is related to image quality, label accuracy, and data imbalance. While some studies have implemented data augmentation techniques such as SMOTE, it remains unclear how well algorithms can process low-quality images captured under field conditions. Furthermore, the generalizability of the models is often confined to the tested datasets, and performance tends to degrade with data from external sources. The weak correlation observed between molecular data and visual classification results also poses methodological challenges for the biological validation of image-based predictions.

In light of these considerations, integrating deep learning–based image classification methods into honey bee biology holds significant potential. However, fully realizing this potential will require the development of more diverse, representative, and well-labeled datasets, the inclusion of subspecies from varied geographic and genetic backgrounds, and the enhancement of model interpretability. These steps would contribute to both the conservation of biological diversity and the implementation of objective, data-driven breeding programs.

Ethical Statement

The authors declare that ethical approval is not required for this research.

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Declaration of Author Contributions

The authors declare that they have contributed equally to the article. All authors declare that they have seen/read and approved the final version of the article ready for publication.

Declaration of Conflicts of Interest

All authors declare that there is no conflict of interest related to this article.

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