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

Figure 1: Four hypotheses considered.

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 $X_{jst} \sim \mathcal{P}(\lambda_{st})$ denote the number of prey species s that predator j eaten during occurrence $t; j \in \{1, \ldots, J_t\}, s \in \{1, \ldots, S\}, t \in \{1, \ldots, T\}$. Further, let $Y_{ist} \sim \mathcal{P}(\gamma_{st})$ denote the number of prey species s found in trap i during occurrence $t; i \in \{1, \ldots, I_t\}$. We make a formal statistical statements about the relative magnitudes of the parameters λ and γ . The four hypotheses considered provide variations on the relative magnitude of $c_{st} = \lambda_{st}/\gamma_{st}$. Holding c_{st} steady over either s or t provides intuitive statements 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.

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 under that particular hypothesis.

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 a complete data likelihood

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

In some cases one can find analytic solutions for the maximum likelihood estimates, namely when the data are balanced $J_t = J$, $I_t = I$, and $c_{st} = c$ and when estimating λ_{st} , γ_{st} under the hypothesis represented by c_{st} . In all other cases, analytic solutions are not readily available. Instead, we rely on the fact that the log-likelihood $l(\lambda, \gamma) = \log L_{comp}$ is concave and iteratively solve

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

Simulations

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