

How cryptic is cryptic diversity? Machine learning approaches to plastral variation in *Emys marmorata*.

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Abstract

2

1 Introduction

4 Cryptic diversity is when taxa were only first delimited via molecular means and were not or cannot be delimited via morphological identification
6 CITATION. The discovery of this previously unknown diversity has
8 Here, we address the question of how much of cryptic diversity may be a product of sample size as well as methodology used for classifying taxa based solely on morphology. Specifically, we ask if fine scale variation in morphology

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10 can provide corroboration for subspecific assignment, and if it is possible to
determine the best classification hypothesis amongst a few.

12 In this study, we address the subspecific classification scheme of *Emys*
marmorata, or western pond turtle. *E. marmorata* has a distribution from
14 northern Washington State, USA to Baja California, Mexico. Traditionally,
E. marmorata was classified into three subgroups: the northern *E. marmorata*
16 *marmorata*, the southern *E. marmorata palida*, and a central Californian
intergrade zone (Seeliger, 1945). More recently, *E. marmorata* was divided
18 into four subgroups based on mitochondrial DNA: a northern clade, a southern
clade, and two central Californian clades (Spinks and Shaffer, 2005; Spinks
20 et al., 2010).

In this study, we apply multiple machine learning approaches to esti-
22 mate the best classification scheme of *E. marmorata* subspecies based on
morphological variation in plastral shape.

24 **2 Materials and Methods**

2.1 Specimens

26 We collected morphometric data from 524 specimens. Geographic information
was recorded from museum collection information. When precise latitude and
28 longitude information was not known for a specimen, it was inferred from
whatever locality information was presented.

30 Specimens were given a class assignment was based on geographic informa-
tion. Because the exact geographic barriers between different class is unknown
and fuzzy, two assignments for both morphological and molecular hypotheses
32 of class were used.

34 **2.2 Geometric morphometrics**

Following Angielczyk et al. (2011), 19 landmarks were digitized using TpsDig
36 2.04 (Rohlf, 2005). 17 of these landmarks are at the endpoints or intersection
of the keratinous plastral scutes that cover the plastron. These landmarks were
38 chosen to maximize the description of plastral variation. 12 of these landmarks
are symmetrical across the axis of symmetry and in order to prevent degrees
40 of freedom and other concerns (Klingenberg et al., 2007), these landmarks
were reflected across the axis of symmetry and the average position of each

42 symmetrical pair was used. In cases where damage or incompleteness prevented
 44 symetric landmarks from being determined, only the single member of the
 pair was used. Analysis was then conducted on the resulting “half” plastra.
 “Half” plastra landmark configurations were superimposed using general-
 46 ized Procrustes analysis (Dryden and Mardia, 1998) after which, the principal
 components of shape were calculated. This was done using the **shapes** package
 48 for R (Dryden, 2013; R Core Team, 2013).

2.3 Machine learning analyses

50 2.3.1 Unsupervised learning

Because shape space, or configurations after Procrustes superimposition, is a
 52 Riemannian manifold (Dryden and Mardia, 1998) the dissimilarity between
 each landmark configuration was measured as the Riemmanian shape distance
 54 or ρ (Dryden and Mardia, 1998; Kendall, 1984) which should vary between 0
 and $\pi/2$ assuming no reflection invariance.

56 The dissimilarity matrix of shape was divisivly clustering using partitioning
 around mediods (PAM) which is analogous to k -means clustering except that
 58 instead of minimizing the sum of squared Euclidean distances between obser-
 vations and centroids, the sum of squared dissimilarities between observations
 and mediods is minimized (Kaufman and Rousseeuw, 1990). The optimal
 60 number of clusters of shape configurations is unknown being possibly three,
 62 four, or some other value. Clustering solutions were estimated for between 1
 and 40 clusters. Clustering solutions were compared using the gap statistic,
 64 which is a measure of goodness of clustering (Tibshirani et al., 2001). Standard
 errors of the gap statistic for each clustering solution were estimated from
 66 500 bootstrap samples. PAM clustering and gap statistic calculation was
 conducted using the **cluster** package for R (Maechler et al., 2013).

68 2.3.2 Supervised learning

The dataset of 524 plastron landmarks was split into training and testing
 70 datasets. The former was used for model fitting (training) and was 75% of the
 total dataset, split proportionally per class, while the testing dataset was used
 72 to estimate the effectiveness of each classification scheme (i.e. performance in
 the wild).

74 Two types of supervised learning, or classification, models were fit to

the PCs of plastral shape: multinomial logistic regression and random forest.
76 These model types were chosen because of various properties of these models
which allow for useful interpretations about the strength and structure of the
78 classification. Multinomial logistic regression models were fit using the **nnet**
package for R (Venables and Ripley, 2002) while random forest models were
80 fit using the **randomForest** package for R (Liaw and Wiener, 2002).

Multinomial logistic regression is an extension of logistic regression, where
82 instead of a binary response it is possible to have three or more response
classes CITATION. Effectively, this type of model can be viewed as multiple,
84 simultaneous logistic regression models for each class and the final classification
of the observation being the most probable of all the sub-model classifications.
86 From the final model the relative risk of a given classification, with reference
to a given class, can be calculated from the coefficients of the features, or
88 predictors. This is similar to the log-odds calculated from the coefficients of a
logistic regression.

Random forest models are an extension of classification and regression
90 trees (CART) CITATION. Basically, CARTs are built for random subsamples
of both the features of the proposed model and observations. This process is
92 repeated many times, 1000 times here, and the final model is chosen as the
mode of the parameter estimates from the distribution of CARTs CITATION.
94 In addition to fitting a classification model, this procedure allows for the
features to be ranked in order of importance, means that the variables most
96 important for determining a given classification scheme can be estimated.
In the context of predicting class from geometric morphometric data, this
98 identifies the PCs that describe the variation that best distinguishes the
100 different classes.

In order to prevent over fitting each machine learning model, tuning
102 parameters were estimated using 10-fold cross-validation (CV) across a grid
search of all tuning parameter combinations. Optimal tuning parameter values
104 were selected based on area under the receiver operating characteristic curve
(AUC ROC). Multiclass AUC ROC was estimated using the all-against one
106 strategy derived by Hand and Till (2001) in implemented in PROC PACKGE.

For the multinomial logistic regression models, PCs were added sequentially
108 in order to increase the overall amount of variation in shape included in each
model and the final model was that with the lowest AICc (Burnham and
110 Anderson, 2002) AKAIKE AND OTHER CITATION. This procedure was
used because the optimal number of PCs to include is unknown, and while
112 including all of the PCs of shape would mean that all of the variability in

114 plastron shape would be used to estimate class, this may cause the model
to be over fit and not provide an accurate estimate of unsampled plastral
variation. The maximum number of PCs allowed to be used as predictors was
116 10 because of both the number of parameters estimated per model and the
necessary sample size needed to estimate that many parameters accurately.

118 Because random forest models are not fit using maximum likelihood, a
recursive feature selection algorithm was used to choose the optimal number
120 of PCs to include based on the AUC ROC of the model. PCs were sequentially
added as features until the AUC ROC of the model did not increase. After
122 each PC was added, 10-fold CV was used to estimate the optimal values
of the tuning parameters as well as quantify the uncertainty of each model.
124 Like the multinomial logistic regression models, 10 was the maximum number
of PCs that could have been included in the model. The recursive feature
126 selection algorithm used here is that implemented in the `caret` package for
R (Kuhn, 2013).

128 The final selected models were then used to estimate the class assignments
of the training dataset. Model performance was measured using AUC ROC. A
130 distribution of AUC ROC values were estimated for each classification scheme
using 1000 nonparametric bootstrap resamples of the training dataset.

132 3 Results

3.1 Geometric morphometrics

134 3.2 Machine learning analyses

3.2.1 Unsupervised learning

136 Comparison of the gap statistic values for the different PAM solutions indicates
that the optimal number of clusters is 1 (Fig. 1). The second best clustering
138 solution is two clusters, however there is no geographic structure to this
classification scheme SUPPLEMENT?. Increasing the number of clusters does
140 appear to improve the gap statistic enough to merit comparison.

3.2.2 Supervised learning

142 For all classification schemes, the optimal random forest model based on
recursive feature selection by maximizing AUC ROC of the model was one

144 with many features (Fig. 2)

146 Results of the bootstrap resamples of the AUC ROC of the generalization
of the selected multinomial logistic regression and random forest models
demonstrates that one of the molecular classification hypotheses based on
148 Spinks and Shaffer (2005) and Spinks et al. (2010) appears to be the best
classification scheme (Fig. 3). The distribution of bootstrapped AUC ROC
150 for the molecular hypothesis is significantly different MANN-WHITNEY
U TEST and greater than all of the other classification scheme. What is
152 remarkable is that the best classification hypothesis is identical based on both
the multinomial logistic regression and random forest models.

154 When the classification results of the training set for the optimal classification
scheme are compared with the references classes, (Fig. 4)

156 4 Discussion

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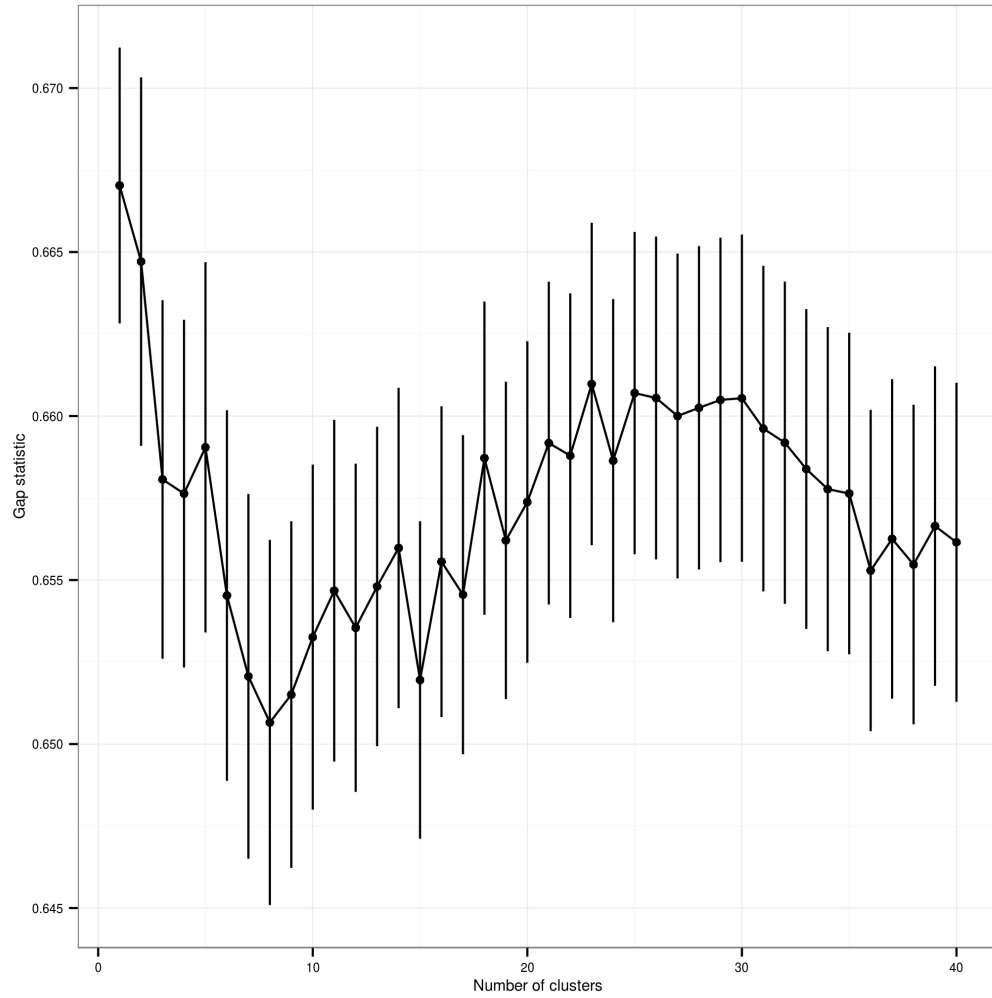


Figure 1: Gap statistic values for PAM clustering results for the ρ dissimilarity matrix of plastron shape. Error bars are standard errors estimated via 500 bootstrap samples.

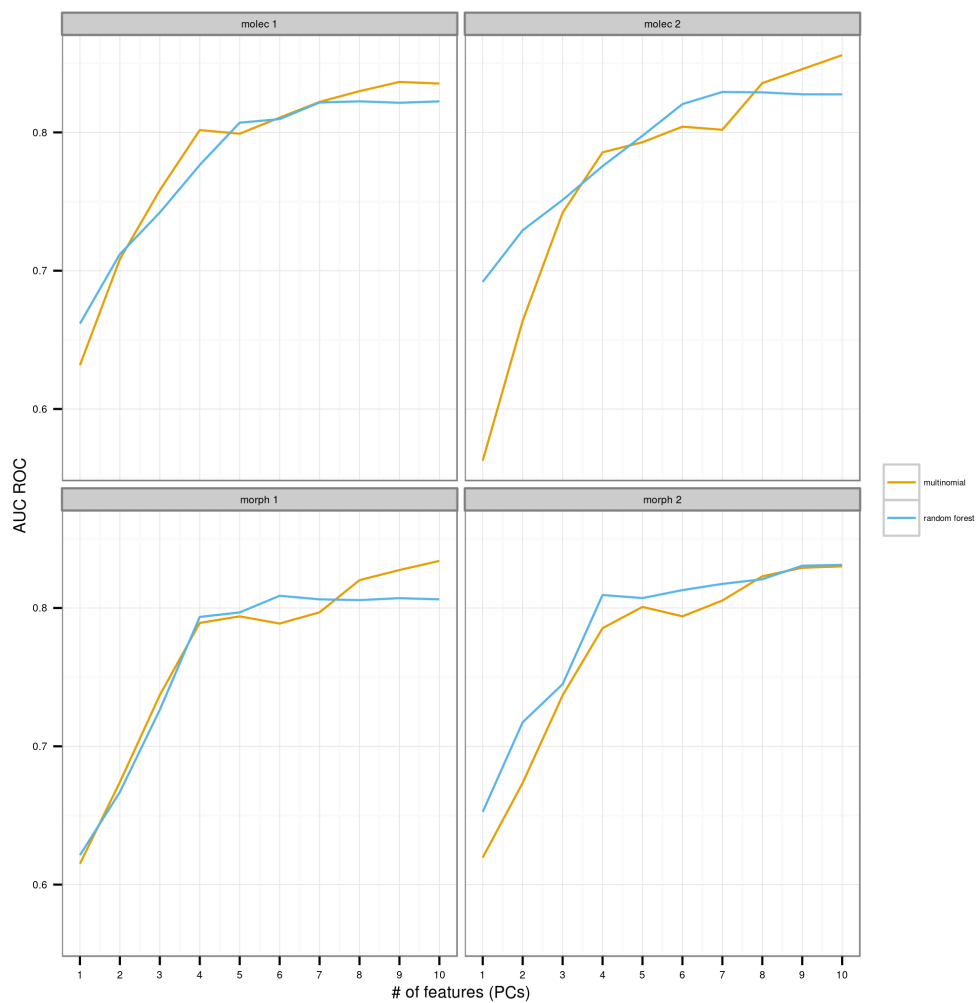


Figure 2: Effect of increasing the number of PCs as features, or predictors, of classification of plastra for all four classification schemes. As the number of PCs increase, AUC ROC increases until eventually leveling off. Both multinomial logistic regression and random forest models are illustrated here, though AUC ROC based model selection was only performed for random forest models.

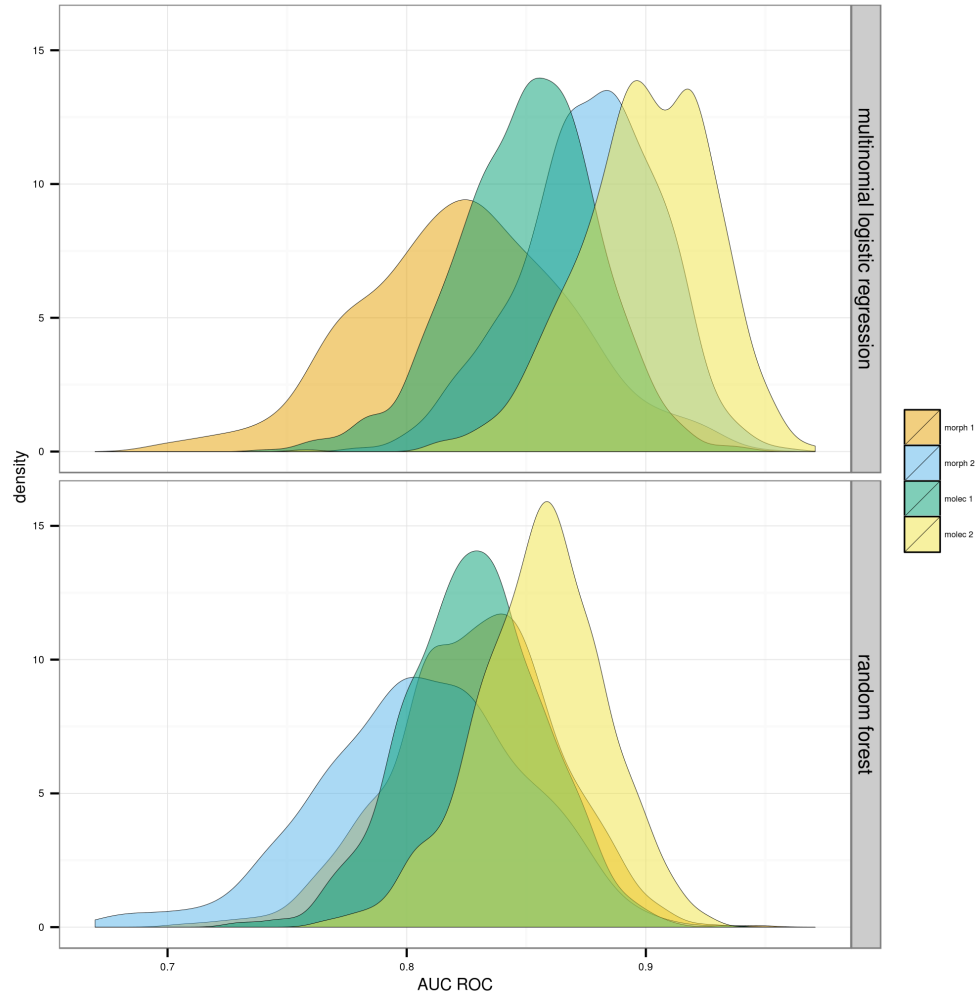


Figure 3: Density estimates of AUC ROC values of predictions of the testing dataset of plastra from 1000 bootstrap resamples. The top facet corresponds to values using the optimal multinomial logistic regression model, as chosen by minimum AICc value. The bottom facet corresponds to the values using the optimal random forest model, as chosen by maximum AUC ROC value.

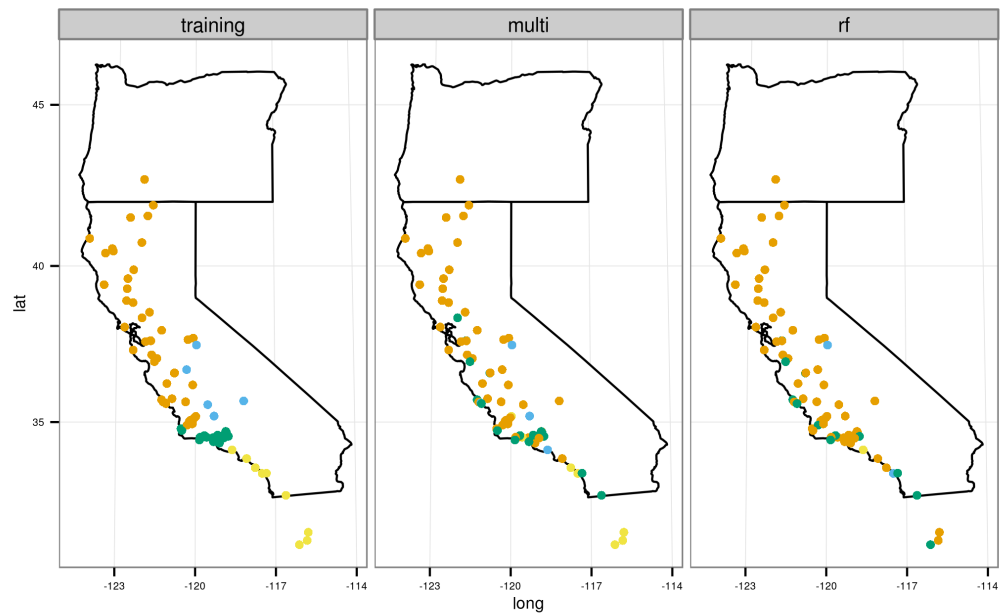


Figure 4: Comparison between reference classification of testing data set and the estimated classifications based on the selected multinomial logistic regression and random forest models, from left to right respectively. Classification corresponds to the four classes as suggested by the hypothesis of Spinks and Shaffer (2005) and Spinks et al. (2010).