As intuitive reflections of biodiversity, morphological characteristics provide valuable taxonomic insights into phenotypic evolution and its underlying genetic mechanisms (Grant & Grant, 2006; Joron et al., 2006; Peichel et al., 2001). Therefore, comparative morphology is generally the indispensable, first step of organismal feature identification and investigation. Yet, quantitatively measuring morphological variation remains challenging.

Fortunately, imaging techniques have advanced so that morphological characteristics can be acquired easily. Commonly, morphological features of interest are measured manually and then classified based on measured data, and the usual geometric morphometrics describes individuals through relative landmark positions (Bookstein, 1996). For example, Drosophila wings are two-dimensional structures with clear venation patterns, so the veins and their crossings are usually considered landmarks whose distances and angles can be measured precisely (Cavicchi et al., 1981; Guerra et al., 1997).
However, using those manual methods with large-scale datasets is both difficult and inefficient. Researchers have developed several advanced methods, such as WINGMACHINE (Houle et al., 2003), DrosoWing (Loh et al., 2017), and FijiWings (Dobens & Dobens, 2013), which detect Drosophila landmark information automatically, and MORPHOJ (Klingenberg, 2011), which performs further morphological analyses based on landmark data. Similarly, some automated systems including machine learning-based methods use fundamental wing morphological features to classify specific insects. For example, using machine learning-based approaches Crnojević et al. (2014) detected vein junctions to discriminate hoverfly species. Yang et al. (2015) developed DAIS, which identifies owlfly species according to wing outlines. Also, color pattern modeling characterizes Heliconius butterfly phenotypes by comparing color patterns (Le Poul et al., 2014); a machine learning-based approach classifies guenon face patterns (Allen & Higham, 2015); and Patternize, another machine learning-based method that works for multiple organisms, uses color pattern variations (Van Belleghem et al., 2018). While those approaches are useful, either for focal organisms or for processing a specific morphological feature, they are not easily used with organisms other than their original targets or for detecting and classifying more complex features that may harbor a wider range of morphological variability in a combination of patterns, shapes, and textures. A comprehensive and efficient solution that considers and handles such integrative features is still required.

As illustrated above, machine learning has recently provided remarkable image processing solutions that can both efficiently identify complex features and accomplish classification tasks (Lürig et al., 2021). Note that although deep-learning algorithms are widely applied to feature extraction and classification, they require relatively larger training sets and cannot appropriately handle classification problems with fewer samples. In contrast, support vector machine (SVM) universally handles generalized problems. SVM-based methods use fundamental wing morphological features further morphological analyses based on landmark data. Several advanced methods, such as WINGMACHINE (Houle et al., 2003), DrosoWing (Loh et al., 2017), and FijiWings (Dobens & Dobens, 2013), which detect Drosophila landmark information automatically, and MORPHOJ (Klingenberg, 2011), which performs further morphological analyses based on landmark data.

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2 | SVMORPH WORKFLOW

We developed SVMorph in the MATLAB environment (MathWorks Inc.). The overall workflow for a typical task generally includes data preprocessing, feature extraction, and classification (Figure 1). When conducting a new task, a classifier must be trained and established before new data may be processed.

3 | DATA ACQUISITION AND PREPROCESSING

While raw images may be captured using digital cameras that can provide better image resolution, we recommend two-dimensional structures, such as insect wings, be photoscanned for better imaging homogeneity. For example, using a regular scanner (HP LaserJet Pro M227fdw) with a resolution of 600 dpi, we obtained a single forewing image of about $1,000 \times 1,000$ pixels. While using a digital camera (NIKON D850) with a 1:1 macro lens, we could acquire a single forewing image of over $3,000 \times 3,000$ pixels with much higher resolution. However, SVMorph or other deep learning-based algorithms only require $256 \times 256$-pixel or $224 \times 224$-pixel images as input, and even lower resolutions work as well. Therefore, the need for image resolution is easily satisfied, so we are more concerned with image homogeneity. When the images come from different sources, it may be difficult to ensure the consistency of the photographing equipment or conditions. Relatively, scanners can provide stable photographing conditions and low operational complexity to obtain images with similar quality. Nevertheless, when digital cameras are properly set up, image homogeneity will not be a critical issue. In addition, data augmentation has the potential to reduce the effects of unstable photographing conditions. Therefore, ordinary photographing devices and normal conditions can satisfy the requirements of SVMorph. After data acquisition, SVMorph requires all input image data be preprocessed as follows. Given that both HOG and LBP feature descriptors extract feature information from eight-bit grayscale images, raw images should be transformed into eight-bit grayscale format (Figure 2a,b) and the appropriate brightness, contrast, and exposure are required (Figure 2a) to ensure optimum classification accuracy. For our sample datasets, we adjusted the butterfly images with the following parameters: brightness 10 and contrast ~50, and we did not adjust the spider images. Note that the adjustments in this step are optional. For photoscanned images, the adjustment in this step is equivalent to setting these parameters correctly when photographing with a digital camera. We want the morphological features we care most about to be well expressed in the images. Therefore, adjustments such as lighting and exposure can depend on the visual effects of the images, that is, whether key morphological features can be clearly distinguished visually. In general, there are no particular restrictions on photographing, but the conditions need to be consistent for a classification task.
Regarding the sample size, as mentioned above, SVM generally performs well compared to other algorithms when faced with a limited or imbalanced sample size, because the decision boundary of SVM is determined only by a few samples (support vectors). Besides, the data augmentation step can improve the classification to some extent as well. Therefore, SVMorph is less affected by the limited sample size. In practice, the criterion of sufficient sample size is difficult to predict and needs to be determined based on the actual model performance. Nevertheless, the model performance generally improves with the increasing sample size, so larger sample size is always preferred. On the other hand, when adding samples, highly imbalanced class distributions of samples should be avoided as well. In practice, we recommend at least 10 samples for each class and the ratio of sample sizes between different classes should be <5. For example, if class A has a sample size of 10 which is the least among all classes, the sample size of other classes should not exceed 50 for each.

4 | DATA AUGMENTATION

For pattern recognition tasks, a set of preprocessed, classified, and labeled image data functions as a training dataset, and many training samples usually produce the most robust model. However, the practical circumstances of morphological studies underline the critical need for a data augmentation step in SVMorph, where the rarity of specific specimens often makes sample collection very challenging. Data augmentation artificially creates synthetic training data with label-preserving transformations by adding slight modifications such as cropping, flipping, rotation, and color jittering, which effectively deal with limited sample size datasets.

Additionally, data augmentation may potentially involve both prior knowledge about the data and task-specific invariances, each of which can regularize the model (Dao et al., 2019). Therefore, to promote task-specific invariances and generalization of classification models, different augmentation methods are needed for different tasks. Based on data-specific invariances and features, the preprocessed training datasets may undergo one or more augmentation methods (Figure 2c,d) by implementing the augmentation.m script in SVMorph. In our sample datasets, the butterfly wing patterns are less sensitive to parameters such as resolution, brightness, and contrast, so we adopted extensive augmentation methods for butterfly images. As for spider images with texture features more susceptible to the abovementioned image factors, we applied fewer methods to avoid distorting the texture features during the augmentation process. Despite the ubiquity of data augmentation in image classification, its underlying theoretical principles are not well understood. Therefore, in practice, the choice of data augmentation methods often depends on the actual performance. Basically, cropping and flipping methods are more reliable and commonly used, which may be considered as the primary choices. We used random parameters for data augmentation, which refer to the specific input arguments of data augmentation methods. For example, in the noise addition step, we introduced Gaussian white noise with random mean values and random variance values. Thus, different images were augmented.
FIGURE 2 Image data preprocessing and augmentation. (a) Examples of preprocessed grayscale images of polymorphic wing patterns of the dead-leaf butterfly, *Kallima inachus*. Morph 1: light-colored main vein; Morph 2: dark-colored main vein; Morph 3: dark-colored main vein with lateral veins; Morph 4: light-colored main vein with dense black dots; and Morph 5: light-colored main vein with black moldy-looking spots. (b) Examples of original images showing the polymorphic body textures of the jumping spider species complex in the *Toxeus* genus. Morph 1: mostly hairless abdomen; Morph 2: abdomen with sparse fine black hair; and Morph 3: abdomen densely covered with white hair. (c) Data augmentation examples of contrast adjustment, noise addition, and random cropping of dead-leaf butterfly wing images. (d) Data augmentation examples showing flipping and image filtering of jumping spider images.
differently, which could increase the diversity of the image datasets and avoid introducing bias during the augmentation process. We also tested the effects of data augmentation on the two sample datasets, subsequently demonstrating that data augmentation significantly improved model accuracies in both cases (Figure 3). Therefore, data augmentation is necessary for optimal model performance.

5 | FEATURE EXTRACTION

SVMorph offers two descriptors for feature extraction from the augmented training dataset: HOG (Dalal & Triggs, 2005) and LBP (Baraldi & Panniggiani, 1995). To classify organisms that display a combination of various elements and that produce local edge and gradient information, we recommend HOG as the major feature descriptor. HOG feature extraction is implemented by the extractHOGFeatures function in the Computer Vision Toolbox in MATLAB 2020b (https://www.mathworks.com/products/computer-vision.html). Once implemented, HOG divides images into small spatial regions called cells, computes discrete histograms for each cell, and then assembles the cells into larger spatial regions called blocks to normalize histograms of all the cells in a block (Dalal & Triggs, 2005), which helps to maintain better invariance and to illuminate changes or shadowing (Figure 4). For texture classification tasks, we recommend LBP be used together with HOG. LBP calculates neighboring pixel gray values to a center pixel and encodes them as a binary number (Baraldi & Panniggiani, 1995), which also endows LBP the advantage of computational simplicity (Figure 5). To further reduce computation time, we use the extractLBPFeatures function in the Computer Vision Toolbox of MATLAB 2020b (https://www.mathworks.com/products/computer-vision.html) to implement a uniform LBP that corresponds to the number of spatial bitwise transitions in LBPs. For example, there would be only 59, instead of 256, total patterns for an eight-bit LBP operator. Finally, both HOG and LBP (if any) feature vectors from each image are extracted and combined for subsequent downstream classification.

6 | CLASSIFIER TRAINING

To train multiclass SVM models, we implement the fitcecoc function in the Statistics and Machine Learning Toolbox (https://www.mathworks.com/products/statistics.html) in MATLAB 2020b. That function adopts a one-versus-one coding design that includes a set of binary SVM classifiers for each possible pair in all classes, so for a model of \( n \) classes, \( n(n - 1)/2 \) binary SVM classifiers are trained. We improve classification accuracy by applying the error-correcting output code multiclass model, which is helpful to deal with multiclass classification problems based on multiple binary classifications (Dietterich & Bakiri, 1994). For the classification tasks using example datasets, all feature extraction and classifier training were performed on a computer with an Intel i7-10700K (3.80G Hz) processor and 32 GB of RAM under a 64-bit Windows operating system.

7 | CLASSIFIER TESTING

During the evaluation step, we used \( k \)-fold cross-validation, which partitions all samples into \( k \) subsets randomly, to examine classifier performances. While a single subset is reserved as test data, the

![Figure 3](https://www.mathworks.com/products/computer-vision.html) Data augmentation effects on model performance. To compare classification performances before and after data augmentation, we calculated accuracy for each replicate (20 replicates for each group) of 10-fold cross-validations for the butterfly (a) and spider (b) datasets, where data are median (SD). The average accuracy for the butterfly dataset increases from 0.9513 (0.0064) to 0.9748 (0.0054) after augmentation and from 0.9196 (0.0154) to 0.9433 (0.0110) for the spider dataset after augmentation. Both (a) and (b) show a significantly higher degree of accuracy with augmentation than without augmentation. Wilcoxon rank-sum test. Boxes enclose scores within the first and third quartiles, and the whiskers show the minimum and maximum values.
remaining \( k - 1 \) subsets are used to train the model. A confusion matrix is an \( n \times n \) table (for \( n \) classes), whose rows represent true labels and columns represent predicted labels. The elements on the main diagonal of a confusion matrix indicate correct predictions and, ideally, all off-diagonal elements equal to zero. The percentage of correct predictions in all test samples defines the classification model's accuracy and, based on the proportion of all main diagonal values in the confusion matrix, is computed as follows:

\[
\text{accuracy} = \frac{(TP + TN)}{(TP + TN + FP + FN)} \tag{1}
\]

where \( TP, TN, FP, \) and \( FN \) stand for true positive, true negative, false positive, and false negative, respectively. To more specifically evaluate a model's performance, we used the precision, recall, and F1 scores that we computed for each class, where

\[
\text{precision} = \frac{TP}{(TP + FP)}, \tag{2}
\]

\[
\text{recall} = \frac{TP}{(TP + FN)}, \tag{3}
\]

\[
F1 \text{ score} = 2 \times \frac{\text{recall} \times \text{precision}}{\text{recall} + \text{precision}}. \tag{4}
\]

For each of our models, we calculated a confusion matrix for each round of 10-fold cross-validations and evaluated the measures calculated from the matrices. We then performed 20 replicates of 10-fold cross-validations for each classifier and used the average of 20 results to calculate an estimate of the model's performance. For each model, we created a receiver operating characteristics (ROC) curve by plotting the true-positive rate against the false-positive rate at various threshold values. For ROC calculation, all samples were randomly halved into a training dataset and a test dataset and then the training dataset's data were augmented. We used the FitPosterior argument of the \textit{fitcecoc} function to obtain posterior probabilities for the test sample labels. For our multiclass classification model, we first computed ROC scores for each class against the rest of the classes by using the \textit{roc_curve} function in the scikit-learn toolbox (Pedregosa et al., 2011) in Python 3.9 and then calculated a macro-averaged ROC as the mean of the binary patterns, which assumes all classes are equally weighted. Area under the curve (AUC) of the macro-averaged ROC for each model was computed to illustrate their performances (Figure 6).

8 | OUTPUT

Our optimally performing, trained and tested classifiers can be used for relevant data classification tasks. Using the \textit{prediction.m} script in SVMorph, we designed classifiers to output predicted labels directly. New data that have undergone preprocessing can be classified using the established classifier, and that results in the most relevant labels being assigned to the image data (Figure 7).
9 | USAGE EXAMPLES

9.1 | Wing pattern classification for dead-leaf butterflies

Dead-leaf butterflies (Kallima spp.) are well known for the leaf patterns on the ventral sides of their wings and are thus a classic example of morphological adaptation (Suzuki et al., 2019). Traditionally, those complex morphological variations have been difficult to quantify precisely and efficiently, so we employed SVMorph to establish an SVM model and to classify those polymorphic leaf wing characters. According to the prior knowledge, we labeled them from Morph 1 to Morph 5 (Figure 2a).

During data acquisition and preprocessing, we photoscanned (HP LaserJet Pro M227fdw) ventral forewing images from 230 K. inachus individuals. The subsequent RGB PDF images each had <600 dpi resolution, were extracted using Adobe Photoshop (Adobe Photoshop CC 2018 v19.1.9, Adobe Systems Inc.), and were merged together for batch operations. Then, we preprocessed all the images by first transforming them into eight-bit grayscale format with brightness and contrast adjusted to 10 and −50, respectively, and then cropped them into separate wing images using the `imagecrop.m` script in SVMorph. Then, the images used for the training dataset were classified and labeled manually according to our a priori knowledge ($n_{\text{Morph 1}} = 77$, $n_{\text{Morph 2}} = 56$, $n_{\text{Morph 3}} = 60$, $n_{\text{Morph 4}} = 18$, and $n_{\text{Morph 5}} = 19$). During data augmentation, preprocessed 256 × 256-pixel wing images were randomly cropped to 224 × 224 (Figure 2c). Then, we randomly introduced Gaussian white noise with means ranging from 0.1 to 0.2 and variances ranging from 0.02 to 0.05 (Figure 2c). Contrast values used as input limits were randomly adjusted at low intensity values ranging from 0.0 to 0.1 and high intensity values ranging from 0.9 to 1.0 (Figure 2c). Since the butterfly wing patterns appear in a combination of various elements, we selected HOG as the major feature descriptor. In order to capture relative large-scale wing pattern information while saving computation time, we set 32 × 32-pixel cells and 2 × 2-cell blocks for butterfly images of 256 × 256 pixels. We used nine orientation bins that were evenly spaced from 0 to 180 degrees to encode oriented gradient information (Figure 4) and extracted 1,764-dimensional HOG feature vectors from each image. Considering those high-dimensional feature vectors, we selected the SVM model with the linear kernel function to reduce computational complexity and overfitting, which also guarantees that the model has fine generalization properties. To evaluate the butterfly classifier’s performance, we evaluated accuracy, precision, recall, and F1 scores (Table 1) by using 20 replicates of 10-fold cross-validation. Using data augmentation, the butterfly classifier’s overall accuracy
**FIGURE 6** Receiver operating characteristic (ROC) curves for multiclass classifications. Macro-averaged ROCs and areas under the curve (AUCs) illustrate the predictive abilities of the trained butterfly (a) and spider (b) classifiers. ROC curves plot the true-positive rate against the false-positive rate at various threshold settings, and the threshold settings are determined by posterior probability distributions of all the samples. Both ROC curves in (a) and (b) are far from the diagonals, indicating a high level of model performance relative to random guessing.

**FIGURE 7** Classifier output that can be used for classification tasks. Examples of the output labels predicted by the trained classifiers for dead-leaf butterflies (a) and jumping spiders (b) using test data. Labels M1–M5 correspond, respectively, to butterfly morphs 1–5 shown in Figure 2a, and labels M1–M3 correspond, respectively, to spider morphs 1–3 shown in Figure 2b.
complex of T. maxillosus with which to test SVMorph. Among them, members of the species vantage (Yamasaki & Ahmad, 2013), providing an excellent example data augmentation in the same way as we did for the butterfly data more sensitive than the previous butterfly wing data, we performed $n$ images manually according to their phenotype information ($n_{\text{Morph}} = 19$, $n_{\text{Morph}} = 42$, and $n_{\text{Morph}} = 38$). Since the spider data were more sensitive than the previous butterfly wing data, we performed data augmentation in the same way as we did for the butterfly data except for noise addition and contrast adjustment (Figure 2d). The images were filtered using an averaging filter with a hsize of [3 3] and the convolution option. During feature extraction, we used the same HOG parameters that we had used for the butterfly wing images and extracted 8,100-dimensional HOG feature vectors from each image. In addition, we introduced LBP to extract local texture information. To preserve more local details, we divided the original $512 \times 512$-pixel images into $64 \times 64$-pixel spatial regions and then calculated uniform LBP histograms for each cell (Figure 5). Specifically, a one-radius circular pattern was used to compute the LBP of eight neighbors for each pixel, and rotationally invariant features were not considered. Then, L2 normalization was applied to each cell’s LBP histogram. As a result, 3,776-dimensional LBP feature vectors were extracted from each image of the spider dataset, and both HOG and LBP descriptors were combined into 11,876-dimensional feature vectors for spider image classification. As with the butterfly data, we applied the SVM model with the linear kernel function to those high-dimensional feature vectors. By using 20 replicates of 10-fold cross-validations, we calculated accuracy, precision, recall, and F1 scores that helped us evaluate the jumping spider classifier’s performance (Table 2). With data augmentation, the overall accuracy of the jumping spider classifier was over 94.3% and, as it was with the butterfly classifier, jumping spider Morph 1, which had the smallest sample size, also had a relatively low recall value (83.4%). These results suggest that as training sample size increases, classification performance should improve. The macro-averaged ROC curve showed a considerable predictive ability for spider classification, comparable to that of the butterfly classification model performance (Figure 6).

9.2 | Body texture classification in jumping spiders

Toxeus spp. jumping spiders are highly polymorphic mimics that resemble unpalatable Polyrrachis ants and thus have a protective advantage (Yamasaki & Ahmad, 2013), providing an excellent example with which to test SVMorph. Among them, members of the species complex of T. maxillosus, T. magna, and T. globose are closely related and have three mimicry morphs according to the body texture features that we named from Morph 1 to Morph 3 (Figure 2b).

Using a microscope (Nikon SMZ18) with an attached digital camera (Nikon DS-Ri2), we photographed 99 individual spiders. Raw images were captured using SHR Plan Apo 1x, at zoom magnification of 0.75x with Nikon C-FLED2 LED Light Source. We directly transformed the images into eight-bit grayscale format and zoomed into the abdominal areas (Figure 2b). Finally, we classified and labeled the images manually according to their phenotype information ($n_{\text{Morph}} = 19$, $n_{\text{Morph}} = 42$, and $n_{\text{Morph}} = 38$). Since the spider data were more sensitive than the previous butterfly wing data, we performed data augmentation in the same way as we did for the butterfly data except for noise addition and contrast adjustment (Figure 2d). The images were filtered using an averaging filter with a hsize of [3 3] and the convolution option. During feature extraction, we used the same HOG parameters that we had used for the butterfly wing images and extracted 8,100-dimensional HOG feature vectors from each image. In addition, we introduced LBP to extract local texture information. To preserve more local details, we divided the original $512 \times 512$-pixel images into $64 \times 64$-pixel spatial regions and then calculated uniform LBP histograms for each cell (Figure 5). Specifically, a one-radius circular pattern was used to compute the LBP of eight neighbors for each pixel, and rotationally invariant features were not considered. Then, L2 normalization was applied to each cell’s LBP histogram. As a result, 3,776-dimensional LBP feature vectors were extracted from each image of the spider dataset, and both HOG and LBP descriptors were combined into 11,876-dimensional feature vectors for spider image classification. As with the butterfly data, we applied the SVM model with the linear kernel function to those high-dimensional feature vectors. By using 20 replicates of 10-fold cross-validations, we calculated accuracy, precision, recall, and F1 scores that helped us evaluate the jumping spider classifier’s performance (Table 2). With data augmentation, the overall accuracy of the jumping spider classifier was over 94.3% and, as it was with the butterfly classifier, jumping spider Morph 1, which had the smallest sample size, also had a relatively low recall value (83.4%). These results suggest that as training sample size increases, classification performance should improve. The macro-averaged ROC curve showed a considerable predictive ability for spider classification, comparable to that of the butterfly classification model performance (Figure 6).

Finally, the preprocessed spider test data were classified using the trained classifier and labeled accordingly (Figure 7b). The feature extraction and classification process for the spider dataset with 11,876-dimensional feature vectors took approximately 0.04 s per image to compute. Our results showed that the spider image data were precisely classified and assigned to the abovementioned morphs, thus suggesting that these spiders could be classified according to their body textures and without any intermediate morph.

9.3 | Performance of SVMorph and other methods

To evaluate the performance of SVMorph, we compared the accuracy and running time for SVMorph and other methods including the morphology-based taxonomy and three established deep learning (Convolutional Neural Network, CNN)-based models such as AlexNet (Krizhevsky et al., 2012), GoogLeNet (Szegedy et al., 2015), and VGG...
both datasets. The SVMorph method performed better with consider-
CNN-based methods showed relatively lower accuracy in analyzing
focus on the generalization ability instead of specificity.
complex classification tasks, and the deep learning-based algorithms
the two datasets, suggesting its application potential on specific and
CNN-based methods and SVMorph cost less time. However, one of the
the manual morphology-based taxonomy, all the
(time was the mean value of ten separate runs. For the butterfly data-
set, we have not established a reliable morphology-based taxonomy;
whereas for the spider dataset, we quantified the spider body textures
using a scanning electron microscope (SEM). The SEM images showed
that the different body textures were due to different cuticle struc-
tures and seta lengths. We collected six individuals for each phenoe-
type and measured three setae for each individual, which took about
two days. Relative to the manual morphology-based taxonomy, all the
CNN-based methods and SVMorph cost less time. However, one of the
the CNN-based methods showed relatively lower accuracy in analyzing
both datasets. The SVMorph method performed better with consider-
ably high accuracy and the least amount of running time when handling
the two datasets, suggesting its application potential on specific and
complex classification tasks, and the deep learning-based algorithms
focus on the generalization ability instead of specificity.

10 | DISCUSSION

The scales and setae of invertebrates are single-cellular cuticular
structures extending from the cuticle, which play an important role
in generating phenotypic diversity and can have a profound impact
on fitness (Tian et al., 2019). Taken the two sample datasets as an
example, the dead-leaf butterflies in K. inachus display a remarkable
diversity of leaf wing patterns for masquerade (Protas & Patel, 2008),
whereas different morphs of Toxeus jumping spiders mimic different
ant species to gain a protective advantage (Yamasaki, 2015). These
cuticular structures accommodate not only color variation but also
shape variation such as length, width, and diameter of a cross sec-
tion, and pilosity variation (Matsuoka & Monteiro, 2018). Therefore,
the complexity in cuticular structures makes it difficult to classify the
phenotypes and understand the underlying mechanisms of pheno-
typic diversity. To characterize the wing coloration of butterflies, one
may measure wavelength reflectance in at least three locations: the
main vein, lateral veins, and spots. To quantify the texture patterns,
one may need to place setae on scanning electron microscopy (SEM)
stubs, sputter-coat them with gold–palladium, and measure their
length and width under SEM. However, it is difficult and inefficient
to apply these quantifying methods to large-scale datasets. SVMorph
is a convenient and efficient method for identifying variations of cu-
ticular structures such as setae and scales. The method obtained in
this study can be used for analyzing wing patterns and body textures,
which could fully develop identification systems of phenotypic poly-
morphism for such nonmodel organisms and bridge the gap between
genotype and phenotype. Furthermore, due to the generality of the
proposed method, it can be used with no major modification for other
tasks, such as analyzing cuticular structures in other invertebrates.

11 | CONCLUSIONS

SVMorph, a fast and accurate pipeline for handling classification
tasks with complex patterns and textures, is particularly helpful
for batch processing large image data applications. Also, based on
the performance of a trained classifier, it can be used to examine
a priori hypotheses of organismal classifications or to extract and
investigate images with rare morphological features that cannot
be appropriately labeled. Moreover, SVMorph is very modular and
easy to schedule, thus giving the researcher the ability to perform
each step independently and interactively with other applications. In
summary, SVMorph efficiently characterizes and classifies morpho-
logical characters of nonmodel organisms.

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CONFLICT OF INTEREST

None declared.

AUTHOR CONTRIBUTION

Dequn Teng: Conceptualization (supporting); Data curation (equal);
Formal analysis (lead); Methodology (lead); Resources (lead); Software
(lead); Validation (equal); Visualization (lead); Writing-original draft
(lead); Writing-review & editing (supporting). Fengyuan Li: Data cura-
tion (equal); Formal analysis (supporting); Funding acquisition sup-
porting); Resources (supporting); Software (supporting); Validation
(equal); Visualization (supporting); Writing-original draft (supporting);
Writing-review & editing (supporting). Wei Zhang: Conceptualization (lead);
Data curation (equal); Formal analysis (supporting); Funding acquisi-
tion (lead); Investigation (lead); Methodology (equal); Project admin-
istration (lead); Resources (equal); Software (supporting); Supervision
(lead); Validation (equal); Visualization (equal); Writing-original draft
(lead); Writing-review & editing (lead).

OPEN RESEARCH BADGES

This article has been awarded Open Data, Open Materials Badges. All
materials and data are publicly accessible via the Open Science
Framework at https://github.com/TDQ233/SVMorph.
SVMorph is available at GitHub (https://github.com/TDQ23/SVMorph) and Dryad (https://doi.org/10.5061/dryad.tdz08kq0g).

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