

1 Modelling Predator Preferences using
2 Expectation-Maximization Algorithm and Molecular
3 Gut-Content Analysis

4 Edward A. Roualdes¹, Simon Bonner¹, Thomas D. Whitney², and James D.
5 Harwood³

6 ¹Department of Statistics, University of Kentucky, Lexington, KY 40536,
7 USA

8 ²Warnell School of Forestry and Natural Resources, University of Georgia,
9 Athens, GA 30602, USA

10 ³Department of Entomology, University of Kentucky, Lexington, KY 40546,
11 USA

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Abstract

14 The literature on modeling a predator's prey selection includes many intuitive indices, few
15 of which have both reasonable statistical justification and tractable asymptotic properties.
16 Here, we provide a simple model that meets both of these criteria, while extending previ-
17 ous work to include an array of multiple species and time points. Further, we apply the
18 Expectation-Maximization algorithm to cases where exact counts of the number of prey
19 species eaten in a particular timer period is not observed. We conduct a simulation study
20 to demonstrate the accuracy of our method, and a real dataset, collected on the wolf spider,
21 illustrates how to apply our methods.
22 *Keywords: moar words*

1 Introduction

The indices most commonly used to estimate a predator’s food preferences, or selectivity, are relatively old (Ivlev, 1964; Jacobs, 1974; Chesson, 1978; Strauss, 1979; Vanderploeg and Scavia, 1979; Chesson, 1983), and yet many applied papers continue to use them; a quick search of just 2014 returns hundreds of publications that cite these fundamental papers, a few being Clements et al. (2014); Hansen and Beauchamp (2014); Hellström et al. (2014); Lyngdoh et al. (2014); Madduppa et al. (2014). These indices, though intuitive, lack the statistical rigor of a model, focus on a snapshot in time, and rarely allow more than one prey species to be considered (Lechowicz, 1982). We propose an intuitive statistical model to determine and statistically test differences in a predators’ prey preferences across an array of time points and between multiple prey species.

A comprehensive overview by Lechowicz (1982), which was later summarized by Manly et al. (1992), details the benefits and faults of the most popular indices. According to these reviews, a majority of the indices give comparable results, save Strauss’ linear index L , despite the fact that most of the methods differ by range and linearity of response. While Lechowicz (1982) recommends one index, E^* by Vanderploeg and Scavia (1979) as the “single best,” albeit imperfect, index, Manly et al. (1992) instead take the approach of suggesting the indices which estimate biologically meaningful values. Lechowicz (1982) recommends the index E^* , an element of the Manly et al. (1992) suggested indices, because the index value 0 denotes random feeding, the index has a range restricted to $[-1, 1]$ (though $E^* = 1$ is nigh impossible), and because the index is based on the predator’s choice of prey as a function of both the availability of the prey as well as the number of available prey types (assumed known). The downside to this index is its lack of reasonable statistical properties (Lechowicz, 1982), thus making the computation of standard errors, and hypothesis testing difficult. This is, in fact, a common fault amongst most of the indices.

To encourage more formal statistical inference, and simultaneously generalize predators’ selectivity to animal resource selection, Manly et al. (1992) proposed the use of generalized linear models (GLM). The well established literature on GLMs allows for hypothesis testing to replace the indices, by estimating the proportion of eaten prey species to that which is available while using environmental variables as predictors. The model we present here, while restricted to predators’ preferences, is a compromise between these two extremes, indices and GLMs. Our model offers formal hypothesis testing and inference similar to the GLMs of Manly et al. (1992), but also provides meaningful single number summaries of the predator’s dietary preferences. To do this, we estimate the rate at which a predator consumes the prey of interest instead of estimating the proportion of consumed to available prey. An outcome of our model, is that we give up the somewhat arbitrary preference for an index to have the range $[-1, 1]$, and random feeding, now denoted by 1, is formally testable across time points and across prey species.

Our model enables formal hypothesis testing and statistical inference, while being general enough to perform statistical tests across multiple species and time points. This provides researchers a more detailed analysis of the predator’s eating preferences. Further, because our model is based on underlying Poisson distributions, members of the well studied exponential family, we are able to estimate the parameters of interest even when exact tallies of the number of each prey species eaten within any given time period is not observed. Instead, we

rely on the researcher being able to DNA sequence the contents of the predator’s gut and make a simple binary conclusion: this predator ate some of that prey species during this time period, or did not.

This paper is organized as follows. Section 2 describes our statistical model, for both fully observed count data, and for the non-observed count data for which we use the Expectation-Maximization (EM) algorithm, and the statistical tests used to make statements about the population parameters of interest. In section 3, we offer a simulation study that demonstrates the accuracy of our methods. Section 4 provides a real dataset, which investigates the eating preferences of the wolf spider, found in the Berea College Forest in Madison County, Kentucky, USA, to demonstrate how interested practitioners could apply our methods. A brief discussion concludes the paper in section 5. Alongside our model, we offer an R (Core Team, 2014) package named `spiders` that fits all the methods discussed.

2 Methods

2.1 Data

We assume data are collected in the following manner. Traps are dispersed, for T time periods, throughout the habitat of the predator and prey of interest. Prey species, indexed by $s \in \{1, \dots, S\}$, are collected in the traps and counted at each time period. The number of prey species s the predator will encounter on average during time period $t \in \{1, \dots, T\}$ are considered random draws from a Poisson distribution with rate parameter γ_{st} . We further assume that the number of prey species found in the gut of the similarly trapped predators follows a Poisson distribution with rate λ_{st} . Here, the parameter λ_{st} represents the rate at which the predator ate prey species s during time period t . By modeling λ_{st} and γ_{st} we are able to test claims about a predator’s eating preferences.

The use of Poisson distributions make the following implicit assumptions: 1) traps independently catch the prey species of interest, 2) predators eat prey species independently, 3) predators eat independent of each other.

We denote the number of predators and the number of prey species caught, in each time period t , by J_t and I_t , respectively. Let $X_{jst} \stackrel{\text{iid}}{\sim} \mathcal{P}(\lambda_{st})$ represent the number of prey species s that predator j ate during occurrence t , where $j \in \{1, \dots, J_t\}$. Let $Y_{ist} \stackrel{\text{iid}}{\sim} \mathcal{P}(\gamma_{st})$ represent the number of prey species s found in trap i during occurrence t , $i \in \{1, \dots, I_t\}$. Formal statistical statements about the relative magnitudes of the parameters $\boldsymbol{\lambda}$ and $\boldsymbol{\gamma}$ offer insights to the relative rates at which predators eat particular prey species.

We consider five variations on the relative magnitude of $\lambda_{st}/\gamma_{st} = c_{st}$. These five hypotheses each allow c_{st} to vary by time, prey species, both, or neither. Because the five hypotheses are nested, a natural testing order is suggested in Figure 1.

1. $c_{st} = 1$

2. $c_{st} = c$

3. $c_{st} = c_s$

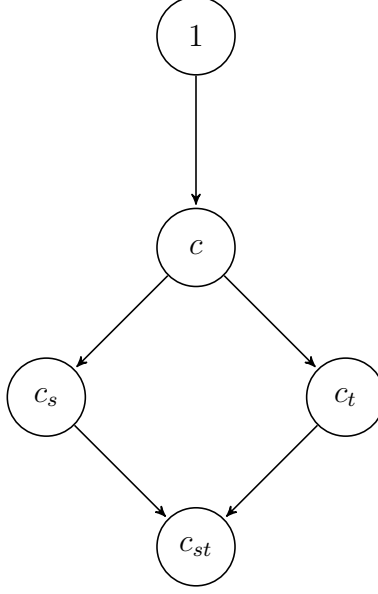


Figure 1: Hierarchy of hypotheses.

4. $c_{st} = c_t$

5. $c_{st} = c_s$

The first hypothesis states that predators and traps sample all prey species at the same rate. One imagines this is the case if the predator simply eats that which comes within its reach, thus suggesting a diet indifference. The second says that predators sample prey proportionally across all time periods. The third hypothesis says that predators sample different prey species at different rates, but each rate is steady across time. This implies that the predator expresses preferences for one prey species over another, but is unresponsive to changes due to time. Conversely, the forth hypothesis implies that each prey species is sampled similarly within each time period, while the rates across time are allowed to change. The fifth assumes a predator's selection varies by both time and prey species. This would make sense if environmental variables, say weather, or prey availability, and taste were affecting predators' selection strategies.

2.2 Fully Observed Count Data

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

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

Writing all five hypotheses as $\lambda_{st} = c_{st} \gamma_{st}$, we can, in the simplest cases, find analytic solutions for the maximum likelihood estimates of c_{st} and γ_{st} . Under the hypothesis $c_{st} = 1$,

124 and when the data are balanced $J_t = J$, $I_t = I$, and $c_{st} = c$ analytic solutions exist. Namely,
 125 these solutions are

$$\hat{\gamma}_{st} = \frac{X_{\cdot st} + Y_{\cdot st}}{J_t + I_t}, \quad \text{and} \quad \hat{c} = \frac{I \sum_{s,t} X_{\cdot st}}{J \sum_{s,t} Y_{\cdot st}}, \quad \hat{\gamma}_{st} = \frac{X_{\cdot st} + Y_{\cdot st}}{I \left(\frac{\sum_{st} X_{\cdot st}}{\sum_{st} Y_{\cdot st}} + 1 \right)}$$

126 respectively, where $X_{\cdot st} = \sum_{j=1}^{J_t} X_{jst}$ and $Y_{\cdot st} = \sum_{i=1}^{I_t} Y_{ist}$.

127 In all other cases, analytic solutions are not readily available and instead we rely on the
 128 fact that the log-likelihood $l(\boldsymbol{\lambda}, \boldsymbol{\gamma}) = \log L$ is concave. We maximize the log-likelihood, using
 129 coordinate descent (Luo and Tseng, 1992), by iteratively solving partial derivatives of l , with
 130 respect to c_{st} and γ_{st} , set equal to zero

$$\hat{c} = \frac{\sum_{s,t} X_{\cdot st}}{\sum_t J_t \sum_s \gamma_{st}}, \quad \hat{c}_t = \frac{\sum_s X_{\cdot st}}{J_t \sum_s \gamma_{st}}, \quad \text{or} \quad \hat{c}_s = \frac{\sum_t X_{\cdot st}}{\sum_t J_t \gamma_{st}}, \quad \text{and} \quad \hat{\gamma}_{st} = \frac{X_{\cdot st} + Y_{\cdot st}}{J_t c_{st} + I_t}.$$

131 2.3 Unobserved Counts

132 Many times it may not be possible to count the number of individuals of each prey species
 133 that are in a predator's gut. Instead, it may only be possible to detect whether or not
 134 a predator consumed the prey species during a given period. In this case we can still
 135 make inference about the predators' preferences for the different prey species by using the
 136 Expectation-Maximization (EM) algorithm to compute maximum likelihood estimates.

137 We denote the binary random variable indicating that the j^{th} predator did in fact eat
 138 at least one individual of prey species s in time period t by $Z_{jst} = 1(X_{jst} > 0)$. The
 139 variables are independent Bernoulli observations with success probability $p_{st} = P(Z_{jst} =$
 140 $1) = 1 - \exp\{-\lambda_{st}\}$. Despite not observing X_{jst} , we can compute maximum likelihood
 141 estimates of the parameters $\boldsymbol{\lambda}, \boldsymbol{\gamma}$ through the EM algorithm using the complete data log-
 142 likelihood

$$l_{comp}(\boldsymbol{\lambda}, \boldsymbol{\gamma}) = \log f_{X,Y,Z}(\mathbf{x}, \mathbf{y}, \mathbf{z} | \boldsymbol{\lambda}, \boldsymbol{\gamma}) = \sum_{s=1}^S \sum_{t=1}^T \left[\sum_{j=1}^{J_t} \log f_{X,Z}(x_{jst}, z_{jst} | \boldsymbol{\lambda}) + \sum_{i=1}^{I_t} \log f_Y(y_{ist} | \boldsymbol{\gamma}) \right].$$

143 The density of Y_{jst} is exactly as in section 2.2 and so we focus on deriving the joint density
 144 of X_{jst} and Z_{jst} . With the distribution of Z_{jst} given above, we can compute $f_{X,Z}(x_{jst}, z_{jst} | \boldsymbol{\lambda})$
 145 by noting that $X_{jst} = 0$ with probability 1 if $Z_{jst} = 0$, and that $[X_{jst} | Z_{jst} = 0]$ has a
 146 truncated Poisson distribution with density

$$f_{X|Y,Z,\boldsymbol{\lambda},\boldsymbol{\gamma}}(x_{jst} | z_{jst}) = \frac{\exp\{-\lambda_{st}\} \lambda_{st}^{x_{jst}}}{(1 - \exp\{-\lambda_{st}\}) x_{jst}!} 1(x_{jst} > 0)$$

147 and expected value

$$\mathbb{E}_{X|Y,Z} X_{jst} = \frac{\lambda_{st} \exp\{\lambda_{st}\}}{\exp\{\lambda_{st}\} - 1}.$$

The joint density of X_{jst}, Z_{jst} is then

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

The EM algorithm works by iterating two steps, the E-step and M-step, until the optimum is reached (Dempster et al., 1977; McLachlan and Krishnan, 2007). Let k index the iterations in the EM algorithm so that $\boldsymbol{\lambda}^{(k)}$ and $\boldsymbol{\gamma}^{(k)}$ denote the estimates computed on the k^{th} M-step. The E-step consists of computing the expectation of l_{comp} with respect to the conditional distribution of X given the current estimates of the parameters

$$Q^{(k)}(\boldsymbol{\lambda}, \boldsymbol{\gamma}) = \mathbb{E}_{X|Y,Z,\boldsymbol{\lambda}^{(k)}} l_{comp}$$

in order to remove the unobserved data. The M-step then involves maximizing $Q = \mathbb{E} l_{comp}$ with respect to the parameters in the model to obtain updated estimates of the parameters,

$$(\boldsymbol{\lambda}^{(k+1)}, \boldsymbol{\gamma}^{(k+1)}) = \arg \max_{(\boldsymbol{\lambda}, \boldsymbol{\gamma})} Q^{(k)}(\boldsymbol{\lambda}, \boldsymbol{\gamma}).$$

These steps are then alternated until a convergence criterion monitoring subsequent differences in the parameter estimates/likelihood is met.

The calculation of $Q^{(k)}(\boldsymbol{\lambda}, \boldsymbol{\gamma})$ is not difficult and is given by:

$$\begin{aligned} Q^{(k)}(\boldsymbol{\lambda}, \boldsymbol{\gamma}) &= \mathbb{E} \log f_{X,Z|\boldsymbol{\lambda}}(X_{jst}, z_{jst}) + \log f_{Y|\boldsymbol{\gamma}}(y_{ist}) \\ &= \sum_{s=1}^S \sum_{t=1}^T \sum_{j=1}^{J_t} \mathbb{E} \log f_{X,Z|\boldsymbol{\lambda}}(X_{jst}, z_{jst}) + \sum_{s=1}^S \sum_{t=1}^T \sum_{i=1}^{I_t} \log f_{Y|\boldsymbol{\gamma}}(y) \\ &\propto \sum_{s,t,j} (-\lambda_{st} + z_{jst} \log \lambda_{st} \mathbb{E} X_{jst}) + \sum_{s,t} (-I_t \gamma_{st} + Y_{.st} \log I_t \gamma_{st}) \\ &\propto \sum_{s,t} \left(-J_t \lambda_{st} + z_{.st} \log \lambda_{st} \mathbb{E}(X_{jst} | \lambda_{st}^{(k)}, \gamma_{st}^{(k)}) \right) + \sum_{s,t} (-I_t \gamma_{st} + Y_{.st} \log I_t \gamma_{st}). \end{aligned} \tag{2}$$

No analytic solution to the M-step exists, however, so we chose to maximize Q with coordinate descent (Luo and Tseng, 1992). In fact, as we only need find parameters that increase the value of Q on each iteration, we forgo fully iterating to find the maximum and instead perform just one step uphill within each EM iteration. Since $Q^{(k)}$ is concave and smooth in the parameters $\boldsymbol{\lambda}, \boldsymbol{\gamma}$, we are able to use the convergence of parameter estimates, $\|(\boldsymbol{\lambda}^{(k)}, \boldsymbol{\gamma}^{(k)}) - (\boldsymbol{\lambda}^{(k+1)}, \boldsymbol{\gamma}^{(k+1)})\|_{\infty} < \tau$, for some $\tau > 0$, as our stopping criterion.

As we show in our simulation study, this generalized EM algorithm accurately estimates the parameters when values of λ_{st} are relatively small, such that zeros are prevalent 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 $1 = \mathbb{E} Z_{jst} 1 - \exp\{-\lambda_{st}\}$. As the proportion of ones in the observed data increases, we expect λ_{st} to grow exponentially large. When no zeros are present in the data, so that where only ones are observed, the likelihood can be made arbitrarily large by sending the parameter off to infinity.

2.4 Testing

The likelihood ratio test statistic is

$$\Lambda(X, Y) := -2 \log \frac{\sup_{\theta_0} L(\theta_0 | X, Y)}{\sup_{\theta_1} L(\theta_1 | X, Y)},$$

where θ_0, θ_1 represent the parameters estimated under the null and alternative hypotheses, respectively. It is well known that the asymptotic distribution of Λ is a χ^2_ρ distribution with ρ degrees of freedom (Wilks, 1938). When the observations X_{jst} are not observed, we use $L_{obs}(Z, Y)$ as the likelihood in the calculation of Λ .

The degrees of freedom ρ equal the number of free parameters available in the stated hypotheses under question. If we put the null hypothesis to be $H_0 : \lambda_t = c_t \gamma_t$, for all t and contrast this against $H_1 : \lambda_{st} = c_{st} \gamma_{st}$ then there are $\rho = 2(S \cdot T) - S \cdot T - T = S \cdot T - T$ degrees of freedom.

A set of hypotheses is determined by the p-value of the χ^2_ρ distribution. Hence, with a level of significance, α , the null hypothesis is rejected in favor of the alternative hypothesis if $\mathbb{P}(\chi^2_\rho > \Lambda) < \alpha$.

2.5 Linear Transformations of c_{st}

After determining which model best fits the data, more detail can be extracted through a hypothesis test of the elements of c_{st} , or in vector notation as $\mathbf{c} \in \mathbb{R}^{S \cdot T}$. Let the elements of $\hat{\mathbf{c}}$ be the maximum likelihood estimates, \hat{c}_{st} , as found via the framework above. Since $\hat{\mathbf{c}}$ is asymptotically normally distributed, any linear combination of the elements is also asymptotically normally distributed. For instance, let a be a vector of the same dimension of $\hat{\mathbf{c}}$. Then $a^t \hat{\mathbf{c}}$ is asymptotically distributed as $\mathcal{N}(a^t \mathbf{c}, a^t \Sigma a)$, where Σ is the covariance matrix of the asymptotic distribution of $\hat{\mathbf{c}}$.

Suppose, for example, that the hypothesis c_s is determined to best fit the data with s ranging $s = 1, 2, 3$. We can test to see whether or not two species are statistically equally preferred under the null hypothesis $c_1 = c_2$. This hypothesis is alternatively written in vector notation as $a^t \mathbf{c} = 0$, where $a = (1, -1, 0)^t$. Tests of the following form $H_0 : a^t \mathbf{c} = \mu$ against any alternative of interest are then approximate Z -tests. Confidence intervals of any size are similarly, readily obtained. Of course, one could also use a t distribution as a small sample size correction.

3 Simulations

Our simulations assume two prey species and five time points, throughout. Of the hierarchy of hypotheses, we generate data under three models: c, c_s, c_t . Sample sizes for both prey species and predator gut count observations are randomly chosen from four overlapping levels: “smallest” sample sizes are randomly sampled numbers in $[20, 50]$, “small” $[30, 75]$, “large” $[50, 150]$, and “largest” $[100, 200]$. This is repeated for each level of sample size. We simulate 500 replicate datasets for each of the twelve scenarios above for both types of data, fully observed count data, X_{jst} , and for non-count data, when we observe only a binary

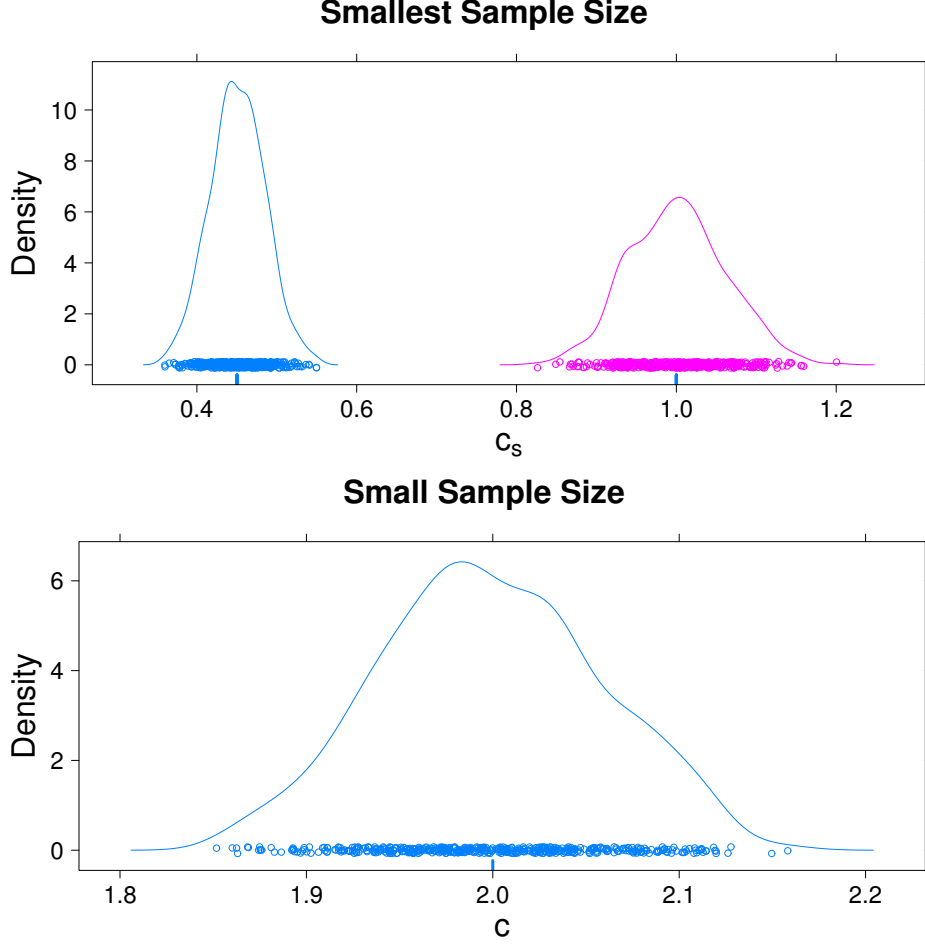


Figure 2: Density plots of all 500 estimates of fitting the true model to the data generated from models c_s, c are shown with sample sizes smallest and small, respectively.

response, $Z_{jst} = 1(X_{jst} > 0)$. Each scenario is then fit with the true model that generated the data. All simulations of non-count data use $\tau = 10^{-5}$ as the convergence tolerance. A subset of the examples are provided here; the interested reader is referred to the supplementary materials for the complete simulation results. For the simulations we used the R Core Team (2014) package **BatchExperiments** by Bischl et al. (2014).

For all simulated data, the true parameter values for the rate at which prey species are encountered in the wild are fixed to be $\gamma_{st} = \pi, \forall s, t$. The values of λ_{st} are set with respect to each data generating model. For model $c_{st} = c$, where predator preferences don't vary by either time or species, we put $\lambda_{st} = 2\pi, \forall s, t$. Under model c_s , the ratio of rates vary by species only, so we put $\lambda_{1t} = \sqrt{2}$ and $\lambda_{2t} = \pi$. Hence, $c_1 = \sqrt{2}/\pi \approx 0.45$ and $c_2 = 1$. For the last model, c_t , the ratio of rates vary by time t . Here, we put $\lambda_{st} = t$ for $t \in \{1, \dots, 5\}$.

Figure 2 shows density plots of the estimates of c_s, c when fitting the true model to the fully observed count data generated under models c_s and c . The plots provide evaluations of parameter estimates under each scenario. In the first display, the parameters $c_1 \approx 0.45$ and $c_2 = 1$ are on average, across all 500 simulations, estimated as $\hat{c}_1 = 0.45$ and $\hat{c}_2 = 1.00$,

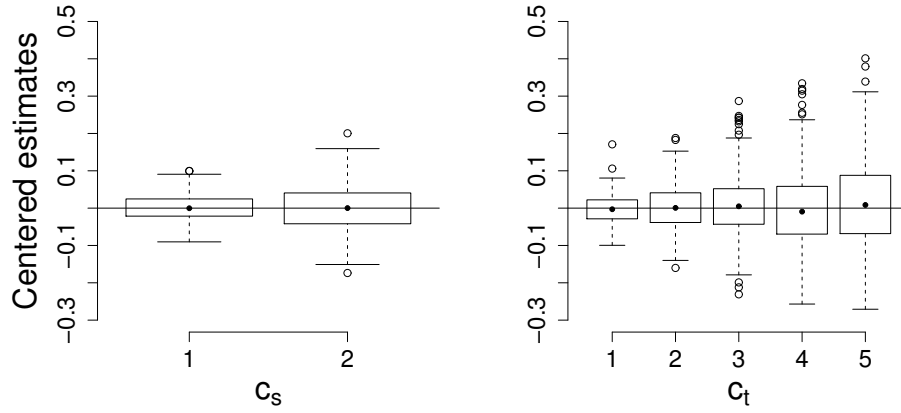


Figure 3: Shown are all 500 estimates, centered at the true parameter values, from fitting the true model to the data generated from models c_s, c_t with sample sizes smallest and small, respectively.

with standard errors of $\text{se}(\hat{c}_1) = 0.03$ and $\text{se}(\hat{c}_2) = 0.06$. The second display provides results for model $c_{st} = c$. Averaging across all 500 simulations, the parameter $c = 2$ is estimated as $\hat{c} = 2.00$. This is further seen in figure 3, where box plots of the parameter estimates, centered at true parameter values, of the correct model fit to data generated from both c_s and c_t show empirically very little bias.

We next generated data with unobserved counts. As noted above under certain circumstances our unobserved counts model accurately estimates the parameters of interest, and at other times can infinitely over-estimate parameters. To investigate this issue further, we consider the same scenarios mentioned above, but now we reduce all of the count data down to binary observations. For each scenario, we fit the unobserved counts model as if we knew the true underlying model that generated the observed data.

Figure 4 contains density plots for all 500 replications of the data generating models c_s, c_t with the smallest and the largest sample sizes, respectively. When data are generated under the model c_s and the true model fit to the non-count data, we find even for the small sample size that point estimates are only very slightly biased. When parameter values are of sufficient size to make zeros in the simulated data less common, the estimates from fitting the correct model to the generated data are occasionally over-estimated. This effect is easily seen in the bottom panel of figure 4 for larger values of c_t despite the increased sample size, but is also seen, less dramatically, in the density plot for the c_s generated data.

The cluster of estimates for c_5 between 3.5 and 4.0 in the bottom panel of figure 4 comes from datasets in which $X_{js5} > 0$ so that $Z_{js5} = 1$ for all j, s . For the data shown in figure 4, this happened 73 times out of the 500 replicated datasets. As mentioned above, the estimate of c_5 is infinite in this case. However, the EM algorithm will always provide a finite estimate for all parameters when it terminates. In this case, we set $\tau = 10^{-5}$ and it just happened that this caused the algorithm to terminate with \hat{c}_5 between 3.5 and 4.0. To confirm that this is due to the arbitrary choice of τ , we repeated the algorithm with smaller values of τ for several datasets. As expected, \hat{c}_5 increased without bound as we refit the model with

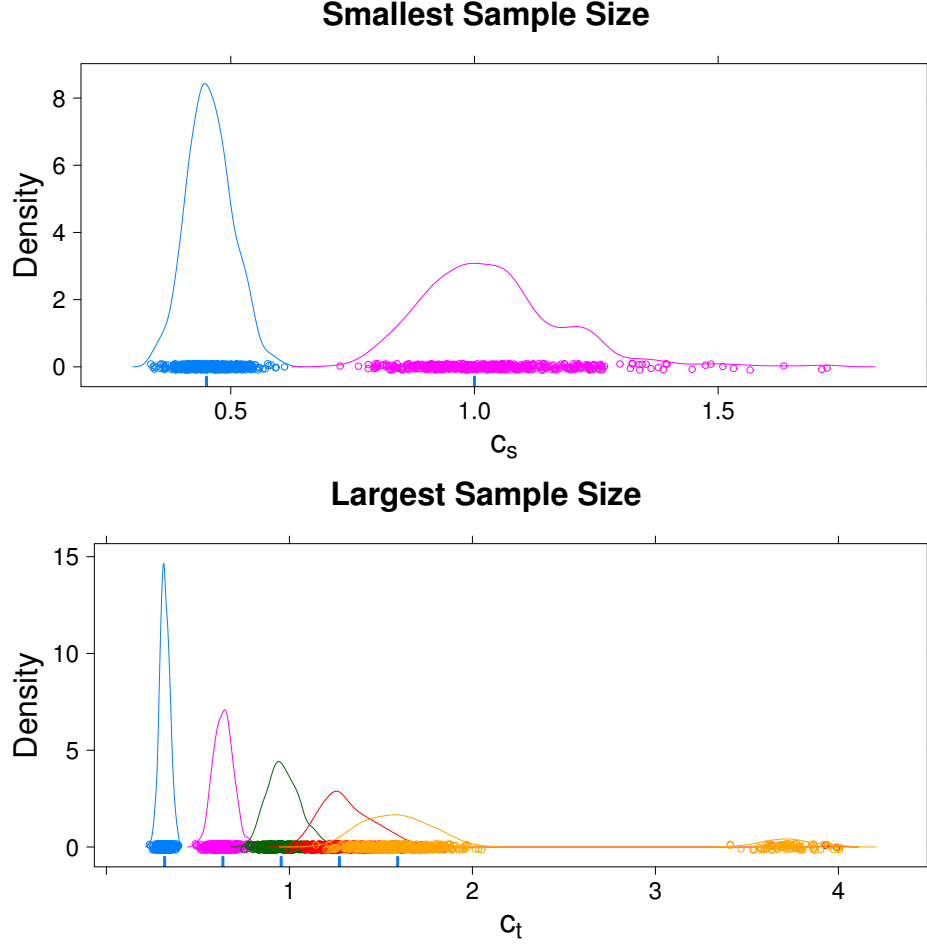


Figure 4: Density plots of all 500 estimates of fitting the true model to the data generated from models c_s, c_t , when counts are not observed, are shown with sample sizes smallest and largest, respectively.

increasingly small values of τ .

The over-estimation of parameters, a symptom of the loss of information due to the unobserved counts, can also be seen with box plots of the 500 point estimates centered at their respective true parameter values. Figure 5 contains box plots of the same scenarios in Figure 4. For the 73 cases in which $Z_{js5} = 1$ for all j, s under model c_t with the largest sample size, the bias is infinite since parameter estimates will, theoretically, be infinite. The finite bias shown in these plots is due to the finite estimates provided by the termination of the EM algorithm. Thus, conditional on a mixture of 0s and 1s in the data the corresponding estimators are unbiased, but when no 0s exist in the data the theoretical bias is infinite.

4 Real Data

We analyzed a dataset that was collected to investigate the eating preferences of the wolf spider, genus *Schizocosa*, towards the prey orders Diptera and Collembola. Predators were

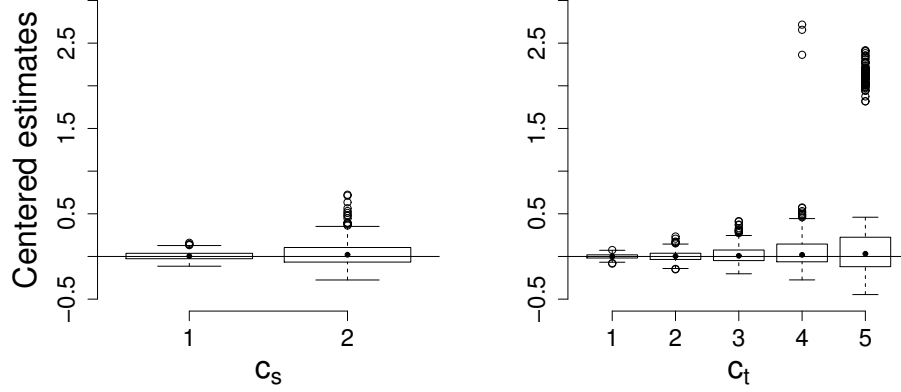


Figure 5: Shown are all 500 estimates, centered at the true parameter values, from fitting the true model to the data generated from models c_s, c_t , when counts are not observed, with sample sizes smallest and largest, respectively.

collected in traps within the deciduous Berea College Forest in Madison County, Kentucky, USA and had their gut-contents analyzed to determine whether or not the spiders ate any Diptera or Collembola within each time period. The left panel of figure 6 plots the percentage of spiders that had the prey in their guts across time. Prey were also collected in traps from the same area. These data were collected for each month from October 2011 to March 2013. On average, 69 spiders, and 111 and 297 Diptera and Collembola, respectively, were caught in each time period. The range of the sample sizes, across all 18 months is, 11 to 181 for caught spiders, from 7 to 322 for trapped Diptera, and from 101 to 755 for trapped Collembola. The right panel of figure 6 plots the total number of each order that was caught during each time period.

These data provide an example of our hierarchy of hypotheses. First, we tested model $c_{st} = c$ against $c_{st} = c_s$, to determine whether or not the wolf spider has different preferences for the two orders Diptera and Collembola. With, one degree of freedom, this likelihood ratio test indicated, $p - value < 0.0001$, that two parameters, one for each order, fits these data better than one parameter for both. Similarly, we tested whether or not there was a significant effect across time by testing model $c_{st} = c$ against $c_{st} = c_t$. Here, the likelihood ratio test, with 17 degrees of freedom, implies that the wolf spiders of the Berea College Forest eat these prey orders at different rates across the months of the year, $p - value < 0.0001$. In fact, we find that the most parameter rich model, $\lambda_{st} = c_{st}\gamma_{st}$ fits these data better than is expected by chance, $p - value < 0.0001$. Model c_{st} estimates 72 parameters in total; since, in this case, there are two prey of interest and 18 time periods, it takes 36 parameters to estimate each c_{st} and γ_{st} . Figure 7 plots the point estimates and 95% confidence intervals of c_{st} , for both prey across all time periods.

With point estimates of c_{st} under the model $\lambda_{st} = c_{st}\gamma_{st}$, we can test any number of linear contrasts. For instance, $c_{1t} = c_{2t}$, for $t \in \{1, \dots, 18\}$. Using a level of significance of 0.05, and after making a Bonferroni multiple comparisons adjustment, the data can not say that the two prey are differently preferred in October, November, and December of 2011 and for

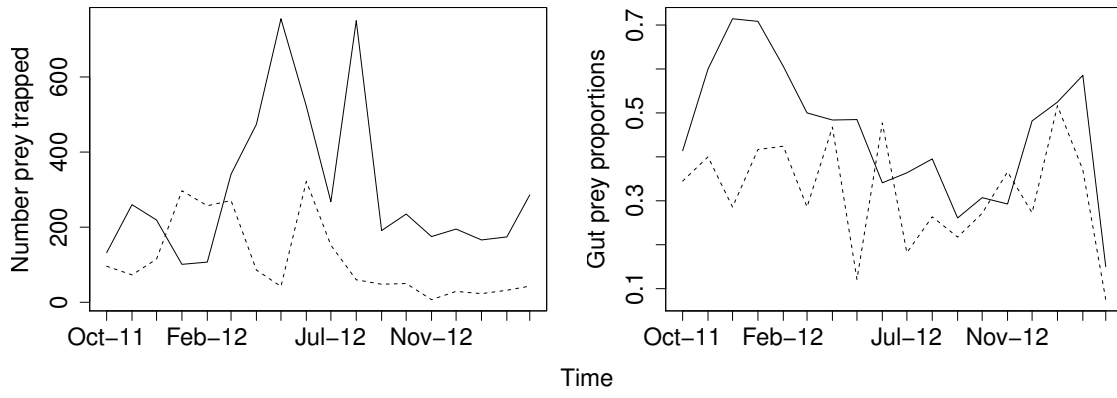


Figure 6: For both Diptera and Collembola, the plots show the proportion of spiders with these orders found in their guts, and the number of these orders trapped in each time period.

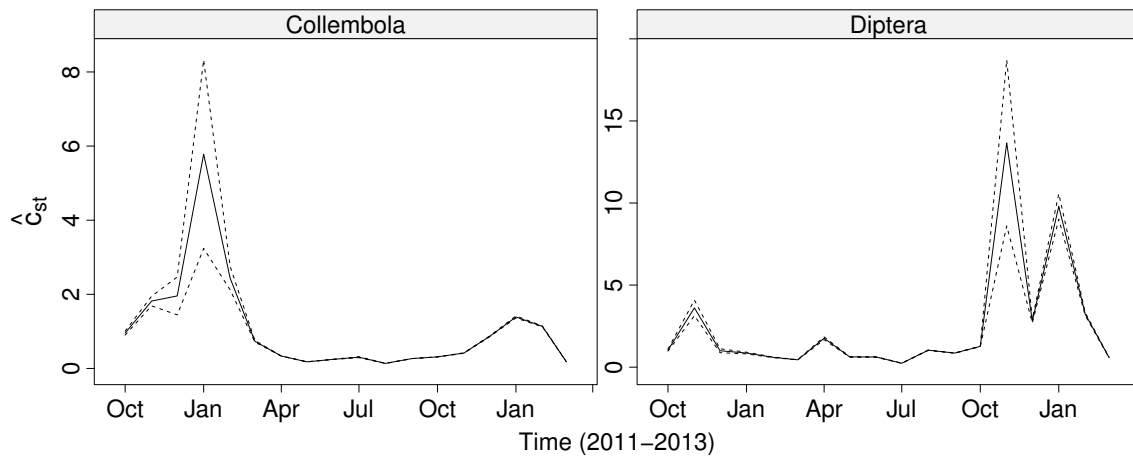


Figure 7: One plot for each prey order displays the point estimates and 95% confidence intervals as estimated from the model c_{st} .

290 March and July of 2012.

291 5 Discussion

292 The model developed here allows predators’ preferences by testing simultaneously across an
293 array of multiple prey species and time points. This is achieved via a simple, but statistically
294 powerful, likelihood ratio test. Further testing of the ratio of rates for which predators eat
295 to encounter prey species allows researchers to make specific conclusions about predators’
296 preferences. For instance, rates across time can be estimated to make statements about
297 seasonal effects on a predator’s eating habits, or relative rates across species groups allows
298 for statements about the relative preferences for different species.

299 When counts of predators’ gut contents are not fully observed, and instead only a binary
300 response indicating the existence of the prey species in the gut is observed, we are able to
301 treat the counts as missing data. By modeling all of the observed data, both the binary
302 responses and the number of prey species caught, and the missing count data, we are able
303 to use the EM algorithm to extract as much information from the data as possible. Though
304 this is nice in theory, in practice the success of this modification to our original model is
305 limited by the magnitude of the unknown parameters λ_{st} .

306 Further developments of our model could be beneficial. Taking into account other envi-
307 ronmental variables that might effect a predator’s eating habits, such as rain or temperature
308 might be advantageous.

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315 7 Data Accessibility

316 An R package, named `spiders`, is available on CRAN at [http://cran.r-project.org/](http://cran.r-project.org/web/packages/spiders/index.html)
317 [web/packages/spiders/index.html](http://cran.r-project.org/web/packages/spiders/index.html) and fits all the methods discussed above.

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