

Trialling a convolution neural network for the identification of Braconidae in New Zealand

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Abstract

Computer vision approaches, such as deep learning, potentially offer a range of benefits to entomology, particularly for the image-based identification of taxa. An experiment was conducted to gauge the ability of a convolution neural network (CNN) to identify genera of Braconidae from images of forewings. A deep learning CNN was trained via transfer learning from a small set of 488 images for 57 genera. Three-fold cross-validation achieved an accuracy of 96.7%, thus demonstrating that identification to genus using forewings is highly predictive. Further work is needed to increase both the coverage to species level and the number of images available.

Keywords

Braconidae, computer vision, diagnostics, identification, model

Introduction

Insect populations are challenging to study. One of the main problems is the identification of species, particularly in hyper diverse groups such as Hymenoptera, and because knowledge of biodiversity around the world is uneven (Amano and Sutherland 2013; Hoye et al. 2020). However, advances in computer vision approaches provide potential new solutions to this global challenge (Hoye et al. 2020; Greeff et al. 2022). Computer vision approaches, such as machine learning and deep learning, are currently

influencing a wide range of scientific disciplines but are only relatively recently being applied to entomology (Boer and Vos 2018; Marques et al. 2018; Hansen et al. 2019).

Recent studies on image-based insect identification are showing that deep learning models can extract features from images and learn to differentiate species to an accuracy approaching, or exceeding, human expertise (Valan et al. 2019; Hoyer et al. 2020). For example, over half of British ground beetles (Carabidae) can be identified to species, and 74% to genus using convolutional neural networks trained on an image set of over 19,000 images (Hansen et al. 2019). Boer and Vos (2018) used over 10,000 images from AntWeb (www.antweb.org) (to classify ants at species level based on dorsal, head, and profile images. Accuracy of identification was between 62–92% for species and 79–95% for genus, depending on different configurations of the models. Marques et al. (2018) also examined the classification of ants, and achieved an accuracy of 80–90%, demonstrating that high confidence and robustness in ant genera identification can be achieved.

Further to identification and diagnostics, the use of images is also being combined with additional automation and/or robotics to undertake sampling in the field, routine laboratory sample processing, or extracting data from images (Ärje et al. 2020). For example, Bjerge et al. (2021) have developed an automated light trap to monitor moths and identify the species using computer vision-based tracking and deep learning. An automated field trial over 48 nights captured more than 250,000 images, an average of 5675 images per night, with a high validation score for the identification of the 8 most common moth species. Machine learning methods have been used to automate the extraction of data on insect herbivore damage from plant specimens in museums, including the ability to identify different types of herbivores (Meineke and Davies 2018).

In this paper, we test the ability of a convolutional neural network to classify genera of Braconidae that are present in New Zealand using images of the forewing.

Methods

Specimens

All specimens are from the New Zealand Arthropod Collection (NZAC), where the family Braconidae is well curated with almost all specimens (~18,000) sorted to at least genus level. However, relatively few endemic or native species have been described (Berry 2010).

Pinned specimens were selected that represent genera of Braconidae which have been recorded from New Zealand. This includes genera which are either endemic (restricted to New Zealand); native (in New Zealand but also naturally occur elsewhere); have been accidentally introduced through human trade; or intentionally introduced for biological control.

Taxa (and the number of images) are: *Aleoides* (10); *Alysia manducator* (Panzer, 1799) (10); *Apanteles* (12); *Aphaereta aotea* Hughes & Woolcock, 1976 (8); *Aphidius colemani* Viereck, 1912 (11); *Ascogaster elongata* Lyle, 1923 (10); *Asobara persimilis* (Papp, 1977) (10); *Aspicolpus* (10); *Aspilota parecur* Berry, 2007 (8); *Austrohormius* (10);

Bracon phylacteophagus Austin, 1989 (4); *Bracon variegator* Spinola, 1808 (10); *Caenophanes* sp5 (11); *Choeras helespas* Walker, 1996 (9); *Chorebus rodericki* Berry, 2007 (10); *Cotesia* (10); *Cryptoxilos thorpei* Shaw & Berry, 2005 (10); *Dacnusa areolaris* (Nees, 1811) (10); *Diaeretiella rapae* (McIntosh, 1855) (10); *Dinocampus coccinellae* (Schrank, 1802) (10); *Dinotrema longworthi* Berry, 2007 (10); *Diolcogaster* (10); *Dolichogenidea tasmanica* (Cameron, 1912) (10); *Doryctomorpha antipoda* Ashmead, 1900 (10); *Eadya daenerys* Ridenbaugh, 2018 (2); *Eubazus* (10); *Glyptapanteles* (10); *Habrobracon hebetor* (Say, 1836) (10); *Kauriphanes* (6); *Kiwigaster variabilis* Fernandez-Triana & Ward, 2011 (9); *Lysiphlebus testaceipes* (Cresson, 1880) (5); *Macrocentrus rubromaculata* (Cameron, 1901) (10); *Metaspathius* (7); *Meteorus pulchricornis* (Wesmael, 1835) (9); *Microctonus hyperodae* Loan, 1974 (9); *Microplitis* (10); *Monolexis fuscicornis* Förster, 1862 (3); *Neptihormius* (10); *Notogaster charlesi* Fernandez-Triana & Ward, 2020 (10); *Ontsira antica* (Wollaston, 1858) (10); *Opius* sp2 (10); *Pauesia nigrovaria* (Provancher, 1888) (8); *Pholetesor* (5); *Pronkia* sp4 (9); *Pseudosyngaster pallidus* (Gourlay, 1928) (10); *Rasivalva* (2); *Rhyssaloides* (9); *Sathon* sp1 (7); *Schauinslandia* (10); *Shireplitis bilboi* Fernandez-Triana & Ward, 2013 (2); *Shireplitis frodoi* Fernandez-Triana & Ward, 2013 (3); *Spathius exarator* (Linnaeus, 1758) (10); *Syntretus* (10); *Taphaeus* (10); *Therophilus* (5); *Trioxys* (10); *Venanides* (10); and *Xynobius* (10).

Some genera were not included because they are wingless, have very reduced wings, or there was an insufficient number of specimens.

An attempt was made to get 10 specimens from each genus. However, this was not always possible. The average number of forewings removed from a genus was 8.6 (range 5–12, median 10). To remove wings, a specimen was placed in a specimen manipulator and a micropin was used to gently move the tegula up and down until the forewing fell off. Wings were not ‘pulled’ because the membrane rips easily. Static electricity meant the wing stuck to the micropin and forceps, making it easy to put into a gelatin capsule. After all wings had been removed, wings were slide mounted with Euparal.

The specimen records, all images (zip folder), and one representative image of each genus are freely available via the datastore repository (<https://doi.org/10.7931/xftx-6w25>).

Imaging and image preparation

Images of the slide mounted wings were taken on a Nikon MZS25 scope with a Nikon DS-Ri2 camera (16.25 megapixels). There was no photo stacking. Images were cropped and edited using Adobe Photoshop (Fig. 1A).

The following pre-processing corrections were applied to each image (Fig. 1B) so that the convolutional neural network focused on diagnostic features and not on irrelevant differences between the images (such as aspect ratios, colour balance, etc.): 1) colour converted to grayscale; 2) blurred to reduce image grain noise; 3) brightness and contrast standardised (to mean = 0.5, contrast range = -2 standard deviations to + 2 standard deviations, with the extreme values clipped); 4) aspect ‘squashed’ to be a square and down sampled to 299 by 299 pixels to match the network input filter size.

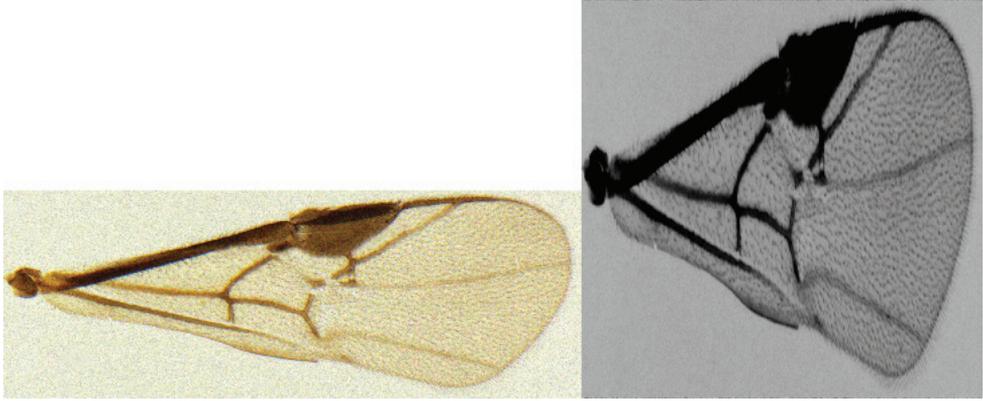


Figure 1. Examples of images: slide mounted forewing (left) and image with pre-processing corrections (right).

A few images were excluded from analyses as they had become ripped during the slide mounting process or were deemed poor quality (colouration, debris on wing) which was not spotted when wings were initially removed.

Model training and validation

Transfer learning was used to train an Xception network that had been initially trained on the Imagenet image set (www.image-net.org). The total number of images were split into three sets (folds) of 2/3 train, 1/3 test, via stratified round-robin cross-validation. The fully connected classification layers were trained for 200 epochs, followed by a further 200 epochs fine-tuning of all parameters. The learning rate was fixed at 0.0001 and the ADAM optimiser used to automatically adjust the update magnitude; this scheme resulted in a very smooth learning curve for this dataset that plateaued at around 200 epochs, reducing the need for validation sets to determine the optimal cut-off. Images were randomly augmented during training to reduce the chance of overfitting and to allow for variations in image conditions that may arise in future cases. Augmentation was conservative because the images were quite highly standardised. The augmentations used were (randomly shift the image up to 10% horizontally and vertically; randomly zoom the image up to +/-10%; randomly rotate the image up to +/-25 degrees).

Results and discussion

A total of 488 wings were used representing 57 genera. Results from cross-validation gave an overall accuracy of 96.7% (472/488; Table 1). Of the 16 misclassified images, 14 images had low confidence scores (<0.9), indicating the network struggled to classify them (Table 2), many of these are from the subfamily Microgastriinae.

Table 1. Accuracy of cross-validation runs on correct predictions to genus.

Cross-validation	Number of correct images / Total images	Percent accuracy
1	182/188	96.81%
2	152/156	97.44%
3	138/144	95.83%

Table 2. List of errors where the correctly identified image was incorrectly predicted. Scores represent the confidence of the model that the prediction is correct. Sorted by highest score.

Catalog number	Correct	Predicted	Confidence score
NZAC02012114	<i>Glyptapanteles</i>	<i>Dolichogenidea</i>	0.997
NZAC02011921	<i>Doryctomorpha</i>	<i>Caenophanes</i>	0.964
NZAC02012115	<i>Glyptapanteles</i>	<i>Sathon</i>	0.765
NZAC02011668	<i>Aphaereta</i>	<i>Asobara</i>	0.65
NZAC02012085	<i>Shireplitis</i>	<i>Venanides</i>	0.649
NZAC02012113	<i>Glyptapanteles</i>	<i>Dolichogenidea</i>	0.597
NZAC02012063	<i>Pholetesor</i>	<i>Sathon</i>	0.567
NZAC02012084	<i>Shireplitis</i>	<i>Venanides</i>	0.56
NZAC02012039	<i>Sathon</i>	<i>Glyptapanteles</i>	0.545
NZAC02011790	<i>Caenophanes</i>	<i>Doryctomorpha</i>	0.535
NZAC02011933	<i>Neptihormius</i>	<i>Metaspathius</i>	0.525
NZAC02012117	<i>Glyptapanteles</i>	<i>Dolichogenidea</i>	0.508
NZAC02011792	<i>Caenophanes</i>	<i>Doryctomorpha</i>	0.497
NZAC02012038	<i>Sathon</i>	<i>Shireplitis</i>	0.471
NZAC02012088	<i>Shireplitis</i>	<i>Venanides</i>	0.395
NZAC02011984	<i>Aleoidea</i>	<i>Doryctomorpha</i>	0.293

This small experiment demonstrated that forewings appear to be highly predictive of genus level identifications. The model accuracy is particularly impressive given the very small number of images. Often hundreds or even thousands of images are needed to build these models. For example, Hansen et al. (2019) had a set of over 19,000 images for ground beetles (Carabidae), and Boer and Vos (2018) used over 10,000 images from AntWeb. We suggest our trial was successful because the forewing morphology (veins/cells) are already recognised as key diagnostic characters for Braconidae, and the images of a forewing are quite simple with considerably less ‘noise’ than dorsal and lateral habitus images of an insect body (Valan et al. 2019).

Two main questions need to be addressed in future work. Firstly, how well does only one species (or morphospecies) represent a genus. Several of the genera above are monotypic, and for some genera the forewing morphology will differ very little between species, but for genera with higher species diversity this condition is unlikely to hold. However, this was an initial trial of the technology, and as the number of species-level image sets increases then genus-level identification becomes less relevant. Secondly, how well will the model perform when additional species or genera are added. An increase in the number of ‘classes’ (taxa) will likely increase the morphological variability in the dataset, perhaps affecting model accuracy and consequently needing

more source images to overcome (Greener et al. 2021). A related issue is the level of image standardisation required. The images used in this study were all photographed and processed with the same equipment setup; adding subsequent imagery (either for the same taxa or novel ones) has the potential to cause the model to focus on spurious photographic differences during training. Similarly, the model has only been tested on images held out from the same set; how well it performs on other image sets (for the same taxa) needs to be tested to determine how well the model ‘transfers’ to novel image sets and whether further refinement of the training process is required, such as more aggressive image pre-processing and augmentation or the inclusion of more images.

Machine learning tools, particularly convolutional neural networks (CNNs), are fast becoming a valuable tool for the identification of insects (Valan et al. 2019; Hoye et al. 2020). Identifications are a vital part of making insects visible and accessible (Greeff et al. 2022). An increase in the number and level of taxa being identified offers many benefits, including accelerating the discovery and increasing the awareness of a greater proportion of biodiversity, providing informed information for applications such as other academic research, conservation, and biosecurity, and may free time for more research tasks.

At present, the major hurdle is the shortage of images (Valan et al. 2019; Greeff et al. 2022), particularly many images of the same species, rather than just one representative photo for a publication. Digitization efforts are underway in many countries that involve taking images of specimens, and large image libraries are available such as those on iNaturalist and for specific taxa (e.g., Antweb, www.antweb.org), however, these will not always cover, or be suitable for, every taxonomic group. Although the above model has been built for use in New Zealand, from a distinct set of genera of which several are endemic, the images from this project could be used for Braconidae in other countries or regions, albeit with very careful interpretation of the results. Consequently, it is vital that researchers facilitate sharing and exchange of their images (Valan et al. 2019), and that collaborative and user-friendly software be developed (Greeff et al. 2022).

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References

- Amano T, Sutherland WJ (2013) Four barriers to the global understanding of biodiversity conservation: wealth, language, geographical location and security. *Proceedings of the Royal Society B* 280: e1756. <https://doi.org/10.1098/rspb.2012.2649>
- Ärje J, Melvad C, Jeppesen MR, Madsen SA, Raitoharju J, Rasmussen MS, Iosifidis A, Tirronen V, Gabbouj M, Meissner K, Høye TT (2020) Automatic image-based identification and biomass estimation of invertebrates. *Methods in Ecology & Evolution* 11: 922–931. <https://doi.org/10.1111/2041-210X.13428>
- Berry JA (2010) Hymenoptera. In: Godron DA (Ed.) *New Zealand Inventory of Biodiversity (Vol. 2): Kingdom Animalia. Chaetognatha, Ecdysozoa, Ichnofossils*. Canterbury University Press, Christchurch, 350–359.
- Bjerge K, Nielsen JB, Sepstrup MV, Helsing-Nielsen F, Høye TT (2021) An automated light trap to monitor moths (Lepidoptera) using computer vision-based tracking and deep learning. *Sensors* 21: e343. <https://doi.org/10.3390/s21020343>
- Boer MJA, Vos RA (2018) Taxonomic classification of ants (Formicidae) from images using deep learning. *bioRxiv*, 1–36. <https://doi.org/10.1101/407452>
- Greff M, Caspers M, Kalkman V, Willemse L, Sunderland BD, Bánki O, Hogeweg L (2022) Sharing taxonomic expertise between natural history collections using image recognition. *Research Ideas and Outcomes* 8: e79187. <https://doi.org/10.3897/rio.8.e79187>
- Greener JG, Kandathil SM, Moffat L, Jones DT (2021) A guide to machine learning for biologists. *Nature Reviews Molecular Cell Biology* 23: 40–55. <https://doi.org/10.1038/s41580-021-00407-0>
- Hansen OLP, Svenning J-C, Olsen K, Dupont S, Garner BH, Iosifidis A, Price BW, Høye TT (2019) Species-level image classification with convolutional neural network enables insect identification from habitus images. *Ecology and Evolution* 10: 737–747. <https://doi.org/10.1002/ece3.5921>
- Marques ACR, Raimundo MM, Cavalheiro EMB, Salles LFP, Lyra C, Von Zuben FJ (2018) Ant genera identification using an ensemble of convolutional neural networks. *PLoS ONE* 13(1): e0192011. <https://doi.org/10.1371/journal.pone.0192011>
- Meineke EK, Davies TJ (2018) Museum specimens provide novel insights into changing plant–herbivore interactions. *Philosophical Transactions of the Royal Society B* 374: e20170393. <https://doi.org/10.1098/rstb.2017.0393>
- Valan M, Makonyi K, Maki A, Vondráček D, Ronquist F (2019) Automated taxonomic identification of insects with expert-level accuracy using effective feature transfer from convolutional networks. *Systematic Biology* 68: 876–895. <https://doi.org/10.1093/sysbio/syz014>