



The DeepFaune initiative: a collaborative effort towards the automatic identification of European fauna in camera trap images

Noa Rigoudy^{1,2} · Gaspard Dussert² · Abdelbaki Benyoub³ · Aurélien Besnard¹ · Carole Birck⁴ · Jérôme Boyer⁵ · Yoann Bollet⁶ · Yoann Bunz³ · Gérard Caussimont⁷ · Elias Chetouane^{8,9} · Jules Chiffard Carriburu¹⁰ · Pierre Cornette¹¹ · Anne Delestrade¹² · Nina De Backer¹³ · Lucie Dispan¹⁴ · Maden Le Barh¹⁴ · Jeanne Duhayer^{2,10} · Jean-François Elder¹⁵ · Jean-Baptiste Fanjul^{6,16} · Jocelyn Fonderflick¹⁷ · Nicolas Froustey¹⁸ · Mathieu Garel¹⁹ · William Gaudry¹⁹ · Agathe Gérard²⁰ · Olivier Gimenez¹ · Arzhela Hemery¹ · Audrey Hemon²¹ · Jean-Michel Jullien²² · Daniel Knitter²³ · Isabelle Malafosse¹⁷ · Mircea Marginean²⁴ · Louise Ménard²⁵ · Alice Ouvrier²⁶ · Gwennaëlle Pariset²⁵ · Vincent Prunet²⁷ · Julien Rabault²⁸ · Malory Randon²⁹ · Yann Raulet³⁰ · Antoine Régnier¹¹ · Romain Ribière³¹ · Jean-Claude Ricci¹⁸ · Sandrine Ruetten¹⁹ · Yann Schneylin³² · Jérôme Sentilles³³ · Nathalie Siefert²⁷ · Bethany Smith³⁴ · Guillaume Terpereau^{8,9} · Pierrick Touchet³⁵ · Wilfried Thuiller^{8,9} · Antonio Uzal³⁴ · Valentin Vautrain¹³ · Ruppert Vimal²⁶ · Julian Weber²³ · Bruno Spataro² · Vincent Miele² · Simon Chamailé-Jammes¹

Received: 12 July 2023 / Revised: 26 September 2023 / Accepted: 3 October 2023

© The Author(s), under exclusive licence to Springer-Verlag GmbH Germany, part of Springer Nature 2023

Abstract

Camera traps have revolutionized how ecologists monitor wildlife, but their full potential is realized only when the hundreds of thousands of collected images can be readily classified with minimal human intervention. Deep learning classification models have allowed extraordinary progress towards this end, but trained models remain rare and are only now emerging for European fauna. We report on the first milestone of the DeepFaune initiative (<https://www.deepfaune.cnrs.fr>), a large-scale collaboration between more than 50 partners involved in wildlife research, conservation and management in France. We developed a classification model trained to recognize 26 species or higher-level taxa that are common in Europe, with an emphasis on mammals. The classification model achieved 0.97 validation accuracy and often > 0.95 precision and recall for many classes. These performances were generally higher than 0.90 when tested on independent out-of-sample datasets for which we used image redundancy contained in sequences of images. We implemented our model in a software to classify images stored locally on a personal computer, so as to provide a free, user-friendly, and high-performance tool for wildlife practitioners to automatically classify camera trap images. The DeepFaune initiative is an ongoing project, with new partners joining regularly, which allows us to continuously add new species to the classification model.

Keywords Camera trap · Classification · Deep learning · Europe · France · Software

Introduction

Camera traps have revolutionized the way ecologists monitor biodiversity and population abundances (O'Connell et al. 2011; Howe et al. 2017). Camera traps enable to scale-up monitoring efforts dramatically, both in space and time, as they are relatively cheap, easy to deploy, and autonomous tools (Steenweg et al. 2017). The continuous monitoring

capacity they provide also facilitates the detection of rare species. Therefore, and unsurprisingly, it has become common practice to deploy tens to hundreds of camera traps in monitoring programs.

The full potential of camera traps is however only realized when the hundreds of thousands of images, many being empty from spurious detections, can be rapidly classified with minimal human intervention (Chen et al. 2014; Schneider et al. 2018; Wearn et al. 2019; Tuia et al. 2022). Since the beginning, machine learning approaches, and in particular deep learning models, have held the promise to solve this issue. Recent works have confirmed their power:

Noa Rigoudy and Gaspard Dussert contributed equally

Extended author information available on the last page of the article

for instance, deep learning models developed by different research teams (Willi et al. 2019; Tabak et al. 2019; Whytock et al. 2021) have obtained > 0.90 recall and precision for a number of mammal species in North American ecosystems, African savannas, and tropical forests. The recurring leading approach, as assessed in recent iWildcam competitions (Beery et al. 2021), consists in two steps: (step 1) detecting animals, humans, and vehicles and filtering out empty images using a robust detection model such as MegaDetector (<https://github.com/microsoft/CameraTraps>; Beery et al. 2019) and (step 2) using a CNN classification model to identify the species in the images when an animal was detected. While MegaDetector is efficient in detecting animals in various environments and geographical regions, there is still a need for tailored CNN classification models dedicated to the species and regions of interest.

The number of image classification models available to ecologists currently remains low and their taxonomic coverage is still limited. So far, most of the image classification models developed on camera trap data have been trained, even when based on millions of pictures, using images collected by a few partners in one or two sites. For example, Norouzzadeh et al. (2018) trained their model on 3.2 million images taken from the Serengeti Snapshot project (Swanson et al. 2015) to identify 48 African mammals, yet all the data was collected from one large study area in the Serengeti National Park as part of the same monitoring project. Although this can lead to highly accurate models when tested on data collected in the same sites or applied to similar systems, such models may fall short from generalizing to other fauna or contexts (Beery et al. 2018). For the European fauna, we believe there is potential in aggregating multiple small datasets from a large number of partners to build sufficiently large training, validation, and test datasets to develop efficient classification models. The pros and cons of a cross-partner image aggregation strategy, and its ability to lead to successful models, have yet to be investigated. Recent initiatives such as Wildlife Insights (www.wildlifeinsights.org) or Agouti (www.agouti.eu), online platforms to manage and classify camera trap images, have embraced this strategy. Naturally, each initiative will have its own terms of participation, which may not be acceptable for certain institutional partners. For example, online platforms require the users to upload their images, and sometimes have non-optional data-sharing policies. This approach may not be suitable for certain institutional partners which have legally bounding contracts on data collection or privacy concerns. Some other initiatives offer user solutions to run models on their own servers or computers (Trapper: <https://trapper-project.readthedocs.io>; Project Zamba: <https://zamba.drivendata.org>; our work).

Developing a classification model is however not only a question of collecting a large amount of data. Many issues

appear when going beyond proof-of-concept and proposing a model that should be of high-enough quality in practice (e.g., data leakage, lack of transferability, shortcut learning, sensitivity to background, out-of-domain predictions, calibration, unbalanced data, and biases for rare species; Desprez et al. 2023). Therefore, we advocate that releases of species-classification models for the ecological community must be accompanied by a reliable performance analysis to help ecologists understand how well the proposed classification model is expected to perform in practical situations (e.g., on new camera trap images).

We report here on the DeepFaune initiative (<https://www.deepfaune.cnrs.fr>). This initiative aims at (1) aggregating camera trap images from many French institutions or research groups to create a collective and large-scale dataset, (2) developing a deep learning-based species classification model, using a clearly explained methodology to circumvent the issues mentioned previously, (3) performing a rigorous performance analysis on out-of-sample datasets to assess how well our model performs on novel images from sites that are not included in the training set, (4) releasing the model to the community as a software component that can be integrated in other tools, and (5) providing a free, open-source, user-friendly, and efficient software for practitioners to run the identification pipeline on self-hosted images with standard personal computers.

Methods

Partners and data collection

At the time of writing, the initiative brings together over 50 partners (see the complete list at <https://www.deepfaune.cnrs.fr>) representing institutions managing protected areas, hunting federations, or academic research groups across France. A few partners also joined from other European countries. Partners provided camera trap images or videos, originating from various monitoring projects (e.g., general monitoring of Alpine fauna, monitoring of the burrows of badgers) or opportunistic surveillance (e.g., to assess the presence of wolves). Among these partners, five partners joined the project after initial data collection, providing annotated pictures to use as out-of-sample data for a stringent test of the classification model accuracy (see below).

Original dataset

We gathered and sorted more than 2 million annotated pictures and 20 thousand annotated videos, after removal of corrupted or other problematic files. These pictures and videos included either one of the animal species originally identified by the partners, a human, and a vehicle or were

empty (less than 1%), i.e., had no animal, human or vehicle visible. In some instances, annotations had been made at a higher taxonomic level than the species level (e.g., bird, rodent). The amount of data provided by each partner varied a lot, ranging from 20 videos to hundreds of thousands of images. Many partners shared data from camera traps set to take a series of images for a single detection event. We thereafter defined these consecutive images as “sequences”, considering that two images taken within 10 s, at the same site, belonged to the same sequence. Finally, as we wanted to train our model to classify camera trap images, we converted videos into images by retaining one frame per second out of the first 4 s of each video.

Targeting 26 animal species or higher-order taxonomical groups

We restricted our dataset and model to 26 animal species or higher-order taxonomical groups that were common enough and well sampled in our original dataset. Our model was trained on the following 19 species: European badger (*Meles meles*), bear (*Ursus arctos*), cow (*Bos Taurus*), dog (*Canis familiaris*), red fox (*Vulpes vulpes*), common genet (*Genetta genetta*), goat (*Capra sp.*), hedgehog (*Erinaceus europaeus*), ibex (*Capra ibex*, alpine only), lynx (*Lynx lynx*), marmot (*Marmota marmota*), mouflon (*Ovis gmelini*), nutria (*Myocastor coypus*), red deer (*Cervus elaphus*), roe deer (*Capreolus capreolus*), sheep (*Ovis aries*), squirrel (*Sciurus vulgaris*), wild boar (*Sus scrofa*), and wolf (*Canis lupus lupus*), and 7 higher-order taxa: bird, chamois (Alpine, *Rupicapra rupicapra*, and Pyrenean, *Rupicapra pyrenaica*), cat (domestic and wild *Felis catus*), *Equidae sp.*, lagomorph, micromammal, and *Mustelidae sp.*

Non-technical outline of the deep learning methodology

Our approach relied on the following steps (described in more detail in the “[Training and validation datasets](#)”, “[Training and validation phases](#)”, “[Estimating classification performance on out-of-sample data using sequences](#)” and “[The DeepFaune software](#)” sections): we first used a high-performance detection model to detect the presence of any animal, human, or vehicle in the full-size and annotated images that we collected through our partner network. This model allowed us to crop the annotated images so that they mostly contained the animals that were detected, with only little background remaining. We then used these cropped images to train a Convolutional Neural Network (CNN) classification model. CNN models are complex models that automatically learn the most relevant features within images that optimize a classification task (here the recognition of species or higher-order taxa). To do so, the model first learns the classification task on a training set

composed of annotated images and its performance is then optimized using a new set of images called the validation set. Finally, we tested whether the trained CNN model’s performance was maintained when it was used to classify images that were quite different from those used for training and validation. These novel images are commonly called “out-of-sample” and allow for the robust assessment of model performance on new datasets. Along the modeling process, we paid attention to common biases and pitfalls that are common when dealing with ecological datasets and followed technical tips to deal with such issues (Desprez et al. 2023).

Training and validation datasets

Avoiding shortcut learning

We prepared the training and validation datasets using MegaDetectorV5, developed by Beery et al. (2019) (model v5a), on our original dataset to filter out empty images and images containing humans and/or vehicles. MegaDetector v5a is based on the image detection model YOLOv5 (Redmon et al. 2016) and allowed us to produce one cropped image per animal that was detected (there were potentially multiple individuals in a given image). We retained cropped images that had a confidence score higher than 0.8 to decrease the risk of false detection. Since the images in the original dataset were annotated, it was possible to annotate any cropped image in the training and validation datasets using the annotation of its parent image. For instance, if MegaDetectorV5 detected two animals in an image originally annotated as “wild boar”, we considered that the two resulting cropped images contained a wild boar to train the model. After this step, we remained with a dataset of 787,575 cropped animal images.

In addition to often having images taken in dozens of different settings thanks to the numerous contributors, for most species, the “cropping” step described above also enabled us to avoid shortcut learning (Geirhos et al. 2020) as we trained and validated our CNN classification model on annotated images for which the background had been mostly removed.

Avoiding data leakage

CNN models require independent training and validation datasets to learn successfully (Kapoor and Narayanan 2022), and as commonly done, we split the whole image dataset into a training dataset containing 90% of the images, and a validation dataset containing the remaining 10%. One issue that could arise during this split is that pictures collected within the same sequence are used in both the training and validation datasets, which would threaten their independence (Desprez et al. 2023). As our original dataset contained pictures and videos collected with many different camera trap

models, there was no consistency in how the date and time stamps were stored. We thus chose to identify sequences through image filenames instead. We used a heuristic based on text mining in the R package *stringdist* (van der Loo 2014) to compare filenames to each other. We considered that two files were not independent if their filenames were too similar, i.e., if their similarity was above 0.9. This conservative threshold ensured that no image, from the same sequence or video, was present both in the training and the validation datasets.

Dealing with class imbalance

Class imbalance may occur when the number of images differs between classes, and it is known to affect both training and validation (Johnson and Khoshgoftaar 2019). Here, we propose a novel approach that combines downsampling and upsampling during the training and validation phases. At each epoch of the training phase, we downsampled the class which was overrepresented down to a multiple of the rarest class. We chose to have a ratio of 5 between the number of images of the most common class and the number of images of the rarest class. This was estimated for every epoch, such that every image is seen by the model if we fit the model for enough epochs. As a consequence, images of the rarest classes were used in many epochs and can thus be considered upsampled whereas those of the most common classes are downsampled. This way, the optimization problem was different at every epoch, but more balanced. We considered that the stochasticity induced by the sampling process at each epoch had a positive impact on the model fit procedure and we observed a continuous reduction in model loss through epochs. We used the same idea to handle imbalance during validation. This enabled us to compute what we called a balanced validation accuracy.

Training and validation phases

We used transfer learning starting from a ConvNext-Base model (Liu et al. 2022) that was pre-trained on Imagenet 22 K, with a resolution of 224×224 , using PyTorch. We performed image augmentation using the *imgaug* Python library (<https://github.com/aleju/imgaug>) during the training phase. Each image in each batch was modified with a random set of transformations such as horizontal flip, affine transformations, gray scale transformation, blurring, brightness, or contrast changes. We used the softmax output as a prediction score. We used the SGD optimizer with a learning rate of $4e-4$. We then estimated the model for a maximum of 100 epochs, monitored the overall balanced validation accuracy, and stopped the estimation when it did not increase with a patience of 10 epochs.

For each processed image, the model computed a prediction score for each class (these scores sum to 1). The prediction score expresses the certainty on the attribution of the image to a given class. In the following, we considered as a prediction the class that maximized these scores. To estimate the quality of the model, we computed global accuracy (i.e., the probability that a prediction is correct), precision (i.e., the probability that an image classified as showing species i actually has species i present), and recall (the true positive rate, i.e., the probability that an image having species i present is actually classified as showing species i).

Estimating classification performance on out-of-sample data using sequences

Building an out-of-sample dataset

We investigated the ability of the pipeline (i.e., the detection model followed by the classification model) to perform an accurate identification of species in an out-of-sample dataset, i.e., on images taken in contexts that have never been seen during the training stage (Schneider et al. 2020). Our out-of-sample dataset originated from five partners plus a public dataset from the Peneda-Gerês National Park in Portugal (Zuleger et al. 2023). We explored the classification accuracy of the CNN-based classification step after using MegaDetector V5 (model v5a) to retrieve cropped images around animals using a threshold of 0.8. The final out-of-sample contained 213,059 cropped animal images of 23 of the 26 species or higher taxonomic groups on which the Deepfaune pipeline focuses (lynx, hedgehog, and nutria were lacking).

Using sequence information to enhance prediction

We predicted the species present at the level of the sequence and not at the level of the individual image. We remained with an out-of-sample dataset of 36,033 sequences. We chose to predict on the sequence level for two reasons: camera traps are now often set to take images in bursts, and animals commonly stay several seconds near the camera, triggering it multiple times in a row. To do so, we extracted the date and time of each image of the out-of-sample dataset using the EXIF information. We obtained the prediction score at the sequence level by first computing the prediction score for each image of the sequence that was not predicted as empty. We then summed these scores and considered that the class with the highest total prediction score was the predicted class for the sequence. Images that were not in a sequence were classified using their own prediction score. Sequences with a score lower than 0.5 were considered as “undefined”.

The DeepFaune software

We found that MegaDetectorV5 created a bottleneck in terms of speed when used on a CPU (about 2 to 3 s per image in our experiments on various personal computers) due to its high image resolution (1280) and large model size based on YOLOv5x (<https://github.com/ultralytics/yolov5>). We therefore developed a much faster alternative using YOLOv8s (<https://github.com/ultralytics/ultralytics>), which is a high-performance medium-sized detection model with a resolution of 640. We trained the YOLOv8s-based detector using the cropping information given by MegaDetectorV5 in images previously used in this study (to limit the computing needs, we took a subset of our full dataset). We obtained a detection performance that is generally similar to the one of MegaDetectorV5, but at a much higher speed (see Online Resource 1 Table S.1). We then implemented this alternative detector (which needs only about 0.3 s per image) and our CNN classifier inside a free, user-friendly, and independent software. The detector automatically crops the image around the animal if one is detected, so users can upload their full-size images, stored locally and directly in the software, and classify these images either as empty, human, vehicle, or one of the 26 animal classes on which the CNN classifier was trained. Users can decide on a threshold on the prediction score below which the images will not be classified and will be set aside in a “undefined” class for visual inspection. The software only requires the installation of Python v3 and its PyTorch module. To overcome the common difficulties associated with the installation of Python libraries on Windows operating systems, we created a standalone and ready-to-use .exe program for these systems. The software processing time depends on the machine’s CPU and is linear with the number of images to be processed. In our experiments, it processed 1000 images in 2 min with an Intel Octa-Core i7-10,700 CPU. Its memory footprint is also small (around 2 GB) as images are loaded on the fly in small batches. Consequently, there is no memory limit with respect to the number of images to treat in one run. The software is available on the project’s website: <https://www.deepfaune.cnrs.fr>.

Results

Performance of the classification model on the validation dataset

We obtained an overall balanced validation accuracy of 97.3%. Recall and precision were > 0.9 for most classes (Table 1) and notably above 0.95 for many classes for which the number of training images was high (e.g., cow

or wild boar). Interestingly, we obtained high performance scores for lynx regardless of the small training sample size (806 images) for this species. This may be due to its characteristic coat color and spotted pattern which facilitates recognition and classification.

We did not observe many identification mismatches between the different ungulate species (Online Resource 1, Fig. S.1). For instance, performance for red deer and roe deer was excellent, despite some objective visual similarities. Precision for mouflon was not great (0.72), but this was because of the imbalance in the validation set: since there was at least twice as many chamois or sheep as mouflon images, having only a few of the chamois and sheep misclassified as mouflon was enough to lead to a low precision for mouflon. The same reason explained the low precision for goat (0.83). Surprisingly, we obtained a moderate performance for ibex: indeed, mismatches appeared on images where ibex’s distinctive horns were not visible on the images. Finally, we observed a lower-than-desired precision for wolf. This was due to some confusion between wolf and fox and dog, mostly on night images in which species identification was intrinsically challenging. Again, this precision is also driven by the aforementioned imbalance in the validation set.

Performance of the classification model on the out-of-sample dataset

The classification model achieved an overall accuracy of 93.6% on individual images and 96.7% on the out-of-sample dataset when predicting at the level of image sequences. Class-specific results were also generally significantly better when identification was done at the sequence level (Table 2). For instance, the recall for roe deer increased from 0.92 to 0.96 using sequences. This suggested that fine-grained species identification was facilitated by having different views of the same moving animal (see an example in Fig. 1). The performance using sequences is overall close to those obtained on the validation dataset (without sequences).

High performance was achieved for large ungulates, with precision and recall being about 0.95 for red deer, roe deer, chamois, and wild boar (Table 2), with the exception of ibex and mouflon for which the model made some confusion with other species (e.g., goat). There remained some mismatches between classes (Online Resource 1 Fig. S.2); for instance, 155 sequences of roe deer were classified as red deer. Performance remained excellent for smaller animals, including marmots, lagomorphs, micromammals, and birds. As in the validation dataset, inspection of the confusions revealed that they mostly occurred in night-time images or when the animal was partially visible (see examples in Fig. 2).

Table 1 Performance metrics of the classification model computed on the validation dataset

Class	<i>N</i> Training	<i>N</i> Validation	Precision	Recall
Badger (<i>Meles meles</i>)	9263	1227	0.96	0.98
Bear (<i>Ursus arctos</i>)	6672	1362	0.91	0.98
Bird	26,575	4069	0.99	0.99
Cat (wild and domestic <i>Felis catus</i>)	5013	926	0.90	0.94
Chamois (<i>Rupicapra rupicapra/pyrenaica</i>)	113,527	14,465	0.99	0.96
Common genet (<i>Genetta genetta</i>)	340	52	0.89	0.92
Cow (<i>Bos Taurus</i>)	44,773	7241	0.99	1.00
Dog (<i>Canis familiaris</i>)	9413	1202	0.94	0.93
<i>Equidae sp.</i>	1211	80	0.91	0.99
Goat (<i>Capra sp.</i>)	3459	235	0.83	0.93
Hedgehog (<i>Erinaceus europaeus</i>)	231	2	0.50	1.00
Ibex (<i>Capra ibex</i>)	6168	756	0.83	0.97
Lagomorph	4655	764	0.94	0.96
Lynx (<i>Lynx lynx</i>)	806	89	0.95	1.00
Marmot (<i>Marmota marmota</i>)	1934	228	0.95	0.98
Micromammal	3265	444	0.99	1.00
Mouflon (<i>Ovis gmelini</i>)	967	72	0.60	0.96
<i>Mustelidae sp.</i>	4515	619	0.87	0.95
Nutria (<i>Myocastor coypus</i>)	382	63	0.94	0.97
Red deer (<i>Cervus elaphus</i>)	130,753	11,468	0.96	0.96
Red fox (<i>Vulpes vulpes</i>)	47,064	4558	0.98	0.95
Roe deer (<i>Capreolus capreolus</i>)	81,923	8167	0.95	0.95
Sheep (<i>Ovis aries</i>)	113,691	15,566	1.00	0.99
Squirrel (<i>Sciurus vulgaris</i>)	4771	576	0.94	0.98
Wild boar (<i>Sus scrofa</i>)	70,616	13,300	0.98	0.99
Wolf (<i>Canis lupus lupus</i>)	7096	959	0.87	0.96

N Training and *N* Validation refer to the number of images of a given class within the training and validation datasets, respectively

Thresholding prediction scores to balance error rate vs. increased manual labeling effort

Most of the prediction errors are associated with a moderate to low or very low score (see Fig. 2 for example). To improve the likelihood that species are correctly predicted by the classification model, one can therefore consider as correct only predictions that have a score above a certain threshold and change the predictions that have a lower score to an “undefined” class. Images with predictions being “undefined” would have to be inspected manually to be correctly labeled. As the score for threshold predictions is increased, the number of errors is reduced, but the number of images to be annotated manually increases. Figure 3 shows how these numbers vary with the score threshold for the classification model presented in this work. In the DeepFaune software, we use a score threshold of 0.8 by default, leading to an error rate of less than 1% on the out-of-sample dataset, at the cost of having to manually annotate approximately 30% of the images. This score threshold can be modified by the user.

Discussion

The DeepFaune initiative represents a successful multi-partner collaboration to build a large-scale camera trap image dataset and develop a machine learning model, fully tested and evaluated, readily available to automatically classify camera trap images collected in Europe. Our current model allows for predicting the presence of 26 different species or higher order taxa in camera trap images, with an emphasis on mammals. Although we did use the standard approach of transfer learning, we implemented a combination of heuristics to deal with class imbalance and the independence of training and validation datasets that could be useful to others. Ultimately, our species classification model performed extremely well on the validation dataset and provided robust results on out-of-sample data. Additionally, we built a graphical user interface (GUI) that is freely available online (<https://www.deepfaune.cnrs.fr>) so that practitioners can easily run the model locally on a personal computer and automatically sort their images

Table 2 Performance metrics of the classification model computed on out-of-sample data, when predicting at the level of individual images or image sequences. Model performance at the image level is expected to be lower than at the sequence level as people who annotated the images had the complete 3-image sequences available and could use previous or subsequent images to clarify uncertainties. Images and sequences that had a prediction score lower than 0.5 were not considered and classified as “undefined” (4.07% and 5.59% of the images and sequences, respectively)

Class	Recall at the sequence (image) level	Precision at the sequence (image) level
Badger (<i>Meles meles</i>)	0.99 (0.97)	0.98 (0.92)
Bear (<i>Ursus arctos</i>)	0.98 (0.96)	0.70 (0.46)
Bird	0.99 (0.98)	0.99 (0.99)
Cat (domestic and wild <i>Felis catus</i>)	0.96 (0.93)	0.88 (0.83)
Chamois (<i>Rupicapra rupicapra/pyrenaica</i>)	0.94 (0.93)	0.95 (0.85)
Common genet (<i>Genetta genetta</i>)	0.91 (0.92)	1.00 (0.99)
Cow (<i>Bos Taurus</i>)	0.95 (0.88)	0.99 (0.98)
Dog (<i>Canis familiaris</i>)	0.93 (0.86)	0.89 (0.68)
Equidae sp.	0.95 (0.90)	0.98 (0.96)
Goat (<i>Capra sp.</i>)	0.73 (0.64)	0.83 (0.39)
Ibex (<i>Capra ibex</i>)	0.83 (0.77)	0.45 (0.22)
Lagomorph	0.98 (0.96)	0.99 (0.97)
Marmot (<i>Marmota marmota</i>)	0.99 (0.98)	1.00 (0.98)
Micromammal	0.96 (0.92)	1.00 (0.98)
Mouflon (<i>Ovis gmelini</i>)	0.91 (0.89)	0.92 (0.66)
Mustelidae sp.	0.97 (0.96)	0.94 (0.88)
Red deer (<i>Cervus elaphus</i>)	0.98 (0.96)	0.95 (0.94)
Red fox (<i>Vulpes vulpes</i>)	0.97 (0.94)	0.99 (0.99)
Roe deer (<i>Capreolus capreolus</i>)	0.96 (0.92)	0.97 (0.95)
Sheep (<i>Ovis aries</i>)	0.99 (0.98)	0.94 (0.80)
Squirrel (<i>Sciurus vulgaris</i>)	0.67 (0.43)	0.75 (0.34)
Wild boar (<i>Sus scrofa</i>)	0.99 (0.97)	0.98 (0.96)
Wolf (<i>Canis lupus lupus</i>)	0.95 (0.96)	0.69 (0.58)

or videos based on model predictions. The model is also available as a software component to be integrated in other tools, in particular in online platforms for the management of camera trap images, such as Agouti (www.agouti.eu), in which the Deepfaune classification model can already be used.

Model performance and relevance for ecological studies

There are currently few species-recognition models available for the European fauna, and our results could therefore be used to benchmark future studies. The quality of our model appears very good, even by deep learning classification standards, and compares favorably with results from similar exercises conducted on fauna from other continents.

For instance, overall accuracies of 0.97, 0.78, and 0.94 on validation datasets were respectively reported in studies on North American fauna (Tabak et al. 2019), Central African fauna (Whytock et al. 2021), and East African fauna (Norouzzadeh et al. 2018). Our model also performs better than those reported by Carl et al. (2020) and Simões et al. (2023) (0.71 accuracy and 0.74 mAP, respectively), which are the rare published models focused on European fauna and for which performance metrics are available. We note however that these performance metrics were computed on different datasets than ours, so that direct comparison between performance values across studies should be interpreted with caution.

We managed to obtain good results with a moderately sized dataset (by deep learning standards), by overcoming a number of obstacles. Firstly, the large imbalance (e.g., two orders of magnitude more images of chamois than ibex) would have biased the classification towards the most common species. We therefore implemented an original approach combining downsampling and upsampling techniques that successfully prevented the emergence of a relationship between identification performance and the number of images per class. Secondly, deep learning models are known to be able to learn “shortcuts” (Geirhos et al. 2020) and can misclassify images due to spurious similarities (e.g., similar image backgrounds). In our context, this would correspond to learning contextual elements (e.g., snow and vegetation structure) that would be associated with the species, rather than learning to recognize the species itself. To avoid this potential issue, we chose to classify cropped images and not full-size images (as opposed to Whytock et al. 2021), with an additional procedure of image augmentation.

Overall, class-specific recall and precision are high enough for the model to be useful for many specific studies, some of which we highlight now: (1) automated monitoring of large ungulates, a guild of important management interest in Europe. Ungulates are indeed generally very well classified by the model, with recall and precision values above 0.9 for most species (as explained in the “Results” section, performance for ibex and mouflon are low, but will likely improve as new pictures are continuously added in the database). These results suggest that our model could be a useful tool to facilitate studies investigating the effects of management practices on locally abundant ungulates (e.g., can wild boar population dynamics be controlled by hunting?) or the dynamics of prey under predation (e.g., do roe deer populations decrease as wolves return?); (2) monitoring large mammalian communities. Although model accuracy levels were generally lower for classes other than ungulates, the model’s performance and taxonomic coverage suggest that it could be useful to automatically sort out hundreds of thousands of pictures for a range of taxonomic groups. This could prove especially



Fig. 1 Using sequences decreases the false positive rate in classification predictions. A sequence of three images of a chamois, taken over a 3-s interval (and cropped by MegaDetectorV5). The two first images (**a**, **b**) are predicted as chamois (with scores 0.91 and 0.96).

The third image (**c**) is misclassified as a mouflon with a lower score (0.81), but the score at the sequence-level is highest for chamois. The three images are therefore predicted to show a chamois by the Deep-Faune pipeline

useful in studies looking at the impact of anthropization on large mammal communities for example. A human intervention would still be required to manually verify the pictures for which prediction scores are low or to identify the species present in images where the model classifies at a higher taxonomic level (e.g., *Mustelidae sp.*), but this effort should be dramatically reduced when using our model; (3) quantifying human disturbance levels, as our pipeline is able to distinguish images containing humans, vehicles, and/or domestic animals such as cattle (sheep, cow) and dogs. The current model performances should therefore enable us to build reliable metrics estimating human activities along wide gradients.

Importantly, the general high quality of the model results was conserved when applied to out-of-sample datasets. It is

a common error to take model results on validation datasets at face value and assume similar accuracies will be observed in new applications. Previous studies (Whytock et al. 2021) have shown that this is not the case and observed dramatic declines in accuracy when tested on out-of-sample datasets, to the point where the usefulness of the model could sometimes be called into question. Our out-of-sample tests, based on heterogeneous images from new and unseen locations, suggest that our model performances are robust to new applications. Additionally, these out-of-sample tests were designed to test the applicability of our model to real-world scenarios. It revealed that using the average prediction score over temporally-close pictures (i.e., sequence) can improve classification results if classification at the sequence-level is sufficient. Our results also show that the common approach

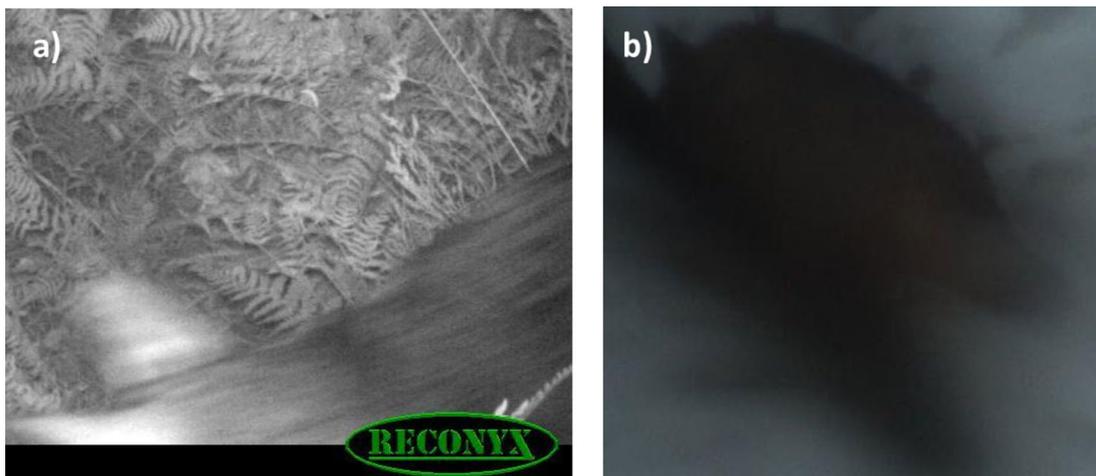


Fig. 2 Examples of images in which a wolf is not correctly identified, possibly due to poor image quality. A wolf was classified as a roe deer, with a low prediction score of 0.51 in a sequence with only

one non-empty image (**a**), and as a fox with a moderate score of 0.82 in a sequence of 1 image (**b**). Both images were cropped by MegaDetectorV5

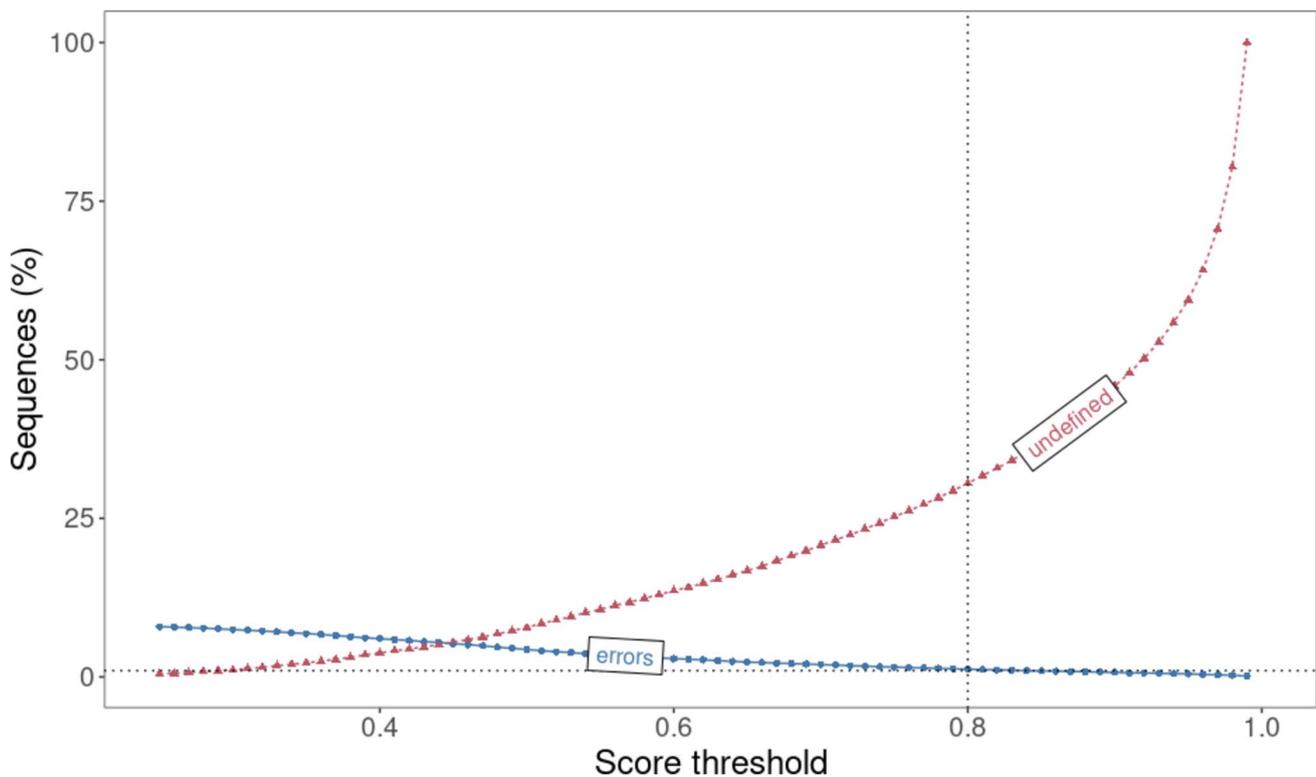


Fig. 3 Effect of increasing the prediction score threshold value on the percentage of image sequences that are wrongly classified (“errors”; in blue squares) or classified as “undefined” (red triangles). The anal-

ysis is conducted on the out-of-sample dataset. The vertical dotted line is at 0.8, the default score threshold value used in the DeepFaune software. The horizontal dotted line indicates 1% of the sequences

of field practitioners to set up camera traps to take several images at each trigger can be leveraged when using classification models. Our work also highlights that the reported performance of a classification model trained without sequence information is likely an under-estimation of the performance it could achieve at the sequence-level. Whether there are better ways to aggregate image-level scores into sequence-level scores remains to be studied. We also note that sequence or temporal information could be directly integrated into the training step, as done in context CNN models (Beery et al. 2020; Tuia et al. 2022), but we could not use this approach here as many partners who provided images for training the models provided batches of images that did not come from the same sequences.

Lessons learned from a successful multi-partner initiative

One of the main strengths of the DeepFaune initiative lies in the creation of a nation-wide network among key actors in French and European biodiversity research, conservation, and management. Under the lead of an academic research group originating from two distinct laboratories, over 50 partners have shared camera trap pictures and videos allowing to build what is likely to be one of the largest databases

of camera trap medias in France, in both, number of files (more than 2 million annotated pictures and 20 thousand annotated videos) and location heterogeneity (e.g., mountains, wetlands).

This success should not hide the technical challenges of working with such a large number of actors. Building the original database clearly revealed the intricacies of dealing with multiple, high-volume data transfers as well as with the strong heterogeneity in data acquisition and organization among the partners. The devil is in the details, and harmonizing directory, file and species names were all very time-consuming tasks that had to be dealt with by combining automatic and manual interventions. Partner-specific data management appears as one of the strongest barriers to creating efficient large-scale datasets that do not depend on a single monitoring program (as opposed to the Serengeti Snapshot (Swanson et al. 2015) dataset for instance). Interestingly, however, some of our individual partners were members of the same institution but worked in different sites. For example, we received data from several national parks that all belonged to the same institution (Parc Nationaux de France). Similarly, several teams from the Office Français de la Biodiversité shared data, all having different formats. In such cases, it would seem beneficial for the

master institution to provide detailed data management guidelines that would allow standardized data management internally. In this context, centralized data management platforms that enforce data standardization, developed either within institutions or at national or international levels, might facilitate future studies.

Having numerous and diverse partners is key however to ground our work in the reality of end-users, as the DeepFaune initiative was originally conceived to develop a free and easy-to-access tool of sufficient quality for field practitioners. Beyond the data collection stage, regular communication between the leading academic team and the partners was critical to identify key expectations and potential difficulties in appropriation. Expectations shared by all partners were that the machine learning approach should be easy to implement and run on a standard personal computer. This is a long-standing issue regarding deep learning models, as even when training is not required and only predictions are expected, the installation of libraries necessary for computation (e.g., Tensorflow and PyTorch) can be difficult. Uploading pictures on an online platform running its own servers naturally solves this issue. We however found that many partners were reluctant to follow this approach either because of the need to upload gigabytes of images online or because the data-sharing policies were too stringent. We thus decided to implement our approach in a freely available, cross-platform (Windows, macOS, Linux), Python-based software whose developments can be followed at <https://www.deepfaune.cnrs.fr>. These developments also include regularly adding new taxa to the list of species that can be identified (e.g., training to add fallow deer is underway). In general, we feel that the diversity of users and their needs will prevent finding a one-size-fits-all solution and will allow for numerous initiatives, cloud- or desktop-based, to co-exist.

Expectations of our partners differed regarding the classification model and how to use its prediction to sort out images. What makes an “optimal” sorting strategy might in fact vary between partners. Some partners are interested in minimizing false negatives over false positives. This can be the case when studying sensitive species, such as wolves, as positive classifications will be verified manually in any case. For other studies, the balance between false positives and false negatives matters less. This is generally the case in occupancy modeling studies of common species (Gimenez et al. 2022). We also foresee that, in a near future, prediction scores will be directly used in the inference process allowing the uncertainty of the classification to be propagated into the estimation of any metric of interest. Irrespective of whether this will be successful or not, in response to this diversity of needs, we decided to let the users decide on a threshold on the prediction score below which the images will not be classified and requires manual inspection. We believe that

this approach gives an important level of flexibility and that users will be able to learn what threshold works best for them by trial-and-error.

Conclusion

In conclusion, our work provides a rather successful classification model of the European fauna in camera trap images, which can be easily used by practitioners through the DeepFaune software on self-hosted images using a standard personal computer. Such an approach contrasts with some recent developments that favor cloud-computing. Our work however remains a work-in-progress and feedback on the use of the model and the associated software, as well as annotations of images for which the model failed, should allow us to improve the model’s performances and increase the number of taxa that are recognized in the near future.

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1007/s10344-023-01742-7>.

Acknowledgements This work was performed using the computing facilities of the CC LBBE/PRABI. This work has benefited from discussions initiated within meetings of the GDR “Ecologie Statistique” of the CNRS. V. Miele would like to thank the LECA laboratory for having hosted him in Chambéry and L. Humblot for insightful discussions about the software. Also, for many partners, field technicians and students contributed largely to data collection, and they are acknowledged for their critical work. Some partners could not share images at the time of our study but actively participated in the discussions around future model developments: PNR des Ardennes, PNR de Chartreuse, PNR du Haut-Languedoc, PNR du Haut Jura, PNR du massif des Bauges, PNR de Préalpes d’Azur, PN de la Vanoise, and PN des Calanques, FNC.

Author contribution N. Rigoudy and S. Chamailé-Jammes initiated the project and the collaborative network. V. Miele developed the models and the graphical-user-interface with G. Dussert. G. Dussert performed all the experiments to validate the models’ performance. B. Spataro supervised the use of the CC LBBE/PRABI computing servers for storage and computation. All five make up the DeepFaune team and all contributed to organize the data collection, clean-up and management. E. Chetouane and J. Rabault contributed significantly to the model and software development. Other authors contributed data on their behalf or on behalf of their institutions.

Funding The DeepFaune team is funded by the CNRS, the University Lyon 1, the “Ecole Normale Supérieure de Lyon” and the “Programme National de Recherche en Intelligence Artificielle”. The CNRS provided additional financial support through its “Mission pour les Initiatives Transverses et Interdisciplinaires”. The following funders supported data collection through various programs (supported partners in parenthesis): Région Auvergne-Rhône-Alpes (FDC Drôme, Ain, Jura; CREA; PNR Baronnies Provençales), Région Sud-PACA (NR Baronnies Provençales), Réseau de Transport d’Electricité (CEFE), Fédération Nationale des Chasseurs (FDC Ain, Jura, Office Français de la Biodiversité (through the Ecocontribution, FDC Ain, Jura)), Conseils Départementaux de l’Ain et du Jura (FDC Ain, Jura), Fonds européens FEDER/POIA (CREA), Département de la Haute Savoie (CREA), Département de la Drôme (PNR Baronnies Provençales), Département des Hautes-Alpes (PNR Baronnies Provençales), Communauté de

Communes Vallée de Chamonix (CREA), DREAL Bourgogne-Franche-Comté (FDC Jura), DREAL Auvergne-Rhône-Alpes (FDC Ain), DREAL Normandie (PNR Perche), DREAL Centre-Val-de-Loire (PNR Perche), DREAL Occitanie (UMR GEODE), Fondation François Sommer (UMR GEODE), Fédération Départementale des Chasseurs de la Marne (CERFE), Réseau SNCF (CERFE), Autoroutes SANEF (CERFE), Nottingham Trent University, and Fauna & Flora International (B. Smith & A. Uzal & M. Marginean). Programme National de Recherche en Intelligence Artificielle.

Availability of data and materials The pictures used in this study are available upon request to each partner. The DeepFaune software code and the model parameters are freely available at <https://www.deepfaune.cnrs.fr>. The code is released under the CeCILL license. The model parameters are protected by the CC BY-NC-SA 4.0 license (Attribution-NonCommercial-ShareAlike 4.0 International).

Declarations

Competing interests The authors declare that they have no financial nor intellectual conflicts of interest with the content of this article.

References

- Beery S, van Horn G, Perona P (2018) Recognition in terra incognita. arXiv preprint. <https://doi.org/10.48550/arXiv.1807.04975>
- Beery S, Morris D, Yang S (2019) Efficient pipeline for camera trap image review. arXiv preprint. <https://doi.org/10.48550/arXiv.1907.06772>
- Beery S, Wu G, Rathod V et al (2020) Context R-CNN: long term temporal context for per-camera object detection. Proc IEEE Comput Soc Conf Comput Vis Pattern Recognit 13075–13085
- Beery S, Agarwal A, Cole E, Birodkar V (2021) The iWildCam 2021 competition dataset. arXiv preprint. <https://doi.org/10.48550/arXiv.2105.03494>
- Carl C, Schönfeld F, Profft I et al (2020) Automated detection of European wild mammal species in camera trap images with an existing and pre-trained computer vision model. Eur J Wildl Res 66:62. <https://doi.org/10.1007/s10344-020-01404-y>
- Chen G, Han TX, He Z et al (2014) Deep convolutional neural network based species recognition for wild animal monitoring. In: 2014 IEEE Int Conf Image Process (ICIP) 858–862
- Desprez M, Miele V, Gimenez O (2023) Nine tips for ecologists using machine learning. <https://doi.org/10.48550/arXiv.2305.10472>
- Geirhos R, Jacobsen J-H, Michaelis C et al (2020) Shortcut learning in deep neural networks. Nat Mach Intell 2:665–673. <https://doi.org/10.1038/s42256-020-00257-z>
- Gimenez O, Kervellec M, Fanjul J-B et al (2022) Trade-off between deep learning for species identification and inference about predator-prey co-occurrence. Computo. <https://doi.org/10.57750/yfm2-5f45>
- Howe EJ, Buckland ST, Després-Einspinner M-L, Kühl HS (2017) Distance sampling with camera traps. Methods Ecol Evol 8:1558–1565. <https://doi.org/10.1111/2041-210X.12790>
- Johnson JM, Khoshgftaar TM (2019) Survey on deep learning with class imbalance. J Big Data 6:27. <https://doi.org/10.1186/s40537-019-0192-5>
- Kapoor S, Narayanan A (2022) Leakage and the reproducibility crisis in ML-based science. arXiv preprint. <https://doi.org/10.48550/arXiv.2207.07048>
- Liu Z, Mao H, Wu CY, Feichtenhofer C, Darrell T, Xie S (2022) A ConvNet for the 2020s. Proceedings IEEE/CVF Conf Comput Vis Pattern Recognit (CVPR) 11976–11986
- Norouzzadeh MS, Nguyen A, Kosmala M et al (2018) Automatically identifying, counting, and describing wild animals in camera-trap images with deep learning. Proc Natl Acad Sci USA 115:E5716–E5725. <https://doi.org/10.1073/pnas.1719367115>
- O’Connell AF, Nichols JD, Karanth KU (eds) (2011) Camera traps in animal ecology. Springer Japan, Tokyo
- Redmon J, Divvala S, Girshick R, Farhadi A (2016) You only look once: unified, real-time object detection. arXiv preprint. <https://doi.org/10.48550/arXiv.1506.02640>
- Schneider S, Greenberg S, Taylor GW, Kremer SC (2020) Three critical factors affecting automated image species recognition performance for camera traps. Ecol Evol 10:3503–3517. <https://doi.org/10.1002/ece3.6147>
- Schneider S, Taylor GW, Kremer SC (2018) Deep learning object detection methods for ecological camera trap data. arXiv preprint. <https://doi.org/10.48550/arXiv.1803.10842>
- Simões F, Bouveyron C, Precioso F (2023) DeepWILD: wildlife identification, localisation and estimation on camera-trap videos using deep learning. Eco Inform 75:102095. <https://doi.org/10.1016/j.ecoinf.2023.102095>
- Steenweg R, Hebblewhite M, Kays R et al (2017) Scaling-up camera traps: monitoring the planet’s biodiversity with networks of remote sensors. Front Ecol Environ 15:26–34. <https://doi.org/10.1002/fee.1448>
- Swanson A, Kosmala M, Lintott C et al (2015) Snapshot Serengeti, high-frequency annotated camera trap images of 40 mammalian species in an African savanna. Sci Data 2:150026. <https://doi.org/10.1038/sdata.2015.26>
- Tabak MA, Norouzzadeh MS, Wolfson DW et al (2019) Machine learning to classify animal species in camera trap images: applications in ecology. Methods Ecol Evol 10:585–590. <https://doi.org/10.1111/2041-210X.13120>
- Tuia D, Kellenberger B, Beery S et al (2022) Perspectives in machine learning for wildlife conservation. Nat Commun 13:792. <https://doi.org/10.1038/s41467-022-27980-y>
- van der Loo MPJ (2014) The stringdist package for approximate string matching. The R Journal 6:111–112
- Wearn OR, Freeman R, Jacoby DMP (2019) Responsible AI for conservation. Nat Mach Intell 1:72–73. <https://doi.org/10.1038/s42256-019-0022-7>
- Whytock RC, Świeżewski J, Zwerts JA et al (2021) Robust ecological analysis of camera trap data labelled by a machine learning model. Methods Ecol Evol 2041–210X:13576. <https://doi.org/10.1111/2041-210X.13576>
- Willi M, Pitman RT, Cardoso AW et al (2019) Identifying animal species in camera trap images using deep learning and citizen science. Methods Ecol Evol 10:80–91. <https://doi.org/10.1111/2041-210X.13099>
- Zuleger AM, Perino A, Wolf F, Wheeler HC, Pereira HM (2023) Long-term monitoring of mammal communities in the Peneda-Gerês National Park using camera-trap data. Biodivers Data J 11:e99588

Publisher’s Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Springer Nature or its licensor (e.g. a society or other partner) holds exclusive rights to this article under a publishing agreement with the author(s) or other rightsholder(s); author self-archiving of the accepted manuscript version of this article is solely governed by the terms of such publishing agreement and applicable law.

Authors and Affiliations

Noa Rigoudy^{1,2} · Gaspard Dussert² · Abdelbaki Benyoub³ · Aurélien Besnard¹ · Carole Birck⁴ · Jérôme Boyer⁵ · Yoann Bollet⁶ · Yoann Bunz³ · Gérard Caussimont⁷ · Elias Chetouane^{8,9} · Jules Chiffard Carriburu¹⁰ · Pierre Cornette¹¹ · Anne Delestrade¹² · Nina De Backer¹³ · Lucie Dispan¹⁴ · Maden Le Barh¹⁴ · Jeanne Duhayer^{2,10} · Jean-François Elder¹⁵ · Jean-Baptiste Fanjul^{6,16} · Jocelyn Fonderflick¹⁷ · Nicolas Froustey¹⁸ · Mathieu Garel¹⁹ · William Gaudry¹⁹ · Agathe Gérard²⁰ · Olivier Gimenez¹ · Arzhela Hemery¹ · Audrey Hemon²¹ · Jean-Michel Jullien²² · Daniel Knitter²³ · Isabelle Malafosse¹⁷ · Mircea Marginean²⁴ · Louise Ménard²⁵ · Alice Ouvrier²⁶ · Gwennaëlle Pariset²⁵ · Vincent Prunet²⁷ · Julien Rabault²⁸ · Malory Randon²⁹ · Yann Raulet³⁰ · Antoine Régnier¹¹ · Romain Ribière³¹ · Jean-Claude Ricci¹⁸ · Sandrine Ruetter¹⁹ · Yann Schneylin³² · Jérôme Sentilles³³ · Nathalie Siefert²⁷ · Bethany Smith³⁴ · Guillaume Terpereau^{8,9} · Pierrick Touchet³⁵ · Wilfried Thuiller^{8,9} · Antonio Uzal³⁴ · Valentin Vautrain¹³ · Ruppert Vimal²⁶ · Julian Weber²³ · Bruno Spataro² · Vincent Miele² · Simon Chamaille-Jammes¹

✉ Vincent Miele
vincent.miele@univ-lyon1.fr

✉ Simon Chamaille-Jammes
simon.chamaille@cefe.cnrs.fr

¹ CEFE, Université de Montpellier, CNRS, EPHE, IRD, Montpellier, France

² Université Lyon 1, CNRS, UMR 5558, Laboratoire de Biométrie et Biologie Evolutive, Villeurbanne, France

³ Parc National des Ecrins, Gap, France

⁴ Conservatoire d'Espaces Naturels de Haute-Savoie, 60 Avenue de Novel, 74 000 Annecy, France

⁵ Office Français de la Biodiversité, Direction de la Recherche et Appui Scientifique Micropolis, Gap, France

⁶ Fédération Départementale des Chasseurs de l'Ain, 19 Rue du 4 Septembre, Bourg-en-Bresse, France

⁷ Fond d'Intervention Eco-Pastoral (FIEP) Groupe Ours Pyrénées, 1 rue Boyrie, Pau, France

⁸ Université Grenoble Alpes, CNRS, Université Savoie Mont Blanc, LECA, Laboratoire d'Ecologie Alpine, Grenoble, France

⁹ Observatoire Spatio-temporel de la Biodiversité et du Fonctionnement des Socio-écosystèmes de Montagne (ORCHAMP), ORCHAMP, France

¹⁰ Office Français de la Biodiversité, Direction de la Recherche et Appui Scientifique, Service "Santé de la Faune et Fonctionnement des Ecosystèmes Agricoles", Saint-Gaudens, Occitanie, France

¹¹ Institut du Développement et des Ressources en Informatique Scientifique (IDRIS), IDRIS-CNRS Campus Universitaire d'Orsay, Rue John Von Neumann, Orsay, France

¹² Centre de Recherches sur les Ecosystèmes d'Altitude, (CREA Mont-Blanc), Observatoire du Mont-Blanc, Chamonix, France

¹³ Parc Naturel Régional du Perche, Courboyer, Perche-en-Nocé, France

¹⁴ CERFE-URCA, 5 rue de la Héronnière, Boulton-aux-Bois, France

¹⁵ Parc Naturel Régional des Marais du Cotentin et du Bessin, 3 Village Ponts d'Ouve, Saint-Côme-du-Mont, Carentan-les-Marais, France

¹⁶ Fédération Départementale des Chasseurs du Jura, Route de la Fontaine Salée, Arlay, France

¹⁷ Parc National des Cévennes, 6 bis, Place du Palais, 48400 Florac-Trois-Rivières, France

¹⁸ Institut Méditerranéen du Patrimoine Cynégétique et Faunistique, Domaine Expérimental Agri-Environnement, Villa "Les Bouillens", Vergèze, France

¹⁹ Direction de la Recherche et de l'Appui Scientifique, Office Français de la Biodiversité, Montfort 01330 Birieux & 5 allée Bethleem, Gières, France

²⁰ Parc Naturel Régional des Ballons des Vosges, Wildenstein, France

²¹ Etablissement Public du Mont-Saint-Michel, 16 route de la Caserne, Beauvoir, France

²² Chemin de Pré Rond-Les Mariages, Le Châtelard, France

²³ OEKO-LOG field Research Joachimsthaler, Str. 9, 16247 Parlow, Germany

²⁴ Fauna & Flora International, The David Attenborough Building, Pembroke Street, Cambridge CB2 3QZ, UK

²⁵ Parc Naturel Régional des Baronnies Provençales, 575 Route de Nyons, 26510 Sahune, France

²⁶ GEODE, UMR 5602, CNRS, Université Jean-Jaurès, 5 Allée Antonio-Machado, 31058 Toulouse, France

²⁷ Parc National du Mercantour, 23 rue d'Italie, CS 51316 06006 Nice, France

²⁸ Institut de Recherche en Informatique de Toulouse, DPD - Université Toulouse III - Paul Sabatier, 118 Route de Narbonne, Toulouse, France

²⁹ Fédération Départementale des Chasseurs de la Drôme, 3132 Route des Sétéreés, Crest, France

³⁰ 100 rue Barbara, 34730 Prades le Lez, France

³¹ Parc Naturel Régional de l'Aubrac, Place d'Aubrac, Aubrac, France

³² 2 la Place du Château, 34190 Brissac, France

³³ Office Français de la Biodiversité, Direction de la Recherche et Appui Scientifique, Service "Conservation et Gestion des Espèces à Enjeux", Villeneuve de Rivière, France

³⁴ School of Animal, Rural and Environmental Sciences, Nottingham Trent University, Nottingham NG25 0QF, UK

³⁵ Office Français de la Biodiversité, Service Départemental, 12000 Rodez, France