# How cryptic is cryptic diversity? Machine learning approaches to fine scale variation in the morphology of *Emys marmorata*.

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# Cryptic diversity

Crytic species are species delimitated via molecular means. Taxa were not/cannot be identified via morphology.

How much of cryptic diversity is just a function of sample size and/or method?

# *Emys marmorata*

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# Morphological hypothesis

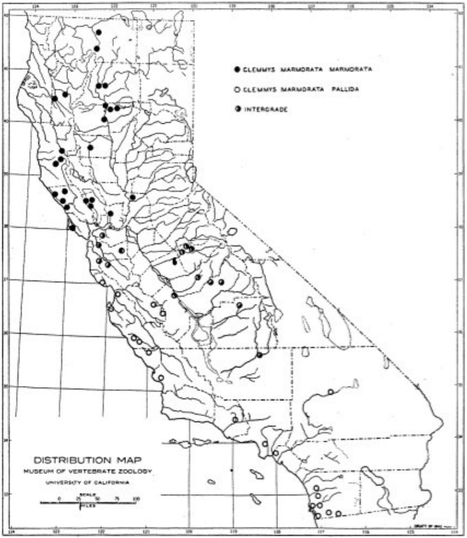
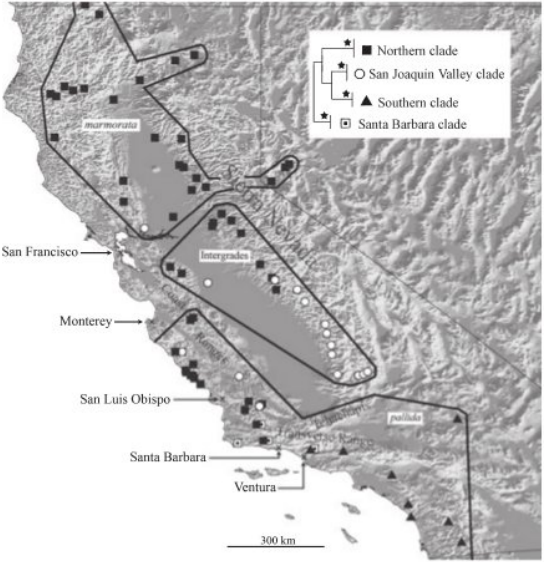



Fig. 4. California localities from which specimens have been examined.

Seeliger 1945 *Copeia*

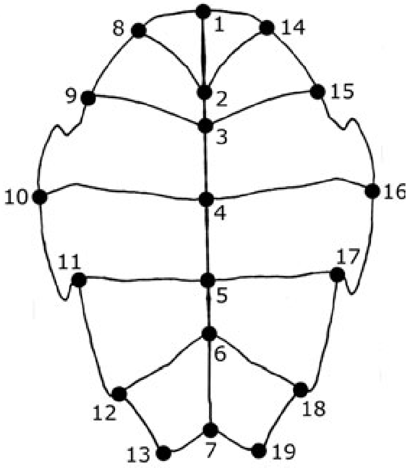
# Phylogenetic hypotheses




Spinks *et al.* 2010 *Molec. Ecol*

# Methods: morphometrics

- 524 adult individuals
- plastral (“belly”) shape
- landmarks averaged across bilat axis
- total 13 landmarks, 7 on bilat axis, 6 off
- geographic information known/inferred




Angielczyk *et al.* 2011 *Evolution*

# Unsupervised learning

Fancy way of saying clustering or density estimation.

Partitioning around mediods (PAM) compared with “gap” statistic.

Analogous to $k$-means clustering, a divisive clustering algorithm.

Minimize sum of dissimilarities between points and medoids.

“Gap” is analogous to goodness-of-clustering.

# Supervised learning

Fancy way of saying classification (and regression).

Features (principal components) predict class (subspecific assignment).

Multinomial logistic regression and random forests.

# Model training and selection

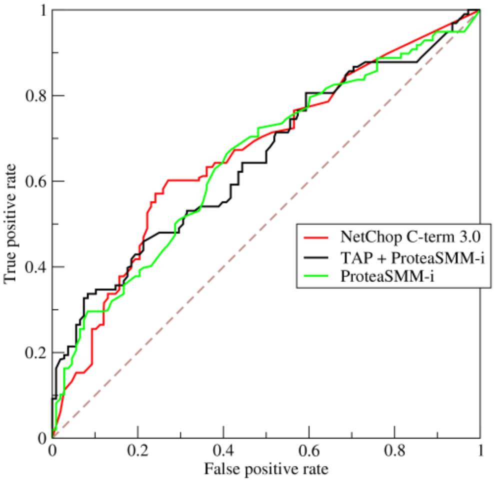
- split into training and testing sets, 75-25.
- tuning parameters via grid-search
- uncertainty via 10-fold CV
- model selection
  - multinomial logistic regression: min AICc
  - random forest: max ROC

# ROC and confusion matrices

| | | Predicted class | |
|---|---|---|---|
| | | 1 | 0 |
| Actual class | 1 | TRUE POSITIVE | FALSE NEGATIVE |
| | 0 | FALSE POSITIVE | TRUE NEGATIVE |

# ROC

- true positive rate or sensitivity: $\frac{TP}{TP+FN}$
- false positive rate or 1 - specificity: $\frac{FP}{FP+TN}$
- multiclass, all-against one (Hand and Till 2001 *Machine Learning*)

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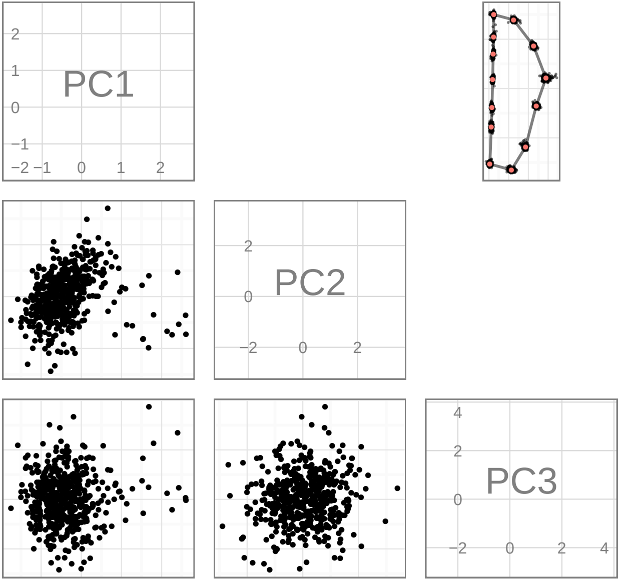
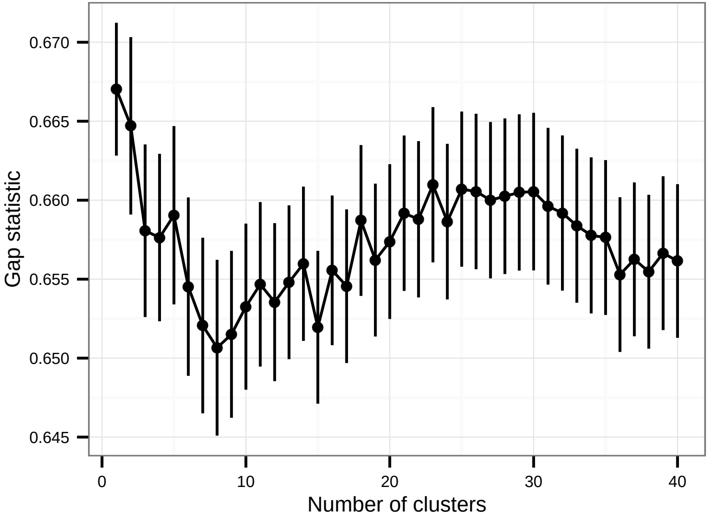
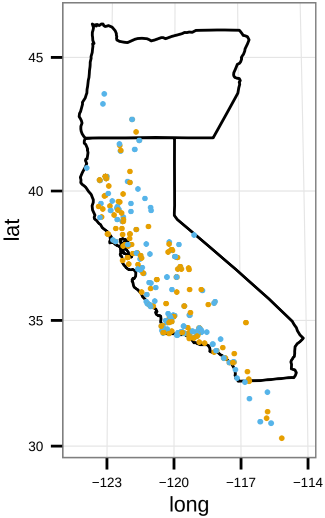
# Results: mophometrics



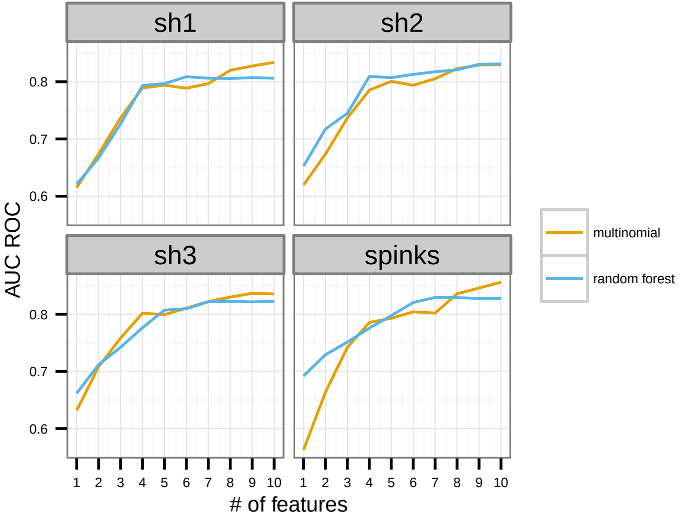
# Results: gap clustering



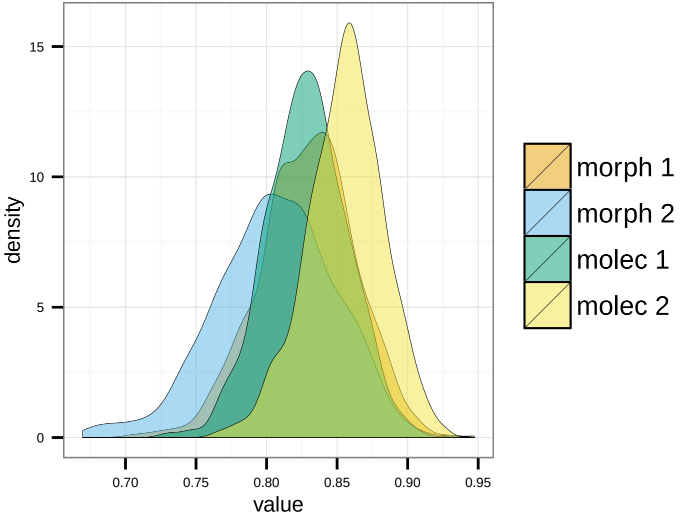
# Second best cluster



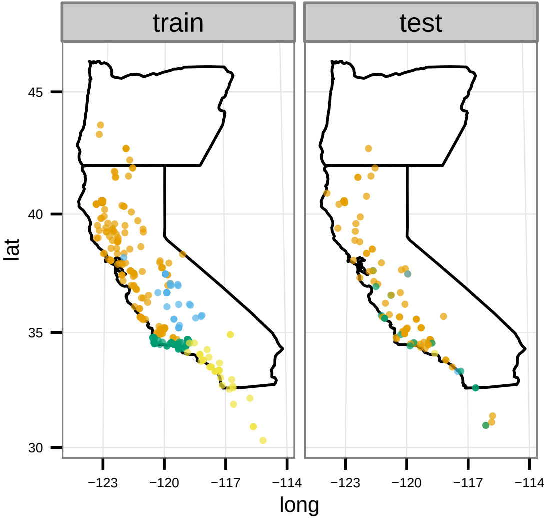
# Model selection via ROC



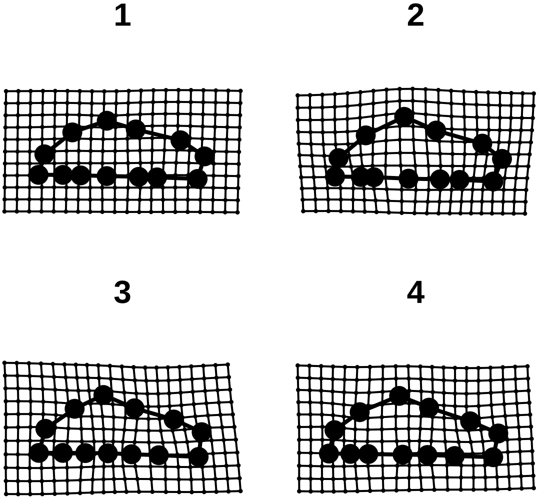
# Generalize using best random forest model



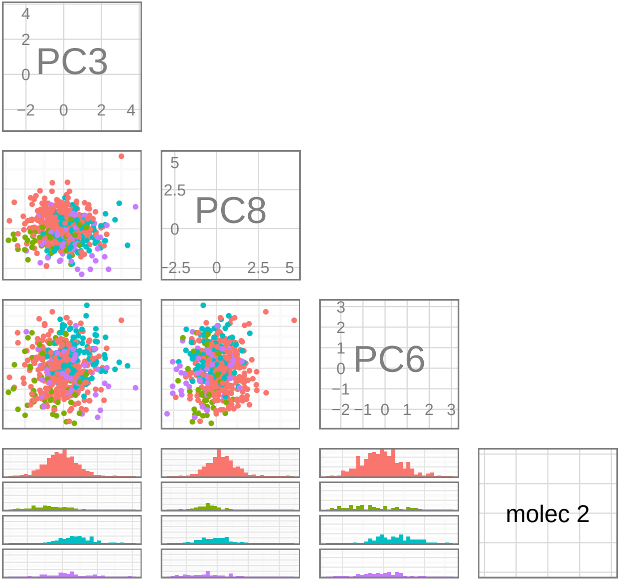
# Best classification scheme via RF model results



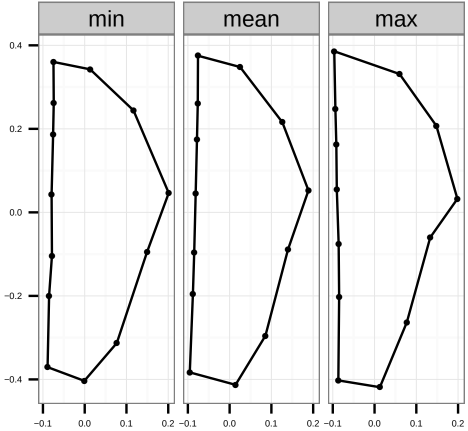
# Mean shape of classes



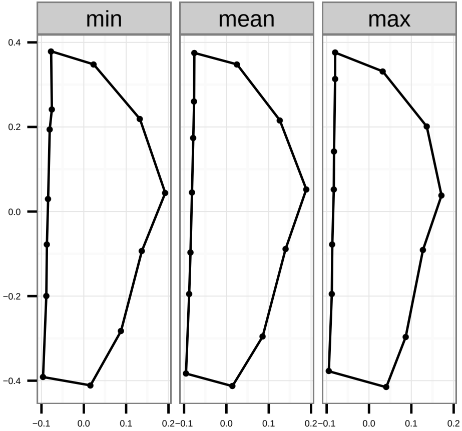
# Variable importance of random forest model



# Shape across PC3



# Shape across PC8



# Future

- illustration of morphological validation of previously cryptic variation
  - the concordance is remarkable
  - large sample sizes can be difficult
- utility of large data, machine learning methods
- unsupervised methods for when no explicit hypothesis – nonparametric Bayes
- cause of interclass variation – local adaptation? pure isolation?

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