

# Determinants of Anuran Distributions

## INTRODUCTION

### Research Question:

Is the distribution of breeding Pacific chorus frogs (*Pseudacris regilla*) determined by factors at local, patch, or landscape scales?

### Hypotheses:

- 1 Local habitat scale: If Pacific chorus frog abundance is high and frog movement in the region is unrestricted, breeding frogs will be found most consistently in wetlands with high emergent plant densities, because frogs with unrestricted mobility tend to aggregate at breeding sites with highest density of egg-attachment structures.
- 2 Local habitat scale: If Pacific chorus frog abundance is high, frog movement is unrestricted, and predation risk is high, then breeding frogs will be found most consistently in wetlands with a large number of vegetation layers, because frogs with unrestricted mobility tend to aggregate at breeding sites with more concealing vegetative cover. (Up to 5 layers: emergent, terrestrial herbaceous, shrub, understory, forest canopy.)
- 3 Habitat patch scale: If Pacific chorus frog movement in the region is relatively unrestricted, breeding frogs will be found most consistently in larger wetlands, because female frogs tend to prefer larger aggregations of calling males.
- 4 Landscape scale: If dispersal barriers obstruct Pacific chorus frog movement in the region, frogs will be found most consistently in wetlands with greatest connectivity to other regional breeding sites because frogs migrating to breeding sites often will not be able to access relatively isolated sites and because well-connected sites are less vulnerable to local extinctions (Trenham et al. 2003).

## FIELD METHODS

### Equipment Needed

data sheets  
pencil/pen  
stopwatch  
thermometer  
GPS receiver

### Sampling Protocol

This protocol is adapted from that used in the Wisconsin Frog and Toad Survey, <http://wiatri.net/inventory/FrogToadSurvey> and described in Heyer et al. (1994).

- 1 Sample at dusk, when wind velocity does not exceed 13 km/hr..
- 2 Approach each sample site quietly, ideally alone or with one companion.
- 3 Listen for 5 minutes (3 minutes if time is short) at each site. For each species, record the highest value of the call index heard during the observation period. See the attached data form for index value definitions.
- 4 After the observation period, record wetland water temperature, and estimate the mean stem density of emergent plants throughout the wetland, and number of vegetation layers in or above the wetland.
- 5 Repeat steps 1–4 at each sample site.

## DATA ANALYSIS

### Model Fitting

In this project, the response variable is categorical and all explanatory variables are continuous. Hence, logistic regression is the appropriate analytical method. To simplify matters, consider detection of any frogs at a site (calling index 1-3) to be a “detection” or  $Y = 1$ . A logistic regression model containing one explanatory variable is given by the following, which relates  $\pi$ , the probability that  $Y = 1$ , to a single explanatory variable,  $x$ .  $\beta_0$  and  $\beta_1$  are fitted constants.

$$\log\left(\frac{\pi}{1-\pi}\right) = \beta_0 + \beta_1 x_1 \quad (1)$$

From this model, the probability of detecting frogs at a give site is the following.

$$\pi = \frac{\exp(\beta_0 + \beta_1 x_1)}{1 + \exp(\beta_0 + \beta_1 x_1)} \quad (2)$$

A measure of fit of the model is obtained by calculating the log-likelihood  $R^2$ :

$$R^2 = 1 - \frac{\text{residual deviance}}{\text{null deviance}} \quad (3)$$

You should fit a logistic regression model for each of the three hypotheses to the data. Use mean emergent stem density, wetland area, and wetland  $x_i^2$  as explanatory variables for local, patch, and landscape scales, respectively.  $x_i$  is  $i^{\text{th}}$  element in the leading eigenvector of metapopulation matrix  $\mathbf{M}$ , as defined in Hanski and Ovaskainen (2000). Values for the response variable and all three explanatory variables are listed in a table linked to the course web site. For instructions on fitting logistic regression models to data, including a worked example, see:

[https://faculty.jmcl.wvu.edu/Biostat/1\\_glm.pdf](https://faculty.jmcl.wvu.edu/Biostat/1_glm.pdf)

### Model Selection

You should evaluate empirical support for each model relative to the others using Akaike’s Information Criterion (AIC). Because the ratio of sample size to number of parameters is less than 40, you should apply an adjustment for small sample sizes,  $AIC_c$ . (For details, see the following course readings: Anderson et al. 2000. *J. Wildl. Manage.* 64:912-923; Anderson and Burnham. 2002. *J. Wildl. Manage.* 66:912-918.

- 1 Enter your data into some electronic format. R or \*.csv formats recommended.
- 2 Fit models for hypotheses 1-3 to the data using logistic regression, as described above. For each model, determine estimates for  $\beta_0$ ,  $\beta_1$ , and residual deviance.
- 3 Calculate an  $AIC_c$  score for each model, using residual deviance values. Because all models contain a single explanatory variable, and residuals are assumed to be binomially distributed,  $K = 2$ .
- 4 Identify the model with the smallest  $AIC_c$  score, and subtract it from  $AIC_c$  scores for the other models to determine  $\Delta_i$  values.

$$\Delta_i = AIC_i - \min(AIC)$$

- 5 Use  $\Delta_i$  values to determine Akaike weights,  $w_i$ , which measures the probability that model  $i$  is the best among all models considered.

$$w_i = \frac{\exp\left(-\frac{1}{2}\Delta_i\right)}{\sum_{r=1}^R \exp\left(-\frac{1}{2}\Delta_r\right)}$$

8 Identify the confidence set for best model. The confidence set can be determined in three ways. The simplest in practice is to include all models with  $\Delta_i \leq 2$ . A second method includes models with the largest weights ( $w_i$ ), such that the weights sum to a given fraction (e.g., 95%). For more information, including the third method, see [https://faculty.jmcl.wvu.edu/Biostat/1\\_AICerr3.pdf](https://faculty.jmcl.wvu.edu/Biostat/1_AICerr3.pdf)

9 Calculate log-likelihood  $R^2$  for each model in the confidence set:

$$\text{log-likelihood } R^2 = 1 - \frac{RD}{ND}, \quad \text{where } RD = \text{residual deviance, and } ND = \text{null deviance.}$$

10 Interpret results of your analysis to answer the research question. Consider the following questions in your interpretation. Which model(s) best explained patterns in frog distribution? How confident are you in your selection of best model(s)? Why might the variable in that model be more informative than the other variables? How strong is the relationship described by your selected model(s)? (How large is the predictor variable coefficient?) How much of the variation in frog site occupancy is explained by the selected model? (e.g., what is the value of log-likelihood  $R^2$ ?)

11 In the Results section of your report about this project, you should include the following quantities for each model considered: (1) log-likelihood, number of estimated parameters ( $K$ ), the value of the selection criterion ( $AIC_c$ ), difference ( $\Delta_i$ ), and the Akaike weight ( $w_i$ ). In addition, you should report the following for each model in the confidence set: log-likelihood  $R^2$ , model parameters ( $\beta_0, \beta_i$ ), and standard errors of model parameters. Do not report  $P$ -values or other results of statistical hypothesis testing, which are not relevant in this model selection/information-theoretic approach.

12 Please note that logistical constraints in this project limited sample size to a value much smaller than statistical guidelines recommend. If you were to determine  $P$ -values for model parameter estimates, those values likely would exceed conventional standards. Because this project does not involve testing statistical null hypotheses,  $P$ -values are not relevant here. Nevertheless, small sample sizes are likely to cause considerable uncertainty in data analysis and result interpretation.

## REFERENCES

- Anderson, DR, KP Burnham, WL Thompson. 2000. Null hypothesis testing: Problems, prevalence, and an alternative. *J.Wildl.Manage.* 64:912-923.
- Anderson, DR and KP Burnham. 2002. Avoiding pitfalls when using information-theoretic methods. *J.Wildl.Manage.* 66:912-918.
- Hanski I and O Ovaskainen. 2000. The metapopulation capacity of a fragmented landscape. *Nature* 404:755-758.
- Heyer, WR, et al., eds. 1994. *Measuring and Monitoring Biological Diversity: Standard Methods for Amphibians*. Smithsonian Institution Press, Washington, D.C.
- Trenham PC, et al. 2003. Regional dynamics of wetland-breeding frogs and toads: turnover and synchrony. *Ecol. Appl.* 13:1522-1532.

Date \_\_\_\_\_ Recorder \_\_\_\_\_  
 Location \_\_\_\_\_  
 Weather \_\_\_\_\_

Instructions: Conduct surveys at dusk, when wind velocity is less than 13 km/hr. Listen 5-10 minutes at each site and record a call index of 1, 2, or 3 (see below) for each species heard.

First Visit				Call Index (1, 2, 3)*			
SITE NAME	H <sub>2</sub> O Temp	# Veg. Layers	Stem density (stems/m <sup>2</sup> )	<i>Pseudacris regilla</i> Pacific Chorus Frog	<i>Rana aurora</i> Red-Legged Frog	<i>Rana catesbeiana</i> Bullfrog	<i>Bufo boreas</i> Western Toad
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
Mean							

Second Visit				Call Index (1, 2, 3)*			
SITE NAME	H <sub>2</sub> O Temp	# Veg. Layers	Stem density (stems/m <sup>2</sup> )	<i>Pseudacris regilla</i> Pacific Chorus Frog	<i>Rana aurora</i> Red-Legged Frog	<i>Rana catesbeiana</i> Bullfrog	<i>Bufo boreas</i> Western Toad
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
Mean							

\* The call index is a rough measure of the abundance of calling males of a species, scored as follows.

- 1 Individuals can be counted; there is a gap between calls.
- 2 Calls of individuals can be distinguished, but there is some overlap of calls.
- 3 Full chorus; calls are constant, continuous, and overlapping.