

Modeling Predator Preferences

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Abstract

Words

Introduction

Methods

One can imagine that a predator eats prey species s upon each encounter, but prey species s' less frequently. Further, predator preferences could change by

Let $X_{jst} \stackrel{\text{iid}}{\sim} \mathcal{P}(\lambda_{st})$ denote the number of prey species s that predator j ate during occurrence t ; $j \in \{1, \dots, J_t\}$, $s \in \{1, \dots, S\}$, $t \in \{1, \dots, T\}$. Further, let $Y_{ist} \stackrel{\text{iid}}{\sim} \mathcal{P}(\gamma_{st})$ denote the number of prey species s found in trap i during occurrence t ; $i \in \{1, \dots, I_t\}$. We make formal statistical statements about the relative magnitudes of the parameters $\boldsymbol{\lambda}$ and $\boldsymbol{\gamma}$. The four hypotheses considered provide variations on the relative magnitude of $\lambda_{st}/\gamma_{st} = \xi(c_{st})$, for a mapping $\xi : c_{st} \mapsto \{1, c, c_s, c_t, c_{st}\}$. When ξ maps to a constant with respect to one of the indexing variables, s or t , intuitive statements are realized about the predator's preferences. Table 1 depicts the ways in which the proportionality constants can vary, or not, for each of the four hypotheses.

		Time	
		constant	varies
Species	constant	c	c_t
	varies	c_s	c_{st}

Figure 1: The four hypotheses considered are shown by their symbolic representations, highlighting which indices are allowed to vary. This is essentially the range of the mapping ξ .

All hypotheses are evaluated via a likelihood ratio test, essentially an asymptotic χ^2_ρ distribution with ρ degrees of freedom set equal to the number of free parameters available

in the stated hypotheses under question. For instance, if we state under the null hypothesis that $H_0 : \lambda_t = c_t \gamma_t, \forall t$ and contrast this against $H_1 : \lambda_{st} = c_{st} \gamma_{st}$ then there are $\rho = 2 \cdot S \cdot T - S \cdot T - T = S \cdot T - T$ degrees of freedom. The alternative hypothesis previously stated is not in fact fit by estimating c_{st} , but is instead fit as if $c_{st} \gamma_{st}$ were $S \cdot T$ unique parameters independent of λ_{st} for all s, t , thus providing $2 \cdot S \cdot T$ total parameters for the hypothesis we denote by c_{st} .

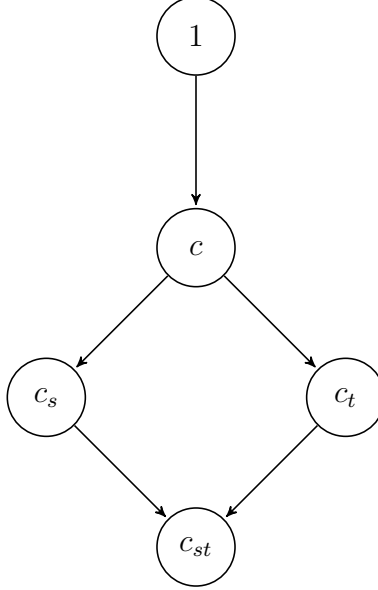


Figure 2: Hierarchy of hypotheses.

The likelihood function that allows for estimation of these parameters is as follows. Since we assume $X_{jst} \perp Y_{ist}$ we can simply multiply the respective Poisson probability density functions together, and then form products over all s, t to get the likelihood

$$L(x_{jst}, y_{ist} | \boldsymbol{\lambda}, \boldsymbol{\gamma}) = \prod_{t=1}^T \prod_{s=1}^S \left\{ \prod_{j=1}^{J_t} f_X(x_{jst} | \boldsymbol{\lambda}) \prod_{i=1}^{I_t} f_Y(y_{ist} | \boldsymbol{\gamma}) \right\}. \quad (1)$$

In some cases analytic solutions for the maximum likelihood estimates are available, namely when the data are balanced $J_t = J$, $I_t = I$, and $\xi(c_{st}) = c$ or when estimating $\lambda_{st}, \gamma_{st}$ under the hypothesis represented by c_{st} . In all other cases, analytic solutions are not readily available. In this case, we rely on the fact that the log-likelihood $l(\boldsymbol{\lambda}, \boldsymbol{\gamma}) = \log L$ is concave and iteratively solve

$$c = \frac{\sum_{s,t} X_{.st}}{\sum_t J_t \sum_s \gamma_{st}}, \quad c_t = \frac{\sum_s X_{.st}}{J_t \sum_s \gamma_{st}}, \text{ or } \quad c_s = \frac{\sum_t X_{.st}}{\sum_t J_t \gamma_{st}}, \text{ and } \quad \gamma_{st} = \frac{X_{.st} + Y_{.st}}{J_t \xi(c_{st}) + I_t}$$

depending on the hypothesis chosen.

Unobserved Counts

Probably need some words about why we might not observed the count data.

When the data X_{jst} are observed as a binary response, instead of count data representing the number of prey species s that the predator ate in time period t , we can still estimate the parameters of interest λ, γ . Because some information is observed, we can treat the counts as missing and use the EM algorithm to find the maximum likelihood estimates of the observed data likelihood.

Let's define some new notation. We denote the binary response that the predator did in fact eat at least one prey species s in time period t by $Z_{jst} = 1(X_{jst} > 0)$. Now, the observed data $Z_{jst} \stackrel{\text{iid}}{\sim} \text{Bern}(1 - \exp\{-\lambda_{st}\})$ are Bernoulli observations. Using this we can find the complete (inclusive of all observed and unobserved) data likelihood, by first noting that the conditional distribution of the unobserved data X_{jst} given everything else is a truncated Poisson distribution

$$f_{X|Y,Z,\lambda,\gamma}(x_{jst}) = \frac{\exp\{-\lambda_{st}\}\lambda_{st}^{x_{jst}}}{(1 - \exp\{-\lambda_{st}\})x_{jst}!} \quad \text{where} \quad \mathbb{E}_{[X|Y,Z]}X_{jst} = \frac{\lambda_{st} \exp\{\lambda_{st}\}}{\exp\{\lambda_{st}\} - 1}.$$

From this conditional distribution we get the joint distribution of X_{jst}, Z_{jst}

$$f_{X,Z|\lambda}(x_{jst}, z_{jst}) = \begin{cases} \exp\{-\lambda_{st}\}, & x_{jst} = 0 \text{ and } Z_{jst} = 0 \\ \frac{\exp\{-\lambda_{st}\}\lambda_{st}^{x_{jst}}}{x_{jst}!}, & x_{jst} > 0 \text{ and } Z_{jst} = 1 \\ 0 & \text{otherwise} \end{cases}$$

From standard EM theory we can now formulate the complete data log-likelihood and take the expectation of it with respect to $f_{X|Y,Z,\lambda,\gamma}(x_{jst})$ to get

$$\begin{aligned} \mathbb{E}l_{comp} &= \mathbb{E} \log f_{X,Z|\lambda}(X_{jst}, z_{jst}) + \log f_{Y|\gamma}(y_{ist}) \\ &= \sum_{s=1}^S \sum_{t=1}^T \sum_{j=1}^{J_t} \mathbb{E} \log f_{X,Z|\lambda}(X_{jst}, z_{jst}) + \sum_{s=1}^S \sum_{t=1}^T \sum_{i=1}^{I_t} \log f_{Y|\gamma}(y) \\ &= \sum_{s,t,j} (-\lambda_{st} + z_{jst} \log(\lambda_{st}) \mathbb{E}X_{jst}) + \sum_{s,t} (-I_t \gamma_{st} + Y_{.st} \log I_t \gamma_{st}) + \text{const} \\ &= \sum_{s,t} (-J_t \lambda_{st} + z_{.st} \log(\lambda_{st}) \mathbb{E}X_{jst}) + \sum_{s,t} (-I_t \gamma_{st} + Y_{.st} \log I_t \gamma_{st}) + \text{const}. \end{aligned}$$

This EM algorithm works well when values λ_{st} are relatively small and zeros are common in the data Z_{jst} . In this case, not too much information is lost since estimation of $\mathbb{E}Z_{jst}$ can be estimated well by the proportion of observed zeros. On the other hand, if the predator consistently eats a given prey species, few to no zeros will show up in the observed data and $\mathbb{E}Z_{jst}$ is estimated to be nearly 1. The loss of information is best seen by attempting to solve for λ_{st} in the equation $1 = \mathbb{E}Z_{jst} = 1 - \exp\{-\lambda_{st}\}$; essentially λ_{st} is sent off to $+\infty$.

Simulations

Our simulations hypothesize two prey species, and five time points. Of the hierarchy of hypotheses, we consider the four most interesting cases $\{c, c_s, c_t, c_{st}\}$. Sample sizes are

chosen randomly from four overlapping levels. We put “small” sample sizes to be randomly sampled numbers in $[20, 50]$, “medium” encompasses $[30 : 75]$, “large” $[50, 150]$, and “huge” $[100, 200]$. Hence, we randomly sample trap and predator observations for each occurrence from one of the sample size levels, then cycle through all hypotheses. This is repeated for each level of sample size. We simulate data for each of the 16 scenarios above under both the standard maximum likelihood theory and under the EM algorithm. Only the details of the EM algorithm are presented here, as the other simulations are standard theory of point estimation.

Conclusion