Deep-learning technology provides insights into the morphological evolution of birds (preprint v1)

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Abstract

The evolution of biological morphology is critical for understanding the diversity of the natural world, yet traditional analyses often involve subjective biases in the selection and coding of morphological traits. This study employs deep learning techniques, utilizing a pretrained ResNet34 model capable of recognizing over 10,000 bird species, to explore avian morphological evolution. We extracted weights from the model's final fully connected (fc) layer to create vector representations of avian species and assessed their similarities using cosine similarity metrics. The results demonstrated multiple clustering patterns with or without biological meaning. Some clustering results are consistent with traditional classifications based on morphology, some are consistent with modern cladistic classifications, and some show behavioural and ecological similarities. Despite these insights, some clusters indicated the influence of non-biological image features on clustering outcomes. This study underscores the potential and limitations of using deep learning approaches in morphological evolution studies.

Key words: bird, biodiversity, clustering, deep learning, morphological evolution.

Introduction

The evolution of biological morphology plays a crucial role in shaping the diverse natural world we observe today. It provides insight into the adaptation and survival of species over time, influencing various ecological interactions and the functioning of ecosystems. Traditionally, analyses of morphological evolution have involved subjective elements, as even quantitative analyses based on morphological traits require human intervention in the selection and coding of these traits (Clark et al., 2023). This subjectivity can introduce biases, affecting the accuracy and reliability of evolutionary interpretations.

To address these limitations, our research employs advanced deep learning technologies, specifically Convolutional Neural Networks (CNNs). CNNs, popularized by LeCun et al. (1989), are designed to automatically learn hierarchical features from image data, making them exceptionally suited for visual recognition tasks. By utilizing pretrained image recognition models, we can leverage the learned weights as indicators of morphological traits of various species, providing a more objective basis for understanding biological evolution.

In our study, we utilized the model trained by Sun (2025) and calculated the cosine similarity between classes using the weights extracted from the fully connected layer (fc). This methodology enabled us to perform hierarchical clustering based on the cosine similarities, yielding insights into the morphological evolution of avian species. While this approach shows promise, it is important to note that it has significant limitations; some results may lack biological meaning. However, as the development of deep learning technologies and citizen science contributes to the vast accumulation of biological imagery, there is substantial potential for these methods to enrich our understanding of morphological evolution in the future.

Materials and Methods

Materials

In our study, we utilized the model provided by Sun (2025), which is based on the ResNet34 architecture and is capable of recognizing over 10,000 bird species with an accuracy of approximately 90%. The original weight data for this model is available on Hugging Face, a popular platform for sharing machine learning models and datasets.

Methods

We began by extracting the weights from the final fully connected layer (fc) of the ResNet34 model. Each class's weights were treated as a vector to analyze the relationships between different avian species based on these representations.

To assess the similarity between various species, we employed cosine similarity. Initially, all vectors were subjected to L2 normalization to ensure that they each had a unit length. Following this normalization, we performed dot product calculations on the normalized vectors. This method is equivalent to computing the cosine similarity of the original vectors, providing a meaningful metric for evaluating the relationships among the species. For this implementation, we utilized built-in functions from the PyTorch library, which facilitated efficient computation (Ansel et al., 2024).

Next, we conducted agglomerative hierarchical clustering using the average linkage method to merge clusters. This was executed with the hierarchical clustering functionalities implemented in the SciPy library (Gommers et al., 2025). The hierarchical structure of the clusters was output in Newick format, a widely used format in computational biology for tree structures. Finally, we utilized ETE3 to export the clustering dendrogram in SVG format and conducted manual analysis (Huerta-Cepas et al., 2016).

Result

Our methodology was successfully applied in the completion of the clustering process, resulting in a comprehensive hierarchical clustering output. The agglomerative clustering technique applied to the cosine similarity measures of the weight vectors yielded a dendrogram that illustrates the relationships between the different avian species based on their morphological features learned by the ResNet34 model.

Discussion

The results of our clustering analysis highlight some critical insights as well as important limitations of deep learning techniques in studying morphology. One significant concern is the issue of interpretability in deep learning models. These models often seek local optima rather than global solutions, leading to clustering outcomes that may not possess real biological meanings.

Currently, the discussion section covers only a limited number of taxa, and we aim to report potential patterns that may carry biological relevance. Notably, the four genera referred to as “fulvetta,” which were traditionally considered similar and related (Pasquet et al., 2006), did not fall into a single cluster. Instead, we found that *Fulvetta* and *Lioparus* clustered with most parrotbills (Paradoxornithidae), aligning with their modern taxonomic classification. On the contrary, the genera *Schoeniparus* (Pellorneidae) and *Alcippe* (Alcippeidae) fell into separate clusters, which suggests that deep neural networks can tell the morphological differences among the “fulvettas.”

Another intriguing finding involves the *Pseudopodoces humilis*, a species morphologically similar to the genus *Podoces*, while is classified within the family *Paridae* based on molecular phylogeny. Yet, this species clustered with the “snowfinches” (*Onychostruthus*, *Pyrgilauda*, *Montifringilla*), indicating possible behavioural and ecological similarities. Both are secondary cavity-nesting birds, often found cohabiting with members of the family Ochotonidae in the Tibetan Plateau (Lu et al., 2011).

We observed that Galliformes and Tinamiformes were nested into a single cluster, pointing to similar morphology traits according to the model. Moreover, the clustering of most species of Strigiformes and Caprimulgiformes into adjacent clusters. However, some nightjar species were incorrectly placed within the owl cluster, potentially suggesting morphological convergence due to adaptations for nocturnality. Alternatively, this could merely reflect that most images were captured at night, leading the deep learning model to perceive them as similar.

Nonetheless, several groupings identified in our analysis evidently lack biological significance. For instance, the close clustering of the *Nymphicus hollandicus* and *Melopsittacus undulatus*, while not aligned with other members of Psittaciformes, is likely due to their wide captivity, leading the model to learn human presence or man-made objects in the images. Additionally, many extinct species clustered together, possibly due to their representation via skeletal images, artistic reconstructions, or other non-biological patterns. Furthermore, some of the recently described species or newly separated cryptic species grouped together, which might reflect insufficient image data, leading to underfitting of the model.

Looking ahead, we plan to expand our analysis by developing code to assess the morphological disparity among different orders. We believe that this methodology may also contribute to the study of avian vocalizations.

Code accessibility

Code: https://github.com/sun-jiao/osea_morpho_evo
Model: https://huggingface.co/sunjiao/osea

Conflict of interests

The author has no conflict of interests.

Author contribution statements

JS designed the project, programmed the python script and drafted the manuscript.

Supplementary files

- class_similarity.csv: similarity matrix of all “classes” (species)
- morphology_clustering.tre: the clustering result
- tree_output.svg: the image version of the clustering result

References

Ansel, J., Yang, E., He, H., Gimelshein, N., Jain, A., Voznesensky, M., Bao, B., Bell, P., Berard, D., Burovski, E., Chauhan, G., Chourdia, A., Constable, W., Desmaison, A., DeVito, Z., Ellison, E., Feng, W., Gong, J., Gschwind, M., … Chintala, S. (2024). PyTorch 2: Faster Machine Learning Through Dynamic Python Bytecode Transformation and Graph Compilation. *Proceedings of the 29th ACM International Conference on Architectural Support for Programming Languages and Operating Systems, Volume 2*, 929 – 947. https://doi.org/10.1145/3620665.3640366

Clark, J. W., Hetherington, A. J., Morris, J. L., Pressel, S., Duckett, J. G., Puttick, M. N., Schneider, H., Kenrick, P., Wellman, C. H., & Donoghue, P. C. J. (2023). Evolution of phenotypic disparity in the plant kingdom. *Nature Plants*, *9*(10), 1618 – 1626. https://doi.org/10.1038/s41477-023-01513-x

Gommers, R., Virtanen, P., Haberland, M., Burovski, E., Reddy, T., Weckesser, W., Oliphant, T. E., Cournapeau, D., Nelson, A., alexbrc, Roy, P., Peterson, P., Polat, I., Wilson, J., endolith, Mayorov, N., van der Walt, S., Colley, L., Brett, M., … Striega, K. (2025). scipy/scipy: SciPy 1.15.0. *Zenodo*. https://doi.org/10.5281/zenodo.14593523

Huerta-Cepas, J., Serra, F., & Bork, P. (2016). ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. *Molecular Biology and Evolution*, *33*(6), 1635 – 1638. https://doi.org/10.1093/molbev/msw046

LeCun, Y., Boser, B., Denker, J. S., Henderson, D., Howard, R. E., Hubbard, W., &

Jackel, L. D. (1989). Backpropagation Applied to Handwritten Zip Code Recognition. *Neural Computation*, *1*(4), 541 – 551. Neural Computation. https://doi.org/10.1162/neco.1989.1.4.541

Lu, X., Huo, R., Li, Y., Liao, W., & Wang, C. (2011). Breeding ecology of ground tits in northeastern Tibetan pla- teau, with special reference to cooperative breeding system. *Current Zoology*, *57*(6), 751 – 757.

Pasquet, E., Bourdon, E., Kalyakin, M. V., & Cibois, A. (2006). The fulvettas (Alcippe, Timaliidae, Aves): A polyphyletic group. *Zoologica Scripta*, *35*(6), 559 – 566. https://doi.org/10.1111/j.1463-6409.2006.00253.x

Sun, J. (2025). OSEA, a deep learning-based bird classification tool, with pre-trained model, mobile and command line applications. *EcoEvoRxiv*. https://doi.org/10.32942/X2FP6T